

# **Understanding pathogenesis of gallbladder cancer: Role of Th17 and Regulatory T cells**

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*A thesis submitted to the  
Board of Studies in Life Sciences  
In partial fulfillment of requirements  
for the Degree of*

**DOCTOR OF PHILOSOPHY**  
*of*  
**HOMI BHABHA NATIONAL INSTITUTE**





**December, 2016**

# Homi Bhabha National Institute

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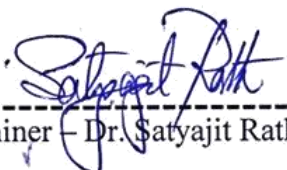
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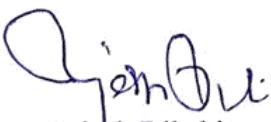
  
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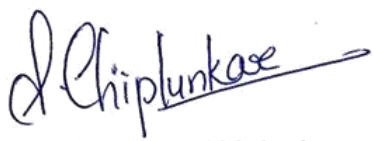
  
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## DECLARATION

I, hereby declare that the investigation presented in the thesis has been carried out by me. The work is original and has not been submitted earlier as a whole or in part for a degree/diploma at this or any other Institution or University.

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## LIST OF PUBLICATIONS ARISING FROM THE THESIS

### **Journal**

1. **Patil RS**, Shalini KS, Chiplunkar SV, “Immunosuppressive role of  $\gamma\delta$  T cells in cancer: The other side of the coin”, **Translational Cancer Research**. 2016 Dec (Manuscript accepted for publication)
2. **Patil RS**, Shah SU, Shrikhande SV, Goel M, Dikshit R, and Chiplunkar SV, “IL17 producing  $\gamma\delta$  T cells induce angiogenesis and are associated with poor survival in gallbladder cancer patients”, **International Journal of Cancer**. 2016 Apr 8. doi: 10.1002/ijc.30134
3. **Patil RS**, Bhat SA, Dar AA, Chiplunkar SV, “The Jekyll and Hyde story of IL17 producing  $\gamma\delta$ T (T $\gamma\delta$ 17) cells”, Feb4 2015, **Frontiers in Immunology**. 2015 Feb 4;6:37. doi: 10.3389/fimmu.2015.00037
4. Dar AA, **Patil RS**, Chiplunkar SV, “Insights into the relationship between toll like receptors and gamma delta T cells responses”, **Frontiers in Immunology**. 2014 Jul 31;5:366. doi: 10.3389/fimmu.2014.00366.

### **Conferences (Abstracts published)**

1. **Patil RS**, Shah SU, Shrikhande SV, Goel M, Dikshit R, and Chiplunkar SV, “Pro-tumor role of IL17 producing  $\gamma\delta$ T cells in gallbladder cancer”, **European Journal of Cancer** Volume 54, Supplement 1, Pages S1-S78 (February 2016). doi: 10.1016/S0959-8049(16)31954-2.

2. **Patil RS**, Shah SU, Shrikhande SV, Goel M, Dikshit R, and Chiplunkar SV, “Role of IL17 producing  $\gamma\delta$  T cells (T $\gamma\delta$ 17) in gall bladder cancer pathogenesis”, Feb10 2015, *J Carcinog*,14:21.

### **Presentations at conferences**

1. Oral presentation on “T $\gamma\delta$ 17 is a proangiogenic subtype of  $\gamma\delta$ T cells and associates with poor survival of gallbladder cancer patients” at “**13<sup>th</sup> FIMSA advanced Immunology Course**” held at ‘Department of Immunopathology, PGIMER, Chandigarh from 17-19 March 2016.
2. Oral presentation on “Paradox of immune system in Gallbladder Cancer: Role of T $\gamma\delta$ 17 cells” at ‘**Society of biological chemists (India) Mumbai chapter meeting**’ held at NIRRH Mumbai (22 August 2015).
3. Oral presentation on “Role of IL17 producing  $\gamma\delta$ T cells (T $\gamma\delta$ 17) in gallbladder cancer pathogenesis” in international conference “**Carcinogenesis-2015**” on ‘Molecular pathways to therapeutics: Paradigms and challenges in oncology’ at ACTREC, Tata Memorial Centre, Navi Mumbai from 11-13 February 2015.
4. Oral presentation on “IL17 producing  $\gamma\delta$ T cells (T $\gamma\delta$ 17) contribute to tumorigenesis of gallbladder cancer” at “**41<sup>st</sup> annual conference of Indian Immunology Society-Immunocon-2014**”at Madurai Kamaraj University, Madurai, from 12-14 December 2014.
5. Poster was presented on “Dynamics of T $\gamma\delta$ 17 and Regulatory T cells in Gallbladder cancer” in international conference “**Keystone Symposium on Infection**

**inflammation and cancer joint with immune evolution in cancer”** at Fairmont Chateau Whistler, Whistler, British Columbia, Canada from 9-14 March 2014.

6. Poster was presented on “Immune dysfunctions in Gallbladder cancer : Imbalance of  $T\gamma\delta 17$  and Regulatory T cells” at **“IX DAE-BRNS Life Sciences Symposium (LSS-2013) on Current advances in immunobiology and cancer”** at BARC, Anushaktinagar, Mumbai from 28-30 November 2013.
7. Poster was presented on “Dynamics of Th17 and regulatory T cells in pathogenesis of Gall Bladder cancer” at **“ 39<sup>th</sup> Annual Conference of Indian Immunology Society- IMMUNOCON 2012”** at Banaras Hindu University, Varanasi from 9-11 November 2012.
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9. Poster was presented on “Imbalance of Th17 and regulatory T cells in gall bladder cancer : implications in pathogenesis” at **“31<sup>st</sup> Annual Convention of Indian Association for Cancer Research & International Symposium on Cancer Genomics and its Impact in the Clinics”** at ACTREC, Navi Mumbai from 26-29 January 2012.

## **Awards**

- **Travel award** for oral presentation at 13<sup>th</sup> FIMSA advanced Immunology Course at PGIMER, Chandigarh (March 2016)
- **Dr. G.P. Talwar Young Scientist Award** in 41<sup>st</sup> Annual Conference of Indian

Immunology Society (IMMUNOCON-2014), Madurai Kamaraj University. (December 2014)

- **Travel fellowship** from Homi Bhabha National Institute, (February 2014)
- Sam Mistry **travel fellowship** award from Sam Mistry Foundation, Mumbai (February 2014)
- 2<sup>nd</sup> Poster presentation award in conference on “National Education Day”, NMIMS School of Science, Mumbai. (2012)

Navi Mumbai

Date: 06/01/2017



Rushikesh Sudam Patil

*I dedicate this dissertation to my late brother and my parents.  
The unconditional support provided by them made my PhD  
journey easy and successful.*

## **Acknowledgements**

*It gives me an immense pleasure to express my gratitude to all of them who directly or indirectly contributed for successful completion of my PhD dissertation work. After an exhaustive tenure of almost six years, when I recollect the memories, it has been a period of intense learning for me, not only in the scientific arena, but also on a personal level. This journey has a big impact on me. I have received a great deal of help from many individuals during the course of this study, but several are noteworthy of special attention.*

*First of all I pay my sincere reverence to my mentor Professor Shubhada V. Chiplunkar. This work would not have been possible without her guidance, support and encouragement. Her continuous support, patience, encouragement, enthusiasm and immense knowledge were the key motivations during my PhD. Her valuable suggestions during tough times and the freedom she gave to conduct experiments helped me to grow intellectually and develop my research skills throughout this journey. Her scientific and ethical approach towards research has influentially shaped my interest in my work. I am truly thankful to her for my personal and academic development. Her selfless dedication towards research, unflinching courage and assertive conviction will always inspire me for my future endeavours. I feel privileged to have her as my mentor.*

*I have also honoured greatly to have eminent scientists as my Doctoral Committee members. I am thankful to Dr. Dalal, Dr. Gupta, Dr. Dikshit, Dr. Sainis, and Dr. (late) Kalraiya for their criticisms and valuable suggestions.*

*I am indebted to our clinical collaborators Dr. Shrikhande, Dr Goel and Dr. Dikshit for providing the clinical samples of gallbladder cancer patients. I am also thankful to Dr. Baretto for his help during initial phase of the study.*

*Special thanks to Dr. Dikshit lab members at Tata Memorial Hospital for the help extended by them for patient sample collection. I also thank Dr. Indap and her lab members at Ruparel College Mumbai; especially Dr. Shweta Agarwal and Mr. Sachin Chaugule for chick chorioallantoic membrane assay.*

*I would like to thank Advanced Centre for Treatment Research and Education in Cancer (ACTREC) and Department of Atomic Energy (DAE) for providing research scholarship to me during this tenure. I acknowledge Department of Biotechnology (DBT), India for*

*providing the financial support to conduct this research. For scholarships and conference funding, I would like to thank DBT project grant, Homi Bhabha National Institute, Sam Mistry foundation, Mumbai.*

*I appreciate the generosity and cooperation shown by all the healthy volunteers and gallbladder cancer patients for donating their blood and consenting to be a part of the study. Special thanks to Mr. Anand and Ms. Lalita, Tumor Tissue Repository TMH, for their help and support during sample collection.*

*I acknowledge the rich and supportive environment provided by Chiplunkar Lab members. I feel lucky to be a part of “Chiplunkar lab” group. The friendly and healthy atmosphere in the lab nourished me to grow and develop my personality. I would like to thank Dr. Jyoti Kode, Trupti Pradhan, Shamal Vetale, Meena Patkar, Rekha Gour, Dakaveji, Desaiji, Sawantji, Kalpesh, Ram, Preeta Menon, Lata, Maya Dolas, and Sujata Hake. Special thanks to Shamal Vetale for introducing me to the field of flowcytometry in a friendly atmosphere. Thanks to Meena Patkar for being a great help to withdraw blood from healthy donors and for placing purchase orders.*

*I found students in Chiplunkar Lab group immensely knowledgeable and dedicated. I am thankful to them for friendly and collegial atmosphere in the lab. They were wonderful colleagues in every sense. In person, I would like to thank Bhairav, Nirmala, Dimpu, Babita, Swati, Aparna, Asif, Gauri, Sajad, Sachin, Shalini, Neha, Siddhesh, Sagar, Pradeep, Atul, Devanand, Priyanka, Pravin, Prasad, for all the happy moments. I thank Bhairav, Dimpu and Asif for their brotherly support and guidance as philosopher in hard and good times.*

*I specially thank Sagar for collecting patient samples from TMH and initial standardization experiments. It was my benefit to have Sagar as my colleague on the project. Special thanks to Saleha who worked with me as summer trainee.*

*I acknowledge the academic environment of ACTREC, supporting the scientific careers of young minds. I thank people from Flowcytometry, Microscopy, Genomics, Common Instrument facility, Library, Photography, IT department, Security and Administration for their timely support. A special thanks to Mr. Shyam Chavan from Photography for his help in the art related material during my PhD tenure.*

*I would like to thank Chiplunkar Sir for being a wonderful host for diverse lab parties at his home or at outside venues. I would also like to thank the group of Shamal, Meena, Asif, Sachin, Sajad, Dakave, Desai, Ram and Siddhesh for making my time outside the lab memorable by arranging picnics and parties.*

*Huge thanks go to my batchmates (Abira, Aditi, Asif, Crismita, Gauri, Indrajit, Madhura, Nikhat, Piyush, Poonam, Prasad, Raja, Rajan, Ram, Richa, Saikat, Satish, Shyam, and Yasser) for all the fun time, get-togethers and other good times besides supporting wholehearted during difficult times.*

*I want to thank those who took the time to finalize the drafts of this thesis and paper manuscript. I thank Asif, Shalini, Sandeepa and Sachin who took their time to read and re-read very early drafts of the thesis/manuscripts and provided helpful comments.*

*Eventually I am thankful to my parents for their sacrifices for me and being a constant source of love. Without them I am nobody. I am grateful to them for the values they taught me to live as human. I also pay sincere respect to my late brother who always used to wish for my best. I thank my uncle, aunt and my cousins where I stayed for long during PhD tenure. I thank them for all the happy time I spent. I would also like to thank my wife Sandeepa for her love and constant moral support during thesis writing.*

*Last but not the least I am grateful to the Almighty, for this wonderful life!*

*Rushikesh Sudam Patil*

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# Synopsis



## Homi Bhabha National Institute

### Ph. D. PROGRAMME

<b>1. Name of the Student:</b>	Rushikesh Sudam Patil
<b>2. Name of the Constituent Institution:</b>	Tata Memorial Centre, Advanced Centre for Treatment, Research and Education in Cancer
<b>3. Enrolment No. :</b>	LIFE09201004010
<b>4. Title of the Thesis:</b>	“Understanding pathogenesis of gall bladder cancer: Role of TH17 and Regulatory T cells”
<b>5. Board of Studies:</b>	Life Sciences

### SYNOPSIS

**Introduction:** Gallbladder Cancer (GBC) is a relatively uncommon but lethal biliary tract related cancer. Its occurrence shows ethnic and geographical variations and is prevalent in Peru, Ecuador, Poland, Chile, Pakistan, Japan and northern India [1]. GBC is 2-3 times common in women than men and highest incidences are reported in north Indian women [2]. Its anatomic location, elusive symptoms and diagnosis at advanced stage renders 5 year survival less than 5% [1]. Cholelithiasis (gallstone) is a major risk factor of GBC. 70-80% patients are associated with gallstone disease. Chronic inflammation associated with cholelithiasis leads to dysplastic changes in gallbladder resulting into high grade premalignant carcinoma *in situ* [3]. Complete surgical resection is the only curative option available, but more than 90% GBC patients are with un-resectable disease. Despite improved results of chemotherapy and surgery, the long term outcome remains disappointing [4].

Therefore, efforts are needed to identify other etiological factors contributing to pathogenesis of GBC.

The inflammatory microenvironment is an essential component of a tumor and plays a decisive role at different stages of tumor development. It modulates host immune response to facilitate tumor growth [5]. Interleukin-17 (IL17) is a potent proinflammatory cytokine and its elevated levels have been found to be detrimental in autoimmune diseases and cancers [6]. IL17 is known to induce, chemoresistance, neoangiogenesis and activation of matrix metalloproteinases which in turn enhances tumor progression [7, 8]. However, the cellular source of IL17 and its clinical relevance in GBC is not well studied.

$CD4^+IL17^+$  (Th17) is a subset of  $CD4^+$  T cell, characterized by the production of IL-17A. Th17 cells and its related cytokines are reported to be present in tumor environment of prostate, ovarian, colorectal, head and neck, gastric cancer and other malignancies [9]. The proinflammatory cytokines such as IL6, IL1 $\beta$ , IL23 and TGF $\beta$  induce the differentiation and/or stabilization of Th17 cells [10]. Th17 generation is controlled by the master transcription factors retinoic acid-related orphan receptor (ROR) $\gamma$ t, ROR $\alpha$ , aryl hydrocarbon receptor (AHR) and interferon regulatory factor 4 (IRF4). Increased intra-tumor Th17 density associates with higher blood vessel density and poor prognosis of cancer patients [11].

In contrast, another subset of  $CD4^+$  T cells, characterized as  $CD4^+CD127^{low/-}CD25^+Foxp3^+$  regulatory T cells (Treg), are known to play a critical role in immune tolerance and control of autoimmunity [12]. They express Foxp3 as lineage determining transcription factor and actively engage in inhibiting the activation of tumor specific CD4 and CD8 T cells [13]. Treg cells suppress target cell types by applying various mechanisms including secretion of suppressor cytokines (TGF $\beta$ , IL10), IL2 sequestration, expression of co-inhibitory molecules (CTLA4, PDL1, TIM3) or cytotoxicity [13]. The elevated proportions of Tregs present in peripheral blood and tumor microenvironment are associated with poor prognosis of head and

neck, lung, liver, gastrointestinal tracts, pancreas, ovary, breast and several other cancer patients [12].

The tumor infiltrating immune cells are engaged in extensive crosstalk with cancer cells. The type, functional orientation, density and location of infiltrating immune cells determine the fate of tumor progression and response to anti-tumor therapy. An expanding body of literature has highlighted the functional relevance of Th17 and Treg cells in tumor environment [14]. The crosstalk of pro and anti-inflammatory immune response mediated by Th17 and Treg cells, determining disease outcome, is not investigated in GBC. The present prospective study aims at understanding the dynamics of Th17 and Treg contributing to inflammation and thereby progression of GBC.

### **Aims and Objectives:**

1. Analysis of the immunophenotypes and effector functions of peripheral blood lymphocytes of GBC patients in comparison to healthy individuals
2. Understanding the functional dynamics of pro-inflammatory (Th17, Tc17 and T $\gamma\delta$ 17) and anti-inflammatory regulatory T cells (CD4<sup>+</sup>CD127<sup>low/-</sup>CD25<sup>+</sup>Foxp3<sup>+</sup>; Tregs) in peripheral blood and tumor microenvironment of GBC patients
3. Protumor role of IL17 producing  $\gamma\delta$  T (T $\gamma\delta$ 17) cells in GBC

### **Methodology**

**Patient samples:** Heparinised peripheral blood was collected from GBC patients (n=52) prior to chemotherapy/radiotherapy or surgery after obtaining written informed consent. The study protocol was approved by ACTREC-TMC Institutional review board. The patients were grouped according to the TNM classification as stage II, stage III and stage IV. Tumor tissues (n=17) were obtained from GBC patients undergoing cholecystectomy. Heparinised blood and clotted blood was collected from healthy individuals (n=30) who participated voluntarily.

**Cell isolation and culture:** Peripheral blood mononuclear cells (PBMCs) were isolated from heparinised blood using Ficoll Hypaque (Sigma-Aldrich, St. Louis, MO). Single cell suspension of surgically resected tumor was prepared by enzyme digestion (0.05%

collagenase, 0.02% DNase and 5U/ml hyaluronidase [Sigma-Aldrich]) and the cells were cultured in serum-free medium and tumor supernatants were collected after 24 h. To isolate T $\gamma$  $\delta$ 17 cells, purified  $\gamma$  $\delta$ T cells were stimulated with PMA and Ionomycin for 5 h and labelled with IL17 catch reagent followed by secretion phase of 45 minutes at 37<sup>0</sup>C. After labelling with anti-IL17 detection antibody, cells were sorted for IL17-PE positive cells (purity > 90%). Gallbladder cancer cell lines [OCUG-1 (poorly differentiated) and NOZ (moderately differentiated)] were purchased from Japan Health Science Research Resources Bank (Osaka, Japan). Cells were cultured in William's E medium (Sigma Aldrich, USA) supplemented with 10% FBS (37<sup>0</sup>C, 5% CO<sub>2</sub>).

**Flow cytometry:** Flow cytometric analysis was performed using FACS Aria flow cytometer (Becton Dickinson, CA, USA) and analysed by FlowJo software (Tree Star, Ashland, OR). Fluorescence minus one control was used in all experiments to determine background fluorescence. For intracellular cytokines staining, PBMCs were stimulated with PMA (50 ng/ml) and ionomycin (1 $\mu$ g/ml) for 5 h in presence of Brefeldin A (5  $\mu$ g/ml). Minimum 50,000 events were acquired on FACS Aria flow cytometer and analyzed by FlowJo.

**Regulatory T cells suppression assay:** Tregs were isolated from PBMCs using immunomagnetic separation kit (BD Biosciences). CD4<sup>+</sup>CD25<sup>-</sup> T cells were used as responder T cells (Tres) and labelled with carboxyfluorescein succinimidyl ester (CFSE; 5 $\mu$ M) (Life technologies). Tres cells (1x10<sup>4</sup>) were co-cultured with Tregs for 5 days at different ratios (Tres: Treg = 1:2, 1:1, 1:0.5, 1:0). Co-cultures were stimulated with anti-CD3/anti-CD28 coated beads (1bead: 1cell) (Treg suppression inspector, Miltenyi biotech). Cells were acquired on FACS Aria and analyzed by FlowJo software.

**Cytokines and chemokines measurement:** Cytokines and chemokines in sera samples of GBC patients and culture supernatants were measured by Th1/Th2/Th17 cytometric bead array kit and flex sets for IL8, IL1 $\beta$ , IL12p70, CXCL9, CCL5, CXCL10, CCL2 (BD

Biosciences) as per manufacturer's instructions. Samples were acquired on FACS Aria and analysed using BD FCAP Array (BD Biosciences). TGF $\beta$  (BD Biosciences) and IL23 (eBiosciences, CA, USA) were determined by ELISA.

**Cell migration assay:** Migration was studied by trans-well assay using Millicell cell-culture inserts (Merck Millipore, MA) with pore size 8.0 $\mu$ m. OCU-G-1 cells ( $5 \times 10^4$ ) were cultured in 600 $\mu$ l serum-free William's E medium. In some experiments rhCXCL9 (100ng/ml; PeproTech, NJ, USA) or tumor supernatants were added to the lower chamber. Isolated T $\gamma$  $\delta$ 17 cells ( $5 \times 10^4$ /100 $\mu$ l medium) or  $\gamma$  $\delta$ T cells ( $1 \times 10^5$ /100 $\mu$ l medium) were added onto the trans-well filter. Migrated cells from lower chamber were counted using haemocytometer after 7 h. For blocking experiments, T $\gamma$  $\delta$ 17/ $\gamma$  $\delta$ T cells were incubated with anti-CXCR3 antibody (10 $\mu$ g/ml; R&D Systems, USA), 30 minutes before trans-well co-culture.

**Angiogenesis array:** Cell-free supernatant of T $\gamma$  $\delta$ 17 was incubated with OCU-G-1 cells ( $2 \times 10^4$ /well) in presence / absence of neutralizing anti-IL17 antibody (10 $\mu$ g/ml; R&D Systems, MN, USA). After 48 h, supernatants were collected and analysed for vascular endothelial growth factor (VEGF) by ELISA (R&D systems, MN, USA) or angiogenesis related proteins by human proteome profiler angiogenesis array (R&D systems, MN, USA). The data was evaluated using Image J 1.48V software (NIH, USA) and expressed as mean pixel density.

**Chorioallantoic membrane (CAM) assay:** On embryonic day 5 of fertilized chicken eggs, a small window was made in the shell and 200 $\mu$ l medium/ T $\gamma$  $\delta$ 17 supernatant/ rhIL17 (100ng/ml, R&D systems, MN, USA) was added onto the CAM of growing embryo. After 48 h, eggs were cracked open and embryos were carefully transferred to 100 mm petri dish and images were captured. Angiogenesis was quantitatively evaluated by scoring number of branching points in control and treated CAMs.

**Cell proliferation assay:** OCUG-1 cells ( $1 \times 10^4$ ) were cultured in serum-free medium with rhIL17 (R&D systems, MN, USA in different concentrations.  $0.5 \mu\text{Ci}/10 \mu\text{l}/\text{well}$   $^3\text{H}$ -Thymidine (specific activity  $240 \text{GBq}/\text{mmol}$ ; Radiation and Isotope Technology, India) was added during last 18 h of the assay. After 72 h, cells were harvested and radioactivity was measured on liquid  $\beta$ -scintillation counter (Packard USA) as counts per minute (CPM).

**Wound healing assay:** OCUG-I and NOZ GBC cell lines were treated with Mitomycin C ( $10 \mu\text{g}/\text{ml}$ ) for 2 h. Three scratches were made precisely with the help of T-10 micro tips. The rhIL-17 ( $50 \text{ng}/\text{ml}$ ,  $100 \text{ng}/\text{ml}$ ) was added and cell migration was monitored for 21 h using time lapse inverted microscope. Images were analysed using Image J1.48V software.

**Matrigel invasion assay:** In a 24 well transwell assay ( $8.0 \mu\text{m}$  pore size), the upper chambers were coated with the matrigel (BD Biosciences, USA). OCUG-1 ( $5 \times 10^4$ ) and NOZ ( $3 \times 10^4$ ) cells were suspended in  $200 \mu\text{l}$  plain William's E medium containing IL17 ( $50 \text{ng}/\text{ml}$  or  $100 \text{ng}/\text{ml}$ ). The invasion of cells was monitored towards William's E medium with 10% FBS added to the lower chamber. Unmigrated cells were removed using cotton swabs. The cells were stained by 1% crystal violet and observed using 10 X objective.

**Statistical analysis:** Statistical significances were calculated by two-tailed student's t-test or Mann-Whitney test (GraphPad Prism software, Lake Forest, CA). Overall patient survival was calculated by Kaplan-Meier curve and compared by Log-rank test. Survival time was defined as the interval between date of diagnosis and date of death or last follow-up, whichever occurred earlier.  $p < 0.05$  was considered statistically significant.

### **Results: 1. Immunophenotyping and effector functions of peripheral blood lymphocytes of GBC patients**

The prevalence of immune infiltrates in the tumor microenvironment has significant influence on development of cancer. The focus of the present prospective study was to investigate immune infiltrates of GBC and to study the functional characteristics of adaptive

and innate immune cells contributing to tumor progression. It was observed that the immune cells contributing to adaptive immunity ( $CD3^+$ ,  $CD3^+CD4^+$ ,  $CD3^+CD8^+$ ,  $CD19^+$ ,  $CD3^+CD56^+$ ) were decreased in the peripheral blood of GBC patients compared to HI. The expression of  $CD3\zeta$  chain, vital signalling molecule in T cell receptor (TCR) mediated signalling of T cells, was downregulated in PBMCs of GBC patients compared to healthy individuals (HI). The compromised signalling through TCR resulted in low lymphocyte proliferative response to anti  $CD3$  mAb or mitogen (phytohaemagglutinin; PHA) stimulation as studied by  $^3H$ -Thymidine incorporation assay. Moreover, the PBMCs of GBC patients showed decreased secretion of effector cytokines upon stimulation anti- $CD3$  mAb or PHA. Thus the data suggests that the systemic immune dysfunction may result in insufficient activation of anti-tumor immune response in GBC patients.

## **2. Dynamics of pro inflammatory (Th17, Tc17 and $T\gamma\delta17$ ) and anti-inflammatory (Tregs) immune cells in peripheral blood and tumor environment of GBC patients**

Chronic inflammatory condition of cholelithiasis is a vital risk factor of GBC. However, the crosstalk of immune cells contributing to inflammation is not well understood in GBC. Using multicolour flowcytometry, it was observed that IL17 producing  $CD4^+$  (Th17),  $CD8^+$  (Tc17), and  $\gamma\delta^+$  ( $T\gamma\delta17$ ) cells were significantly increased in PBMCs of GBC patients compared to HI. Levels of these cells were further elevated in tumor compartment than peripheral blood of GBC patients. Interestingly, the relative percentages of  $T\gamma\delta17$  appeared to be higher in tumor infiltrating lymphocytes (TILs) compared to Th17 and Tc17. In contrast,  $\gamma\delta^+IFN\gamma^+$  cells were significantly decreased in TILs compared to PBMCs of GBC patients and HI. A significant decrease was also observed in  $CD8^+IFN\gamma^+$  cells in TILs compared to PBMCs of GBC patients. However, no changes were observed in  $CD4^+IFN\gamma^+$  cells in GBC patients compared to HI. Interestingly, it was observed that the  $T\gamma\delta17$  and  $\gamma\delta^+IFN\gamma^+$  cells showed a negative

correlation. It is reported that  $\gamma\delta$ T cells expressing CD27 produce IFN $\gamma$  and CD27<sup>-</sup>  $\gamma\delta$ T cells secrete IL17 [15]. In GBC patients, the levels of CD27<sup>-</sup>  $\gamma\delta$ T cells were significantly elevated than CD27<sup>+</sup>  $\gamma\delta$ T cells. Overall the data suggests that the cytokine profile of  $\gamma\delta$ T cells in GBC patients is skewed towards production of IL17.

To study the anti-inflammatory and immunosuppressive arm of immune response in GBC patients we investigated the levels of regulatory T cells (Tregs; CD4<sup>+</sup>CD25<sup>+</sup>CD127<sup>low/-</sup> expressing Foxp3 more than 80%). Studies demonstrated that Tregs were significantly decreased in peripheral blood of GBC patients than HI. However, the percentages of Tregs in TILs were higher than PBMCs of GBC patients but comparable to HI. The median fluorescence intensity (MFI) of Foxp3 expression on Tregs was significantly increased in TILs than PBMCs of GBC patients. Moreover, the suppressive potential of Tregs, as analyzed by CFSE dye dilution method, in peripheral blood of GBC patients was comparable to HI. This indicates that although Tregs were decreased in PBMCs of GBC patients, their suppressive potential was not compromised. Study of dynamics of these cells revealed that the ratios of T $\gamma\delta$ 17/Treg, Th17/Treg and Tc17/Treg were significantly increased in PBMCs as well as in TILs of GBC patients indicating an inverse correlation of IL17 producing cells and Tregs. T $\gamma\delta$ 17, Th17 and Tc17 cells showed no correlation with clinical stage (II to IV) of GBC patients. However, their levels remained high in all stages of GBC patients compared to HI. In contrast, the levels of Tregs in GBC patients of all stages (II to IV) remained lower than HI. This clearly indicates that the immune response is skewed towards IL17 producing cells in GBC patients.

As increased levels of T $\gamma\delta$ 17 were observed in GBC patients, we reasoned that the cytokine milieu promoting T $\gamma\delta$ 17 differentiation should be present in sera and tumor environment. Cytokine profile of GBC patients revealed that the cytokines (IL6, IL23, IL1 $\beta$ ) required for polarization and/or stabilization of IL17 producing cells were elevated in sera and tumor

environment of GBC patients thus making the environment conducive for differentiation of T $\gamma$  $\delta$ 17 cells.

To investigate the clinical significance of T $\gamma$  $\delta$ 17, Th17, Tc17 and Tregs, the survival time of patients was analyzed with frequency of these cells in peripheral blood of GBC patients. Cox proportional regression analysis revealed that patients with high T $\gamma$  $\delta$ 17 showed poor overall survival than patients with low levels of T $\gamma$  $\delta$ 17. In contrast, the patients with high levels of  $\gamma\delta^+$ IFN $\gamma^+$  had longer overall survival than patients with low levels of  $\gamma\delta^+$ IFN $\gamma^+$  cells. Similarly, Th17 and Treg cells in peripheral blood were associated with poor survival of GBC patients. Tc17 were not associated with survival of patients. Altogether, the data suggests that T $\gamma$  $\delta$ 17, Th17 and Treg cells might serve as biomarkers for prediction of risk and prognosis of GBC. Interestingly, our data revealed that in GBC patients, T $\gamma$  $\delta$ 17 cells are emerging as an important phenotype in cancer progression.

### **3. Protumor role of T $\gamma$ $\delta$ 17 cells in GBC patients**

The increased levels of T $\gamma$  $\delta$ 17 cells observed in tumor environment of GBC patients suggest that these cells have the propensity to migrate to the tumor. To test this hypothesis, expression of chemokine receptors (CCR6, CCR7, CXCR4 and CXCR3) on Th17, Tc17 and T $\gamma$  $\delta$ 17 cells were analyzed in peripheral blood of GBC patients. It was observed that T $\gamma$  $\delta$ 17 expressed elevated levels of CXCR3 than Th17 or Tc17. However, CCR6, CCR7 and CXCR4 were expressed at comparable levels by T $\gamma$  $\delta$ 17, Th17 and Tc17. Next, to investigate migration of T $\gamma$  $\delta$ 17 cells, purified T $\gamma$  $\delta$ 17 cells were cultured with GBC cells in transwell assay. Enhanced migration of T $\gamma$  $\delta$ 17 cells was observed towards OCU-1 or rhCXCL9 or tumor supernatants. In the presence of neutralizing anti-CXCR3 antibody, the migration of T $\gamma$  $\delta$ 17 cells was significantly curtailed. The data suggests that tumor environment induces infiltration of T $\gamma$  $\delta$ 17 cells to the tumor bed through CXCL9-CXCR3 axis. Similar results

were obtained with purified  $\gamma\delta$ T cells suggesting total  $\gamma\delta$ T cells are also recruited towards tumor environment using CXCL9 as chemoattractant. In order to investigate whether the elevated levels of T $\gamma\delta$ 17 in GBC patients, contribute to tumor progression, the cytokine profile of T $\gamma\delta$ 17 was analysed. It was observed that T $\gamma\delta$ 17 primarily secretes high levels of IL17 and low levels of IL2 and TNF $\alpha$  but did not produce other cytokines (IL4, IL6, IL10 and IFN $\gamma$ ). The presence of IL17 receptor on the GBC cells (OCUG-1 and NOZ) was confirmed by flow cytometry and immunofluorescence staining. The data showed that more than 80% of GBC cells (OCUG-1 and NOZ cell lines) expressed IL17 receptor on the surface.

The proangiogenic action of T $\gamma\delta$ 17 cells on GBC was studied by human protein profiler angiogenesis array. Cell-free supernatants from T $\gamma\delta$ 17 cells significantly upregulated secretion of angiogenesis promoting factors from OCUG-1 cells such as VEGF, uPA, MMP9, MCP1, GM-CSF, CXCL16, coagulation factor III, angiogenin, etc. compared to OCUG-1 cells cultured with medium alone. This effect was abrogated by addition of anti-IL17 mAb. Further, the proangiogenic effects of T $\gamma\delta$ 17 were validated by chorioallantoic membrane (CAM) assay. Cell-free supernatants of T $\gamma\delta$ 17 enhanced vascularization of CAM compared to medium alone. The effect was curtailed after addition of anti-IL17 mAb to the assay. Collectively, the data suggests that T $\gamma\delta$ 17 cells are proangiogenic subtype of  $\gamma\delta$ T cells and may contribute to carcinogenesis of GBC.

Next, to study whether IL17 has direct role in GBC promotion, poorly differentiated (OCUG1) and moderately differentiated (NOZ) cell lines of GBC were treated with rhIL17 and analysed for their proliferation, migration and invasion potential. It was observed that addition of recombinant IL17 to GBC cells induced proliferation, migration, matrigel invasion and VEGF production in concentration dependent manner. However, the effect was

more pronounced on poorly differentiated GBC cells. In conclusion, the data suggests that the cytokine IL17 significantly contributes to progression of GBC.

### **Summary and Conclusion**

Despite conventional treatments modalities, GBC remains a highly lethal malignancy. 70-80 % GBC patients are associated with inflammatory condition of cholelithiasis. However, the mediators of inflammatory circuits in GBC remain unexplored. The current study has shown that low lymphocyte proliferative response, decreased cytokine secretion upon stimulation with anti CD3 mAb and down regulated CD3 $\xi$  chain expression in PBMCs demonstrate immune-dysfunction and incapability to mount optimum antitumor immune response in GBC patients. The increased levels of Tregs were reported in cancer patients as strategy of tumor immune evasion [16]. In GBC patients, the multicolour flowcytometry showed that Tregs were decreased in peripheral blood of GBC patients at all stages of disease compared to HI. However, their suppressive potential was not compromised suggesting that Tregs in GBC patients are functionally normal. We observed that GBC patients with high peripheral blood Treg cells have decreased survival compared to those with low levels. In addition, Tregs were increased in tumor compartment and express elevated levels of Foxp3 compared to peripheral blood of GBC patients. In contrast, the analysis of inflammatory immune cells revealed that compared to HI, Th17, T $\gamma$  $\delta$ 17 and Tc17 cells were increased in PBMCs and TILs of GBC patients. Serum cytokines profile of GBC patients showed elevated levels of cytokines (IL6, IL23 and IL1 $\beta$ ) that are required for polarization and/or stabilization of IL17 producing cells. It was shown that the tumor environment of GBC recruits T $\gamma$  $\delta$ 17 cells to the tumor bed through CXCL9-CXCR3 axis and T $\gamma$  $\delta$ 17cells induce angiogenesis in GBC cells by secretion of IL17 as confirmed by CAM assay. Further, the data provide evidence that rhIL17 enhance proliferation, migration and invasion potential of GBC. Thus the present study provides

strong evidence that IL17 and T $\gamma$  $\delta$ 17 cells are emerging as important signatures of GBC and holds significance for targeted therapies.

Currently there are many drugs under clinical trial targeting IL17 inflammatory axis including monoclonal antibodies specific for IL17 (Secukinumab), IL17R (brodalumab), IL23 p40 subunit (ustekinumab), IL23 p19 subunit and small molecules with inverse agonist activity against ROR $\gamma$ t, etc.[17]. Moreover, the increased levels of Tregs observed in GBC tumors could also be targeted using depleting antibodies or their migration to the tumor can be inhibited.

In conclusion, T $\gamma$  $\delta$ 17 and Th17 are emerging as predictive markers in GBC. Our data suggests that T $\gamma$  $\delta$ 17 mediated angiogenesis and Treg cells mediated immunosuppression may contribute to the negative clinical outcome of GBC patients. Thus, future immunotherapeutic treatment modality for GBC may use a combined approach to block the trafficking of T $\gamma$  $\delta$ 17 cells to the tumor, inhibit functions of IL17 and reverse the immunosuppression mediated by Treg cells.

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### **Publications in Refereed Journal**

#### **A) Published manuscripts**

5. Dar AA, **Patil RS**, Chiplunkar SV, “Insights into the relationship between toll like receptors and gamma delta T cells responses”, **Front Immunol**. 2014 Jul 31;5:366. doi: 10.3389/fimmu.2014.00366.
6. **Patil RS**, Bhat SA, Dar AA, Chiplunkar SV, “The Jekyll and Hyde story of IL17 producing  $\gamma\delta$ T (T $\gamma\delta$ 17) cells”, Feb4 2015, **Front Immunol**. 2015 Feb 4;6:37. doi: 10.3389/fimmu.2015.00037
7. **Patil RS**, Shah SU, Shrikhande SV, Goel M, Dikshit R, and Chiplunkar SV, “IL17 producing  $\gamma\delta$  T cells induce angiogenesis and are associated with poor survival in gallbladder cancer patients”, **Int J Cancer**. 2016 Apr 8. doi: 10.1002/ijc.30134

#### **B) Communicated Manuscript**

#### **C) Manuscripts in preparation**

1. **Patil RS** and Chiplunkar SV, “Interleukin 17 promotes proliferation, invasion and angiogenesis of gallbladder cancer”

#### **D) Other Publications / Conference Presentations:**

#### **Conference Proceedings:**

3. **Patil RS**, Shah SU, Shrikhande SV, Goel M, Dikshit R, and Chiplunkar SV, “Pro-tumor role of IL17 producing  $\gamma\delta$ T cells in gallbladder cancer”, **European Journal of Cancer** Volume 54, Supplement 1, Pages S1-S78 (February 2016). doi: 10.1016/S0959-8049(16)31954-2.
4. **Patil RS**, Shah SU, Shrikhande SV, Goel M, Dikshit R, and Chiplunkar SV, “Role of IL17 producing  $\gamma\delta$  T cells ( $T\gamma\delta 17$ ) in gall bladder cancer pathogenesis”, Feb10 2015, *J Carcinog*, 14:21.

#### **Awards:**

- Received **Travel award** for oral presentation at 13<sup>th</sup> FIMSA advanced Immunology Course at PGIMER, Chandigarh (March 2016)
- **Dr. G.P. Talwar Young Scientist Award** in 41<sup>st</sup> Annual Conference of Indian Immunology Society (IMMUNOCON-2014), Madurai Kamaraj University. (December 2014)
- Received **travel fellowship** from Homi Bhabha National Institute, (February 2014)
- Received Sam Mistry **travel fellowship** award from Sam Mistry Foundation, Mumbai (February 2014)
- 2<sup>nd</sup> Poster presentation award in conference on “National Education Day”, NMIMS School of Science, Mumbai. (2012)


#### **Presentations:**

1. Oral presentation on “ $T\gamma\delta 17$  is a proangiogenic subtype of  $\gamma\delta$ T cells and associates with poor survival of gallbladder cancer patients” at “**13<sup>th</sup> FIMSA advanced Immunology Course**” held at ‘Department of Immunopathology, PGIMER, Chandigarh from 17-19 March 2016.
2. Oral presentation on “Paradox of immune system in Gallbladder Cancer: Role of  $T\gamma\delta 17$  cells” at ‘**Society of biological chemists (India) Mumbai chapter meeting**’ held at

NIRRH Mumbai (22 August 2015).

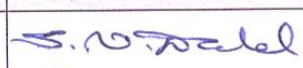
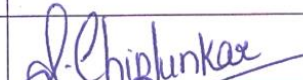
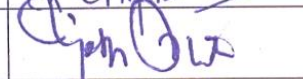
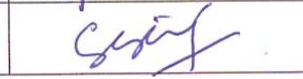
3. Oral presentation on “Role of IL17 producing  $\gamma\delta$ T cells ( $T\gamma\delta 17$ ) in gallbladder cancer pathogenesis” in international conference **“Carcinogenesis-2015”** on ‘Molecular pathways to therapeutics: Paradigms and challenges in oncology’ at ACTREC, Tata Memorial Centre, Navi Mumbai from 11-13 February 2015.
4. Oral presentation on “IL17 producing  $\gamma\delta$ T cells ( $T\gamma\delta 17$ ) contribute to tumorigenesis of gallbladder cancer” at **“41<sup>st</sup> annual conference of Indian Immunology Society-Immunocon-2014”** at Madurai Kamaraj University, Madurai, from 12-14 December 2014.
5. Poster was presented on “Dynamics of  $T\gamma\delta 17$  and Regulatory T cells in Gallbladder cancer” in international conference **“Keystone Symposium on Infection inflammation and cancer joint with immune evolution in cancer”** at Fairmont Chateau Whistler, Whistler, British Columbia, Canada from 9-14 March 2014.
6. Poster was presented on “Immune dysfunctions in Gallbladder cancer : Imbalance of  $T\gamma\delta 17$  and Regulatory T cells” at **“IX DAE-BRNS Life Sciences Symposium (LSS-2013) on Current advances in immunobiology and cancer”** at BARC, Anushaktinagar, Mumbai from 28-30 November 2013.
7. Poster was presented on “Dynamics of  $Th17$  and regulatory T cells in pathogenesis of Gall Bladder cancer” at **“ 39<sup>th</sup> Annual Conference of Indian Immunology Society-IMMUNOCON 2012”** at Banaras Hindu University, Varanasi from 9-11 November 2012.
8. Poster was presented on “Imbalance of  $Th17$  and regulatory T cells in gall bladder cancer: implications in pathogenesis” at **“National Education Day”** SVKM’s NMIMS School of Science, Mithibai College, Mumbai on 1 November, 2012.

9. Poster was presented on “Imbalance of Th17 and regulatory T cells in gall bladder cancer : implications in pathogenesis” at “31<sup>st</sup> Annual Convention of Indian Association for Cancer Research & International Symposium on Cancer Genomics and its Impact in the Clinics” at ACTREC, Navi Mumbai from 26-29 January 2012.

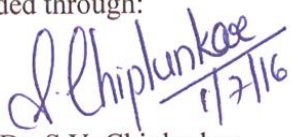
Signature of Student: 

Date: 30/06/2016

**Doctoral Committee:**

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## Abbreviations

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<sup>3</sup> H-TdR	Tritiated Thymidine
ADCC	Antibody dependent cellular cytotoxicity
Ag	Antigen
Act1	NF-κB activator 1
ATP	Adenosine triphosphate
ADP	Adenosine diphosphate
APC	Antigen Presenting Cell
APC	Allophycocyanin
AP-1	Activator protein 1
AJCC	American Joint Committee on Cancer
AKT	Protein kinase B
AID	Activation-induced cytidine deaminase
BTLA	B and T lymphocyte attenuator
BSA	Bovine serum Albumin
Bcl-6	B-cell lymphoma 6 protein
GBq	Giga Becquerel
CBA	Cytometric Bead Array
Cbl-b	Casitas B cell lymphoma-b
CCL	Chemokine Ligand
CCR	C-C motif chemokine receptor
CD	Cluster of Differentiation
cDNA	Complementary Deoxyribonucleic acid
CFSE	Carboxyfluorescein succinimidyl ester
CAM	Chorioallantoic membrane
cm	Centimeter
COX	Cyclooxygenase
cpm	Counts per minute
C/EBPβ	CCAAT-enhancer-binding protein β
CXC	Chemokine (C-X-C motif)
CTL	Cytotoxic T lymphocyte
CTLA4	Cytotoxic T lymphocyte associated protein 4
CTLA8	cytotoxic T lymphocyte associated antigen 8
DAMP	Damage associated molecular patterns
DAPI	4,6-diamidino-2-phenylindole
DC	Dendritic Cell
DEPC	Diethyl Pyrocarbonate
DN	Double negative
DMSO	Dimethyl sulphoxide
DP	Double positive
SP	Single positive
DNA	Deoxyribonucleic acid
dNTP	Deoxyribonucleotide triphosphate
DTT	Dithiothreitol

EAE	experimental autoimmune encephalomyelitis
EDTA	Ethylene Diamine tetra acetic acid
EGF	Epidermal growth factor
EGFR	Epidermal growth factor receptor
ELISA	Enzyme Linked Immunosorbent Assay
FACS	Fluorescence-activated cell sorting
FasL	Fas ligand
FBS	Fetal bovine serum
FCS	Fetal calf serum
FH	Ficoll Hypaque
FITC	Fluorescein isothiocyanate
5-FU	5-Fluorouracil
FSC	Forward Scatter
Foxp3	Forkhead box P3
GBC	Gallbladder cancer
GMCSF	Granulocyte macrophage colony-stimulating factor
G-CSF	Granulocyte colony-stimulating factor
GRAIL	gene related to anergy in lymphocytes
GWAS	genome-wide association study
GSK-3 $\beta$	Glycogen synthase kinase-3 $\beta$
HRP	Horseradish peroxidase
HIF	Hypoxia inducing factor
HIs	Healthy Individuals
HLA-DR	Human leukocyte antigen- D related
HNSCC	head and neck squamous cell carcinoma
HPC	hematopoietic progenitor cells
HPV	Human papillomavirus
h	Hours
HRPO	Horse radish peroxidase
HMGB1	High mobility group box 1
HSP	Heat shock proteins
IDO	Indoleamine 2,3-dioxygenase
IFN- $\alpha/\beta$	Interferon alpha/beta
IFN- $\gamma$	Interferon gamma
iNOS	inducible nitric oxide synthase
IL	Interleukin
IPP	Isopentenyl pyrophosphate
IKKi	I kappa B kinase I
JAK	Janus tyrosine kinase
kDa	Kilo Dalton
LXR $\beta$	Liver X receptor $\beta$
LT $\beta$ R	lymphotoxin- $\beta$ receptor
mAb	Monoclonal antibody
MACS	Magnetically activated cell sorting
MAPK	Mitogen Activated Protein Kinase
MCA	methylcholanthrene
MCP-1	monocyte chemoattractant protein 1
MCSF	macrophage colony-stimulating factor
MDSCs	myeloid-derived suppressor cells

mg	microgram
MHC	Major histocompatibility complex
MIC	MHC class I chain-related molecules
min	minutes
ml	millilitre
mM	milli molar
mm	milimeter
MMP	matrix metalloproteinases
Mo-MDSC	monocytic MDSC
mRNA	Messenger Ribonucleic acid
NF- $\kappa$ B	Nuclear factor kappa B
NKT	Natural killer T
NK	Natural killer
NKG2D	Natural Killer Group 2D
nM	Nano Moles
OGG1	8-Oxoguanine glycosylase
OD	Optical Density
PAMP	Pathogen-associated molecular pattern
PBMCs	Peripheral Blood Mononuclear Cells
PBS	Phosphate buffer Saline
PCR	Polymerase chain reaction
PD1	programmed death-1
PDL1/2	programmed death ligand 1/2
PE	Phycoerythrin
PerCP	Peridinin Chlorophyll Protein
pg	Pico gram
PGE2	prostaglandin E2
PHA	Phytohaemagglutinin
PTGS	Prostaglandin-endoperoxide synthase
PRR	pattern recognition receptors
PMA	Phorbol 12-myristate 13-acetate
PTK	protein tyrosine kinases
rIL-2	Recombinant Interleukin 2
RANTES	regulated on activation, normal T cell expressed and secreted
Rag	Recombination activating gene
RNA	Ribonucleic acid
RNAase	Ribonuclease
ROS	Reactive Oxygen Species
RNI	Reactive nitrogen intermediates
rpm	Revolutions per minute
RPMI	Roswell Park memorial Institute
RT	Room temperature
RT-PCR	Real Time-Polymerase chain reaction
ROR	retinoid-related orphan receptor
SCC	Squamous cell carcinoma
SEFIR	Similar Expression of Fibroblast growth factor genes and IL17Rs
SD	Standard deviation
SDS-PAGE	Sodium dodecyl sulphate-polyacrylamide gel electrophoresis
SEM	Standard error mean
SLAP	Src-like adaptor protein

Sec	Seconds
SSC	Side scatter
STAT	signal transducer and activator of transcription
TAA	Tumor associated antigen
TAK1	TRAF6 dependent TGF $\beta$ activated kinase
TAMs	tumor-associated macrophages
TCR	T-cell receptor
TLR	Toll like receptor
TGF- $\beta$	Transforming growth factor beta
Th	T helper
Tc	T cytotoxic
TIL	Tumor infiltrating lymphocytes
TLR	Toll like receptor
TNF- $\alpha$	Tumor necrosis factor alpha
TIM-3	T-cell immunoglobulin and mucin-domain
TRAIL	tumor necrosis factor-related apoptosis inducing ligand
TRAF	TNF receptor associated factor
Tregs	Regulatory T cells
Tres	Responder T cells
VEGF	Vascular endothelial growth factor
WHO	World Health Organization
$\alpha\beta$	Alpha beta
$\gamma\delta$	Gamma delta
$\mu\text{Ci}$	Micro-Curie
$\mu\text{g}$	Microgram
$\mu\text{l}$	Microliter
UICC	International Union Against Cancer



# Chapter 1

## Introduction

## Introduction

In India, more than 1 million new cancer cases are diagnosed every year and this number is expected to double in next 20 years [1]. Nearly 0.7 million deaths occurred in India due to cancer, which is home to about 17% of the global population with mortality to incidence ratio 68.6 [2]. Over the years, the burden of cancer has shifted to less developed countries, which currently account for about 57% of cases and 65% of cancer deaths worldwide. Although incidence rates for all cancers combined are twice in more developed compared with developing countries, mortality rates are only 8% to 15% in more developed countries [3]. This disparity highlights the lack of sophisticated cancer care system in developing countries and the need to pursue comprehensive understanding of cancer in local setting. The burden of cancer is linked to socioeconomic inequalities to access health care thus it is a major health care challenge in India. It leads to catastrophic healthcare expenditure and push entire family below poverty line [2]. Thus, the current cancer care system in India demands extensive research focusing on basic understanding of molecular mechanisms of cancer progression as well as technological improvements providing affordable, equitable, and universal cancer care for the entire population.

Gallbladder cancer (GBC) is one of the uncommon types of cancer but is highly lethal with 5 year survival of patients less than 5%. The increasing incidences of GBC in India are giving alarming signals that the search for new therapeutic targets with the hope of improving survival in patients with GBC is much needed. First described by Maximillian de Stoll in 1777, it is the fifth most common malignancy of gastrointestinal cancer worldwide and 4<sup>th</sup> most common cancer (following breast, cervix and ovary) and commonest gastro-intestine related cancer in India (accounting for 80 to 90% of biliary tract cancer) [4, 5]. The incidence of GBC displays striking differences on the basis of gender, ethnicity and geography. Though it is common in the Indian subcontinent (India, Pakistan), South America (Chile, Bolivia,

Columbia), East Asia (Korea, Japan) and central Europe (Slovakia, Poland, and Czech Republic), it is relatively infrequent in most parts of Europe, North America and Australia/New Zealand. The prevalence of GBC is three times higher among women than men in almost all populations (7.5 per 100,000 for men and 23 per 100,000 for women). The highest GBC incidence rate worldwide is reported for women in north India followed by Pakistan, Ecuador and Chile [6]. The incidence of GBC varies within India. It is much higher in northern parts specifically in gangetic belts than in southern parts of India. The risk of GBC increases with increase in age. The incidence increases after age of 45 and peaks after age of 65 years [4, 7].

The major risk factor of GBC is cholelithiasis. More than 70% of GBC patients are associated with gall stone disease. However, a very small fraction of patients with cholelithiasis develop GBC. Increasing stone size (>3 cm), number, volume, and weight, all are associated with an increased risk of cancer [8]. Cholelithiasis and GBC frequently coexist in the same population suggesting gallstones may function as cofactor in GBC. It is hypothesized that gallstones might cause direct mechanical irritation to the surrounding mucosal surface or they might affect gallbladder function, leading to delayed or incomplete emptying of bile with subsequent bile stasis and dilation of the gallbladder, which predisposes to inflammation. The chronic inflammation associated with cholelithiasis leads to dysplastic changes in gallbladder wall resulting into high grade premalignant carcinoma *in situ* [9].

Patients diagnosed with GBC show dismal prognosis with median survival of 3 to 6 months irrespective of treatment [10]. Anatomical location of gallbladder in the abdomen and elusive early symptoms, render diagnosis of these patients at an advanced stage. Complete surgical removal of gallbladder is the only curative treatment available [11]. However, more than 90% of patients present with an unresectable advanced disease. In addition, among patients undergoing “curative” resection, recurrence rates are high since GBC represents most

aggressive type of cancer among biliary tract related cancers. There is lack of suitable biomarkers for early diagnosis of the disease and established adjuvant treatments are unavailable in this setting [12, 13]. Despite improved results of chemotherapy and surgery, the long term outcome remains disappointing [14]. Therefore, for successful management of GBC, efforts are needed to identify other etiological factors contributing to pathogenesis of the disease.

The inflammatory microenvironment is an essential component of a tumor and plays a decisive role at different stages of tumor development. In GBC, chronic persistence of gallstones leads to inflammatory condition of chronic cholecystitis [15]. In murine models of gallstone disease, chronic gallbladder inflammation occurs at early stages as a local response to the presence of lithogenic bile (i.e. cholesterol supersaturated bile) [16]. Although the histological changes in gallbladder wall are induced by chemical stimulus (lithogenic bile), presence of microbiota of intestinal origin is also reported in gallbladder milieu [17]. The epidemiological evidence indicates a definite relation of GBC with infection of *Salmonella typhi* and *Helicobacter pylori* which result in chronic inflammation [10]. Liver flukes, particularly *Clonorchis sinensis* and *Opisthorchis viverrini*, have been implicated in patients of biliary tree cancer [18, 19]. The persistent inflammation in gallbladder could promote epithelial hyperplasia, dysplasia and ultimately progression to carcinoma [20]. Polymorphisms in genes related to the immune system, inflammation and oxidative stress namely PTGS2 (Prostaglandin-endoperoxide synthase 2 / cyclooxygenase 2), TLR2 (Toll like receptor 2), TLR4, IL1RN (IL1 receptor antagonist), IL1B, IL10, IL8, CCR5 (C-C motif chemokine receptor 5), LXR $\beta$  (Liver X receptor  $\beta$ ) and OGG1 (8-Oxoguanine glycosylase) have been associated with increased risk of GBC. Enhanced expression of COX2 and VEGF in GBC tissue associates with poor prognosis of GBC patients [21, 22]. A study on immune infiltrates in GBC analysed by immunohistochemistry showed that enhanced expression of

BTLA (B and T lymphocyte attenuator; co-inhibitory receptor) and Cbl-b (Casitas–B-lineage lymphoma protein-b; the anergy cell marker) are involved in inhibition of antitumor immunity and associates with unfavourable outcome in GBC patients [23]. Thus the inflammation-related genes, under the stimulus of gallstones or other insults, may accelerate the development of GBC [20]. The gathered evidence strongly links chronic inflammation with GBC progression. However, the immune players contributing to tumor associated inflammation in GBC are elusive.

Inflammatory cytokines have been observed to increase in pathogenic condition and are associated with disease exacerbation. Interleukin 17 (IL17), a 32 kilo Dalton dimeric protein, is a potent proinflammatory cytokine. [24]. It is predominately produced by CD4<sup>+</sup> (Th17) cells, but also by CD8<sup>+</sup> T cells (Tc17), Natural Killer T cells (NKT cells), macrophages, neutrophils and  $\gamma\delta$  T cells [24, 25]. Originally called cytotoxic T lymphocyte associated antigen 8 (CTLA8), induces the expression of proinflammatory cytokines including Tumor Necrosis Factor (TNF), IL1, IL6, Colony Stimulating Factors, chemokines, antimicrobial peptides and matrix metalloproteinases from endothelial cells, epithelial cells and fibroblasts. IL17 increases the immigration of neutrophils, macrophages and monocytes to inflamed tissues [25]. It acts through the IL17 receptor expressed on nearly every cell type of body [26]. It is shown that fibroblasts, epithelial cells and endothelial cells are the major targets of IL17. The contribution of IL17 to disease progression is thus linked to the role of these cells in disease pathology [26]. IL17 has a protective role against fungi and bacteria but when dysregulated, its elevated levels have been found in many autoimmune diseases and cancers [24]. Several human studies have highlighted the correlation between the level of IL17 and poor prognosis in cancer patients [27, 28]. Increased levels of IL17 in tumor tissue participate in neoangiogenesis and associate with microvessel density in tumors [29]. IL17 has been shown to induce, chemoresistance, neoangiogenesis and activation of matrix

metalloproteinases which in turn enhances tumor progression [30, 31]. However, the cellular source of IL17 and its clinical relevance in GBC is not well studied. Additionally, how IL17 augments progression of GBC is not well understood.

Initial studies on IL17 at mRNA level showed that it is expressed in memory CD4<sup>+</sup> T cells [32]. Later it was shown that IL17 is produced by distinct subset of CD4<sup>+</sup> T cells different from IFN $\gamma$  producing subset called as Th17 (CD4<sup>+</sup>IL17<sup>+</sup>) cells. The proinflammatory cytokines such as IL6, IL1 $\beta$ , IL23 and TGF $\beta$  induce the differentiation and/or stabilization of Th17 cells [33]. Analogous to the differentiation of Th1 and Th2 cell lineages, Th17 cells require both retinoid-related orphan receptor- $\alpha$  (ROR $\alpha$ ) and ROR $\gamma$  as lineage-specific transcription factors [34]. Ubiquitin mediated degradation of ROR $\gamma$ t results into impairment of Th17 differentiation suggesting critical requirement of ROR $\gamma$ t for Th17 functions [35]. IL6 plays an essential role by activating STAT3 (Signal transducer and activator of transcription 3), which directly drives transcription of Th17 lineage-specific genes including Rorc, IL17, and IL23R [36]. IL21 and IL23 induce ROR $\gamma$ t, which in synergy with STAT3 promote IL17 expression [37]. Th17 cells migrate to the tumor environment via CCR6/CCL20 chemokine axis [38]. RANTES and MCP-1 secreted by tumor cells and tumor-derived fibroblasts also mediate the recruitment of Th17 cells to the tumor bed [39]. Th17 cells and its related cytokines are reported to be present in tumor environment of hepatocellular, prostate, ovarian, colorectal, head and neck, breast, gastric cancer and various other malignancies [40, 41]. Th17 cells expressing CCR4 and CCR6 suppress lytic function, proliferation, and cytokine secretion of CD8<sup>+</sup> T cells. Additionally IL17 secreted by Th17 cells promotes not only regular angiogenesis but also lymphangiogenesis and development of lymphatic vessels by inducing expression of the pro-angiogenic factors including VEGF-D [42-44]. In contrast, it was demonstrated that increased levels of Th17 correlated with the number of NK cells, CD4<sup>+</sup>IFN $\gamma$ <sup>+</sup>, IL-17<sup>+</sup>IFN $\gamma$ <sup>+</sup>, CD8<sup>+</sup>IFN $\gamma$ <sup>+</sup> T cells in tumor tissue and were associated with

improved survival of patients with ovarian, oesophageal and lung cancer [38, 45, 46]. Th17 cells can also undergo lineage conversion into regulatory T cells (Treg) which suppress antitumor immune response [47, 48]. Moreover, Th17 cells cultured with TGF- $\beta$ /IL-6 co-express CD39 and CD73 ectonucleotidases on their surface which transforms ATP or ADP into immunosuppressive adenosine hampering antitumor immune response [49]. Thus, although the accumulation of Th17 cells into tumors is commonly observed, their effect on cancer progression remains controversial [50].

In contrast to the proinflammatory subtypes of CD4<sup>+</sup> T cells, another subset characterized as CD4<sup>+</sup>CD127<sup>low/-</sup>CD25<sup>+</sup>Foxp3<sup>+</sup> regulatory T cells (Treg), are known to play a critical role in immune tolerance and control of autoimmunity [51]. They express Foxp3 as lineage determining transcription factor and are actively engaged in inhibiting activation of CD4 and CD8 T cells thereby impairing antitumor immune responses [52]. Treg cells suppress target cell types by using various mechanisms including secretion of suppressor cytokines (TGF $\beta$ , IL10), IL2 sequestration, expression of co-inhibitory molecules (CTLA4, PDL1, TIM3) or cytotoxicity [52]. The tumor environment secretes large amounts of CC-chemokine ligand 22 (CCL22) which recruit Treg cell through CCR4 to the tumor bed [53]. Consequently, elevated proportions of Tregs have been identified in peripheral blood as well as in tumor microenvironment and are associated with poor prognosis of head and neck, lung, liver, gastrointestinal tract, pancreas, ovary, breast and several other cancer patients [51].

An expanding body of literature has highlighted the importance of balance between destructive inflammation and protective immunity determining the direction of malignant progression [54, 55]. The tumor infiltrating immune cells are engaged in extensive crosstalk with cancer cells. The type, functional orientation, density and location of infiltrating immune cells determine the fate of tumor progression and response to anti-tumor therapy [56]. Th17 and Treg are mutually contradictory subtypes of CD4<sup>+</sup> T cells mediating inflammation and

immunosuppression respectively. The cytokines present in tumor environment play decisive role in determining the balance of Th17 and Treg [57]. The altered balance of Th17/Treg is associated with disease progression in patients with lung cancer, pancreatic cancer, cervical cancer, etc. suggesting that interaction of Th17 and Tregs represent important regulatory mechanism in cancer pathogenesis [58-60]. Maintaining an appropriate balance of Th17 and Treg cells may ensure effective immunity against tumor. The molecular mechanisms underlying the involvement and regulation of these two subsets in cancer immunopathology remain largely unknown. Thus understanding the functional relevance of IL17 producing T cells and Treg cells in GBC tumor environment holds significance.

The present prospective study is aimed at investigating how the dynamics of proinflammatory (IL17 producing T cells) and immunosuppressive (Treg cells) contributes to inflammation and thereby progression of GBC.

On the basis of available information as described above, we addressed following objectives in the current thesis

1. Analysis of the immune scenario in peripheral blood of GBC patients
2. Understanding the functional dynamics of pro-inflammatory (Th17, Tc17 and T $\gamma\delta$ 17) and anti-inflammatory regulatory T cells (CD4<sup>+</sup>CD127<sup>low/-</sup>CD25<sup>+</sup>Foxp3<sup>+</sup>; Tregs) in peripheral blood and tumor microenvironment of GBC patients
3. Exploring the pro-tumor role of IL17 producing  $\gamma\delta$ T (T $\gamma\delta$ 17) cells in GBC

## **Chapter 2**

# ***Review of literature***

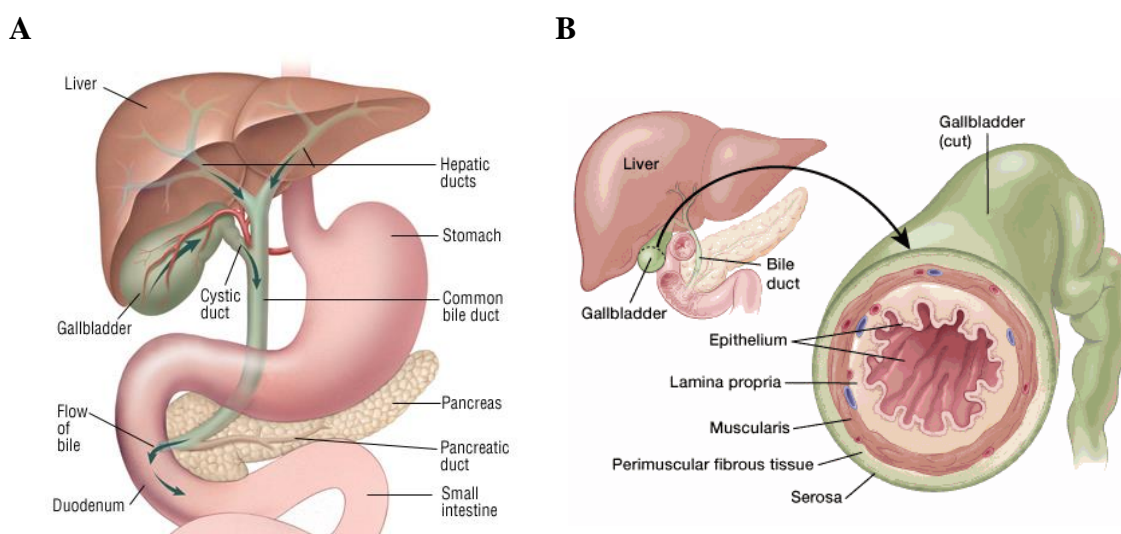
## 2.1 Gallbladder Cancer

Gallbladder cancer (GBC) is the most common malignancy of the biliary tract, representing 80-95% of biliary tract cancers worldwide [4]. The cancers of biliary tract, importantly GBC, are relatively infrequent but highly lethal diseases that are notoriously difficult to diagnose and treat. The biliary tract consists of an interconnected system of intra- and extrahepatic ducts that transport bile secreted from the liver to the digestive tract. Gallbladder is a sac-like structure situated beneath the right lobe of the liver (Figure 2.1 A). It is a vital component of the biliary system that receives bile produced in the liver, modifies its composition and then releases it into the duodenum [9]. The GB has a thin wall ( $< 3$  mm) composed of a single layered columnar lining, a thin lamina propria, a thin muscle layer and serosa (Figure 2.1 B) [61]. The bile secreted into the duodenum facilitates the intestinal absorption of dietary lipids across the absorptive cells of the brush-border membrane of the intestine, either through passive diffusion or by a carrier-mediated mechanism. Filling of the gallbladder with bile is promoted by contraction of the sphincter of Oddi (a junction where common bile duct meets duodenum). Bile, secreted from liver is an isotonic fluid consisting of an electrolyte resembling blood plasma in composition. The gallbladder epithelium is one of the most absorptive epithelial surfaces. The trans-mucosal absorption of water and electrolytes by gallbladder wall concentrates the bile. The evacuation of the gallbladder contents into the duodenum through contraction of the muscular layer is regulated by a peptide hormone cholecystokinin, which is released from the duodenal mucosa in response to the ingestion of fats and amino acids [9].

## 2.2 Anatomical and Physiological Considerations of GBC

GBC originates from the mucosal epithelial lining (adenocarcinoma) of the gallbladder and the cystic duct [12]. Eighty to ninety percent of gallbladder cancers are adenocarcinomas. The remainder are papillary, squamous cell, adenosquamous, undifferentiated or small cell

carcinomas [62]. The development of gallbladder cancer is proposed to occur over a span of 5–15 years, with tissue alterations including metaplasia, dysplasia, carcinoma *in situ*, and invasive cancer [4]. GBC is characterized by local invasion, extensive regional lymph node metastasis, vascular encasement, and distant metastases. It is the most aggressive of the biliary cancers and neither radiation nor conventional chemotherapy significantly improves survival or quality of life [9, 12]. Gallbladder is an out pouching from the gastrointestinal tract and regularly empties more viscous bile material against gravity to prevent stagnation. Thus gallbladder mucosa is constantly exposed to various metabolites excreted by the liver. Progressive physiological concentration of toxic materials in the bile, promote chronic injury and mutagenesis [11]. Thus majority of GBC originate from the fundus (60%) and remaining from body (30%) or neck (10%) of the gallbladder [62].



**Figure 2.1 :** (A) A representative diagram depicting anatomical location of gallbladder along with other visceral organs. (B) A representative image of cut section of gallbladder wall. The images were adapted from google images.

Gallbladder cancer spreads in four modes: 1) local invasion to liver or adjacent organs; 2) lymphatic spread; 3) peritoneal dissemination; 4) haematogenous spread. The propensity of local invasion and lymphatic spread is the highest [62]. The lymphatic drainage follows four

routes: cholecysto-retropancreatic to the retropancreatic group, cholecysto-celiac to the celiac group, cholecysto-mesenteric to the superior mesenteric group and the ascending lymphatics to the hilar group of lymph nodes. The lymphatic drainage of gallbladder is extensive and in multiple directions, facilitating early lymphatic spread [61]. The gallbladder is in an anatomically “busy” area due to presence of adjoining bile duct, portal vein, liver, duodenum and colon, making surgical resection and radiotherapy difficult [11]. Diagnosis of GBC commonly occurs as an incidental finding in the setting of surgical intervention for cholelithiasis (gall stone disease), resulting in advanced disease at the time of initial diagnosis [63]. The local and metastatic spread of GBC is evaluated by surgical staging which helps in planning the treatment.

### 2.3 Surgical staging of GBC

The staging of GBC is based on the depth of penetration and extent of spread. Multiple tumour staging systems (Nevin staging, Japanese Biliary Surgical Society staging system, TNM staging system of the American Joint Committee on Cancer [64]/International Union Against Cancer [UICC]) have been described for gallbladder cancer [5]. In 1976, Nevin *et al.* originally classified patients into five stages combining staging and histological grading of this cancer: Stage 1–*in situ* cancer; Stage 2–cancer not yet transmural; Stage 3–transmural direct liver invasion; Stage 4–lymph node metastases; Stage 5–distant metastases [65].

Table 2.1 Nevin staging system for gallbladder cancer

<b><i>Stage Grouping</i></b>	<b><i>Characteristics</i></b>
Stage I	Intramucosal tumor
Stage II	Tumor extends to muscularis
Stage III	Tumor extends to serosa
Stage IV	Transmural involvement and cystic lymph node involvement

Stage V	Direct extension to the liver and or distant metastasis
---------	---

The Japanese Biliary Surgical Society staging system classified tumours into four stages: Stage I- Cancer spread confined to gallbladder capsule; Stage II– positive N1 lymph nodes and/or minimal liver/bile duct invasion; Stage III– positive N2 lymph nodes and/or marked liver/ bile duct invasion; Stage IV–distant metastases [66]. However, this system is rarely used outside Japan. In 2010, the seventh edition of the American Joint Committee on Cancer has published a simplified tumor node metastasis (TNM) classification [67]. It is presently the most widely used system. This system is also used to stage cancers that start in the cystic duct (the tube that carries bile away from the gallbladder). The TNM system is based on 3 key pieces of information:

- **T** : describes how far the primary tumor has grown into the wall of the gallbladder and if it has grown into other nearby organs or tissues.
- **N** : describes whether the cancer has spread to regional lymph nodes
- **M** : indicates whether the cancer has metastasized to the distant other organs of the body. The most common sites of gallbladder cancer spread are the liver, peritoneum, and the lungs.

Table 2.2 Staging of GBC according to AJCC 7<sup>th</sup> edition

<i>Stage</i>	<i>Characteristics</i>
<b>Primary Tumor (T)</b>	
Tx	Primary tumor cannot be assessed
T0	No evidence of primary tumor
Tis	Carcinoma <i>in situ</i>

T1a	Tumor invades lamina propria		
T1b	Tumor invades muscle layer		
T2	Tumor invades perimuscular connective tissue; no extension beyond serosa or into liver		
T3	Tumor perforates the serosa and/or directly invades liver and/or 1 adjacent organ/structure		
T4	Tumor invades main portal vein or hepatic artery or invades 2 or more extrahepatic organs		
Regional Lymph Nodes (N)			
N0	No regional lymph node metastasis		
N1	Metastasis to nodes along cystic duct, common bile duct, hepatic artery and or portal vein		
N2	Metastasis to periaortic, pericaval, superior mesenteric artery and/or celiac artery lymph nodes		
Distant metastasis (M)			
M0	No distant metastasis		
M1	Distant metastasis		
Stage Grouping			
Stage 0	Tis	N0	M0
Stage I	T1	N0	M0
Stage II	T2	N0	M0
Stage IIIA	T3	N0	M0
Stage IIIB	T1-3	N1	M0
Stage IVA	T4	N0-1	M0
Stage IVB	Any T	N2	M0
	Any T	Any N	M1

GBC categorized as stages I or II are potentially resectable with curative intent; stage III generally indicates locally unresectable disease as a consequence of vascular invasion or involvement of multiple adjacent organs; stage IV represents unresectability with distant metastases. Histologically, GBC is graded according to its cellular differentiation into four grades. The scale used for grading gallbladder cancers goes from G1 (where the cancer looks much like normal gallbladder tissue) to G4 (where the cells are poorly differentiated). The grades G2 and G3 fall somewhere in between. The majority of GBC patients presented with grade 3, exhibit poorly differentiated tumors [68].

## 2.4 Epidemiology of GBC

Gallbladder cancer (GBC) was first described by Maximillian de Stoll in two autopsy cases in 1777, with the first documented cancer resection performed by Keen in 1891 [5]. GBC is the fifth most common cancer of biliary tract. The overall mean survival rate for patients with advanced gallbladder cancer is 6 months, with a 5-year survival rate of less than 5% [8]. Worldwide, GBC has a low occurrence, < 2 per 100,000, but there is a widely variable geographic pattern for GBC occurrence. Prevalence of GBC is rare in developed countries but prevalent in developing countries. Asia is a high risk continent, while the United States and most western and Mediterranean European countries (e.g., UK, France, and Norway) represent low risk areas [62]. Annual incidence rate of GBC is high in north and South American Indians, particularly amongst women: 15.5 per 100,000 in women (vs 7.5/100,000 in men) from La Paz, Bolivia, and 11.3 per 100,000 in women (vs 4/100,000 in men) from New Mexico. The increasing rate of GBC is the leading cause of cancer death in Chilean women, exceeding even breast, lung and cervical cancers [69]. The other high risk regions include Poland (incidence rate is 14/100,000 for women), northern India (21.5/100,000 for women), Ecuador (12.9/100,000) and south Pakistan (11.3/ 100,000 for women) [6, 62].

Other South American countries, Israel, Japan and China show intermediate incidence of GBC.

### **2.4.1 GBC : Indian scenario**

In India, the incidence of GBC is increasing [7]. A comparative study of different cancer registries in India has shown that the Delhi registry has more number of GBC cases but incidence rate of GBC is high in Kamrup urban district (Assam) followed by Imphal district (Nagaland) [7]. Interestingly the prevalence of GBC in India shows a peculiar north-south distribution [70]. The age standardised GBC incidence is high in north and eastern India among both genders compared to south India. Residence in Gangetic belt is one of the important risk factor identified in the epidemiological studies [71]. The presence of low levels of selenium and zinc and high levels of copper, cadmium, nickel, chromium, and lead in the bile and gallbladder tissue may be associated with increased risk of GBC in patients residing in Gangetic belt [72]. The incidence of GBC is higher in rural India compared to urban area [73, 74]. The lower socioeconomic status, illiteracy, poor nutritional diet, tobacco habit and joint family are identified risk factors which may be associated with rural and urban distribution of GBC occurrence [71, 74, 75]. The incidence of GBC cases in India are projected to increase in near future in both males and females [76]. Therefore, the important inputs are required from various health agencies for management of GBC.

### **2.5 Risk factors of GBC progression**

Risk factors responsible for GBC include genetic predisposition, geographic variation, ethnicity, increasing age, female gender, chronic inflammation, congenital developmental abnormalities, low socio-economic status, low frequency of cholecystectomy for gallbladder diseases and exposure to certain chemicals. The most relevant risk factors are discussed here.

### 2.5.1 Age

The incidence of GBC increases with advancing age. The age-adjusted incidence rates of GBC is reported as 0.16/100,000 (for those 20–49 years), 1.47/100,000 (for those 50–64 years), 4.91/100,000 (65–74 years), and 8.69/100,000 for individuals over the age of 75 years [64]. The highest mortality rate was 5.05/100,000, for individuals over the age of 75.

In India, the age standardised incidence rate of GBC revealed an increasing trend after age of 45 years and peaks after age of 65 years [7]. The various epidemiological studies shown that the GBC incidence rate increases with higher age. However, the mean ages of GBC patients (51.5 years in males and 55.5 years in females) in India are lower compared to those of the world population[4, 7, 75]. This might be a reflection of the average low life expectancy in India.

### 2.5.2 Ethnicity

The geographic pattern of GBC occurrence varies widely across the globe. The prevalence also varies in different ethnic populations. The highest rate of GBC incidence is exhibited by Mapuche Indians from Valdivia, Chile, South America (12.3/100,000 for males and 27.3/100,000 for females). American Indians in New Mexico, USA, follow, with an average annual rate of 8.9/100,000 [4]. Asia is a high risk continent, where an increased frequency of GBC occurs in northern Indian females, Pakistani females and Korean males. In India there exist differences in the GBC occurrence between north and south India which can be related to different ethnic and cultural background [70]. The Korean males have highest incidence rate in Asia than females (8.1 for males and 5.6 for females per 100,000) [4]. The mortality rate of GBC follows the incidence. Worldwide, the burden peaks in the Mapuche Indians of Chile (35 per 100,000 each year), closely followed by Hispanics and North American Indians. However, mortality is declining in some countries, like the USA, Canada, Australia, and parts of Europe (the UK and Hungary), but increasing in others, including Chile and

Japan [77]. The availability of standard healthcare and treatment for GBC may be responsible for the lower mortality in developed countries.

### 2.5.3 Gender

Frequency of GBC occurrence shows a marked predominance in women over men worldwide. The incidence is highest in north Indian women followed by Pakistan and Chile [6]. Women are affected two to six times more often than men [4]. This bias varies greatly in different parts of the world, being highest in countries and regions with the highest rates of GBC. The main victims of the disease are elderly postmenopausal females as compared to the males with median age of 51 to 60 years [78]. The role of estrogen receptor and progesterone receptor expression in gallbladder cancer is not significantly different between men and women [79]. The co-expression of both receptors is increased in females with gallbladder cancer as compared with males. There are contradictory reports on involvement of estrogen and progesterone responsible for high risk of GBC in females [79]. However, greater number of pregnancies in women is one of the risk factors of GBC [78]. The increased use of oral contraceptives among premenopausal female is another serious risk factor for the high occurrence of GBC in females [78].

### 2.5.4 Cholelithiasis (gallstone disease)

Cholelithiasis is a major risk factor of GBC. More than 80% of GBC patients are diagnosed with gallstones [8]. Epidemiological data showed that the occurrence of GBC is high in area prevalent for gallstone disease. The coexistence of GBC and gallstone disease is observed in Pima Indian females (21/100,000 cancer incidence and 75.8% gallstone prevalence), North American Indian females (7.1/100,000 and 64.1%), Chilean Mapuche Indian females (27.3/100,000 and 49.4%), and East Indian females (22/100,000 and 21.6%) [4]. GBC and gallstone disease often share common risk factors including age, gender, parity and ethnicity [8].

Gallstones are formed by the concentration of normal or abnormal bile constituents. There are three main types: cholesterol gallstones, mixed gallstones and pigment gallstones [8]. Cholesterol stones seem to be more common than pigment stones in GBC patients. Cholesterol gallstones contain more than 50% cholesterol monohydrate and a mixture of calcium salts, bile pigments, proteins and fatty acids. In the presence of an excess of cholesterol in relation to phospholipids and bile acids, the unstable, cholesterol-rich vesicles aggregate into larger multi-lamellar vesicles, from which cholesterol crystals precipitate [9]. These cholesterol crystals transform into stones by aggregation and compaction of cholesterol and calcium bilirubinate. Thus excessive cholesterol secretion and gallstone synthesis is associated with obesity, ageing, pregnancy, hyperlipidaemia and use of oral contraceptive and hypolipodaemic agents [9]. It has been suggested that increase in number, volume, and weight of stones have a greater impact on the risk of developing gallbladder cancer [80, 81]. In case-control studies, the relative risk for gallbladder cancer in patients with gallstones  $\geq$  3cm was shown to be 9-10 times higher, compared with patients with stones smaller than 1cm [81-83]. A polymorphism at the ABCG5/G8 (hepatocanicular cholesterol transporter) heterodimer partner was the first genetic risk factor of cholesterol gallstone disease discovered by a GWAS study [84]. This polymorphism allows increased sterol secretion leading to cholesterol hyper saturation and thereby promoting gallstone formation [85]. Thus the genetic predisposition to the gallstone formation increases the risk of GBC incidence.

It is suggested that chronic persistence of gallstones might cause direct mechanical irritation to the surrounding mucosal surface which leads to inflammation. Chronic inflammation leads to intermediate low-grade dysplastic changes in the gallbladder epithelium followed by increased stratification of the atypical epithelium, results in late high-grade premalignant changes, called as carcinoma *in situ* [10]. Gallstones may also obstruct the release of bile leading to delayed or incomplete emptying with subsequent bile stasis and dilation of the

gallbladder, which predisposes to inflammation. It is reported that in gallbladder specimens excised for cholelithiasis or cholecystitis, 83% exhibited epithelial hyperplasia, 13.5% atypical hyperplasia and 3.5% *in situ* carcinoma, suggesting cholelithiasis and cholecystitis could produce a series of epithelial pathologic changes [86]. Therefore, cholelithiasis is a well-established risk factor for GBC although only 1–3% of patients with gallstones develop GBC.

## 2.6 Inflammation and GBC

### 2.6.1 Cholelithiasis induced inflammation

Given the association between chronic cholecystitis and gallbladder cancer, chronic inflammation is probably the most common causative factor for GBC. Gallstone related gallbladder carcinogenesis occurs mainly through the metaplasia–dysplasia–carcinoma pathway. Epithelial metaplasia is characterised by a transformation of a differentiated epithelium and is associated with tissue damage and chronic inflammation [87]. The metaplastic gallbladder epithelium is often infiltrated with denser populations of T and B lymphocytes and macrophages correlated with an increase in the average gallbladder wall thickness [20, 88]. Cyclooxygenase-2 (COX2) is an enzyme involved in prostaglandin biosynthesis and inflammation is overexpressed in high grade lesions of GBC [89]. Treatment of patients with aspirin showed reduced risk of GBC suggesting the vital role of inflammation in GBC development [90].

Polymorphisms in genes related to the immune system, inflammation and oxidative stress namely PTGS2 (Prostaglandin-endoperoxide synthase 2 / cyclooxygenase 2), TLR2 (Toll like receptor 2), TLR4, IL1RN (IL1 receptor antagonist), IL1B, IL10, IL8, CCR5 (C-C motif chemokine receptor 5), LXR $\beta$  (Liver X receptor  $\beta$ ) and OGG1 (8-Oxoguanine glycosylase) have been reported to be associated with increased risk of GBC. Thus, variants in inflammation related genes may, under the stimulus of gallstones or other insults, accelerate

the development of GBC [20]. In a murine study, presence of cholesterol crystals in gallbladder developed local changes in the gallbladder characterized by increased mucus layer thickness, IL1 and myeloperoxidase activity [91]. In another study, mice on lithogenic diet showed infiltration of inflammatory cells composed of eosinophils, macrophages, neutrophils and lymphocytes within the lamina propria and granulocyte infiltration in the gallbladder with progressive impairment of gallbladder emptying [16, 92]. Interestingly, it is shown that Rag2<sup>-/-</sup> mice (deficient for B and T cells) were resistant for development of gallstones [93]. In addition, gallbladder tissue from patients with gallstones has been observed to contain higher levels of infiltration of COX-2/iNOS positive macrophages, granulocytes and mast cells compared to controls (patients without gallstones) suggesting the role of inflammatory immune infiltrates in gallstone formations [94]. The ethnic differences in the population also contribute to the gallstone formation and inflammation. The bile samples of patients from Chile and The Netherlands showed the differences in lithogenic process and degree of gallbladder inflammatory response [95]. Thus the chronic inflammatory infiltrates are involved in the early stages of gallstone formation and seem to contribute to GBC.

### 2.6.2 Infection associated inflammation in GBC

#### *Salmonella* infection in gallbladder

Another important risk factor for GBC is the chronic carriage of infectious microorganisms in the gallbladder. Up to 20% of cases of cancer worldwide are associated with microbial infection [96]. The bacterial genera identified by culture or by PCR in the gallbladders of patients with cholecystitis and cholelithiasis, include *Salmonella*, *Escherichia*, *Klebsiella* and *Helicobacter* [97]. The epidemiological evidence indicates a definite relationship between *S. typhi* and GBC. About 3–5% of GBC patients are chronic carriers of *S. typhi* infection as the bacteria are known to persist in the biliary system [98]. Studies performed in north India, for

both typhoid fever and GBC, have reported odds ratios for GBC of 8.5 [99], 9.2 [100], 14 [98] and 22.8 [101] among chronic typhoid carriers, supporting the strong association between these pathologies. Recently, molecular evidence linking *Salmonella* infection with GBC development has shown that infection with *Salmonella enterica* induced malignant transformation in predisposed mice, murine gallbladder organoids, and fibroblasts, with TP53 mutations and c-MYC amplification. It involved the activation of MAPK and AKT pathways mediated by *Salmonella enterica* effectors secreted during infection [102]. This suggests the importance of *Salmonella* infection as significant risk factor of GBC.

### ***Helicobacter* infection in gallbladder**

Infection of *Helicobacter* species is another risk factor of GBC. Several PCR-based studies showed that *Helicobacter* species were identified in resected gallbladder tissue and bile collected from patients with cholecystitis or cholelithiasis [103-105]. The infection rate of *H. bilis* is 2-3 times higher in patients with biliary tract cancer compared to healthy individuals. *H. bilis* infection activates transcription factor nuclear factor-kappa B (NF- $\kappa$ B) in human bile duct cancer cells and stimulates production of vascular endothelial growth factor (VEGF) and leads to enhancement of angiogenesis [106]. *H. pylori*, classified as a class I carcinogen by the World Health Organization, is a well-established cause of gastric cancer and recently proved to be associated with GBC. The presence of *H. pylori* in the gallbladder tissue was more frequent in patients with biliary tract carcinoma compared with the control group [105]. Another study showed the association of *H. pylori* infection and increase in serum inflammatory cytokines in patients with GBC [107]. However, other studies failed to demonstrate any increase in risk of GBC in presence of *H. bilis* [108] or *H. pylori* [109]. The disparities in the reports associating *Helicobacter* with GBC may be due to small sample sizes and various detecting methods that have different sensitivity and specificity.

### Parasite infection in gallbladder

The association of biliary tract cancers and infection of parasite liver fluke are also reported. High incidence of cholangiocarcinoma is well correlated with the presence of the liver fluke, *Opisthorchis viverrini* and *Clonorchis sinensis* [18]. Liver fluke infection causes pathological changes mainly to the bile ducts where the worms can be found, as well as to the liver and gall bladder in both humans and animals. In the chronic phase of infection, when the parasites develop into the adult stage leads to hyperplasia and adenomatous formations of the bile duct epithelium resulting into periductal fibrosis and scarring. The inflammatory responses become less severe in chronic infection than in the acute phase, suggesting that immune modulation may occur and there is marked humoral immunity in *O. viverrini*-infected humans. However, there is scanty literature detailing the relationship of liverfluke infection and GBC. Thus, the infection by liver fluke is one of the important risk factor of biliary tract cancer [19].

### 2.7 Clinical management of GBC

GBC is highly aggressive disease. The diagnosis and pre-operative assessment of the extent of gallbladder cancer is important in determining the management plan. Early gallbladder carcinoma does not have any specific symptoms. Patients with early disease are operated for acute cholecystitis and have improved survival. The patients with biliary-tract disease show symptoms of jaundice, weight loss, general weakness, and pain in the right upper quadrant. The patients with malignant tumours outside the biliary tract, exhibit symptoms like anorexia, weight loss, general weakness, and local complications of the tumour such as a fistula or invasion of adjacent organs. Jaundice is common and is an indicator of poor prognosis [110]. Complete surgical resection (cholecystectomy) remains the only potentially curative treatment for primary adenocarcinoma of the gallbladder. However, only 10% of patients present with early stage disease and are considered surgical candidates. Ultrasonography,

computed tomography scan, magnetic resonance imaging with magnetic resonance cholangiography or endoscopic retrograde cholangiopancreatography provides information for tumour staging and resectability. Patients with T1 disease have a disease-specific survival rate of 100% at 5 years after simple cholecystectomy. Unfortunately, few cases of GBC are identified at these early, curable stages [111]. Systemic therapy is the mainstay of treatment for patients who present recurrent or metastatic disease. Gallbladder cancer is likely to have spread to loco-regional sites at the time of diagnosis. It is therefore necessary to administer adjuvant chemotherapy in all patients with advanced GBC. Gemcitabine, cisplatin and 5-FU are the widely prescribed chemotherapeutic drugs to GBC patients [12]. Various randomised trials using combined treatment of cisplatin, 5-FU, Oxaliplatin and gemcitabine have improved benefits to the patients. However, the long term survival is disappointing [112, 113].

Advances in the understandings of molecular pathogenesis of cancers led to the development of targeted therapies. In recent past, target specific antibodies alone or in combination with chemotherapy were evaluated in biliary tract cancer patients in clinical trials. Use of the molecular inhibitors /antibodies targeting EGFR pathway (Erlotinib, Lapatinib, Cetuximab) or VEGF pathway (Bevacizumab, Sorafenib, Sunitinib and Vandetanib) alone or in combination with chemotherapeutic drugs (Oxaliplatin, gemcitabine, etc) are under clinical trials [113]. However, the success rate of these drugs is not promising. Therefore, the discoveries of newer targets are necessary for management of GBC.

## **2.8 Cancer and immune system**

For years it was believed that the development of cancer is restricted to the transformed cells and thus the scientific efforts were focused on understanding the biology exclusively of tumor cells. However, the emerging data in past two decades has unequivocally established the considerable involvement of non-neoplastic cells present in tumor environment such as

cells of immune system and cells of mesenchymal origin [114]. The significance of immune response in cancer was first envisaged by Burnet and Thomas as an “Immunosurveillance hypothesis”, stating that adaptive immunity was responsible for preventing cancer development in immunocompetent hosts [115, 116]. The evidences emerged in recent past stressed the dual host-protective and tumor-promoting actions of immunity on developing tumors, compelled the emergence of new hypothesis by Schreiber et al. called as “Cancer Immunoediting Hypothesis” [117]. During the dynamic process of immune cells – tumor cells interaction, the immune system not only protects against cancer development but also shapes the character of emerging tumours. The interaction is described in three phases — Elimination, Equilibrium and Escape.

In an elimination phase, the coordinated and balanced activation of innate and adaptive immune cells detect and destroy the tumor cells. The damage-associated molecular pattern molecules (DAMPs) released from dying tumor cells [such as high mobility group box 1 (HMGB1)] activates dendritic cells and secretion of interferons. Type I interferons act on  $CD8\alpha^+/CD103^+$  DCs to enhance cross-presentation of tumour antigens to  $CD8^+$  T cells [118]. The immune effector molecules, such as  $IFN-\gamma$ , perforin, Fas/FasL, and TRAIL (TNF-related apoptosis-inducing ligand); recognition molecules such as NKG2D; and an intact lymphocyte compartment altogether contribute in protective anti-tumour immunity and elimination of tumor cells [119].

The tumor cell variants which escape elimination phase exhibit long term state of dormancy with immune responses. The adaptive immunity prevents tumor cell outgrowth and simultaneously sculpts the immunogenicity of the tumor cells maintaining equilibrium. It is observed that adaptive immunity specifically, IL12,  $IFN\gamma$ ,  $CD4^+$ , and  $CD8^+$  T was responsible for maintaining the occult tumor cells in equilibrium [117]. The balance of IL12 promoting elimination, and IL23 promoting persistence, maintains tumor in equilibrium

[120]. In equilibrium phase, the immune system maintains residual tumor cells in a functional state of dormancy which may extend throughout the life of the host. The close interaction of immune cells with tumor cells facilitate the sculpting of tumor cell variants which are resistant to immune recognition and emerge as progressively growing, visible tumor.

The tumor cells deploy various mechanisms to escape from immune recognition. Tumor cells reduce expression of tumor antigen and inhibit cytotoxic effects of immunity ensuing decreased immunogenicity. Alternatively, tumor cells promote secretion of immunosuppressive cytokines such as VEGF, transforming growth factor  $\beta$  (TGF $\beta$ ), galectin, indoleamine 2,3-dioxygenase (IDO), etc. thereby create immunosuppressive state within tumor environment. Recruitment of Treg cells (Regulatory T cells) and MDSCs (Myeloid-derived Suppressor Cells) into the tumor bed inhibits the function of tumor specific T lymphocytes by expressing the negative co-stimulatory molecules CTLA-4 (cytotoxic T-lymphocyte-associated ligand-4), PD-1 (Programmed cell death receptor-1), and PD-L1; and by consuming IL2, a cytokine that is critical for maintaining CTL function [117]. Eventually tumor environment mediates immune system deterioration, circumvents the tumor suppressor mechanisms of immunity and helps to develop into a progressively growing malignant disease. The advances in understanding the molecular pathogenesis of cancer regulated by tumor infiltrating immune cells have provided a scope to intervene the cancer progression using immunotherapeutic drugs. However, the progression of cancer at cellular and molecular level varies among cancer types and patient with different ethnic background. Thus further research is needed exploring the interaction between cancer and immunity specific to cancer type.

## 2.9 Inflammation and cancer

In recent years the emerging evidences have revealed that the tumor progression is not only confined to the cellular proliferation of epithelial cells but significantly regulated by

surrounding microenvironment. Tumor associated inflammation is one of the important hallmark of cancer [121]. Enormous efforts have elucidated that chronic inflammation plays decisive role in initiation, promotion, malignant conversion, invasion, and metastasis of cancer [54]. Initiation of tumorigenesis requires a genetic mutational hit. Activated inflammatory cells serve as sources of reactive oxygen species (ROS) and reactive nitrogen intermediates (RNI) that are capable of inducing DNA damage and genomic instability [122, 123]. Inflammatory cytokines are reported to activate AID (activation-induced cytidine deaminase) enzyme in tumor cells which induces genomic instability and increases mutations in critical cancer genes, including Tp53, c-Myc, and Bcl-6 [124]. TNF $\alpha$  produced by tumor cells or infiltrating lymphocytes stimulates ROS accumulation, DNA damage, oncogene activation and epithelial mesenchymal transition in epithelial cells [125]. Dysregulation of IL6 contributes to tumor promoting effects on cancer cells and stromal cells in tumor environment. IL6 signals through STAT3 that promote cell proliferation, survival, angiogenesis and metastasis [126]. IL6 is reported to be involved in the pathogenesis of colorectal, gastric, liver, pancreatic, esophageal, breast, kidney, prostate and gynaecological cancers [126]. Various murine tumor models have shown that the inflammatory cytokines (IL6, TNF $\alpha$ , IL23 and IL1) activate transcription factors, such as NF- $\kappa$ B, STAT3, and AP-1, in premalignant cells to induce genes that stimulate cell proliferation and tumor promotion [54]. Growth of large tumors requires an increased intra-tumoral blood supply which is triggered by tumor hypoxia. Under hypoxic conditions HIF1 $\alpha$  (hypoxia-inducible factor-1 $\alpha$ ) stimulated recruitment of Tumor associated macrophages (TAMs) and MDSCs induces local VEGF production [127]. Important proangiogenic genes, such as IL8, CXCL1, CXCL8, VEGF, and HIF1 $\alpha$ , are directly regulated by NF- $\kappa$ B, STAT3, and AP-1 in TAMs, MDSCs, and other cell types [127, 128]. During metastasis of cancer, tumor cells undergo epithelial mesenchymal transition. Signalling through TGF $\beta$  activates SMAD transcription factors and

MAPKs, which control expression of other regulators of the epithelial-mesenchymal transition, such as Slug [129]. Signalling through TNF $\alpha$  induces Snail and Twist through activation of AKT/GSK-3 $\beta$  (Protein kinase B/ Glycogen synthase kinase-3 $\beta$ ) or NF- $\kappa$ B pathway respectively [130, 131]. Survival of circulating metastatic cells is regulated by inflammatory mediators (TNF $\alpha$ , IL6, VEGF and epiregulin) released by immune cells [132]. The interaction of circulating cancer cells with platelets or macrophages may protect them from NK cell-mediated killing, thereby overcoming immunosurveillance [133]. Overall it is now appreciated that chronic inflammation orchestrates cancer initiation by generating genotoxic stress, cancer promotion by inducing cellular proliferation, and cancer progression by enhancing angiogenesis and tissue invasion. Given the crucial role of inflammation in cancer progression, understanding the immunological mediators of inflammations including cytokines and immune cells may provide platform for future therapeutic interventions.

## 2.10 Interleukin 17

Interleukin 17 (IL17) is a potent pro-inflammatory cytokine that contributes to the pathogenesis of several inflammatory diseases. The *Il17* gene and IL17 protein were first discovered as a product of T cells in rodents, where they were initially known as cytotoxic T lymphocyte-associated antigen 8 (CTLA8) [134]. IL17 was recognized to have homology to an open reading frame encoded within a T cell-tropic  $\gamma$ -herpesvirus, *Herpesvirus Saimiri* [134]. There are five related cytokines that were identified through database searches and degenerative RT-PCR, that share 20–50% homology to IL17 constitute an IL17-family [135]. The six members are designated as IL17A (commonly refer to IL17), IL17B, IL17C, IL17D, IL17E (also called IL25) and IL17F. IL17A is the founding member of the IL17 cytokine family [135]. These cytokines incorporate four conserved C-terminal cysteine residues [136]. IL17 is most homologous to IL17F (~ 60%), and the genes encoding them are proximally located on longer arm of chromosome 6. The distance between these genes is 46 kbp. IL17A

is located on the forward strand and has a length of 4,252 bp, and IL17F is located on the reverse strand and has a length of 7,815 bp. Both genes are comprised of three exons [25]. IL25 has the least homology with IL17A. Little is known about the regulation and function of IL17B and IL17C; however, there is some evidence that these cytokines also regulate inflammatory response [137]. IL17 is a unique cytokine that bears no resemblance to other known interleukins. Furthermore, IL17 bears no resemblance to any other known proteins or structural domains.

### **2.10.1 IL17 structure**

IL17A is a 155 amino acid homodimeric, disulfide linked protein that is secreted as glycoprotein with a molecular mass of 35 kDa. After splitting off the signal peptides (23 amino acids for IL17A and 30 amino acids for IL17F), the secreted polypeptides are 132 amino acids (IL17A) and 133 amino acids (IL17F) long [25]. Each subunit of the homodimer is approximately 15-20 KDa. The structure of IL17 consists of a signal peptide of 23 amino acids followed by a 123 amino acids chain region characteristic of the IL17 family [138]. Comparison of different members of the IL17 family revealed four conserved cysteines that form two disulfide bonds [138].

### **2.10.2 IL17 receptor**

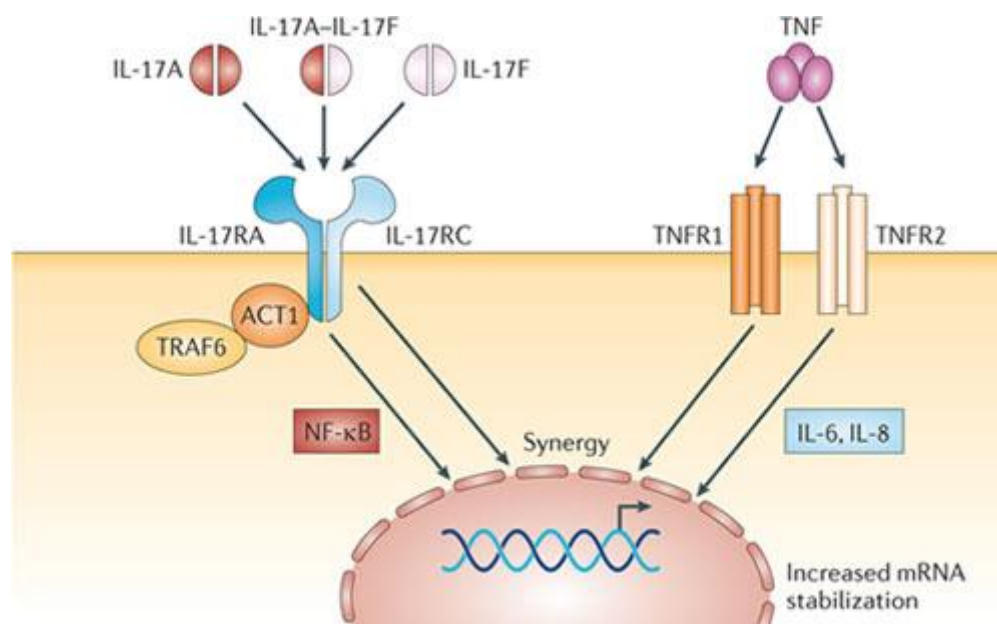
Similar to their cognate cytokines, IL17 receptor complexes are multimeric (Figure 2.2). The IL17 receptor family consists of 5 members (IL17RA, RB, RC, RD and RE), all of which, like their ligands, share sequence homology. IL17RA is ubiquitously expressed on a wide range of tissues and cell types [139]. Upon stimulation with IL17, IL17RA initiates the activation of downstream signalling pathways to induce the production of pro-inflammatory molecules. However, IL17RA alone is insufficient to mediated IL17 signalling. IL17 signals through a heterodimeric receptor complex composed of IL17RA and IL17RC (Figure 2.2). IL17RA subunits are pre-assembled in the plasma membrane prior to ligand binding [140].

The preassembly enables the receptor to respond rapidly and specifically to ligand, while preventing unproductive interactions with other receptors [139]. IL17F also signals through the same receptor complex with ~100 to 1000 times lower affinity than does IL17A [141].

### 2.10.3 IL17 receptor signalling

At the C-terminus of the IL17 receptors is a conserved region known as the SEFIR (Similar Expression of Fibroblast growth factor genes and IL17Rs) domain which is closely related to the TIR (Toll/Interleukin-1 receptor) domain in Toll-like receptors (TLRs) and IL1 receptors [139]. SEFIR domain is also expressed by a cytosolic protein Act1 (NF- $\kappa$ B activator 1) which is recruited to the IL17 receptor complex through homotypic interactions of the SEFIR domains upon IL17 stimulation [139]. Following binding to IL17R, Act1 mediates Lys-63 linked TRAF6 (TNF receptor associated factor-6) ubiquitination through its U-box domain [142]. Poly-ubiquitinated TRAF6 further activates downstream TRAF6 dependent TGF $\beta$  activated kinase 1 (TAK1) for NF $\kappa$ B activation (Figure 2.2). TRAF6 is essential for IL17A dependent activation of NF $\kappa$ B and MAPK cascades whereas TRAF2 and TRAF5 are involved in IL17A dependent chemokine production. Upon IL17A stimulation IKKi (I kappa B kinase I; regulator protein of ACT1) is recruited to the IL17R–Act1 complex, where it specifically phosphorylates Act1 at Ser-311. This generates a docking site that recruits TRAF2 and TRAF5, to form an Act1/TRAF2/TRAF5/arginine - and serine - rich splicing factor SRSF1 (SF2 (ASF)) complex. This complex prevents ASF from binding to the 3' UTR of CXCL1 mRNA for cleavage and thereby enhances CXCL1 mRNA stability [143, 144]. TRAF3 and TRAF4 are the negative regulators of IL17 signalling. They bind directly to the IL17R to interfere with the formation of the IL17R–Act1–TRAF6 complex [145, 146]. IL17 stimulation also triggers the dual phosphorylation of C/EBP $\beta$  (CCAAT-enhancer-binding protein  $\beta$ ) at Thr-188 and Thr-179 by ERK and GSK3 $\beta$ , respectively. These phosphorylation

events on C/EBP $\beta$  lead to inhibition of IL17 dependent pro-inflammatory gene induction [147].



**Figure 2.2 : IL17 receptor signalling.** Heterodimers of IL17A/IL17F interacts with heterodimer of IL17RA. Receptor signalling induces the activation of ACT1, NF- $\kappa$ B and TRAF6 which leads to increased transcription of the target genes. Signalling through TNG-TNFR synergizes the effect of IL17. The figure is adapted from Miossec et al, *Nature reviews drug discovery*,11, 2012

#### 2.10.4 Functions of IL17

IL17RA is expressed in nearly every cell type of the body, including epithelial cells, endothelial cells, fibroblasts and myeloid cells. The contribution of IL17 to disease is thus linked to the role of these cells in disease pathology. IL17 activity contributes to various aspects of acute and chronic inflammation. IL17 induces the production of many neutrophilic granulocyte attracting chemokines, such as CXCL1, CXCL2, CXCL5, CXCL8 and T cell and myeloid cell attracting chemokines CCL20, CCL2, and CCL7 in fibroblasts, epithelial cells, endothelial cells, and keratinocytes [25]. IL17 enhances the expression of G-CSF, GM-CSF, and stem cell factor in tissue cells, macrophages, and T cells and thereby led to strengthened granulopoiesis [148, 149]. This leads to a significant increase in the immigration of

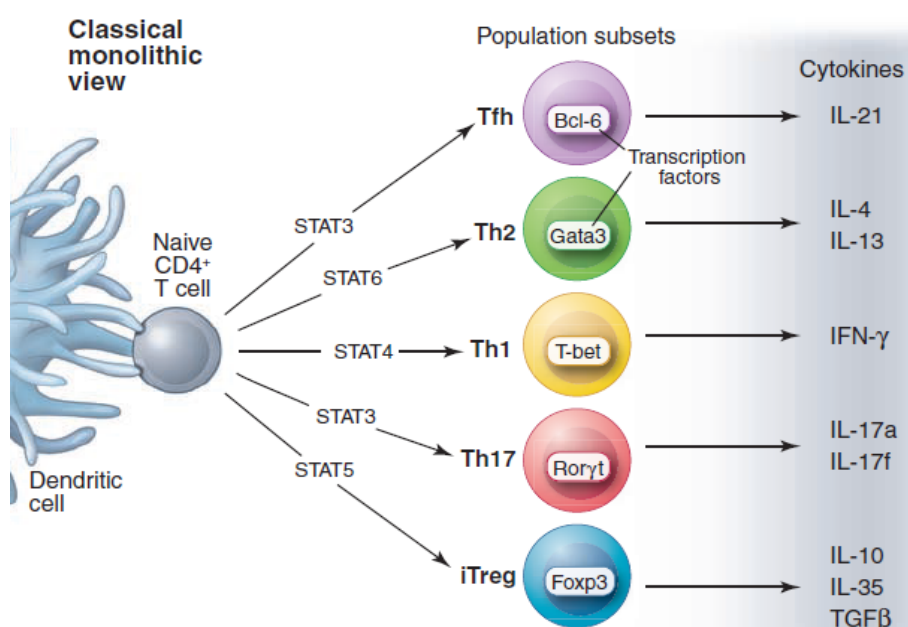
neutrophilic granulocytes to the site of inflammation. The treatment of tissue cells with IL17F induces the expression of IL1 $\beta$ , TNF $\alpha$ , IL6, and a variety of metalloproteinases (MMP1, MMP2, MMP3, MMP9, and MMP13) [150, 151]. IL17 levels have been found increased in colon, ovarian, hepatocellular, esophageal, lung cancer, and glioblastoma [30]. The polymorphism G-197A in the IL17 promoter region is associated with increased gastric cancer risk independently of *Helicobacter pylori* presence [152]. IL17 induces AKT dependent IL6/JAK2/STAT3 activation and tumor progression in hepatocellular carcinoma by enhancing expression of downstream targets IL8, MMP2, and VEGF [153]. In carcinogen induced skin cancer models IL17 is shown to augment myeloid cell recruitment and STAT3 associated local inflammation [154]. IL17 acts synergistically with TNF $\alpha$  to stimulate glycolysis by increasing expression of the glucose transporter SLC2A1 and hexokinase-2 thereby supporting growth of colorectal cancer cells [155]. The major function of IL17 is to promote angiogenesis and invasiveness by stimulating VEGF production in cancer cells [29, 156]. Thus increasing levels of IL17 are reported to associate with poor prognosis of colorectal, Non-small-cell lung carcinoma (NSCLC) cancer patients [28, 29]. Contradictory reports demonstrated that higher levels of IL17 were correlated with progression free survival (PFS), and death rate in glioblastoma patients. The IL17 and PFS were also observed to be independent factors affecting the overall survival. Therefore, in glioblastoma, the IL17 may be modulating the tumor microenvironment as a defence mechanism [157]. Similarly in ovarian cancer, increased levels of IL17 associated with increased PFS and survival [158]. The increased levels of IL17 also associated with chemo-sensitivity of ovarian cancer cells to platinum-based chemotherapy [159].

## 2.11 Th17 cells

### 2.11.1 Differentiation and development of Th17

Th17 is a subset of CD4<sup>+</sup> T cells producing IL17, a lineage distinct from Th1, Th2, and Treg cells and are characterized by a unique molecular and functional signature (Figure 2.3) [160]. Th17 cells are characterized by their capacity to secrete IL17A, IL17F, IL21, IL22, and CCL20 [161, 162]. Th17 generation is controlled by the master transcription factors retinoic acid-related orphan receptor (ROR) $\gamma$ t, ROR $\alpha$ , aryl hydrocarbon receptor (AHR), and interferon regulatory factor4 (IRF4) [163-166]. Differentiation of Th17 cells takes place from naïve CD4<sup>+</sup> T cells. Activation in the presence of TGF $\beta$  and IL6 primes the initial differentiation of naïve CD4<sup>+</sup> T cells to IL17 producing Th17 cells [167, 168]. IL6 plays an indispensable role in initiating this process by activating STAT3, which directly regulate transcription of Rorc (ROR $\gamma$ t), Il17, and Il23r [169, 170]. Recently it was shown that the ratio of activated STAT3 /STAT1 determines the Th17 differentiation program. IL6 and IL21 induce p-STAT3/p-STAT1 ratios > 1, leading to the promotion of Th17 differentiation, whereas IL27 or IL6+IL27 induce p-STAT3/p-STAT1 ratios < 1, resulting in inhibition of Th17 differentiation [171]. Expression of IL23 receptor is essential for the maturation of Th17 cells [172]. Activated ROR $\gamma$ t<sup>+</sup> Th17 cells, but not naïve CD4<sup>+</sup> T cells, express IL23R [173]. Addition of IL23 markedly enhances Il23r gene expression by IL23R<sup>+</sup>ROR $\gamma$ t<sup>+</sup> Th17 cells. Subsequent exposure to IL23 is required for the functional maturation and pathogenic function of Th17 cells and IL23R deficient Th17 cells fail to maintain their IL17 expression [172]. IL23 induces GM-CSF to regulate pathogenic functions of Th17 cells since GM-CSF deficient Th17 cells are unable to induce experimental autoimmune encephalomyelitis (EAE) upon adoptive transfer [174]. TGF $\beta$ 1 plays an indirect role in the initial differentiation of Th17 cells by suppressing T-bet and GATA-3, thus inhibiting CD4<sup>+</sup> T cells from adopting alternate Th1 or Th2 cell fates [175]. Autocrine signalling by TGF $\beta$ 1 also promotes Th17 cell

differentiation [176]. The effect of TGF $\beta$ 1 may be dependent on its concentration in the cytokine milieu where low levels promote Th17 differentiation by inhibiting T-bet while high levels obstruct Th17 differentiation by inhibiting IL23R and inducing IL10 and Foxp3 [177]. However, TGF $\beta$ 3 is shown to upregulate IL23R expression leading to highly pathogenic Th17 cells [178]. IL2 inhibits early Th17 differentiation by inducing STAT5 that displaces STAT3 binding to IL17 promoter and repress transcription [179]. IL23 directly suppresses IL2 signalling suggesting IL23 can prevent destabilization of the Th17 program [172].



**Figure 2.3 : Distinct lineages of CD4<sup>+</sup> T cells.** The figure depicts the differentiation pathways of naïve CD4<sup>+</sup> T cells to different subsets. The subset specific transcription factors determine the effector cytokines secreted by each subtype. The figure adapted from O'shea and Paul, *Science*, 327, 2010.

### 2.11.2 Natural Th17 cells

In mice, Th17 cells developed in the thymus, express IL23R and ROR $\gamma$ t and belong to innate immune cell compartment are natural Th17 cells (nTh17) [177, 180]. nTh17 cells develop in the thymus in the presence of strong interaction of TCR and MHC suggesting nTh17 cells may survive negative selection despite bearing TCRs with high affinity to MHC in the

thymus [181]. It is reported that thymic stromal MHC class II expression and RelB-dependent medullary thymic epithelial cells (mTEC), including Aire<sup>+</sup> mTEC, are an essential requirement for nTh17 development suggesting critical role of the thymic medulla in the differential regulation of nTh17 development [182]. Similar to inducible Th17 (iT<sub>H</sub>17) cells, development of nTh17 cells also require TGF $\beta$  as the deficiency of TGF $\beta$  receptor showed significant reduction in the thymic Th17 cells [181]. However, intracellular developmental pathways vary between two. Although Akt and the downstream mTORC1–ARNT–HIF $\alpha$  axis required for generation of iT<sub>H</sub>17 cells, nTh17 cells developed independently of mTORC1. In contrast, mTORC2 and inhibition of Foxo proteins are critical for development of nTh17 cells. Moreover, AKT2 is critical in development of iT<sub>H</sub>17 cells whereas AKT1 is required for nTh17 [180]. It is reported that IL17 expressing thymocytes are present in the DN1 T cell precursor compartment of Rag1<sup>-/-</sup> mice, indicating naturally occurring IL17 expressing T cell precursors develop in the absence of TCR rearrangement [183]. These data suggest that nTh17 commitment may occur before the process of thymic selection [183].

### 2.11.3 Classical and alternative Th17 cells

During differentiation of Th17, the cytokine milieu determines the functional characteristics as ‘classical’ or ‘alternative’ [184]. Although T-bet and IFN $\gamma$  are classical features of Th1 lineage, *in vitro* or *in vivo* generated Th17 cells also express IFN $\gamma$  in disease condition [184]. These IL17<sup>+</sup>IFN $\gamma$ <sup>+</sup> double producing cells are derived from Th17 cells and show reduced expression of ROR $\gamma$ t as T-bet sequester the transactivation factor Runx-1 required for ROR $\gamma$ t activation [185, 186]. Expression of T-bet and IFN $\gamma$  in Th17 cells is dependent on IL23, but inhibited by TGF $\beta$  and thus is a characteristic of alternative rather than classical Th17 cells [185, 186]. Classical Th17 cell producing both IL17 and IFN $\gamma$  are more plastic than alternative Th17 cells which are more terminally differentiated and therefore maintain a

stable IL17 production [184]. However, it remains to be determined whether the switch to IFN $\gamma$  is actually beneficial or detrimental for the development of tissue inflammation and autoimmunity. In humans, the Th17 cells that convert to Th1 lineage (gain an ability to secrete IFN $\gamma$  and lose their capacity to secrete IL17) express CD161 [187]. When Th17 cells encounter IL12, they convert to a Th17/Th1 phenotype that co-expresses ROR $\gamma$ t, T-bet, CXCR3, CCR6, CD161, and IL23R. The transcription factors Runx1 or Runx3, in combination with T-bet, are crucial for the generation of IFN $\gamma$  producing Th17 cells [188].

Alternative Th17 cells are also reported to produce IL10 [184, 189]. The exposure of Th17 cells to IL23 diminishes IL10 production, whereas TGF $\beta$  promotes the production of IL10 [190, 191]. In addition, IL1 $\beta$  inhibited IL10 production in differentiating and memory Th17 cells, whereas blockade of IL1 $\beta$  *in vivo* lead to increased IL10 production by memory Th17 cells [192]. IL10 may be produced by Th17, suppress Th17 induced inflammation [193]. IL17<sup>+</sup>IFN $\gamma$ <sup>+</sup> T cells express higher levels of IL10R $\alpha$  compared to IFN $\gamma$ <sup>+</sup> T cells and that their proliferation is preferentially suppressed by IL10 signalling [194]. Thus, in the absence of IL23 and IL1 $\beta$ , Th17 cells may eventually start producing IL10 in order to restrain themselves and prevent unnecessary tissue destruction. Another factor that is differentially expressed in 'alternative' vs. classical Th17 cells is GM-CSF [174]. TGF $\beta$  suppresses GM-CSF production in Th17 cells, while IL1 $\beta$  and especially IL23 drive the production of GM-CSF, which stimulates antigen presenting cells to produce more IL23 in a positive feedback loop [195]. In contrast, IL17 and GM-CSF expression are antagonistically regulated by human T cells [196]. Induction of GM-CSF expression by human CD4<sup>+</sup> T cells is constrained by the IL23/ROR $\gamma$ t/Th17 cell axis but promoted by the IL12/T-bet/Th1 cell axis. IL2 mediated STAT5 signalling induce GM-CSF expression in naïve and memory CD4<sup>+</sup> T cells, whereas STAT3 signalling blocks it [196]. The study highlights the difference in the regulation of Th17 cells in mouse and human. GM-CSF not only induces antigen presenting

cells to produce pro-inflammatory cytokines including IL6 and IL23, it also attracts a wave of secondary infiltrating cells primarily macrophages, which then amplify the inflammatory process and promote tissue inflammation [184].

#### **2.11.4 Recruitment of Th17 to the tumor**

The role of Th17 cells in cancer displays complexity in various types of tumor immunity. Although it seems that the pathogenic role of IL23 induced Th17 cells has been consistently documented in autoimmunity, Th17 cells in cancer display both anti-tumorigenic and pro-tumorigenic functions [50]. The emerging evidences reported that the development of Th17 cells in tumor infiltrating lymphocytes is a general feature of cancers [197]. Th17 cells have been found in many different types of human tumors, including lymphoma, myeloma, breast cancer, colon cancer, gastric cancer, hepatocellular cancer, melanoma, ovarian cancer, pancreatic cancer, and prostate cancer [197]. In addition to universal expression of CCR6, Th17 cells can express Th1-associated (CCR2, CXCR3, CCR5, and CXCR6), Th2-associated (CCR4), and nonlymphoid tissue trafficking receptors (CCR4, CCR5, CCR6, CXCR3, and CXCR6), as well as homeostatic chemokine receptors (CD62L, CCR6, CCR7, CXCR4, and CXCR5) that are implicated in T-cell migration to and within lymphoid tissues [198]. The tumor cells, as well as tumor-derived fibroblasts, secrete MCP-1 (the ligand for CCR2 or CCR4) and RANTES (the ligand for CCR1, CCR3, or CCR5) and specifically recruit Th17 cells to the tumor environment [39]. In colorectal cancer and cervical cancer it is reported that Th17 cells are recruited into tumor tissues preferentially through CCR6-CCL20 pathway [199, 200]. Moreover, Th17 cells isolated from melanoma, colon, hepatocellular, ovarian, pancreatic, and renal cell carcinomas express high levels of CXCR4 and CCR6, several CD49 integrins, and CD161 which are involved in the Th17 cell trafficking and migration into the tumor sites [198]. Beside migration of Th17 cells from circulation to the tumor bed, Tumor cells and tumor environment stromal cells produce the proinflammatory cytokines

IL1 $\beta$ , IL6, IL23, and TGF $\beta$ , which can form an optimal proinflammatory cytokine milieu suitable for human Th17 cell differentiation and expansion [39, 42, 45].

### **2.11.5 Contrasting functions of Th17 cells in cancer**

The potential mechanisms responsible for the pro-tumor activity of IL17 or Th17 cells mainly involve angiogenesis and cytokine induction in the tumor microenvironment resulting in the promotion of tumor growth. The accumulation of intra-tumoral Th17 cells enhances human hepatocellular carcinoma, head and neck squamous cell carcinoma, gastric cancer progression by fostering angiogenesis. [27, 42, 201]. In addition to its involvement in angiogenesis IL17 can induce IL6 production, which in turn activates the oncogenic signal STAT3, resulting in up-regulated pro-survival and proangiogenic genes [153]. A comparative study of emerging reports showing correlation of intra-tumoral Th17 cells and clinical outcome of patients showed association of increased Th17 cells with poor survival of patients [197]. However, Th17 cells are also reported to show antitumor immunity. In the murine models deletion of IL17 resulted faster tumor growth and metastasis than wild type mice [202]. Adoptive transfer of Th17 cells also showed elimination of tumor cells [203, 204]. Improved anti-tumor immunity has also resulted from immunotherapies directed towards increasing Th17 activity – these include injection of IL6 [205], blocking indoleamine 2,3-dioxygenase (IDO) [206] or use of IL7 as an adjuvant [207]. Th17 cells are also shown to promote dendritic cell recruitment into the tumor tissues and in draining lymph nodes containing tumor material which activate tumor-specific CD8<sup>+</sup> T cells [204]. In human intra-tumoral Th17 cells are associated with survival of cancer patients. Increased Th17 and IL17 in ovarian tumor predict longer survival of patients [45]. Th17 cells stimulate CXCL9 and CXCL10 production to recruit IFN $\gamma$  producing effector T cells to the tumor microenvironment [45]. Elevated infiltration of Th17 in squamous cell carcinoma is also reported as independent prognostic factor for improved survival [208]. Another study showed that accumulation of Th17 cells in

lung cancer pleural effusion predicted improved patient survival [38, 209]. In patients with acute and chronic lymphocytic leukemia elevated levels of Th17 were also associated with longer survival [210, 211]. The contrasting functions of Th17 observed in cancer may be because of the source of the Th17 cells (arising naturally via tumor growth or adoptively transferred following *ex vivo* manipulation), the functional phenotype of the cells and/or exposure to therapeutic interventions such as chemotherapy. Understanding how Th17 cells cause inflammation in the context of these factors, as well as how these elements impact patient survival, is of considerable interest in the field of oncology.

## 2.12 $\gamma\delta$ T cells

### 2.12.1 Features of $\gamma\delta$ T cells

T cells expressing  $\gamma\delta$ TCR is a separate lineage involved in early immune response in infections, inflammatory diseases, and cancer. Human  $\gamma\delta$  TCR expressing cells constitute 1–5% of total T cells in the peripheral blood but make up a major lymphoid subset (20–50%) in tissues such as the intestine and the dermis [212]. Initially,  $\gamma\delta$ T cells were considered as cells of innate immunity owing to their ability to recognize conserved non-peptide antigens expressed by stressed cells. In addition to this, they recognize pathogen-associated molecular pattern (PAMP) or danger-associated molecular pattern (DAMP) through pattern recognition receptors (PRR) expressed by them [213]. Although activated by innate cytokines  $\gamma\delta$ T cells undergo clonal propagation enhancing the immune response against invading pathogen or danger signal posed by “self” cells. Thus  $\gamma\delta$ T cells are considered to link innate and adaptive immunity [214]. Antigen recognition by murine or human  $\gamma\delta$ T cells does not require antigen presentation by major histocompatibility complex (MHC) class I or class II [215].  $\gamma\delta$ T cells recognise special class of antigens which are small mono- and pyrophosphates of linear C5 isoprenoids called as phosphoantigens [215]. In humans, during cholesterol biosynthesis, phosphorylated precursors such as isopentenyl pyrophosphate (IPP) and DMAPP

(dimethylallyl pyrophosphate) are synthesized by the mevalonate pathway. However, microbial pathogens use non-mevalonate pathway to produce these phosphorylated precursors [216, 217]. Similar to natural killer (NK) cells, human  $\gamma\delta$ T cells also recognize the stress-induced MHC class I related molecules MICA, MICB, and the UL16 binding proteins that are upregulated on malignant or stressed cells [218]. Aminobisphosphonates is a class of drugs which indirectly activate  $\gamma\delta$ T cells by inducing bioaccumulation of mammalian phosphoantigens [219]. The aminobisphosphonates (Zoledronic acid, pamidronate, ibandronate, alendronate, etc) are selective inhibitors of the farnesyl-pyrophosphate synthase enzyme (FPPS) from the mevalonate pathway of cholesterol biosynthesis. bioaccumulation of the FPPS substrate, IPP and DMAPP, which activate  $\gamma\delta$ T cells [219]. In addition to non-protein antigens,  $\gamma\delta$ T cells recognize small peptides such as heat shock proteins (HSPs) [220, 221]. The exclusive response of  $\gamma\delta$ T cells to these phosphoantigens has a potential therapeutic significance and can be used to harness the cytotoxic potential of  $\gamma\delta$ T cells.

### 2.12.2 Development of $\gamma\delta$ T cells

$\gamma\delta$ T cells develop in the thymus from  $CD4^-CD8^-$  (double negative, DN) thymocytes [222]. In humans, sustained notch signalling is required for the development of  $\gamma\delta$ T cells [223]. Differential requirement of notch signalling for  $\gamma\delta$ T cells development in thymus, leads to a scenario of DN, DP, and SP  $TCR\gamma\delta^+$  population, which highlights heterogeneity in human  $\gamma\delta$ T cell development [224]. Notch signalling also regulates extra thymic functions of  $\gamma\delta$ T cells [225] thus validates the requirement of notch signalling in both thymic development and functions of human  $\gamma\delta$ T cells.

### 2.12.3 Functions of $\gamma\delta$ T cells

$\gamma\delta$ T cells perform diverse effector functions determined by the TCR expressed, tissue localization, and activation status.  $\gamma\delta$ T cells are potential cytotoxic cells based on MHC-independent recognition of antigens, production of  $IFN\gamma$ , and expression of cytotoxic

granules [212]. Human  $\gamma\delta$ T cells recognise heat shock proteins (HSP60/70) expressed on tumor cells and enhance its cytolytic activity against the tumors [220, 221, 226]  $\gamma\delta$ T cells support the maturation and activation of other lymphocytes, NK cells and macrophages with the help of secreted chemokines (CCL3, CCL4, CXCL10) [212]. Another chemokine CXC - chemokine ligand 13 (CXCL13) produced by  $\gamma\delta$ T cells can regulate B cell organization within lymphoid tissues and help B cells to produce antibodies [227]  $\gamma\delta$ T cells secrete IL12 and IFN $\gamma$  and influence maturation and antigen presentation of dendritic cells [213, 228]. Activated  $\gamma\delta$ T cells can take up and process the soluble antigens, opsonize target cells and can migrate to lymph nodes through CC-chemokine receptor 7(CCR7) where they upregulate expression of MHCs and co-stimulatory receptors CD80 and CD86 [229, 230]. Moreover, activated  $\gamma\delta$ T cells are licenced to act as antigen presenting cells and activate CD4 and CD8 T cells [231]. Collectively, these observations highlight the multi-faceted role of  $\gamma\delta$ T cells, having both Th and Tc like properties along with their APC like function. These properties of  $\gamma\delta$ T cells aid in generation of an effective immune response in appropriate condition. Thus  $\gamma\delta$ T cells can kill activated, infected, stressed and transformed cells using various strategies such as engagement of death-inducing receptors, such as FAS and TNF-related apoptosis inducing ligand receptors (TRAILR) and the release of cytotoxic effector molecules such as perforin and granzymes [232, 233]. These antitumor properties of  $\gamma\delta$ T cells compelled investigators to undertake clinical trials in cancer patients. Adoptive transfer or *in vivo* expansion of  $\gamma\delta$ T cells were implicated as treatment approaches. Results from Phase I and II clinical trials indicate that the efficacy of  $\gamma\delta$  T cell-based immunotherapy is comparable to that of conventional second-line therapies[234].

In contrast,  $\gamma\delta$ T cells are reported to show pro-tumor activities. Recently, it is shown that  $\gamma\delta$ T cells infiltrating pancreatic ductal adenocarcinoma express elevated levels of T cell exhaustion ligands (PD-L1) and suppress the activity of CD4 and CD8 T cells [235].

Tumour-infiltrating  $\gamma\delta$ T cells are also reported to be the most significant predictor of relapse and poor survival in patients with breast cancer [236]. The pro-tumorigenic role of  $\gamma\delta$ T cells is dependent on their regulatory function in the tumor microenvironment and secondary lymphoid tissues. Foxp3 expressing  $\gamma\delta$ T cells are present in human PBMCs and tumor infiltrating lymphocytes and are reported to suppress T cell activation and proliferation [237, 238]. The suppressive activity of  $\gamma\delta$ T cells did not correlate with Foxp3 but with CD86-CTLA-4 interaction and expression of CD39 [239].

### 2.13 T $\gamma\delta$ 17: a subtype of $\gamma\delta$ T cells

In recent past, the IL17 producing subtype of  $\gamma\delta$ T cell is emerging as important contributor to cancer progression [240]. In humans, upon activation with different cytokines,  $\gamma\delta$ T cells can be polarised towards different effector subtypes like  $\gamma\delta$ 1,  $\gamma\delta$ 2 [241],  $\gamma\delta$ 17 [242, 243],  $\gamma\delta$ Treg [237, 244]. This functional plasticity of  $\gamma\delta$ T cells assists them to tackle the distinct disease conditions and play important role in the early responses to invasive pathogens. Similar to Th17 cells T $\gamma\delta$ 17 cell express ROR $\gamma$ t as a lineage determination transcriptional factor [245]. Like  $\gamma\delta$ T cells human T $\gamma\delta$ 17 cells present in non-lymphoid environment belong to CD27<sup>-</sup> CD45RA<sup>+/+</sup> effector [246] or terminally differentiated (T<sub>EMRA</sub>) [243] memory phenotype.

#### 2.13.1 Development of T $\gamma\delta$ 17 cells

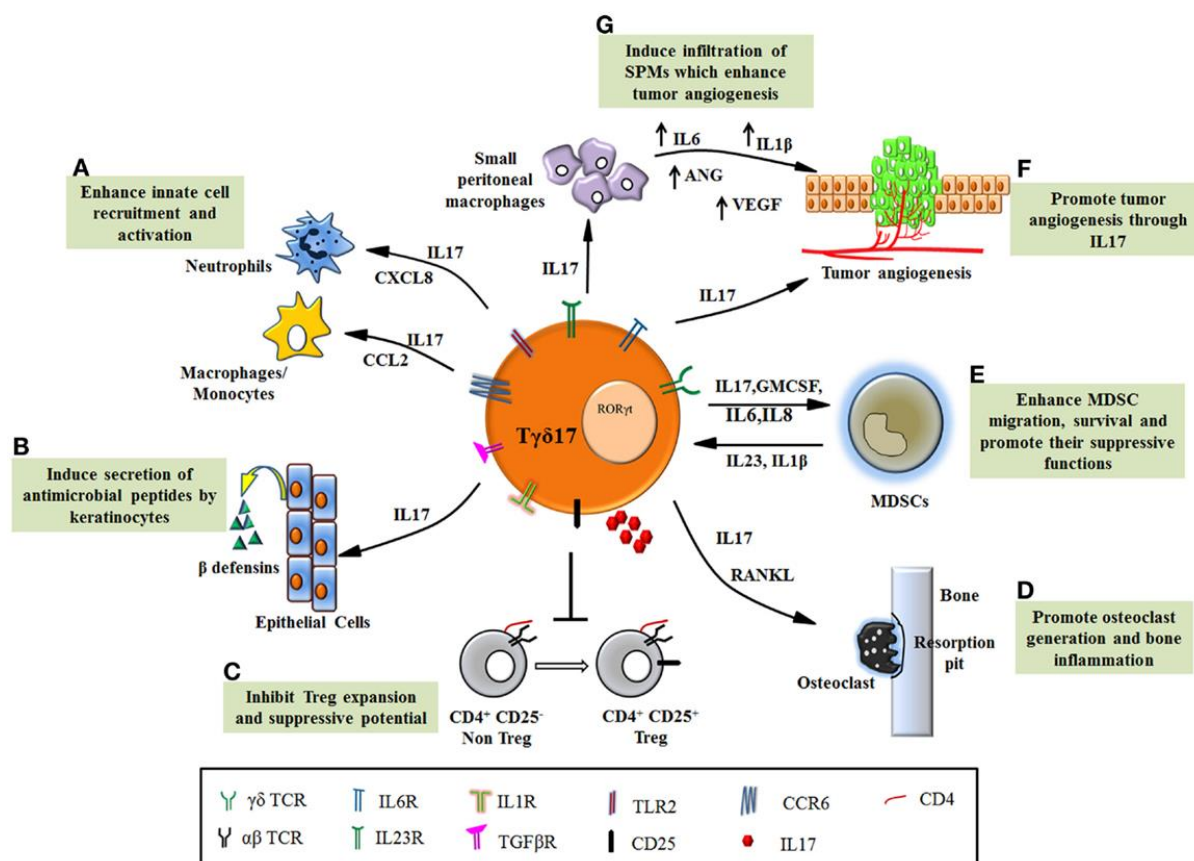
Most of the studies carried out to understand the differentiation mechanisms of T $\gamma\delta$ 17 cells are based on the murine models.  $\gamma\delta$ T cells preferentially localized to barrier tissues are the initial source of IL17 and are likely to originate from the fetal thymus. These are called as the natural IL17 secreting  $\gamma\delta$ T cells.  $\gamma\delta$ T cells that make IL17 within 24 h fall in this category [247]. The  $\gamma\delta$  T cells that have encountered the cognate antigen interaction in thymus, gain the potential to differentiate into the IFN $\gamma$  producing functional phenotype while antigen naïve  $\gamma\delta$  T cells develop into IL17 producing  $\gamma\delta$ T cells [248]. Moreover, CD27<sup>+</sup>  $\gamma\delta$ T cells differentiate into IFN $\gamma$  producing cells whereas IL17 production was restricted to CD27<sup>-</sup> T

cells [249]. Another signalling pathway through lymphotoxin- $\beta$  receptor (LT $\beta$ R) controls T $\gamma\delta$ 17 development by regulating transcription factors ROR $\gamma$ t and ROR $\alpha$ 4, required for IL17 expression in  $\gamma\delta$  thymocytes [250]. Thymic development of human T $\gamma\delta$ 17 cells is poorly investigated. Around 80% circulating human  $\gamma\delta$ T cells are IFN- $\gamma$  producers and express CD27 whereas CD27 negative cells are IL17 producing  $\gamma\delta$  T cells are less than 5% [242]. Human,  $\gamma\delta$  T cells can be polarised to T $\gamma\delta$ 17 cells in periphery upon IPP activation and in presence of cytokines like TGF $\beta$ , IL1 $\beta$ , IL6, and IL23, followed by a week of culture in differentiation medium supplemented with IL2 can induce IL17 in these cells [242, 243]. The kinetics of IL17 production by human  $\gamma\delta$ T cells showed that mRNA expression of IL17 and ROR $\gamma$ t peaks by day 3-6 and decrease by day9 onwards, after stimulation. The expression of cytokine receptors (IL1 $\beta$ R, IL6R, TGF $\beta$ R and IL23R) on V $\gamma$ 9V $\delta$ 2 T cells peaks on day 3 and decrease by day 6 [243].

### 2.13.2 Functions of T $\gamma\delta$ 17 cells

T $\gamma\delta$ 17 cells are reported to exacerbate inflammatory diseases (Figure 2.4) [251]. With the notion that IL17 is a proangiogenic cytokine [252], T $\gamma\delta$ 17 cells promote angiogenesis in tumor model. In IL17<sup>-/-</sup> tumor bearing mice, the blood vessel density was markedly decreased compared to wild type. In addition, IL17 induced the expression of Ang-2 (angiopoietin) and VEGF in tumor cells [253]. T $\gamma\delta$ 17 cells induce mobilization of pro-tumor small peritoneal macrophages (SPM) to the tumor bed which express IL17 dependent proangiogenic profile (*Il1b*, *Il6*, *vegfa*, *tgfb*, *mif*, *cxcl1*, *cxcl8* and *tie2*). SPMs also enhance ovarian cancer growth by stimulating tumour cell proliferation [254]. In hepatocellular carcinoma mouse model, it was reported that IL17, majorly produced by V $\gamma$ 4<sup>+</sup> $\gamma\delta$ T cells, induced CXCL5 production by tumor cells which enhance migration of MDSCs expressing CXCR2 to the tumor site. In addition, IL17 also enhanced suppressive functions of MDSCs by inhibition of T cells proliferation and IFN $\gamma$  and TNF $\alpha$  production [255]. The importance

of  $T\gamma\delta 17$  cells in human cancer is recently appreciated [251].  $T\gamma\delta 17$  cells are reported to secrete IL8, TNF and GM-CSF, which recruit immunosuppressive MDSCs into the malignant microenvironment, further driving progression of colorectal cancer [246].  $T\gamma\delta 17$  cells induce angiogenesis related factors (VEGF, uPA, MMP9, MCP-1, GM-CSF, CXCL16, Coagulation factor III, Angiogenin, etc.) in gallbladder tumor cells through IL17[256].



**Figure 2.4 : Effector functions of  $T\gamma\delta 17$  cells .** The figure illustrates the functions of  $T\gamma\delta 17$  cells in innate cell activation, induction of antimicrobial peptides, inhibition of Treg expansion, promote osteoclast generation, enhance MDSC migration, promote tumor angiogenesis and recruitment of macrophages. The figure is adapted from Patil et. al, *Frontiers in Immunology*,6, 2015.

In contrast, antitumor activity of  $T\gamma\delta 17$  cells was also reported [251]. In a chemotherapeutic approach, in several transplantable tumor models,  $T\gamma\delta 17$  cells are shown to invade the tumor bed early in response after drug treatment. This was followed by infiltration and induction of IFN $\gamma$  producing CD8 (Tc1) cells to the tumor bed. This infiltration of  $T\gamma\delta 17$  and Tc1 cells was correlated and associated with tumor regression post radio or chemotherapy [257].

Collectively, the apparent opposite roles of  $T\gamma\delta 17$  cells in cancer immunity need to be understood in detail to consider it as potential target in immunotherapeutic interventions.

## **2.14 Inflammation and immunosuppression**

Immune response in cancer patients is characterised by impairment of homeostatic levels of immune cells. Given that inflammation is one of the important hallmarks of cancer, the impairment of levels of inflammatory and immunosuppressive immune cells in cancer patients is obvious. The alteration in the Th17 and Treg cells and related cytokines is reported in various cancers. In patients with non-small cell lung cancer the levels of Treg cells were increased and that of Th17 cells decreased with cancer progression [258]. Similar trend was observed in salivary gland tumors [259]. In breast cancer patients analysis of tumor infiltrating lymphocytes showed that Th17 and Treg cell accumulation in the tumour microenvironment occurred in early disease; Th17 cell infiltration gradually decreased and Treg cells accumulated with disease progression [260]. Altered Th17 Treg balance was also reported in lung cancer, prostate cancer, and cervical cancer [58-60]. Thus the reports suggest that the balance of proinflammatory and immunosuppressive cells is crucial in cancer patients and investigation of the dynamics of proinflammatory and immunosuppressive cells is necessary for better understanding the pathogenesis of cancer.

## **2.15 Regulatory T cells**

### **2.15.1 Features of Treg cells**

Regulatory T cells (Tregs) is a subtype of CD4<sup>+</sup> T cell that functionally suppresses an immune response by manipulating the activity of other immune cells [51]. It was first reported by Gershon et. al. that the subset of T cells exhibit suppressive function [261, 262]. Sakaguchi and his colleagues showed that Tregs are a small group of T cells co-expressing CD4 and CD25 (IL2 receptor- $\alpha$  chain) involved in maintaining self-tolerance since depletion of Treg cells lead to autoimmunity [263, 264]. Foxp3, a key transcription factor is crucial for

the development and functioning of  $CD4^+CD25^+$  regulatory T cells [52, 265, 266]. In humans, the low expression of CD127, the  $\alpha$ -chain of the interleukin-7 receptor, was used in combination with  $CD25^+$  and  $Foxp3^+$  to better define the Treg cell population with suppressive function. CD127 expression is reported to be inversely correlated with expression of  $Foxp3$  and the suppressive potential of  $CD4^+$  Treg cells [267, 268]. In the periphery, naturally occurring Tregs represent around 6–10% of total  $CD4^+$  T-cell population. In order to be sustained, Tregs need uninterrupted TCR triggering and co-stimulation in the presence of IL2 [269, 270]. Treg cells can be dissected into three sub-populations by the expression levels of  $Foxp3$  and the cell surface molecules CD45RA and CD25 : (i)  $Foxp3^{lo}CD45RA^+CD25^{lo}$  cells, designated naive or resting Treg cells, which differentiate into  $Foxp3^{hi}CD45RA^-CD25^{hi}$  cells upon antigenic stimulation; (ii)  $Foxp3^{hi}CD45RA^-CD25^{hi}$  cells, designated eTreg (effector Treg) cells, which are terminally differentiated and highly suppressive; and (iii)  $Foxp3^{lo}CD45RA^-CD25^{lo}$  non-Treg cells, which do not possess suppressive activity but can secrete pro-inflammatory cytokines [51].

### 2.15.2 Treg cells in cancer

There is an increased prevalence of  $CD4^+CD25^+$  T cells in a wide spectrum of human malignancies like skin, lung, head and neck, ovarian, and gastrointestinal. These cells are found in relatively higher numbers in blood, ascites, within the tumor draining lymph nodes and tumor tissue of cancer patients [271, 272]. Importantly, the numbers of  $CD4^+CD25^+$   $Foxp3^+$  Tregs present in tumors and in particular, decreased ratios of  $CD8^+$  T cells to  $CD4^+CD25^+Foxp3^+$  Tregs in tumors, correlate with poor prognosis in breast cancer [273], gastric cancer [274], head and neck cancer [275] and ovarian cancer patients [276]. The accumulation of Tregs in the tumor takes place by three different, but not mutually exclusive, modes: (i) increased trafficking, (ii) preferential Treg expansion and (iii) de-novo differentiation, where the latter two can occur either locally within the tumor

microenvironment. The chemokine receptors CCR4 and CCR8 are expressed by Tregs and the CCR4 ligand CCL22 has been shown to be produced by both tumor cells and tumor-infiltrating macrophages [277, 278]. An inflammatory condition in tumors also recruits Tregs in CCL20-CCR6 dependent fashion [279]. Other combinations of chemokines and chemokine receptors, such as CCR10-CCL28 and CXC chemokine receptor (CXCR) 3-CXCR3 ligands (such as CXCL9, 10, and 11), also reportedly contribute to Treg cell infiltration [280, 281]. A second mechanism could be through expansion of Tregs in the presence of IL2 and TGF $\beta$  within the tumor mass or in the tumor draining lymph nodes (TDLNs). Presence of IL2 and TGF $\beta$  within the tumor mass could promote Treg proliferation, development and homeostasis [282-284]. A third mechanism involving *de-novo* conversion of Foxp3<sup>+</sup> T cells into Tregs may play an important role in Treg accumulation in tumors [285]. The role of TGF $\beta$  in the induction of Tregs is well established and tumor cell derived TGF $\beta$  can contribute to the induction of Tregs [286, 287]. Compared with tumor-reactive CD4<sup>+</sup> T cells, natural Treg cells may be better at recognizing tumor-associated self-antigens because of their TCR repertoires are more self-reactive than those of conventional T cells. Moreover, the higher level expression of T cell accessory molecules including adhesion molecules (such as LFA-1) indicate their ‘antigen- primed’ states [51].

### 2.15.3 Mechanism of Treg function

Accumulating evidences have shown that Foxp3<sup>+</sup>CD25<sup>+</sup>CD4<sup>+</sup> natural Tregs suppress the activation and/or expansion of multiple types of immunocompetent cells. Based on these studies, multiple mechanisms have been proposed for Treg-mediated suppression, including soluble factor mediated as well as cell surface molecule dependent inhibition of T cells and antigen presenting cells [52]. Tregs majorly utilize the inhibitory cytokines like IL10, TGF $\beta$ , and IL35 to directly induce immune suppression [288]. Tregs can also use

perforin/granzyme-mediated cytotoxicity as a mechanism to suppress the function of effector T cells [289]. Tregs isolated from cancer patients were found to express Fas ligand (FasL) and mediate killing of CD8<sup>+</sup> T cells on activation via TCR ligation and high-dose IL2 [290]. Another study suggests that *in vitro*-activated mouse Tregs can induce apoptosis of CD4<sup>+</sup> effector T cells in a TRAIL/DR5 (tumor necrosis factor related apoptosis inducing ligand/death receptor dependent fashion [291].

In addition to directly inhibiting effector lymphocytes through inhibitory cytokines or cytotoxic molecules, Tregs may also suppress immune responses by modulating APCs. Foxp3 regulated CTLA-4 (cytotoxic T lymphocyte antigen 4) expression on Tregs can downregulate the costimulatory molecules (CD80, CD86) on antigen-presenting cells to suppress T cell activation [292, 293]. Besides suppressing the ability of APC to activate other T cells, CTLA-4 can induce the production of IDO in APCs, which can degrade the essential amino acid tryptophan, leading to an inhibition of T cell proliferation [294]. In addition, IDO-mediated degradation of tryptophan can generate toxic metabolites that induce apoptosis in lymphocytes [295, 296]. Ectoenzymes like CD39 and CD73 preferentially expressed on the surfaces of Treg cells can catalyse the generation of adenosine from the extracellular nucleotide ATP or ADP [297]. Adenosine inhibits effector T cell function through activation of the adenosine receptor 2A [298]. Tregs harbour high levels of cyclic adenosine monophosphate (cAMP) which can potently inhibit IL-2 synthesis and T cell proliferation [299].

## **Chapter 3**

# **Materials and Methods**

## Materials and methods:

### 3.1 Cell culture medium

RPMI-1640 medium (Invitrogen Life-Technologies, Grand Island, N.Y.) or Williams' E medium (Sigma-Aldrich, St. Louis, USA) powder was dissolved in deionized water and supplemented with sodium bicarbonate (Sarabhai Chemicals, India) as per manufacturer's instructions. The medium was sterilized by membrane filtration (0.45µm, Millipore Co, Bedford, MA). Sterility testing of the filtered media was carried out by adding 1-2ml of medium to the tube containing the sterility medium (Thioglycolate medium) (Annexure) and incubated at 37<sup>0</sup>C. Sterility was monitored for 6 days and stored at -20<sup>0</sup>C until use.

To prepare complete medium, RPMI/ Williams' E plain medium was supplemented with 10% heat inactivated Fetal calf serum, (FCS; Invitrogen Life Technologies, Grand Island, N.Y), Penicillin (100 IU/ml; Alembic Chemicals India), Streptomycin (100 mg/ml; Alembic chemicals India), Mycostatin (5 mg/ml; Sigma, USA), Gentamycin (40 mg/ml; Schering Corp, India) and L-Glutamine (2 mM, Hi Media, India). Williams' E medium was supplemented with L-Glutamine thus it was not added while preparing complete medium.

### 3.2 Maintenance of cell lines

Gallbladder cancer cell lines (OCUG-1; JCRB-0191[300] and NOZ; JCRB-1033[301]) were purchased from Japan health science foundation, Health science research resources bank, Osaka, Japan.

Table 3.1 Characteristics of OCUG-1 cell line

<b>OCUG-1</b>	
Cell No	JCRB0191
Characteristics	Poorly differentiated adenocarcinoma. Cells are tumorigenic in nude mice.

Medium	Williams' E supplemented with 10% FCS
Growth rate	~ 31 h
Growth Temperature	37 <sup>0</sup> C
Lifespan	Infinite
Morphology	Clusters with monolayer cells
Source	Male (age 43)
Metastasis	Yes
Chromosome Number	Chromosome number distribute in a broad range from 52 to 139.

Table 3.2 Characteristics of NOZ cell line

<b>NOZ</b>	
Cell No	JCRB1033
Characteristics	Moderately differentiated adenocarcinoma.
Medium	Williams' E supplemented with 10% FCS
Growth rate	~ 24 h
Growth Temperature	37 <sup>0</sup> C
Life span	Infinite
Morphology	Epithelial like
Source	Female (age 48)
Metastasis	Cells are transplantable to nude mice and the morphology of the transplanted tumor was similar to the original one
Chromosome Number	46

Cells were cultured in Williams' E medium (Sigma Aldrich, USA) supplemented with 10% heat inactivated FBS under standard culture conditions (37°C, 5% CO<sub>2</sub>). The adherent cell lines were maintained in 25cm<sup>2</sup> or 75cm<sup>2</sup> flasks and split when confluent. The cells were trypsinized from the flask with PBS-trypsin (Sigma, USA; 0.3% trypsin in 0.01M PBS pH 7.5, containing 0.02% EDTA, sterilized by Millipore filtration), and washed with plain medium before use. For continuous maintenance of cultures, 0.2 to 0.3 x10<sup>6</sup> cells were reseeded into the flask with 5 ml of complete medium (containing 10% FCS).

GBC cell lines were cryopreserved as main stock and working stock. For cryopreservation of the cultures, cells were pelleted by centrifugation at 1000 rpm. Chilled freezing mixture (10% Dimethyl sulphoxide [DMSO] + 90% FCS) was added drop-wise to the pellet with constant mixing. 2-3x10<sup>6</sup> cells/ml of freezing mixture were transferred to cryotube (Nunc, Denmark) and frozen in liquid nitrogen with gradual decrease in temperature.

GBC cell lines were revived from working stock frozen vials. The vials were thawed rapidly by placing in a beaker containing lukewarm water (~37°C). The cells were transferred to a centrifuge tube containing warm plain medium drop-wise with constant mixing to dilute the DMSO. Cells were washed twice with plain medium and checked for the viability using the trypan blue stain (0.4% trypan blue prepared in normal saline)

### 3.3 Study Group

Newly diagnosed GBC patients (n=52) were recruited from Tata Memorial Hospital, Mumbai. 22 males (mean age = 54±2 years) and 30 females (mean age = 51±2 years) were enrolled in the study group. Peripheral blood was collected prior to chemotherapy/radiotherapy or surgery after obtaining informed consent. The study protocol was approved by ACTREC-TMC Institutional review board for human studies. The patients were grouped according to the TNM classification as stage II (n=5), stage III (n=20) and

stage IV (n=27). Tumor tissue (n=17) were obtained from GBC patients undergoing cholecystectomy without radio or chemotherapy received. Peripheral blood was obtained from age and sex matched healthy individuals (n=30) who participated voluntarily and written informed consent was obtained.

#### **Inclusion criteria for GBC patient accrual**

- ✓ Patients presenting gallbladder as primary site of tumor origin
- ✓ Patient diagnosed with GBC with any clinical stage
- ✓ Treatment naïve patients

#### **Exclusion criteria for GBC patient accrual**

- ✓ Patients treated elsewhere with chemo/radiotherapy
- ✓ Patients refusing consent of the study
- ✓ Patients treated for cholecystectomy elsewhere
- ✓ Patients diagnosed with HIV/ hepatitis infection

### **3.4 Cell isolation and culture**

#### **3.4.1 Isolation of Peripheral blood mononuclear cells (PBMCs)**

PBMCs were isolated from heparinized blood of GBC patients and healthy individuals using Ficoll Hypaque (FH) (Sigma-Aldrich, St. Louis, MO) by density gradient centrifugation. Briefly, peripheral blood collected in heparin (Sigma, USA; 100 IU/ml) was diluted with equal volume of normal saline (0.82% NaCl in double distilled water). 8ml of diluted blood was loaded on 2.5ml of FH [24 parts of 9% Ficoll 400 (Sigma, USA) + 10 parts 33.3% sodium diatrizoate (Sigma, USA), specific gravity adjusted to  $1.077 \pm 0.001$ ] and centrifuged at 1,500 rpm for 20 min at room temperature (RT) using a swing-out rotor in Beckman centrifuge. PBMCs were collected from the interface between FH and plasma and washed

thrice with sterile normal saline. Viability was checked using Erythrosine B or Trypan blue vital dye (0.4%).

### **3.4.2 Preparation of single cell suspension of tumor tissue**

Surgically resected gallbladder tumors were collected in a collection medium (sterile plain RPMI 1640 supplemented with double strength of antibiotics). The freshly collected tumor tissue was processed for preparation of single cell suspension. Briefly, necrotic, hemorrhagic and fatty tissues were removed and tumor tissues were thoroughly washed with RPMI medium containing double strength of antibiotics. Tumor tissues were minced finely and were incubated in RPMI medium containing double strength of antibiotics and enzyme mixture [0.05% collagenase, 0.02% DNase and 5U/ml hyaluronidase (Sigma, USA)] at 37°C for 2 h with intermittent shaking. The minced tumor tissues were then passed through a 200 # wire mesh to obtain single cell suspension of lymphocytes. The cells were washed with plain RPMI medium containing antibiotics. The collected cells were washed twice and the cell viability was checked using Erythrosine B or trypan blue vital dye.

### **3.4.3 Collection of tumor supernatants**

The single cells suspension obtained from freshly collected gallbladder tumor tissue were cultured in 4 well plate as  $1 \times 10^6$  cells/ml in a serum free medium for 24 h. The cell-free culture supernatant were collected, centrifuged and stored at  $-80^\circ\text{C}$  until used.

### **3.4.4 Isolation of $\gamma\delta$ T cells from peripheral blood of HI**

PBMCs were isolated from HI by Ficoll Hypaque density gradient centrifugation.  $\gamma\delta$ T cells were purified by immunomagnetic purification using  $\gamma\delta$ -TCR microbeads (Miltenyi Biotech, Germany). PBMCs were washed with a degassed buffer containing PBS with 0.5% BSA and 2 mM EDTA. Supernatant was removed and cells were suspended in 40  $\mu\text{l}$  of buffer per total  $10^7$  cells. 10  $\mu\text{l}$  of  $\gamma\delta$ -TCR antibody labelled with hapten was added per  $10^7$  total cells. Cells

were mixed and incubated for 10 min at 4°C. 30µl of buffer and 20µl of anti-hapten antibody labelled with micro-beads and FITC were added per  $10^7$  cells, mixed well and incubated for 15 min at 4°C. Cells were then washed by adding buffer 10-20 times of labeling volume and centrifuged at 1000 rpm for 10 min. Supernatant was removed and cells were suspended in 500µl buffer per  $10^8$  cells.

For isolation of magnetically labelled  $\gamma\delta$ T cells, MACS column (MS column for  $10^7$  cells or LS MACS column for  $10^7$  to  $5 \times 10^7$  of target cells) was placed in magnetic field of MACS separator. Column was washed thrice with 500µl of wash buffer. The cell suspension was applied onto the column. Unlabelled cells were washed out from the column as negative selection and collected separately. Column was removed from the separator and magnetically labelled cells (positively selected) cells were collected by flushing the cells from the column into 1 ml of buffer. The purity of positively selected cells was checked by flow cytometry. More than 90-95% pure  $\gamma\delta$ T cells were re-suspended in the culture medium for further assay.  $5-8 \times 10^6$   $\gamma\delta$ T cells were isolated from starting PBMC population of  $60-70 \times 10^6$  cells.

#### 3.4.5 Isolation of T $\gamma\delta$ 17 cells from peripheral blood of HI

T $\gamma\delta$ 17 cells were isolated using IL17 secretion assay-cell enrichment and detection kit (Miltenyi Biotec, Germany) according to manufacturer's instructions. Briefly,  $\gamma\delta$ T cells were purified by positive selection from PBMCs of healthy individuals using anti TCR- $\gamma\delta$  microbeads (Miltenyi Biotec, Germany). Purified  $\gamma\delta$ T cells ( $7-8 \times 10^6$ ) were stimulated with 50ng/ml of PMA (phorbol 12-myristate 13-acetate) and 1µg/ml of Ionomycin for 5 h in RPMI medium supplemented with 10% FCS. Cells were washed at 4°C, and labelled with IL17 catch reagent (5µl) for 5 min on ice. Cells were maintained at cold temperature. Cells were suspended in RPMI containing human AB serum (10ml) and incubated at 37°C for 45 min with constant mixing for secretion phase. Cells were again maintained at 4°C and after

washing labelled with anti-IL17 detection antibody (5 $\mu$ l) labelled with phycoerythrin. The cells were sorted for IL17-PE positive cells. Purity was determined by flow cytometry. Around 5x10<sup>4</sup> T $\gamma$  $\delta$ 17 cells were isolated from 7-8x10<sup>6</sup>  $\gamma$  $\delta$ T cells medium with > 90% purity.

### 3.4.6 Isolation of regulatory T cells

Regulatory T cells were isolated from PBMCs of healthy individuals and GBC patients using BD Imag immunomagnetic separation kit. PBMCs (50-60x10<sup>6</sup>) isolated by ficoll density gradient were first labelled with cocktail of biotinylated antibodies (5 $\mu$ l per 1x10<sup>6</sup> cells). The cocktail of antibodies consist of antibodies that recognize antigens on erythrocytes, platelets and peripheral leukocytes that are not CD4<sup>+</sup> T lymphocytes (CD8, CD11b, CD16, CD19, CD36, CD41a, CD56, CD123, TCR  $\gamma$  $\delta$  and Glycophorin A) and APC-labelled mouse anti-human CD25 antibody. After peripheral blood lymphocytes were labelled with the cocktail, the CD4<sup>+</sup> CD25<sup>+</sup>Treg cells were isolated in two immunomagnetic separation steps. First, the CD4<sup>+</sup>T lymphocytes were enriched by negative selection (depletion of the non-CD4<sup>+</sup> cells) using the Streptavidin Particles (7.5 $\mu$ l per 1x10<sup>6</sup> cells). In the second immunomagnetic separation step, the Anti-APC Particles (5 $\mu$ l per 1x10<sup>6</sup> cells) were used to select the CD25<sup>+</sup> cells, from the enriched CD4<sup>+</sup> cells, which were already labelled with the APC anti-CD25 mAb. The phenotype and purity of regulatory T cells was confirmed using flow cytometry. 1-2x10<sup>5</sup> purified Treg cells were isolated with > 80% purity.

## 3.5 Flow cytometry

### 3.5.1 Multi-colour flow cytometry staining

Flow cytometric analysis was performed using FACS Aria flow cytometer (Becton Dickinson, CA, USA) and data was analysed using FlowJo software (Tree Star, Ashland, OR). Fluorescence minus one control was used in all experiments to determine background fluorescence. For intracellular staining, cells were washed with PBS and cold fixed with 500 $\mu$ l 1% Paraformaldehyde (Sigma Aldrich, USA) for 15 min at 4<sup>0</sup>C, followed by

permeabilization for 5 min with 0.1% saponin (50 $\mu$ l) at room temperature. Cells were incubated with antibodies for 30 min at room temperature. For intracellular cytokines staining, PBMCs (1x10<sup>6</sup> cells per well) were first stimulated with PMA (50ng/ml) and ionomycin (1 $\mu$ g/ml) for 5 h in presence of Brefeldin A (5 $\mu$ g/ml) (All from Sigma Aldrich, USA). Stimulated cells were washed with PBS, fixed with paraformaldehyde, permeabilized with saponin and stained with antibodies. After staining cells were resuspended in FACS buffer (PBS+1% FCS+ sodium azide; Sigma Aldrich, USA) and acquired using FACS Aria flow cytometer (Becton Dickinson). 50,000-100,000 live cells (events) were collected to obtain reliable data.

Frequencies of T helper, cytotoxic T,  $\gamma\delta$ T, B cells, NK cells, NKT cells, Th17, Tc17, T $\gamma\delta$ 17, regulatory T and myeloid derived suppressor cells in PBMCs were compared between healthy individuals and GBC patients. The data was expressed as percent positive cells or MFI (median fluorescence intensity). Range of antibodies was used in multi-color flowcytometry to characterize these cell types in peripheral blood and tumor tissue of gallbladder cancer patients. Following are the antibodies used to characterize different cell subsets.

### **3.5.2 IL17 receptor expression on GBC cell line**

To analyse the IL17 receptor expression on the OCUg-1 and NOZ cells, cells were cultured in the 60 mm petri dish (Nunc, Germany) to attain 70% confluency. The spent medium was removed and cells were washed with PBS. Cells were fixed with 1% paraformaldehyde for 15 min at 4<sup>0</sup>C. After washing, cells were scraped from the plate and stained with IL17R-PE antibody for 30 min at RT. Unbound antibody was removed by washing the cells with FACS buffer and cells were re-suspended in 300 $\mu$ l buffer. Cells were acquired on FACS Aria.

## 3.5.3 Antibodies used

Table 3.3 List of Fluorochrome conjugated antibodies

<i>Antibody</i>	<i>Fluorochrome</i>	<i>Clone</i>	<i>Isotype</i>	<i>Company</i>
<b>CD3<math>\epsilon</math></b>	APCCy7	SK7	<i>Mouse IgG1<math>\kappa</math></i>	BD Biosciences
<b>CD3<math>\epsilon</math></b>	Pacific Blue	SP34-2	<i>Mouse IgG1<math>\lambda</math></i>	BD Biosciences
<b>CD4</b>	PECF594	RPA-T4	<i>Mouse IgG1<math>\kappa</math></i>	BD Biosciences
<b>CD4</b>	APC	RPA-T4	<i>Mouse IgG1<math>\kappa</math></i>	BD Biosciences
<b>CD8</b>	Pacific blue	RPA-T8	<i>Mouse IgG1<math>\kappa</math></i>	BD Biosciences
<b>V<math>\delta</math>2TCR</b>	PE	B6	<i>Mouse IgG1<math>\kappa</math></i>	BD Biosciences
<b>V<math>\delta</math>2TCR</b>	FITC	B6	<i>Mouse IgG1<math>\kappa</math></i>	BD Biosciences
<b>CD19</b>	PE	HIB19	<i>Mouse IgG1<math>\kappa</math></i>	BD Biosciences
<b>CD56</b>	PE	B159	<i>Mouse IgG1<math>\kappa</math></i>	BD Biosciences
<b>CD45RA</b>	PECY5	HI100	<i>Mouse IgG2b<math>\kappa</math></i>	BD Biosciences
<b>CD27</b>	APC	L128	<i>Mouse IgG1<math>\kappa</math></i>	BD Biosciences
<b>CD3<math>\zeta</math></b>	PE	6B10.2	<i>Mouse IgG1<math>\kappa</math></i>	Santacruz Biotech
<b>IL17</b>	Alexa fluor488	N49-653	<i>Mouse IgG1<math>\kappa</math></i>	BD Biosciences
<b>IL17</b>	Alexa fluor 647	SCPL1362	<i>Mouse IgG1<math>\kappa</math></i>	BD Biosciences
<b>IFN<math>\gamma</math></b>	PECY7	B27	<i>Mouse IgG1<math>\kappa</math></i>	BD Biosciences
<b>CD33</b>	PECF594	WM53	<i>Mouse IgG1<math>\kappa</math></i>	BD Biosciences
<b>HLADR</b>	APCH7	G46-6	<i>Mouse IgG2a<math>\kappa</math></i>	BD Biosciences
<b>CD11b</b>	Alexa fluor 488	ICRF-44	<i>Mouse IgG1<math>\kappa</math></i>	BD Biosciences
<b>CD25</b>	PE	M-A251	<i>Mouse IgG1<math>\kappa</math></i>	BD Biosciences

<b>CD127</b>	V450	HIL-7R-M21	<i>Mouse IgG1<math>\kappa</math></i>	BD Biosciences
<b>Foxp3</b>	Alexa fluor 488	259D/C7	<i>Mouse IgG1</i>	BD Biosciences
<b>IL17R</b>	PE	FAB177P	<i>Mouse IgG1</i>	BD Biosciences
<b>CD183 (CXCR3)</b>	PE	1C6	<i>Mouse IgG1<math>\kappa</math></i>	BD Biosciences
<b>CD184 (CXCR4)</b>	PECy7	12G5	<i>Mouse IgG2a<math>\kappa</math></i>	BD Biosciences
<b>CD196 (CCR6)</b>	APC	11A9	<i>Mouse IgG1<math>\kappa</math></i>	BD Biosciences
<b>CD197 (CCR7)</b>	Alexa fluor 647	3D12	<i>Mouse IgG2a</i>	BD Biosciences
<b>CD194 (CCR4)</b>	PerCP-Cy <sup>TM</sup> 5.5	1G1	<i>Mouse IgG1<math>\kappa</math></i>	BD Biosciences

Table 3.4 List of purified antibodies

<i>Antibody</i>	<i>Clone</i>	<i>Isotype</i>	<i>Company</i>
<b>CD3</b>	UCHT1	<i>Mouse IgG1<math>\kappa</math></i>	BD Biosciences
<b>IL17</b>	--	<i>Polyclonal Goat IgG</i>	R&D Systems
<b>CXCR3</b>	49801	<i>Mouse IgG1<math>\kappa</math></i>	R&D Systems

### 3.5.4 Staining panel for immune cells

Table 3.5 List of staining panel of immune subtypes

<i>Immune cell type</i>	<i>Antibody panel</i>
T cell subsets	CD3-Pacific Blue, CD4-APC, CD8-FITC, V $\delta$ 2TCR-PE
B Cells	CD19 -PE
NK and NKT cells	CD3-FITC, CD56-PE

IL17 and IFN $\gamma$ producing cells	CD3-APC-Cy7, CD4-PECF594, CD8-FITC, V $\delta$ 2TCR-PE, IL17-APC, IFN $\gamma$ -PECY7
Regulatory T cells	CD3-APC-Cy7, CD4-PECF594, CD25-PE, CD127-APC, Foxp3-AF488
Myeloid derived suppressor cells	HLADR-APCH7, CD33-PECF594, CD11b-AF488,

Abbreviations: APC: allophycocyanin; FITC: fluorescein isothiocyanate; PE: phycoerythrin; Foxp3: forkhead box P3.

### 3.6 Proliferation assay

#### 3.6.1 Proliferative response of PBMCs to mitogen and TCR agonist

Proliferative response of PBMCs was analysed by tritiated thymidine ( $^3\text{H}$ -Thymidine) incorporation assay. PBMCs were isolated from GBC patients and HI using ficoll-hypaque gradient centrifugation. Anti-CD3 mAb (1 $\mu\text{g}$ /well; 100 $\mu\text{l}$  in normal saline) was pre-coated overnight at 4 $^{\circ}\text{C}$ . Excess antibody was removed and PBMCs ( $1 \times 10^5$ ) were cultured with pre-coated anti-CD3mAb or phytohaemagglutinin (PHA; Sigma Aldrich, USA) (1%) for 72 h at 37 $^{\circ}\text{C}$  in round bottom 96 well plates (Nunc, Denmark). Only lymphocytes in complete medium (RPMI 1640 + 10% FCS) were used as control. 0.5 $\mu\text{Ci}$ /10 $\mu\text{l}$ /well  $^3\text{H}$ -Thymidine (specific activity 240GBq/mmol; Radiation and Isotype Technology, India) was added during last 18 h of the assay. The cells were harvested on glass-fibre filter paper (Titertek, Norway) using cell harvester (Titertek, Norway). The filter paper was dried at 60 $^{\circ}\text{C}$  and each disc corresponding to single well was placed in 3 ml liquid scintillation fluid [0.7% 2, 5 diphenyloxazole + 0.05% 1, 4 bis (5-phenyloxazole)]. Radioactivity was measured on a liquid  $\beta$ -scintillation counter (Model 1900 Packard, USA) as counts per minute (CPM). Stimulation index was calculated by following formula. Stimulation index = (Test CPM /

Control CPM). Proliferation of PBMCs in presence of stimulation was compared with cells cultured with medium alone. Data are presented as mean  $\pm$  SEM.

### 3.6.2. Effect of rhIL17 on proliferation of GBC cell lines

Proliferative response of gallbladder cancer cell lines (OCUG-1 and NOZ) was analysed by tritiated thymidine ( $^3\text{H}$ -Thymidine) incorporation assay. To study the effect of IL17 on proliferation of GBC cells, OCUG-1 and NOZ cell lines were cultured in a 96 well flat bottom plate (Nunc, Denmark). Cells were seeded in triplicates with density  $1 \times 10^4$  per well in presence of complete Williams' E medium for total 72 h. After 24 h, cells were washed with serum-free medium and rhIL17 (R&D systems, MN, USA) was added at different concentrations (100, 10, 1, and 0.1 ng/ml) to the wells. Cells cultured with medium alone were used as control.  $0.5 \mu\text{Ci}/10 \mu\text{l}/\text{well}$   $^3\text{H}$ -Thymidine (specific activity 240 GBq/mmol; Radiation and Isotope Technology, India) was added during last 18 h of the assay. After 72 h, cells were harvested on glass-fibre filter paper (Titertek, Norway) using cell harvester (Titertek, Norway). The filter paper was dried at  $60^\circ\text{C}$  and each disc corresponding to single well was placed in 3 ml liquid scintillation fluid [0.7% 2, 5 diphenyloxazole + 0.05% 1, 4 bis (5-phenyloxazole)]. Radioactivity was measured on liquid  $\beta$ -scintillation counter (Packard USA) as counts per minute (CPM). Proliferation of OCUG-1 and NOZ cells in the presence of rhIL17 was compared with control cells cultured with medium alone by measuring the radioactivity in CPM. Data was presented as mean  $\pm$  SEM.

## 3.7 Estimation of cytokines

### 3.7.1 Cytokine secretion by stimulated PBMCs

PBMCs ( $1 \times 10^5$ ) from HI and GBC patients were stimulated with pre-coated anti-CD3 ( $1 \mu\text{g}/\text{well}$ ;  $100 \mu\text{l}$  in normal saline) or PHA (1%) for 24 h at  $37^\circ\text{C}$  in round bottomed 96 well plates (Nunc, Denmark). The cell free supernatants were collected and stored at  $-80^\circ\text{C}$  until used. Cytokines and chemokines in culture supernatants were measured by Th1/Th2/Th17

cytometric bead array kit (BD Biosciences) and flex sets for IL8, IL1 $\beta$ , IL12p70, CXCL9, CCL5, CXCL10, CCL2 (BD Biosciences) as per manufacturer's instructions. Samples were acquired on FACS Aria and analysed using BD FCAP Array (BD Biosciences). TGF $\beta$  (BD Biosciences) and IL23 (eBiosciences, CA, USA) were determined by ELISA as per manufacturer instructions.

### **3.7.2 Cytokine estimation in serum samples of GBC patients and HI**

Peripheral blood was collected from GBC patients and HI in vacutainers (BD biosciences). Blood was allowed to clot at 4<sup>0</sup>C overnight. Serum was collected in eppendorff tubes after centrifuging the clotted blood. Serum samples were stored at -80<sup>0</sup>C until used. Cytokines and chemokines in sera samples were measured by Th1/Th2/Th17 cytometric bead array, flex sets (BD Biosciences) and ELISA.

#### **Cytometric bead array**

The CBA technique utilizes microparticles or beads labelled with discrete fluorescence intensity. The maximum emission of capture beads is at 650 nm on RED parameter. Cytokine specific capture antibody is covalently attached to beads. The captured cytokines are detected using specific antibodies with phycoerythrin (PE) fluorochrome which emits at 585 nm on yellow parameter. The intensity of fluorescence of yellow parameter is proportional to the amount of cytokines present in test samples. Cytokines were determined in the test samples according to the manufacturer instructions. Briefly test samples (50 $\mu$ l) and PE detection antibody were incubated with capture bead reagent for 3 h in the dark at room temperature. All unbound antibodies were washed (1.0 ml wash buffer), re-suspended in 300 $\mu$ l before acquisition on BD FACS Aria cytometer (BD Bioscience, San Jose, CA, USA). All cytokines exhibited single, well separated peaks. The individual cytokine standard curves (range 20–5000 pg/ml) were run in each assay. The data was presented as pg/ml.

### Enzyme Linked Immunosorbent Assay

ELISA was performed as per the instructions in commercially available kits. Briefly 100µl capture antibody (with required dilution in coating buffer) specific for cytokine (TGBβ / IL23 / VEGF) was coated in flat bottom 96 well plates (Maxisorp, Nunc, Germany) for overnight at 4°C. After three times washing with wash buffer (0.01M phosphate buffered saline + 0.05% Tween 20; 300µl) the wells were coated with assay diluent (PBS + 10% bovine serum albumin or FCS; 200µl) for 1 h at RT. After washing with wash buffer, serially diluted recombinant cytokine (100µl) was added to the wells. The standard and serum/supernatant samples (100µl) were incubated for 2 h at RT. Unbound proteins were removed by washing (3-5 times) with wash buffer. The bound cytokines were determined by detection antibody (100µl with required dilution) labelled with biotin. The wells were washed (5-7 times). The ELISA was developed using HRP tagged streptavidin and chromogenic substrate for 30 min in dark (100µl). The reaction was terminated using 2N H<sub>2</sub>SO<sub>4</sub> (50µl). Optical density was measured at 450nm on ELISA plate reader. The concentrations of cytokines in the supernatants were calculated by extrapolating the OD values of unknown samples on calibration curve of standards. The data was expressed as pg/ml.

### 3.8 Real time Polymerase chain reaction (RT-PCR)

#### 3.8.1 Extraction of RNA

PBMCs isolated from GBC patients and HI were stored at -80°C in TRIzol (Invitrogen Life-Technologies, N.Y.) in the ratio of 1x10<sup>6</sup> cells per 100µl TRIzol solution until further use. During RNA extraction, chloroform was added in 1: 5 ratio of chloroform : TRIzol (eg. 20µl chloroform in 100 µlTRIzol). The mixture was vigorously vortexed and centrifuged at 10,000 rpm for 15 min at 4°C. The aqueous phase was collected in separate tube and treated with chilled Isopropyl alcohol (Qualigens, India) equivalent to half the volume of TRIzol. After mixing gently, the precipitated RNA was centrifuged for 10 min at 10,000 rpm at 4°C.

The pelleted RNA was washed with 75% ethanol (10,000 rpm for 5 min at 4<sup>0</sup>C). The pellet was air dried and dissolved in appropriate volume of DEPC (Diethyl Pyrocarbonate; Sigma, USA) treated water. Optical density (O.D.) readings were taken for quantitation of RNA by NanoDrop spectrophotometer (Thermo Scientific, DE). The RNA was run on a 1.5% agarose gel containing ethidium bromide to confirm its purity and integrity.

### 3.8.2 Complementary DNA (cDNA) synthesis by reverse transcription

Total RNA isolated from PBMCs was used for first strand cDNA synthesis using oligo dT primers (Invitrogen Life-Technologies, N.Y.). 1- 5µg of RNA (10µl volume with DEPC treated water) was reverse transcribed using 1µl of oligo dT and 1µl (10 mM) of dNTP. The mixture was heated at 65<sup>0</sup>C for 5 min and then chilled on ice for 10 min. The mixture for reverse transcriptase containing the components given below was prepared and was added to the previously made RNA-primer mixture.

Table 3.6 Composition of cDNA synthesis PCR reaction

<i>Component</i>	<i>Volume (µl)</i>
5 X first strand buffer	4
0.1M DTT	2
RNAse out inhibitor (40U/µl)	1
MMLV reverse transcriptase enzyme (200U/µl)	1

This total mixture was heated at 37<sup>0</sup>C for 52 min followed by 70<sup>0</sup>C for 15 min in PTC-100TM Programmable Thermal Controller (MJ Research Inc.). The final cDNA volume was 20µl. The reverse transcriptase enzyme used was Murine Moloney Leukemia Virus (MMLV) reverse transcriptase enzyme (Invitrogen Life-Technologies, N.Y.; 200U/µl).

### 3.8.3 Real Time PCR

Quantitative RT-PCR for transcription factors (Foxp3 and RORc) and cytokines (IL6 and TGFβ) was performed using Assays-on-Demand Gene Expression probes (Applied Biosystems). RT-PCR reaction mixture was prepared as follows:

Table 3.7 Composition of real time PCR reaction

<i>Component</i>	<i>Volume (μl)</i>
DEPC water	2.5
Primer probe mixture	0.25
PCR Master-mix	0.25
cDNA (10ng)	2.0

Samples were analysed using QuantStudio™ 12K Flex Real-Time PCR System (Thermo Fisher Scientific). Gene Expression probes for RORC (Hs01076112\_m1), Foxp3 (Hs01085834\_m1), IL6 (Hs00985639\_m1) and TGFβ (Hs00234244\_m1) were purchased from Applied Biosystems. Gene expression was normalized using housekeeping gene β actin (Hs99999903\_m1) (Applied Biosystems). Relative mRNA expression of target genes was calculated as  $2^{(Ct \text{ control RNA} - Ct \text{ test RNA})}$ . The relative mRNA expression of target genes (IL6, IL23, RORc and Foxp3) in PBMCs of GBC patients was compared with HI.

### 3.9 Regulatory T cells suppression assay

Tregs (CD4<sup>+</sup>CD25<sup>+</sup>) were isolated from PBMCs using BD IMag regulatory T lymphocyte separation set-DM (BD Biosciences). Briefly CD4<sup>+</sup> T cells were negatively selected from PBMCs followed by positive selection of CD25<sup>+</sup> T cells. CD4<sup>+</sup>CD25<sup>-</sup> T cells were used as responder T cells (Tres) and labelled with carboxyfluorescein succinimidyl ester (CFSE; 5μM) (CellTrace proliferation kit, Life technologies). Briefly, 1-5 x 10<sup>6</sup> cells suspended in PBS + 5% FCS were incubated with 5μM CFSE for 10 min at RT in dark. After incubation

cells were washed thrice with PBS + 5% FCS. Labelled Tres cells ( $1 \times 10^4$ ) were co-cultured with Tregs for 5 days at different ratios (Tres: Treg = 1:2, 1:1, 1:0.5, 1:0) in round bottom 96 well plate. Co-cultures were stimulated with anti-CD3/anti-CD28 coated beads (1bead: 1cell) (Treg suppression inspector, Miltenyi biotech). CFSE labelled Tres cells cultured without Treg cells in the presence of anti-CD3/anti-CD28 coated beads were kept as control. Cells were acquired on FACS Aria and analysed by FlowJo software. The stimulation of Tres cells was analysed by calculating the number of peaks representing generation of divided cells. The undivided cells having peak with high CFSE intensity were considered as mother population. The suppressive effect of Treg cells on Tres cells was determined by decrease in the number of peaks. The data was presented as division index calculated by the software using percentage of cells in each generation and number of peaks.

### 3.10 Cell migration assay

#### 3.10.1 Migration of $T\gamma\delta 17$ cells

Migration of  $T\gamma\delta 17$  cells was studied by trans-well assay using Millicell cell-culture inserts with pore size  $8.0 \mu\text{m}$  (Merck Millipore, MA, USA). OCUG-1 cells ( $5 \times 10^4$ ), cultured in 24 well plate were washed with plain medium and  $600 \mu\text{l}$  serum-free Williams' E medium was added to the lower chamber. In some experiments rhCXCL9 ( $100 \text{ ng/ml}$ ; PeproTech, NJ, USA) or tumor supernatants of gallbladder tumor tissue were added to the lower chamber. Isolated  $T\gamma\delta 17$  cells ( $5 \times 10^4/100 \mu\text{l}$  medium) were added onto the trans-well inserts.  $T\gamma\delta 17$  cells cultured with medium alone were used as control. Migrated cells from lower chamber were counted using hemocytometer after 7 h. For blocking experiments,  $T\gamma\delta 17$  cells were incubated with anti-CXCR3 antibody ( $10 \mu\text{g/ml}$ ; R&D Systems, MN, USA), 30 min before trans-well co-culture. Migration of  $T\gamma\delta 17$  cells was compared with control wells where  $T\gamma\delta 17$  cells were cultured with medium alone.

### 3.10.2 Migration of $\gamma\delta$ T cells

$\gamma\delta$ T cells were isolated from peripheral blood of HI. Purified  $\gamma\delta$ T cells ( $1 \times 10^5$ ) were cultured to the upper chamber of Millicell cell-culture inserts with pore size  $8.0 \mu\text{m}$  (Merck Millipore, MA, USA). OCU-1 cells ( $1 \times 10^5$ ) were cultured in 24 well plates (lower chamber of trans-well). Cells were washed and  $600 \mu\text{l}$  serum-free Williams' E medium was added to the lower chamber. In some experiments tumor supernatants were added to the lower chamber. Migrated  $\gamma\delta$ T cells to the lower chamber were collected and counted using hemocytometer after 7 h. For blocking experiments,  $\gamma\delta$ T cells were incubated with anti-CXCR3 antibody ( $10 \mu\text{g/ml}$ ; R&D Systems, MN, USA), 30 min before trans-well co-culture. Migration of  $\gamma\delta$ T cells was compared with control wells where T $\gamma\delta$ 17 cells were cultured with medium alone

### 3.11 Estimation of angiogenesis factors

T $\gamma\delta$ 17 cells ( $5 \times 10^4$ ) were cultured in serum-free RPMI medium for 24 h in the presence of anti-CD3/anti-CD28 coated beads. Cell-free supernatant of T $\gamma\delta$ 17 was collected and added to OCU-1 cells ( $2 \times 10^4$  cells/well) cultured in 96 well plate. Neutralizing anti-IL17 antibody ( $10 \mu\text{g/ml}$ ; R&D Systems, MN, USA) was added to some wells. OCU-1 cells cultured with medium alone were used as control. After 48 h, supernatants were collected and analyzed for VEGF by ELISA (R&D systems, MN, USA) or for presence of angiogenesis related proteins by human proteome profiler angiogenesis antibody array (R&D systems, MN, USA) as per manufacturer's instructions.

#### 3.11.1 Angiogenesis Array

The cell free supernatants collected from above experiment were diluted ( $1 \text{ml}$  supernatant +  $500 \mu\text{l}$  array buffer provided in the kit) and mixed with a  $15 \mu\text{l}$  of reconstituted cocktail of biotinylated detection antibodies specific for angiogenesis related proteins. The nitrocellulose membranes coated with array of antibodies (spotted in duplicate with capture antibodies

specific for angiogenesis related proteins) were dipped in 2ml blocking buffer for 1 h on rocking platform. The mixture of supernatant and diluted antibodies was incubated with the nitrocellulose membranes overnight at 4°C with intermittent shaking. Membranes were washed three times on rocking platform shaker to remove unbound material followed by incubation with 2ml HRP-conjugated streptavidin for 30min at room temperature. After washing the membranes, chemiluminescence was used for signal detection using x-ray film with exposure of 10min. The signal produced was proportional to the amount of bound analyte. The data was evaluated using Image J 1.48V software (NIH, USA) and expressed as mean pixel density. The mean pixel density of angiogenesis related factors produced by OCUG-1 cells in presence of T $\gamma$  $\delta$ 17 supernatant was compared with OCUG-1 cells cultured with medium alone.

### 3.11.2 VEGF ELISA

The cell free supernatants collected from above experiment were analyzed for the presence of VEGF using VEGF ELISA as per the manufacturer's instructions. Briefly, the capture antibody was diluted to working concentration in PBS (137 mM NaCl, 2.7 mM KCl, 8.1 mM Na<sub>2</sub>HPO<sub>4</sub>, 1.5 mM KH<sub>2</sub>PO<sub>4</sub>, pH 7.2-7.4). 100 $\mu$ l capture antibody specific for VEGF was coated in flat bottom 96 well plates (Maxisorp, Nunc, Germany) and incubated overnight at room temperature. The wells were washed three times with 300 $\mu$ l wash buffer (PBS + 0.05% Tween 20). The wells were coated with reagent diluent (1% BSA in PBS) for 1 h at room temperature. After washing with wash buffer, serially diluted recombinant VEGF or cell-free supernatants (100 $\mu$ l) was added to the wells. The standard and supernatant samples were incubated for 2 h at room temperature. Unbound proteins were removed by washing (3-5 times) with wash buffer. The VEGF present in the wells was determined by detection antibody labelled with biotin (100 $\mu$ l with required dilution prepared in reagent diluent). The wells were washed to remove unbound detection antibody (3 times). HRP tagged streptavidin

(100µl prepared in reagent diluent) was added to well and incubated for 20min at room temperature. The ELISA was developed using chromogenic substrate (100µl per well) for 30 min in dark. The reaction was terminated using 2N H<sub>2</sub>SO<sub>4</sub> (50µl). Optical density was measured at 450nm on ELISA plate reader. The concentrations of cytokines in the supernatants were calculated by extrapolating the OD values of unknown samples on calibration curve of standards. The data was expressed as pg/ml.

### 3.12 Chorioallantoic membrane (CAM) assay

Fertilized chicken eggs (Central Poultry Development Organization, Goregaon, Mumbai) were incubated in humidified incubator at 37<sup>0</sup>C. On embryonic day 5, the eggs were screened for presence of embryo by exposing against torch. A small window was made in the shell and 200µl medium/ Tγδ17 supernatant/ rhIL17 (100ng/ml, R&D systems, MN, USA) was added onto the CAM of growing embryo. In some eggs, Tγδ17 supernatant pre-incubated with neutralizing anti-IL17 antibody was added. The window was sealed using parafilm (Sigma Aldrich, USA) and the eggs were incubated in humidified incubator at 37<sup>0</sup>C. After 48 h, eggs were cracked open and embryos were carefully transferred to 100mm petri dish and images were captured. CAM was cut and transferred to a glass slide to observe under the microscope. Angiogenesis was quantitatively evaluated by scoring number of branching points in control and treated CAMs.

### 3.13 Immunofluorescence staining

To study the expression of IL17R on OCUg-1 and NOZ cells, OCUg-1 and NOZ cells were cultured in glass bottom plates for 48 h with seeding density of 2x10<sup>4</sup>. Cells were washed with PBS and fixed with 4% paraformaldehyde at 4<sup>0</sup>C for 15-20 min. Bovine serum albumin (5% prepared in PBS; Sigma Aldrich, USA) was used for blocking at room temperature for 1 h. Primary antibody specific for IL17R (1µg/ml, R&D Biosystems) was incubated overnight at 4<sup>0</sup>C in humid chamber. Cells were washed three times with PBS. Secondary antibody

labelled with FITC (1: 200 dilution; Sigma, USA) was incubated for 2 h in humid chamber at room temperature. Cells were washed for three times with PBS and counterstained with DAPI (Sigma, USA) for 2min. Cells were maintained in PBS and images were acquired using Leica STED super resolution microscope (Leica Microsystems, Germany). The images were analysed by Image J1.48V software (NIH, USA).

### **3.14 Effect of IL17 on VEGF production in gallbladder cancer cell lines**

To study the proangiogenic effect of rhIL17 on gallbladder tumor cells, OCUG-1 and NOZ cells were cultured in presence or absence of rhIL17 and levels of VEGF were measured in the supernatant by ELISA. Briefly, OCUG-1 and NOZ cells ( $2-3 \times 10^5$ ) were cultured in 6 well plate in Williams' E medium supplemented with 10% FCS for 48 h. The cells were seeded to attain 80% confluency in 48 h. The cells were washed gently with plain Williams' E to remove FCS. Plain medium with or without rhIL17 (50ng/ml or 100ng/ml) was added to the wells. Cells cultured with plain medium were considered as control. After 48 h, supernatant was collected and levels of VEGF were measured by ELISA (R&D systems, USA) as described in 3.11.2. The effect of rhIL17 on VEGF production in cell lines was analysed by comparing with the control wells where cells were cultured with medium alone.

### **3.15 Wound healing assay**

GBC cell lines were cultured in 6 well plate in complete Williams' E medium. When OCUG-1 and NOZ cell lines formed monolayer with 90% confluency the spent medium was removed and cells were washed twice with plain Williams' E medium. The cells were treated with Mitomycin C (10 $\mu$ g/ml; Sigma Aldrich, USA) in plain medium for 2 h at 37°C with 5% CO<sub>2</sub>. Cells were gently washed two times with plain medium to remove traces of Mitomycin C. Three scratches were made precisely with the help of T-10 micro tips. The scratched cells were removed further by rinsing the wells with plain Williams' E medium. rhIL17 (50ng/ml, 100ng/ml) was added in plain Williams' E medium to the respective wells. Cells with plain

Williams' E medium were used as control. The cell migration was monitored for 21 h using time lapse inverted microscope (Carl Zeiss, Germany). The images were acquired with interval of every 1 h. Images were analysed using Image J1.48V software (NIH, USA). The effect of IL17 on migration of GBC cells was measured by comparing the percent wound closure of cells with the control. The percent wound closure was calculated by the formula

$$\text{Percent (\% ) wound closure} = \frac{\text{Area of wound at 0 h} \times 100}{\text{Area of wound at 21 h}}$$

### 3.16 Matrigel invasion assay

To study the effect of rhIL17 on invasion potential of gallbladder tumor cells, OCUg-1 and NOZ cells were treated with rhIL17 and analysed by matrigel invasion assay. In a 24 well trans-well assay the cell culture inserts (8.0µm pore size, BD Falcon, USA), were coated with the matrigel (20µl of Matrigel [1mg/ml stock] diluted in 140µl of plain Williams' E; BD Biosciences, San Jose, CA) for 2 h at 37°C. The matrigel was maintained at 4°C during coating process. The inserts were washed with plain medium to remove unpolymerised matrigel. OCUg-1 (5x10<sup>4</sup>) and NOZ (3x10<sup>4</sup>) cells were suspended in 200µl plain Williams' E medium containing IL17 (50ng/ml or 100ng/ml). The untreated cells were considered as control. The cells were added to the inserts of trans-well and 600µl of Williams' E medium with 10% FCS was added to the lower chamber. OCUg-1 cells were incubated for 48 h and NOZ cells were incubated for 24 h. The incubation periods were decided by prior standardization experiments. After incubation, the inserts were lifted from the plate and washed by gentle dipping in PBS. The cells were fixed in absolute methanol for 5-10sec followed by washing with PBS for 30sec. The cells were stained by 1% crystal violet (prepared in 70% methanol) for 5min and excess stain was removed by dipping the trans-well in PBS. Cells remained in the upper chamber (unmigrated cells) were removed using cotton swabs. The membrane was cut from inserts and carefully transferred to the glass slide with

cells adhered to the membrane facing upward. The cells were observed using 10X objectives of microscope (Carl Zeiss, Germany). Minimum 10 microscopic fields were photographed and the migrated cells were counted. The fold increase in invasion upon rhIL17 treatment was calculated by normalizing the migrated number of cells with the control.

### 3.17 Survival analysis

The survival analysis was performed using GraphPad Prism software (Prism Software, Lake Forest, CA). The clinical significance of  $T\gamma\delta 17$ , Th17, Tc17, and Treg,  $\gamma\delta^+IFN\gamma^+$  cells and serum IL17 and serum IFN $\gamma$  levels was analysed by comparing with survival time of GBC patients. The survival time of patients was determined from date of diagnosis and date of death. The data was censored for patients alive or lost to follow up at the time of analysis. As there was no clinically defined cut off points for Th17, Tc17,  $T\gamma\delta 17$ , Treg cells, the high-expressing or low-expressing groups of GBC patients were defined based on mean values of expression of these lymphocytes (4.7 for  $T\gamma\delta 17$ , 1.8 for Th17, 1.8 for Tc17 and 3.2 for Treg). Overall patient survival was calculated by Kaplan-Meier curve and compared by Log-rank test.

### 3.18 Statistical analysis

Statistical analysis of data was performed using GraphPad Prism software (Prism Software, Lake Forest, CA). Statistical significances were calculated by two-tailed student's t-test or Mann-Whitney test.  $P < 0.05$  was considered statistically significant. The data was presented as mean  $\pm$  standard error.

## **Chapter 4**

# **Analysis of immune scenario in peripheral blood of GBC patients**

## 4.1 Introduction

Tumor infiltrating immune cells and tumor cells are in continuous crosstalk with each other and significantly contribute in shaping malignant progression of tumor [54, 55]. The studies in cancer patients have shown that modulation of immune response in tumor environment is also reflected in peripheral blood [258, 302-304]. Systemic levels of T cells are reported as a potential prognostic marker and are associated with survival of patients with melanoma, breast cancer, gastric cancer, ovarian cancer, etc. [305-307]. Circulating frequencies of lymphocytes can also serve as a measure of effectiveness of therapeutic treatment of patients [302, 308]. Therefore, understanding the immune scenario in peripheral blood of cancer patients is important for successful therapeutic interventions. The significance of immune response regulating development of gallbladder cancer is not well understood. Knowledge of prognostic or predictive markers could be of great importance for the choice of appropriate individual treatment for GBC patients. The earlier studies in GBC patients have shown the prevalence of CD4 and CD8 T cells in tumor tissue [309, 310]. However, the comprehensive analysis of immune cell types, their response to antigenic stimulus and secretion of effector cytokines by adaptive and innate immune cells in GBC patients is not investigated.

In the present prospective study we used flowcytometry based immunophenotyping of GBC patients to delineate the importance of adaptive and innate lymphocytes. The data highlights functional parameters of peripheral blood lymphocytes of GBC patients in comparison to healthy individuals.

## 4.2 Results

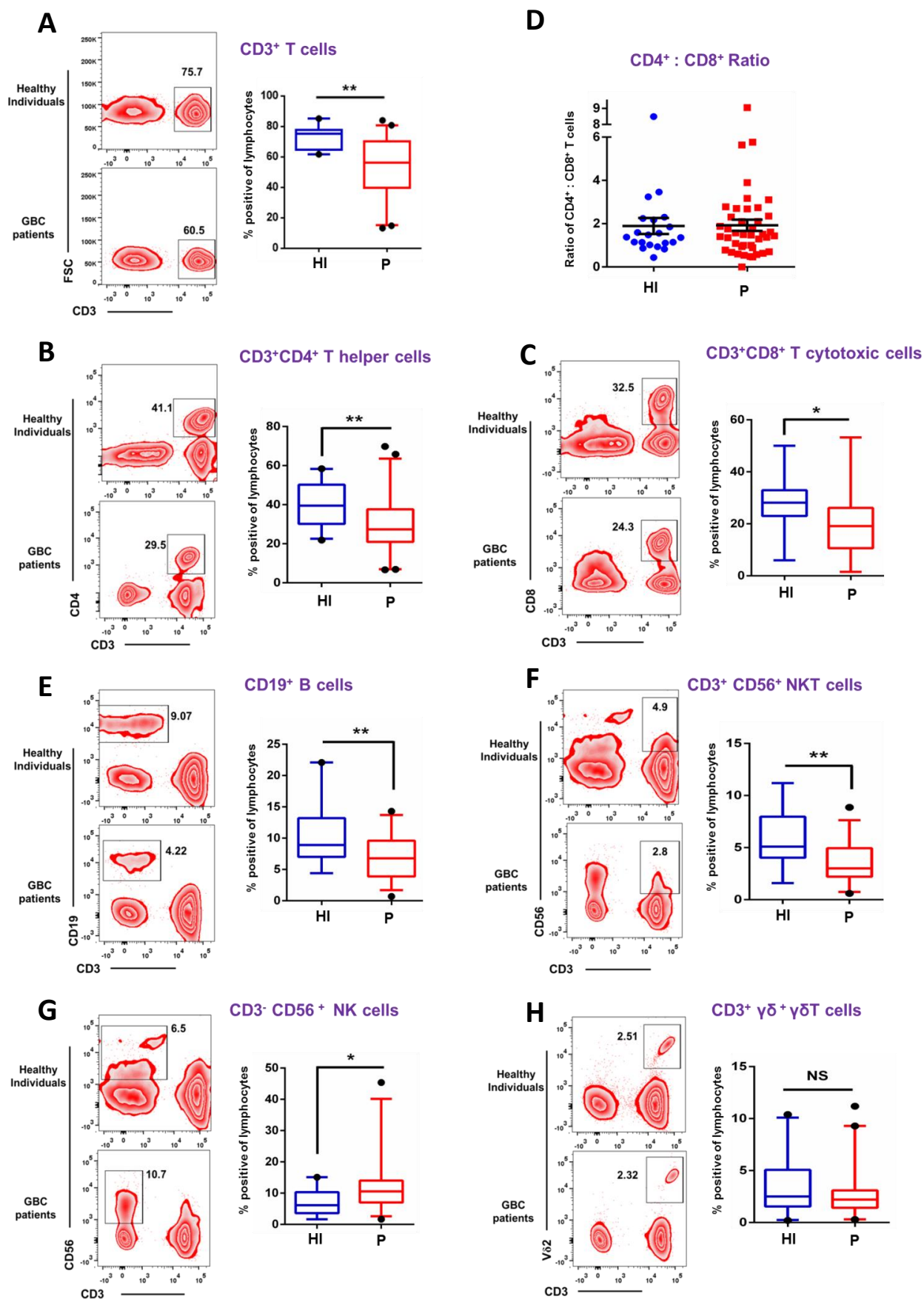
### 4.2.1 Cells contributing to adaptive immunity are decreased in peripheral blood of GBC patients

In order to study the innate and adaptive immune cells in GBC patients, peripheral blood mononuclear cells (PBMCs) were isolated from GBC patients (n=52) and healthy individuals (HI; n=30). For multicolour flow cytometry, PBMCs were surface stained for CD3<sup>+</sup>, CD4<sup>+</sup>, CD8<sup>+</sup>, CD19<sup>+</sup>, and CD56<sup>+</sup> cells. Figure 4.1 describes gating strategy used to analyse T cells (CD3<sup>+</sup>), T-helper cells (CD3<sup>+</sup>CD4<sup>+</sup>), T-cytotoxic cells (CD3<sup>+</sup>CD8<sup>+</sup>), B cells (CD19<sup>+</sup>), natural killer cells (CD3<sup>-</sup>CD56<sup>+</sup>), natural killer T (CD3<sup>+</sup>CD56<sup>+</sup>) cells and  $\gamma\delta$ T cells (CD3<sup>+</sup>V $\delta$ <sub>2</sub>TCR<sup>+</sup>) cells.

The data showed that CD3<sup>+</sup> T lymphocytes were decreased in peripheral blood of GBC patients compared to HI (Figure 4.1 A). The subtype analysis of T cells revealed that CD3<sup>+</sup>CD4<sup>+</sup> helper T cells and CD3<sup>+</sup>CD8<sup>+</sup> cytotoxic T cells were significantly low in peripheral blood of GBC patients compared to HI (Figure 4.1 B and C). However, the ratio of CD4 : CD8 T cells was comparable in GBC patients and HI (Figure 4.1 D). CD19<sup>+</sup> B cells and NKT cells showed marked decrease in percentage compared to HI (Figure 4.1 E and F). In contrast, CD3<sup>-</sup>CD56<sup>+</sup> NK cells were elevated and  $\gamma\delta$ T cells were unaltered in GBC patients compared to HI (Figure 4.1 G and H). The data revealed that decrease in the percentages of lymphocytes contributing to adaptive immunity suggesting inadequate immune response in GBC patients to maintain the immune-surveillance.

### 4.2.2 PBMCs from GBC patients show poor lymphocyte proliferative response

Antigen recognition leads to activation and clonal propagation of lymphocytes. To understand the proliferative response of lymphocytes, the PBMCs from GBC patients (n=26) and HI (n=19) were stimulated in separate sets with anti CD3 mAb (1 $\mu$ g/well) and



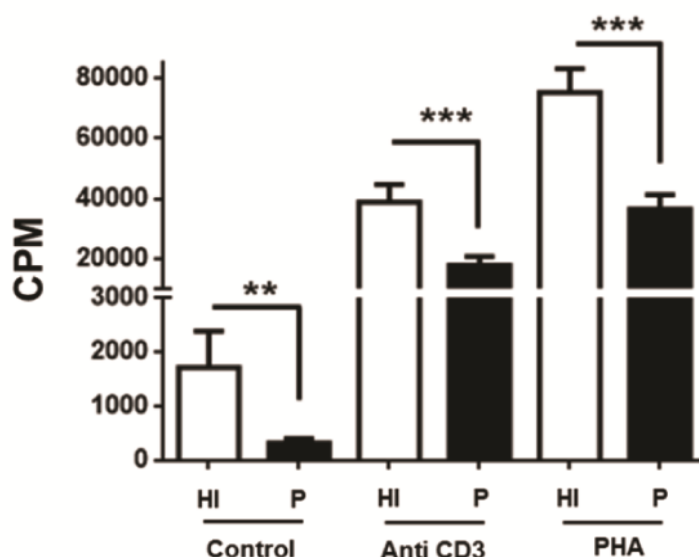
**Figure 4.1 : Immunophenotyping of peripheral blood lymphocytes of GBC patients.** PBMCs from GBC patients (n=52) and HI (n=30) were analysed by flowcytometry for percent levels of lymphocytes in peripheral blood of GBC patients compared to HI. (A-C) A summarized data for the percent levels of  $CD3^+$  (A),  $CD3^+CD4^+$  (B),  $CD3^+CD8^+$  (C) is presented as box whisker plots. Representative figures of flowcytometry analysis are shown as zebra plots. (D) Ratio of  $CD3^+CD4^+ : CD3^+CD8^+$  T cells in GBC patients and HI is presented as dot plot analysis. (E-H) Representative flowcytometry figures and box whisker plots showing expression of B cells (E), NKT cells (F), NK cells (G) and  $\gamma\delta T$  cells (H) in peripheral blood of GBC patients in comparison to HI. The box plots show the median (middle line), 5<sup>th</sup> and 95<sup>th</sup> percentiles (box), the extreme values (whiskers) and the outliers (dark circles). Data are shown as mean  $\pm$  SEM with \* $p < 0.05$  or \*\* $p < 0.01$ .

Phytohaemagglutinin (PHA; 1%) for 72 h. The proliferative responses were monitored by  $^3H$  Thymidine incorporation assay.

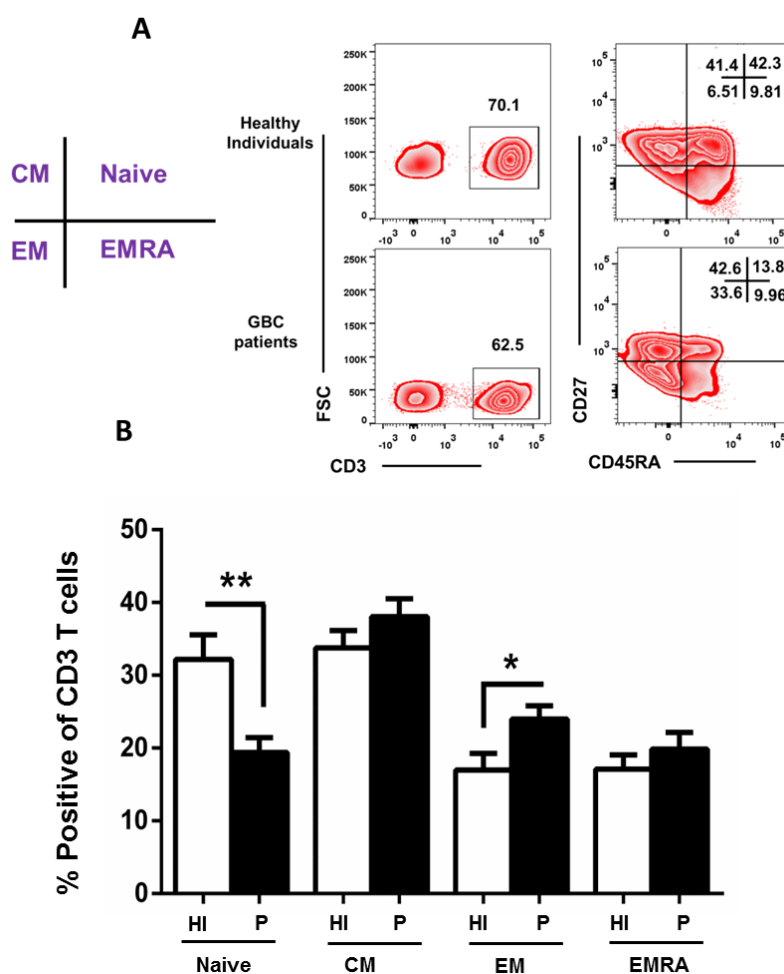
PBMCs from GBC patients showed decreased basal level proliferative potential in comparison to HI (Figure 4.2). Further, stimulation of PBMCs with anti-CD3 mAb, showed decreased proliferative response of lymphocytes from GBC patients compared to HI. Similar results were obtained when PHA was used to stimulate the PBMCs (Figure 4.2). The results indicate that PBMCs from GBC patients exhibit decreased proliferative responses to PHA (mitogen) and anti-CD3 mAb (TCR agonist) as compared to HI.

#### 4.2.3 T lymphocytes in peripheral blood of GBC patients exhibit effector memory phenotype

Activated T cells differentiate into memory phenotype and attain variety of effector functions. To study the memory phenotype of T cells, PBMCs from GBC patients (n=27) and HI (n=14) were analysed by flow cytometry for the surface expression of CD27 and CD45RA. Naïve T cells were defined as  $CD27^+CD45RA^+$  ( $T_{Naïve}$ ), central memory T cells as  $CD27^+CD45RA^-$  ( $T_{CM}$ ), effector memory T cells as  $CD27^-CD45RA^-$  ( $T_{EM}$ ) and terminally differentiated effector memory T cells as  $CD27^-CD45RA^+$  ( $T_{EMRA}$ ) (Figure 4.3 A). The data revealed that the percentages of naïve cells in total T lymphocytes were



**Figure 4.2 : Proliferative response of PBMCs from GBC patients to anti-CD3 and PHA.** PBMCs from GBC patients (n=26) and HI (n=19) were stimulated with anti-CD3 or PHA and proliferation was monitored by  $^3\text{H}$ -Thymidine incorporation assay. The data is shown as bar diagram presenting radiations counted as counts per minutes. Data are shown as mean  $\pm$  SEM with \*  $p < 0.05$ ; \*\*  $p < 0.01$ ; \*\*\*  $P < 0.001$ .



**Figure 4.3 : Memory phenotypes of T lymphocytes in GBC patients.** (A) Representative zebra plot showing expression of CD27 and CD45RA on T lymphocytes of GBC patients and HI. (B) Proportion of naïve and memory T cells in peripheral blood of GBC patients compared to HI are shown as bar diagram.

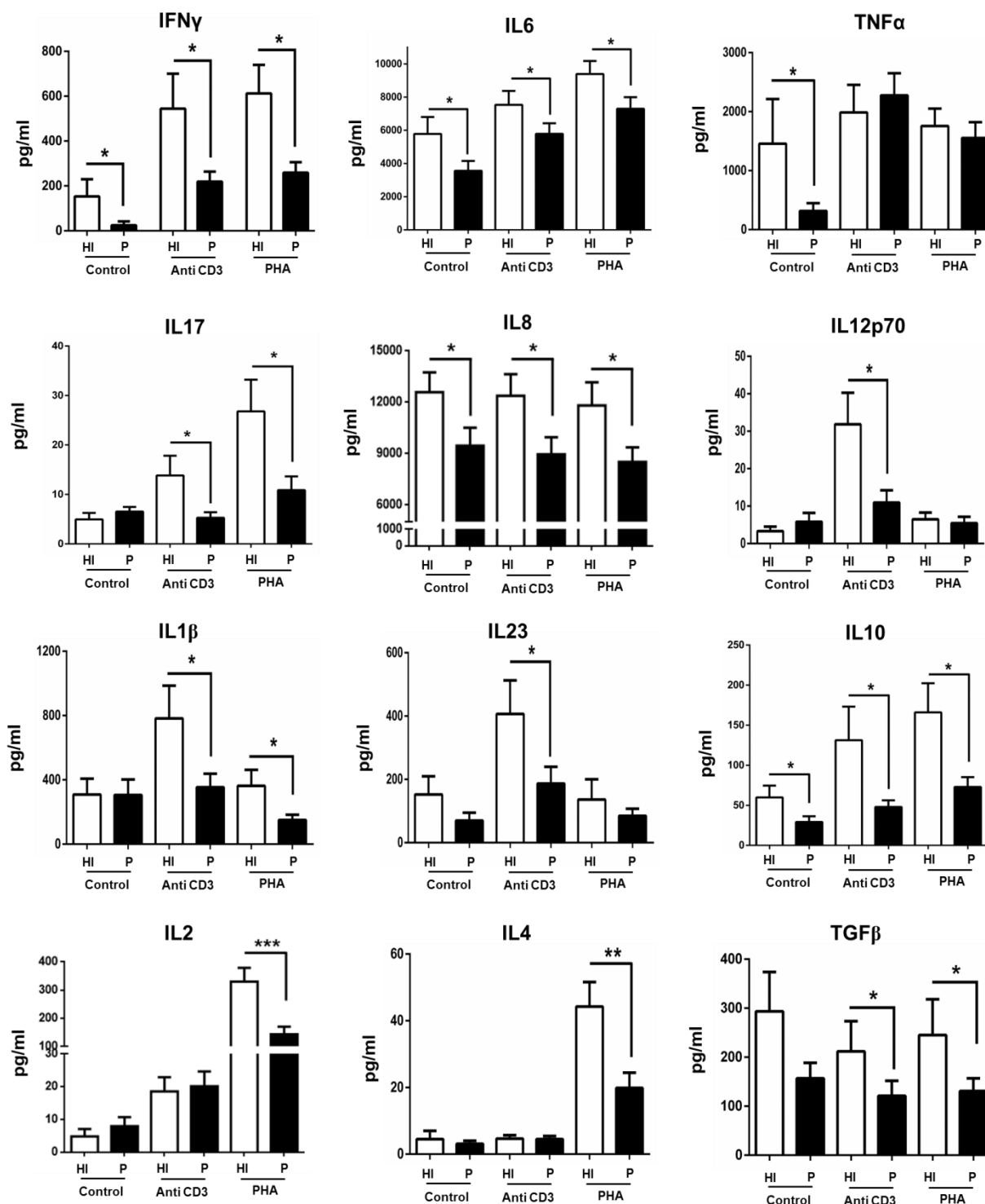
Data are shown as mean  $\pm$  SEM with \*  $p < 0.05$ ; \*\*  $p < 0.01$ .

significantly decreased in peripheral blood of GBC patients. However, T cells exhibiting effector memory phenotype were increased in GBC patients. The percentage of central memory and terminally differentiated effector memory (T<sub>EMRA</sub>) cells were unaltered in GBC patients compared to HI (Figure 4.3 B). The analysis of memory phenotypes indicates that the T lymphocytes may be functionally active in GBC patients.

#### 4.2.4 PBMCs of GBC patients secrete low levels of effector cytokines compared to HI

Activated lymphocytes secrete effector cytokines in response to the antigenic stimulation. To determine the cytokine profile of activated lymphocytes, PBMCs from GBC patients (n=42) and HI (n=21) were stimulated with anti-CD3 mAb and PHA. Cell free supernatants were collected after 24 h and analysed by cytometric bead array.

The PBMCs from GBC patients secreted decreased levels of IFN $\gamma$ , IL6, TNF $\alpha$ , IL8 and IL10 at baseline i.e. without any stimulation compared to HI (Figure 4.4). Upon stimulation with anti-CD3 mAb, PBMCs from GBC patients produced significantly low levels of IFN $\gamma$ , IL6, IL17, IL8, IL12p70, IL1 $\beta$ , IL23, IL10 and TGF $\beta$  whereas levels of IL2, IL4 and TNF $\alpha$  did not alter in comparison to HI. Similar results were observed in GBC patients upon stimulation with PHA that the levels of IFN $\gamma$ , IL6, IL17, IL8, IL1 $\beta$ , IL10, IL2p70, IL4 and TGF $\beta$  were decreased compared to HI (Figure 4.4). Overall, the poor production of effector cytokines by activated PBMCs from GBC patients, suggests that the immune response in GBC patients is defective.

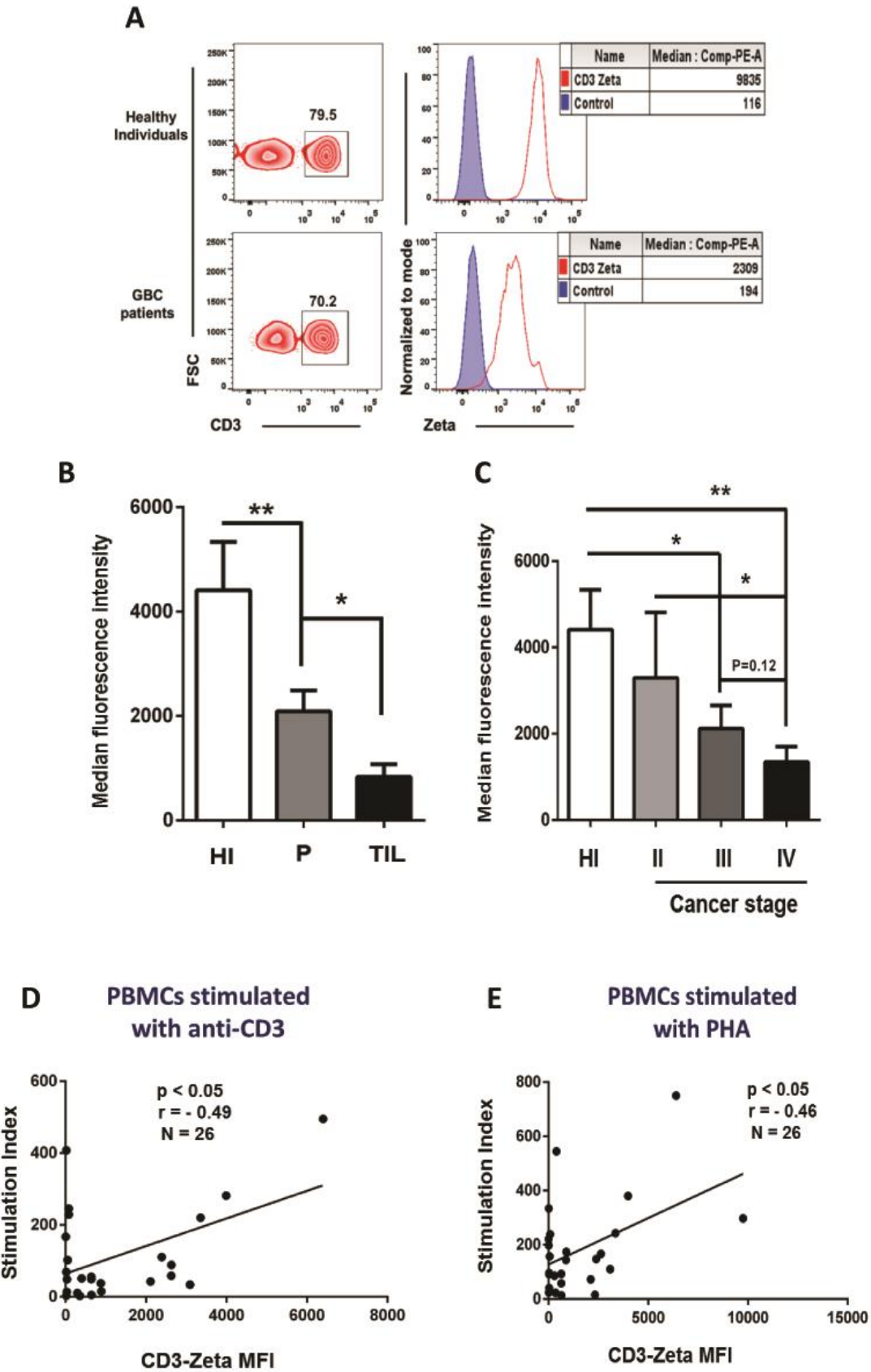


**Figure 4.4 : Cytokines secreted by activated PBMCs of GBC patients.** PBMCs from GBC patients and HI were stimulated with anti-CD3 or PHA and cell-free culture supernatants were collected after 24 hrs. The cytokines were estimated by cytometric bead array. The levels of secreted cytokines are presented as pg/ml. Data are shown as mean  $\pm$  SEM with \*  $p < 0.05$ ; \*\*  $p < 0.01$ .

#### 4.2.5 TCR $\zeta$ chain is downregulated in T lymphocytes of GBC patients

To understand the mechanism of poor effector functions of T lymphocytes, the defects in the T cell receptor (TCR) signalling were analysed. PBMCs from GBC patients (n=50) and HI (n=24) were analysed for expression of TCR  $\zeta$  chain by flow cytometry. It was observed that more than 90% of T lymphocytes from GBC patients expressed TCR  $\zeta$  chain as shown by percent positive expression. However, the median fluorescence intensity of TCR  $\zeta$  chain expression in T cells was significantly low in peripheral blood of GBC patients compared to HI (Figure 4.5 A and B). Investigation of TCR  $\zeta$  chain in tumor infiltrating lymphocytes (n=13) showed further decrease in the expression compared to peripheral blood of GBC patients and HI (Figure 4.5 B). In addition, the classification of GBC patients with clinical stage II (n=5), stage III (n=18) and stage IV (n=27) showed that the TCR  $\zeta$  chain expression in T lymphocytes inversely correlated with clinical stage of the patients (Figure 4.5 C). This suggests that the expression of TCR  $\zeta$  chain is downregulated in T lymphocytes of GBC patients.

Further, correlation analysis revealed that TCR  $\zeta$  chain expression positively correlated with proliferation of T lymphocytes (stimulation index) stimulated with anti-CD3 mAb or PHA (Figure 4.5 D and E). The data suggests that defective TCR mediated signalling may be responsible for poor activation and effector functions in T lymphocytes of GBC patients.



**Figure 4.5 : Expression of TCR  $\zeta$  chain in T lymphocytes of GBC patients.** (A) A representative zebra plot and histogram of expression of TCR  $\zeta$  chain in CD3<sup>+</sup> T lymphocytes of GBC patients and HI. Figures in the histogram indicate median fluorescence intensity (MFI) of TCR  $\zeta$  chain expression (empty histogram) and isocontrol (filled histogram). (B) Bar diagram shows summarised data of expression of TCR  $\zeta$  chain presented as MFI in GBC patients (n=50) and HI (n=24). (C) Expression of TCR  $\zeta$  chain in T lymphocytes of peripheral blood was analysed with clinical stages of GBC patients. (D) Correlation graph of expression of TCR  $\zeta$  chain in T lymphocytes with stimulation index of PBMCs stimulated with anti-CD3 mAb. (E) Correlation graph of Expression of TCR  $\zeta$  chain in T lymphocytes with stimulation index of PBMCs stimulated with PHA. “r” indicate coefficient of correlation and “N” indicate number of pairs in correlation. Data are shown as mean  $\pm$  SEM with \*  $p < 0.05$ ; \*\*  $p < 0.01$ .

### 4.3 Summary

The results described in this chapter revealed dysfunctions in immune response in peripheral blood of GBC patients. The lymphocytes contributing to adaptive immune response were decreased in PBMCs of GBC patients compared to HI. Although T lymphocytes belonging to effector memory phenotype were elevated in GBC patients, the proliferative response of T cells stimulated with mitogen or TCR agonist was decreased compared to HI. Moreover, the PBMCs from GBC patients produced decreased levels of effector cytokines upon stimulation in comparison to HI. The reason behind poor immunological response by PBMCs of GBC patients may be rooted in the downregulated expression of TCR  $\zeta$  chain involved in the signal transduction and T cell activation. Overall, the present data showed that the peripheral blood lymphocytes in GBC patients are dysfunctional.

## **Chapter 5**

**Understanding the  
functional dynamics of  
pro-inflammatory and  
anti-inflammatory T cells  
in peripheral blood and  
tumor microenvironment  
of GBC patients**

## 5.1 Introduction

Chronic inflammation is one of the important hallmark of cancer progression [121]. The tumor microenvironment selects the type of inflammatory reactions most favourable to tumor growth and progression [311]. It also subverts tumor antigen specific adaptive immune responses, and alters responses to chemotherapeutic agents [31]. Infiltration of lymphocytes is an integral part of tumor associated inflammation. Chronic inflammation activates tumor associated macrophages (TAMs), neutrophils (TANs), immunosuppressive cells (regulatory T cells, myeloid derived suppressor cells) which promote cancer progression. In contrast, signals that trigger acute inflammatory reactions often stimulate dendritic cells maturation and antigen presentation thereby trigger antitumor immunity [55]. The expression of various immune modulators and the abundance and activation state of different cell types in the tumor microenvironment dictate the balance of tumor-promoting inflammation and antitumor immunity. Thus it is necessary to study the type, functional orientation and dynamics of lymphocytes, cytokines and chemokines in inflammatory tumor environment.

GBC is an interesting model to understand such nexus of immune infiltrates and inflammation in tumor. GBC is predisposed with chronic inflammatory condition of cholelithiasis but the impact of immune infiltrates on inflammation and tumorigenic events remains largely unknown. Therefore, the efforts are needed to understand the tumor solicited inflammation present in GBC tumor microenvironment regulating the immune response.

The antitumor immune response is dysfunctional in GBC patients as demonstrated in chapter 4. In the present chapter, the dynamics of inflammatory (IL17 producing CD4, CD8 and  $\gamma\delta$ T cells) and immunosuppressive (Treg, MDSCs) lymphocytes in gallbladder tumor environment and peripheral blood of GBC patients were investigated.

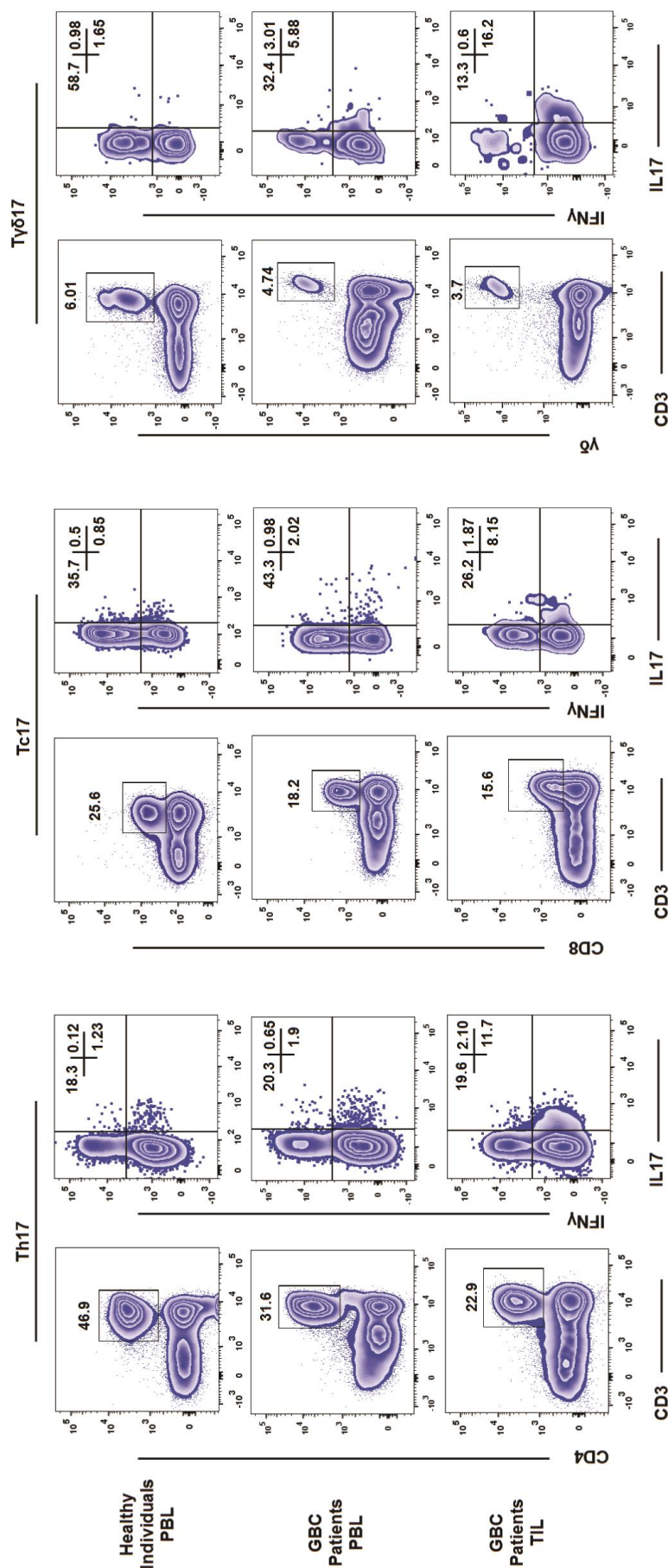
## 5.2 Results

### 5.2.1 IL17 producing CD4, CD8 and $\gamma\delta$ T cells are elevated in tumor environment and peripheral blood of GBC patients

In order to study the prevalence of circulating IL17 producing cells, peripheral blood mononuclear cells (PBMCs) were isolated from GBC patients (n=52) and healthy individuals (HI; n=30). To investigate the tumor infiltrating lymphocytes (TILs) the single cell suspension of tumor tissue (n=17) was prepared by enzyme digestion as discussed in materials and methods. Cells were stimulated with PMA and Ionomycin in the presence of Brefeldin A. T lymphocytes in the peripheral blood and TILs were analysed by staining PBMCs and single cell suspension of tumor tissue using fluorochrome labelled subset specific antibodies.

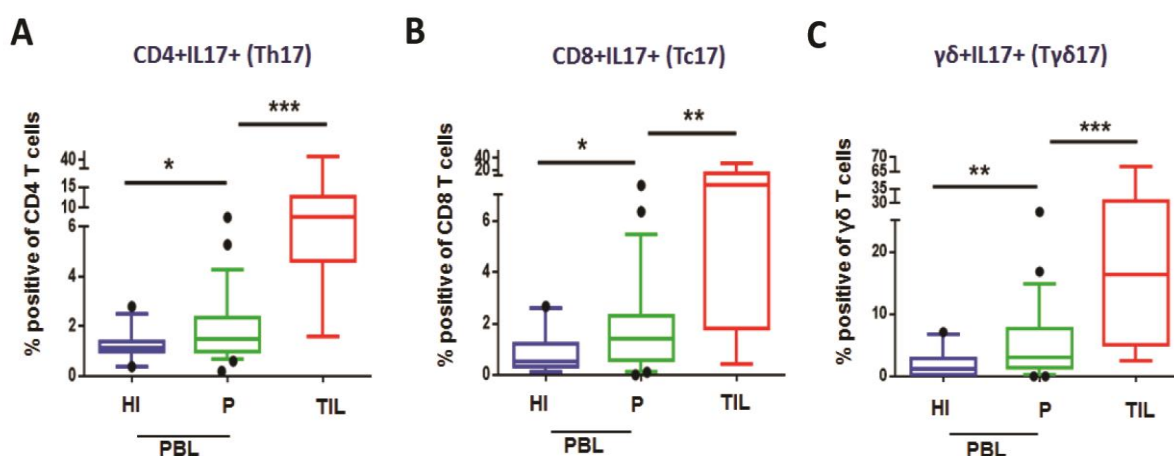
Figure 5.1 describes representative gating strategy to define Th17, Tc17, T $\gamma\delta$ 17 cells as CD4<sup>+</sup>IL17<sup>+</sup>, CD8<sup>+</sup>IL17<sup>+</sup> and  $\gamma\delta$ <sup>+</sup>IL17<sup>+</sup> cells. IL17 producing cells were gated on CD3<sup>+</sup>CD4<sup>+</sup>, CD3<sup>+</sup>CD8<sup>+</sup> and CD3<sup>+</sup>V $\delta$ 2-TCR<sup>+</sup> T cells respectively.

Th17 and Tc17 cells were significantly increased in PBMCs of GBC patients compared to HI (Figure 5.2 A and B). Interestingly, it was observed that IL17 producing  $\gamma\delta$ T cells (T $\gamma\delta$ 17) were also increased in PBMCs of GBC patients (Figure 5.2 C). A marked increase in the levels of these cells (Th17, Tc17 and T $\gamma\delta$ 17) was observed in tumor compartment compared to the peripheral blood of GBC patients (Figure 5.2 A, B and C). It was Interesting to note that the relative percentages of T $\gamma\delta$ 17 were higher compared to Th17 and Tc17 in TILs of GBC patients. Collectively, the data indicates that T $\gamma\delta$ 17 cells are emerging as an important phenotype in GBC patients.



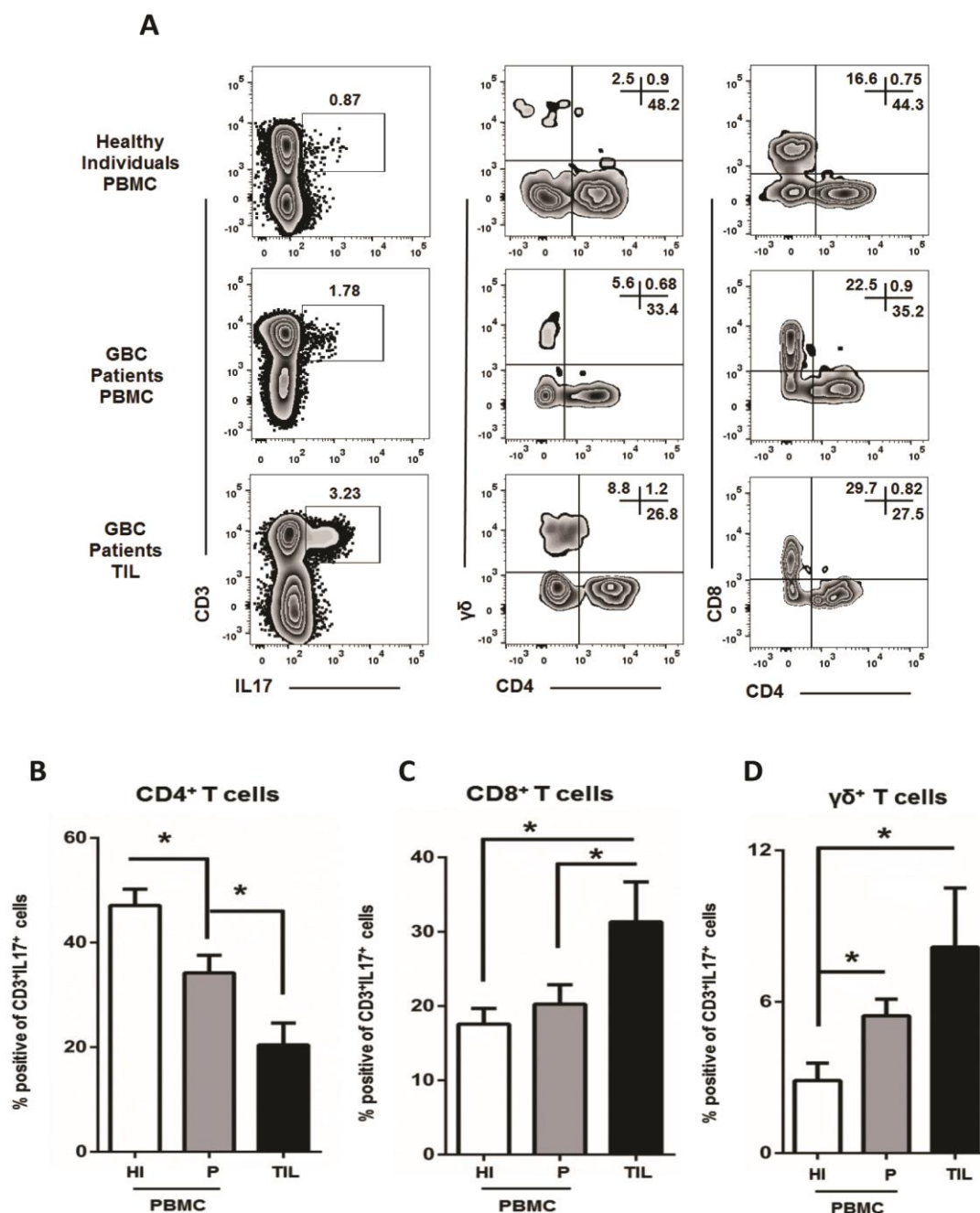
**Figure 5.1. Gating strategy to define IL17 producing cells in GBC patients and HI.** Representative zebra plot analysis of Th17 (left), Tc17 (middle) and Tγδ17 (right) cells from PBMCs (n=52) and TILs (n=17) of GBC patient and HI (n=30). PBMCs and TILs were stimulated with PMA and ionomycin in presence of brefeldin A followed by intracellular staining for IL17 and IFNγ. IL17 and IFNγ producing cells were gated on CD3<sup>+</sup>CD4<sup>+</sup>, CD3<sup>+</sup>CD8<sup>+</sup> and CD3<sup>+</sup>Vδ2TCR<sup>+</sup> population respectively. Numbers in the plot indicate percent positive cells.

To examine which T cell subset have higher propensity to produce IL17 in GBC patients, the data was analysed by another gating strategy.  $CD4^+$ ,  $CD8^+$  and  $V\delta 2TCR^+$  T cells from peripheral blood (n=24) and TILs (n=13) of GBC patients were analysed by gating on  $CD3^+IL17^+$  T cells (total IL17 producing cells) (Figure 5.3 A). It was observed that percentage of  $CD4^+$  cells within  $CD3^+IL17^+$  T cells were significantly decreased in peripheral blood and TILs of GBC patients compared to HI (Figure 5.3 B). In contrast,  $CD8^+$  T cells within  $CD3^+IL17^+$  T cells were increased in TILs of GBC patients (Figure 5.3 C). Next, it was observed that among total  $CD3^+IL17^+$  T cells, the levels of  $\gamma\delta$ T cells were significantly increased in peripheral blood and further elevated in TILs of GBC patients compared to HI (Figure 5.3 D). Thus, the data revealed that the potential of IL17 production by T cell subsets was different at different anatomical locations (peripheral blood and tumor environment) in GBC patients. The  $\gamma\delta$ T cells have higher propensity to produce IL17 compared to  $CD4^+$  T cells in tumor environment of GBC patients.



**Figure 5.2 : Prevalence of Th17, Tc17 and Tγδ17 cells in GBC patients.** (A-C) The levels of Th17, Tc17 and Tγδ17 cells were analysed in PBMCs (n=52) and TILs (n=17) of GBC patients and compared with HI (n=30). Summarised data in box whisker plots show percentages of Th17 (A), Tc17 (B) and Tγδ17 (C) in PBMCs and TILs of GBC patients compared with HI.

HI, healthy individuals; P, GBC patients; TIL, Tumor infiltrating lymphocytes. The box plots show median (middle line), 5<sup>th</sup> and 95<sup>th</sup> percentiles (box), extreme values (whiskers) and outliers (dark circles). Results are analysed by Mann-Whitney test and student's *t* test with \*(*p* < 0.05); \*\*(*p* < 0.01); \*\*\*(*p* < 0.001).

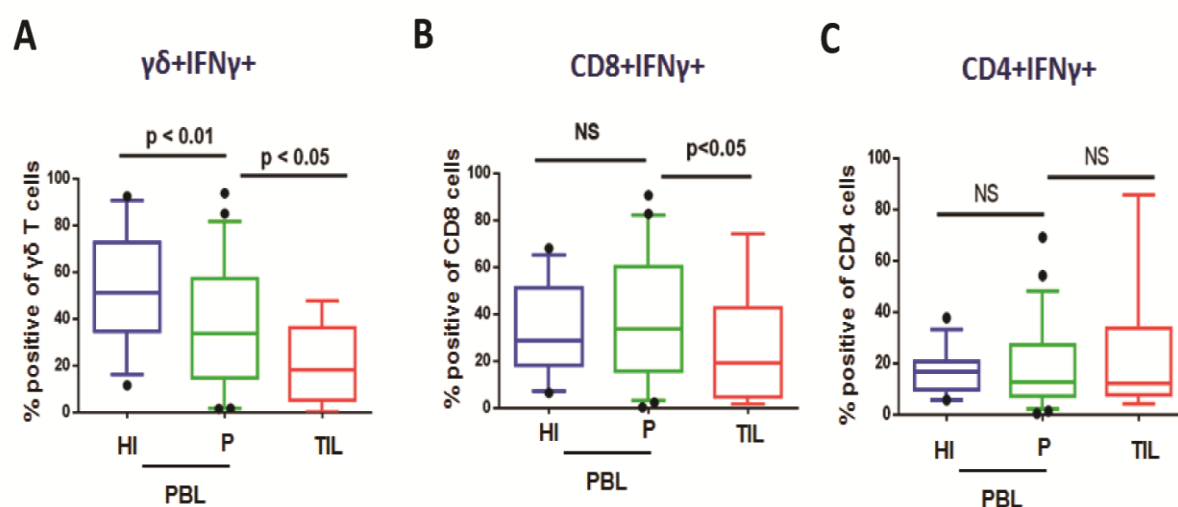


**Figure 5.3 : Propensity of IL17 production in subsets of CD3<sup>+</sup> T cells in GBC patients.** To study the proportion of IL17 produced by T cells subsets, CD4<sup>+</sup>, CD8<sup>+</sup> and γδT cells were gated on CD3<sup>+</sup>IL17<sup>+</sup> cells in peripheral blood (n=24) and TILs (n=13) of GBC patients and compared with HI (n=11). (A) A representative zebra plot analysis show gating strategy of CD4<sup>+</sup>, CD8<sup>+</sup> and γδT cells within CD3<sup>+</sup>IL17<sup>+</sup> population in GBC patients and HI. Numbers in the plot indicate percent positive cells. (B-D) A summarized data of CD4<sup>+</sup> T cells (B), CD8<sup>+</sup> T cells (C) and γδT cells (D) within CD3<sup>+</sup>IL17<sup>+</sup> population in GBC patients and HI. HI, healthy individuals; P, GBC patients; TIL, Tumor infiltrating lymphocytes; PBMCs, peripheral blood mononuclear cells. Data was analysed by Mann Whitney test and student's t test and presented as mean ± SEM with \*p<0.05.

### 5.2.2 IFN $\gamma$ producing $\gamma\delta$ and CD8 $^{+}$ T cells are decreased in tumor environment of GBC patients

IFN $\gamma$  producing T cells are reported to be tumoricidal and are associated with better prognosis of cancer patients [312]. To study the role of IFN $\gamma$  producing cells in GBC patients, PBMCs and single cells suspension of tumor tissue were stained for intracellular expression of IFN $\gamma$  after stimulation with PMA and Ionomycin in presence of Brefeldin A. IFN $\gamma$  producing CD4, CD8 and  $\gamma\delta$ T cells were defined as CD4 $^{+}$ IFN $\gamma^{+}$ , CD8 $^{+}$ IFN $\gamma^{+}$  and  $\gamma\delta^{+}$ IFN $\gamma^{+}$  respectively where IFN $\gamma^{+}$  cells were gated on CD3 $^{+}$ CD4 $^{+}$ , CD3 $^{+}$ CD8 $^{+}$  and CD3 $^{+}$ V $\delta$ 2-TCR $^{+}$  T cells respectively (as shown in Figure 5.1).

The data revealed that  $\gamma\delta^{+}$ IFN $\gamma^{+}$  cells were significantly decreased in TILs compared to PBMCs of GBC patients and HI (Figure 5.4 A). A significant decrease was also observed in



**Figure 5.4 : Frequency of IFN $\gamma$  producing cells in GBC patients.** IFN $\gamma$  producing cells were studied in PBMCs ( $n=52$ ) and TILs ( $n=17$ ) of GBC patients and compared with HI ( $n=30$ ). The cumulative data presented in box whisker plots show  $\gamma\delta^{+}$ IFN $\gamma^{+}$  (A), CD8 $^{+}$ IFN $\gamma^{+}$  (B) and CD4 $^{+}$ IFN $\gamma^{+}$  (C) cells in PBMCs and TILs of GBC patients compared with HI.

HI, healthy individuals; P, GBC patients; TIL, Tumor infiltrating lymphocytes. The box plots show median (middle line), 5<sup>th</sup> and 95<sup>th</sup> percentiles (box), extreme values (whiskers) and outliers (dark circles). Results are analysed by Mann-Whitney test and student's  $t$  test with  $*(p < 0.05)$ ;  $**(p < 0.01)$ .

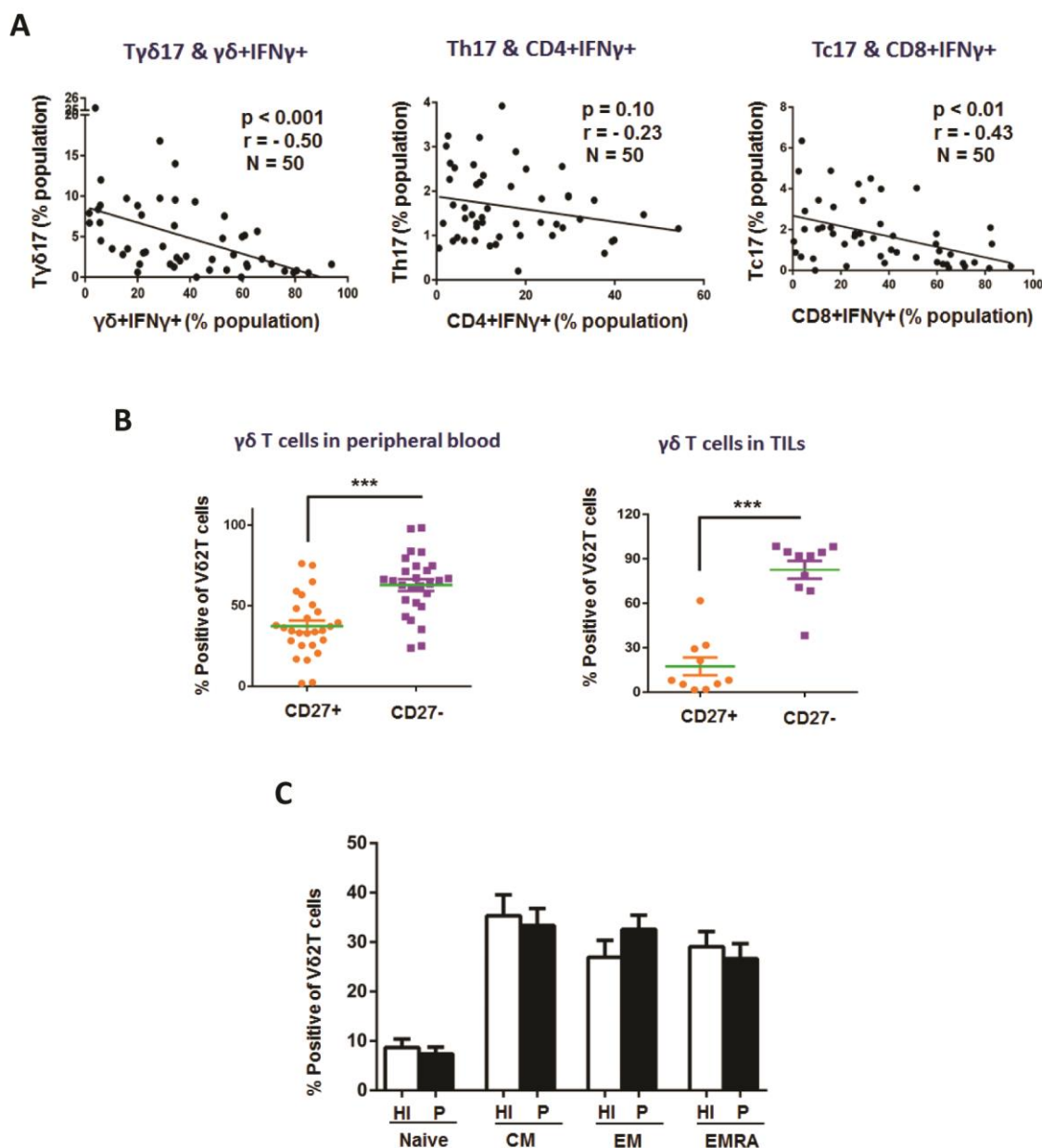
CD8<sup>+</sup>IFN $\gamma$ <sup>+</sup> cells in TILs compared to PBMCs of GBC patients (Figure 5.4 B). However, the levels of CD4<sup>+</sup>IFN $\gamma$ <sup>+</sup> cells were comparable in GBC patients and HI (Figure 5.4 C). The data suggests that the anti-tumor immunity contributed by  $\gamma\delta$ <sup>+</sup>IFN $\gamma$ <sup>+</sup> and CD8<sup>+</sup>IFN $\gamma$ <sup>+</sup> cells may be dysfunctional in GBC patients.

### 5.2.3 Cytokine profile of $\gamma\delta$ T cells is skewed towards IL17 production in GBC patients

The immune-phenotype analysis of  $\gamma\delta$ T cells showed that the levels T $\gamma\delta$ 17 cell were increased and that of  $\gamma\delta$ <sup>+</sup>IFN $\gamma$ <sup>+</sup> cells were decreased in GBC patients in comparison to HI. The correlation analysis of T $\gamma\delta$ 17 and  $\gamma\delta$ <sup>+</sup>IFN $\gamma$ <sup>+</sup> cells in peripheral blood of GBC patients further confirmed the significant negative correlation among these cells (Figure 5.5 A). Th17 and Tc17 cells also negatively correlated with CD4<sup>+</sup>IFN $\gamma$ <sup>+</sup> and CD8<sup>+</sup>IFN $\gamma$ <sup>+</sup> cells respectively (Figure 5.5 A).

It is reported that the expression of CD27 on surface of  $\gamma\delta$ T cells, determine the cytokine profile of  $\gamma\delta$ T cells towards IFN $\gamma$  production.  $\gamma\delta$ T cells lacking the expression of CD27 develop to produce IL17 [249]. In GBC patients, the levels of  $\gamma\delta$ T cells deficient in CD27 expression were significantly elevated in peripheral blood (n=27) and TILs (n=10) compared to CD27<sup>+</sup> $\gamma\delta$ T cells (Figure 5.5 B). Next, the analysis of memory phenotype of  $\gamma\delta$ T cells in peripheral blood revealed that more than 90% of  $\gamma\delta$ T cells were memory T cells. However, the categorization of  $\gamma\delta$ T cells from GBC patients (n=27) into different memory phenotypes (central memory, effector memory and terminally differentiated memory phenotype) did not show significant difference in comparison to HI (n=14) (Figure 5.5 C). In addition, as shown in Figure 4.1 H, the levels of total  $\gamma\delta$ T cells in GBC patients were comparable to HI. Thus the data suggests that although the frequency of total  $\gamma\delta$ T cells and their memory phenotype in

GBC patients did not alter, the cytokine secretion profile of  $\gamma\delta$ T cells was skewed towards IL17 production.



**Figure 5.5 : Cytokine profile of  $\gamma\delta$  T cells in GBC patients.** (A) The correlation of IL17 producing and IFN $\gamma$  producing cells was analysed in peripheral blood of GBC patients. Pearson coefficient of correlation was calculated between T $\gamma\delta$ 17 and  $\gamma\delta$ +IFN $\gamma$  (left), Th17 and CD4+IFN $\gamma$  (centre) and Tc17 and CD8+IFN $\gamma$  (right). “r” indicates Pearson coefficient of correlation and N indicates number of pairs in correlation. (B) Expression of CD27 was analysed on  $\gamma\delta$  T cells in PBMCs (n=27) and TILs (n=10) of GBC patients. The levels of

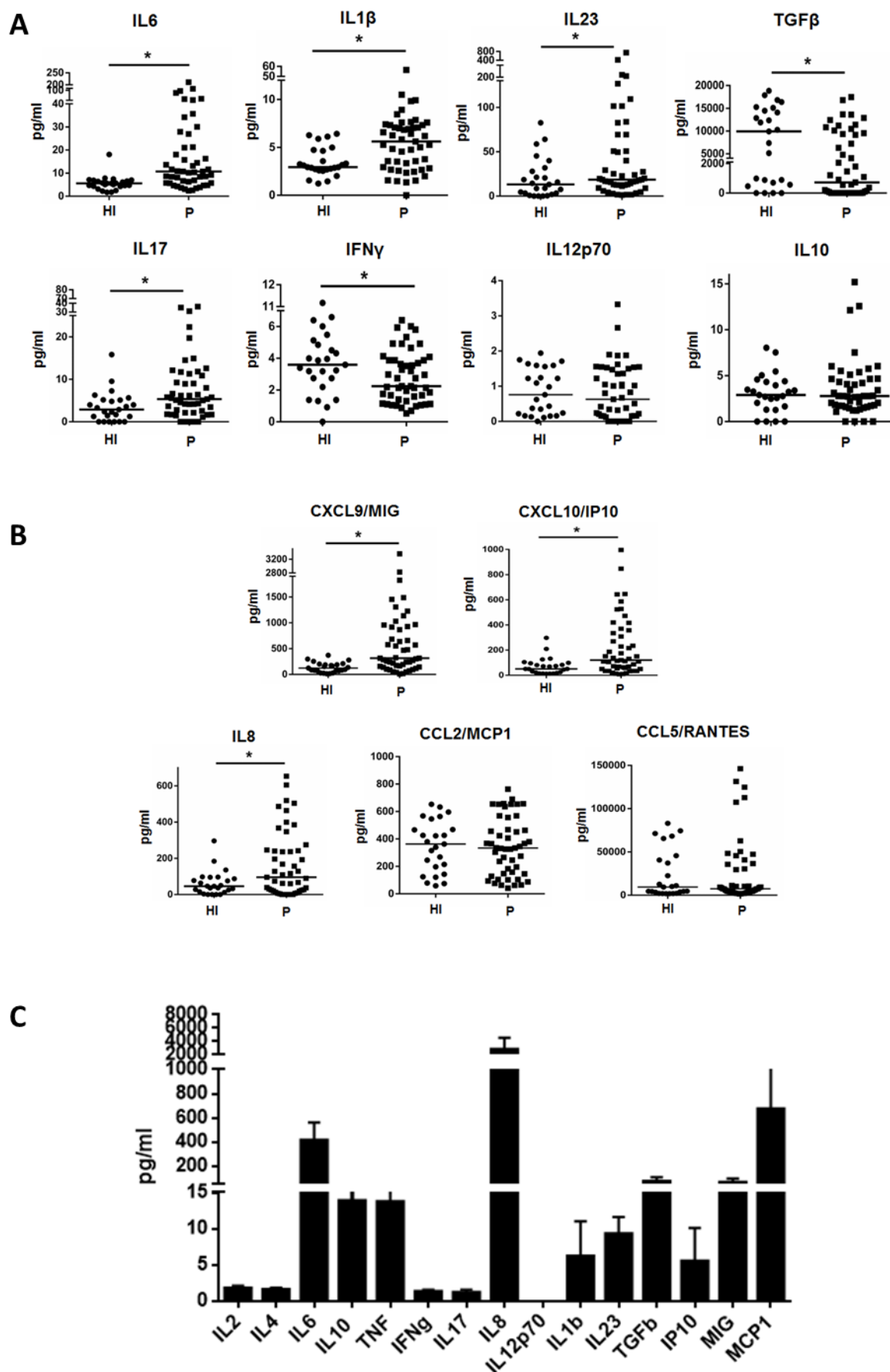
*CD27<sup>+</sup>γδT cells and CD27<sup>-</sup>γδT cells in peripheral blood (left) and TILs (right) are presented as scatter plots. (C) The proportion of memory phenotypes of γδT cells were analysed by expression of CD27 and CD45RA on γδT cells. The levels of naïve and memory (central memory, effector memory and terminally differentiated effector memory) γδT cells in peripheral blood of GBC patients (n=27) and HI (n=14) are presented as bar diagram. HI, healthy individuals; P, GBC patients; TIL, Tumor infiltrating lymphocytes. Data are shown as mean ± SEM with \*  $p < 0.05$ ; \*\*  $p < 0.01$ ; \*\*\*  $P < 0.001$ .*

#### **5.2.4 Cytokines involved in differentiation of Tγδ17 cells are elevated in sera and tumor environment of GBC patients**

Studies have shown that the differentiation of Tγδ17 and Th17 from naïve T cells is facilitated by combinations of IL6, TGFβ, IL1β and IL23 [243, 313]. The serum levels of these and related cytokines and chemokines were evaluated in GBC patients (n=49) and HI (n=25) by cytometric bead array (CBA). The data was analysed by flow cytometry. As shown in Figure 5.6 A, the levels of IL6, IL1β, and IL23 were high in GBC patients whereas TGFβ was low compared to HI. IL17 was significantly elevated in sera of GBC patients. However, IFNγ was decreased and IL12p70 remained unaltered compared to HI. Levels of IL10 also did not alter among HI and GBC patients.

The chemokines in the sera of GBC patients and HI were evaluated by combining individual flex sets of CBA. Analysis of chemokines revealed that monokine induced by gamma interferon (MIG; CXCL9), interferon induced protein 10 (IP-10; CXCL10) and IL8 were increased in sera of GBC patients. Levels of monocyte chemoattractant protein-1 (MCP-1; CCL2) and RANTES (CCL5) in GBC patients were comparable to HI (Figure 5.6 B).

Further to evaluate the cytokine profile in tumor environment, single cell suspension of surgically resected tumor tissue was prepared and cytokines were measured in cell-free culture supernatant collected after 24 h. It was observed that cytokines involved in



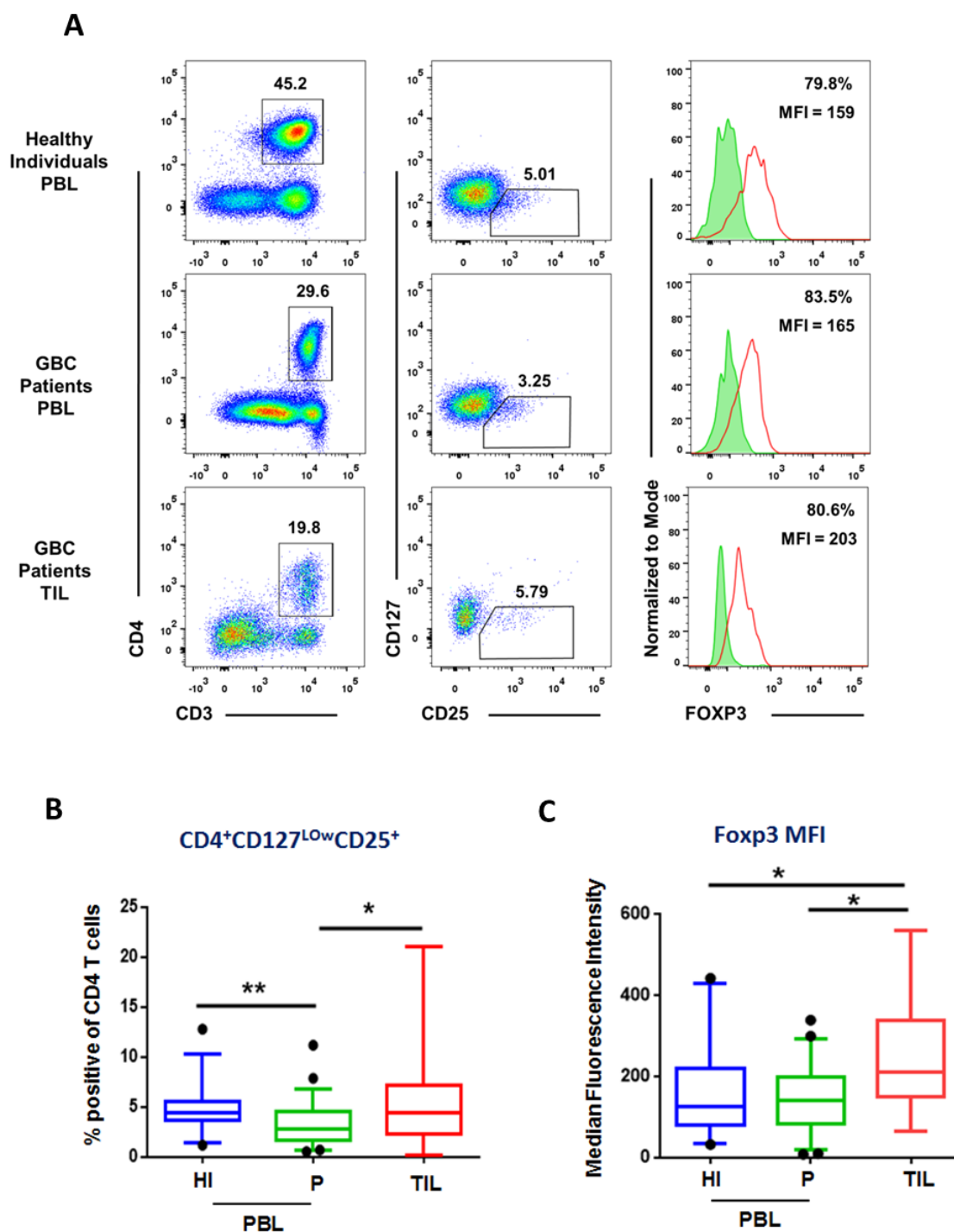
**Figure 5.6 : Cytokine profile in serum and tumor environment of GBC patients.** (A-B) Scatter plots depict concentration of various cytokines (A) and chemokines (B) in sera of GBC patients (n=49) and HI (n=25) analysed by cytometric bead array. Horizontal lines indicate median values. Data was analysed by Mann Whitney test with  $*(p < 0.05)$  (C) Cytokines and chemokines were measured in cell-free tumor supernatants (n=15) by cytometric bead array. Data presented as concentration in pg/ml.

polarization of IL17 producing cells (IL6, TGF $\beta$ , IL1 $\beta$  and IL23) were present in the tumor environment. Levels of IL12, IFN $\gamma$ , IL2 and IL4 were low whereas chemokines such as IL8, CXCL9, CXCL10 and CCL2 were remarkably high (Figure 5.6 C). Taken together, these results suggest that cytokines involved in the polarization of T $\gamma\delta$ 17 are elevated in sera and tumor environment of GBC patients.

### 5.2.5 Regulatory T cells are decreased in peripheral blood of GBC patients

The cytokine profile of sera and tumor environment of GBC patients showed that the levels of TGF $\beta$  were decreased and IL10 were comparable to HI. TGF $\beta$  is required by Treg cells for differentiation from naïve CD4 $^{+}$  T cells [314], and IL10 is secreted by Treg cells [315]. The frequency of Tregs in PBMCs of GBC patients (n=52) and HI (n=30) were analysed by surface staining for CD4, CD25 and CD127 followed by intracellular staining for Foxp3. Figure 5.7 A describes the gating strategy used for Tregs where Tregs were defined as CD25 $^{+}$ CD127 $^{low/-}$  cells within CD4 $^{+}$  T cells with Foxp3 expression of  $\geq 80\%$ .

It was observed that Tregs were significantly decreased in PBMCs of GBC patients compared to HI. However, the percentages of Tregs in TILs were higher than PBMCs of GBC patients but comparable to HI (Figure 5.7 B). The median fluorescence intensity (MFI) of Foxp3 expression on Tregs was significantly increased in TILs than PBMCs of GBC patients (Figure 5.7 C).



**Figure 5.7 : Frequency of regulatory T cells in GBC patients.** (A) A representative dot plot describing Tregs, characterized as CD25<sup>+</sup>CD127<sup>low/-</sup> within CD4<sup>+</sup> T cells. Histograms indicate expression of Foxp3 within CD25<sup>+</sup>CD127<sup>low/-</sup> population. Figures in the histogram indicate median fluorescence intensity of Foxp3 expression (blank histogram) corrected with isocontrol (shaded histogram). (B) Box whisker plots showing composite results of Tregs in PBMCs (n=52) and TILs (n=17) of GBC patients compared with HI (n=30). (C) Comparison of median fluorescence intensity of Foxp3 expression within Tregs in GBC

patients and HI. HI, healthy individuals; P, GBC patients; TIL, Tumor infiltrating lymphocytes; PBMCs, peripheral blood mononuclear cells. The box plots show median (middle line), 5<sup>th</sup> and 95<sup>th</sup> percentiles (box), extreme values (whiskers) and outliers (dark circles). Data was analysed by Mann Whitney test and student's *t* test and presented as mean  $\pm$  SEM with \*  $p < 0.05$ ; \*\*  $p < 0.01$ .

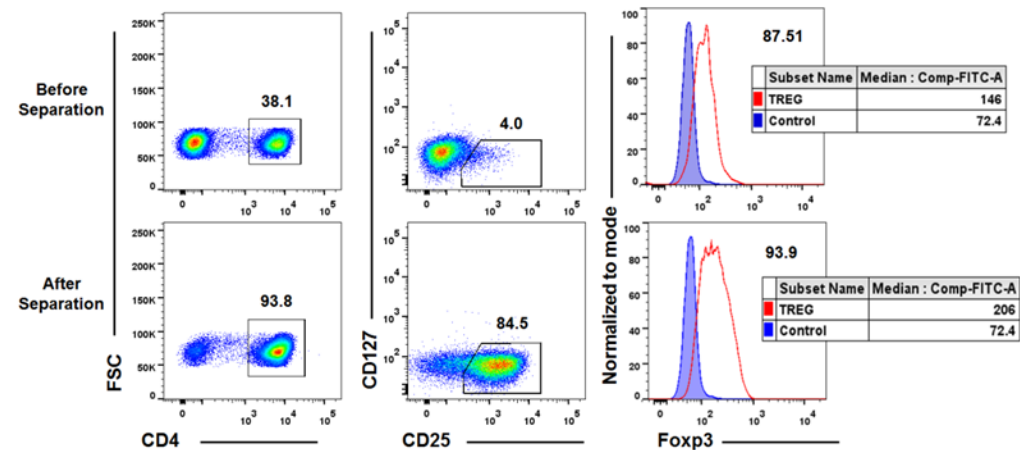
### 5.2.6 Suppressive potential of Tregs is comparable in GBC patients and HI

In order to investigate functional potential of Tregs in GBC patients, Tregs were isolated from peripheral blood of GBC patients and HI with more than 80% purity (Figure 5.8 A). The purified Treg cells were co-cultured with autologous responder T cells (Tres; CD4<sup>+</sup>CD25<sup>-</sup>) labelled with carboxyfluorescein succinimidyl ester (CFSE) and stimulated with anti-CD3/anti-CD28. It was observed that percent dividing Tres cells were decreased with increase in Treg cells in culture. The co-culture of Tres with Treg in 1:2 ratio significantly inhibited the proliferation of Tres. However, the suppressive potential of Tregs in GBC patients was comparable to HI (Figure 5.8 B and C). Thus, the results indicate that although Tregs were decreased in PBMCs of GBC patients, their suppressive potential was not compromised.

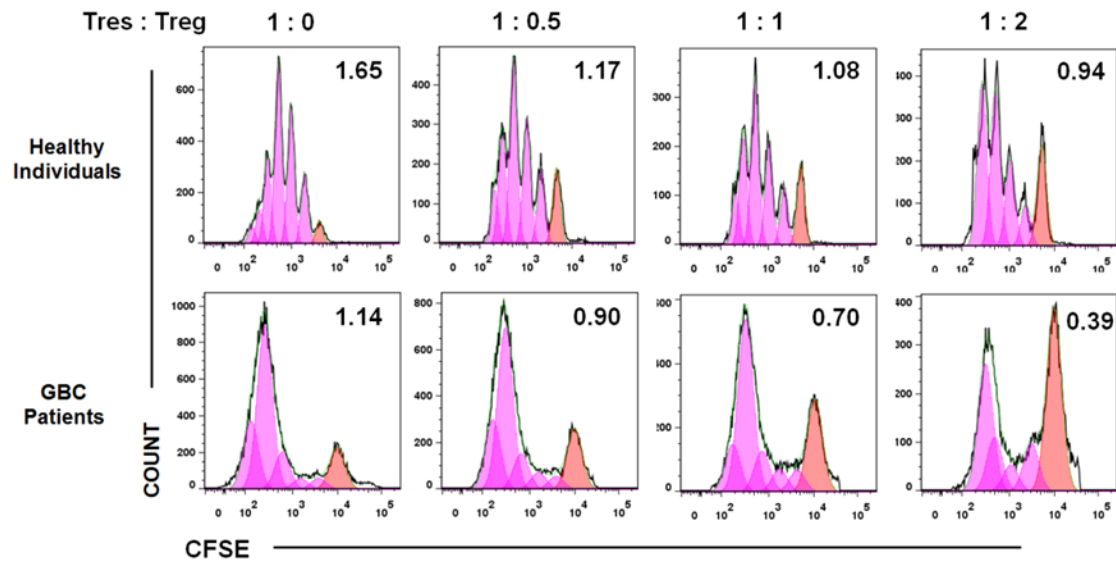
### 5.2.7 Dynamics of T $\gamma$ $\delta$ 17, Th17, Tc17 and Treg cells in GBC patients

We further analyzed the relationship between T $\gamma$  $\delta$ 17, Th17, and Tc17 cells with Tregs in GBC patients. The ratios of T $\gamma$  $\delta$ 17/Treg, Th17/Treg and Tc17/Treg were significantly increased in peripheral blood as well as in tumor environment of GBC patients indicating an inverse correlation of IL17 producing cells and Tregs (Figure 5.9 A). Next, we found that peripheral blood T $\gamma$  $\delta$ 17 cells positively correlated with serum IL17 levels (Figure 5.9 B). However, the levels of Th17 and Tc17 cells in peripheral blood of GBC patients did not correlate with serum IL17 levels. Thus the data highlighted the importance of T $\gamma$  $\delta$ 17 cells in inflammation associated with GBC (Figure 5.9 B).

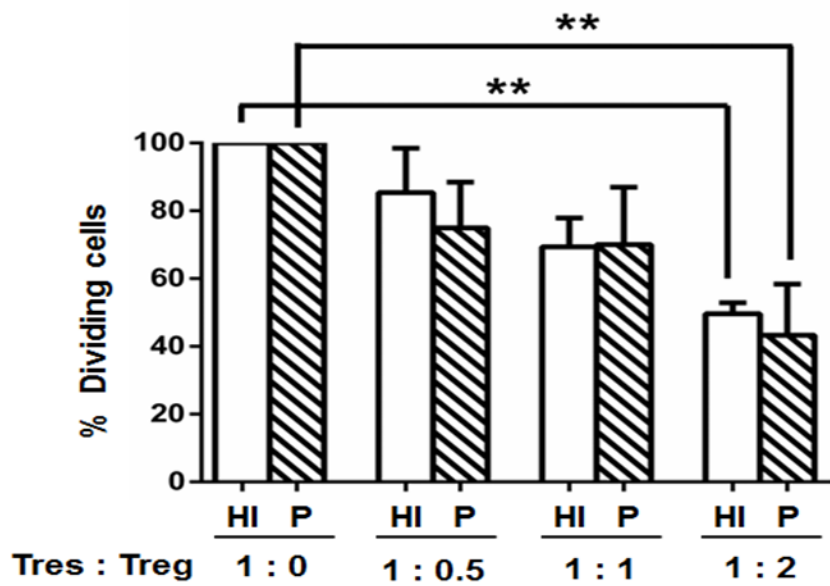
A



B

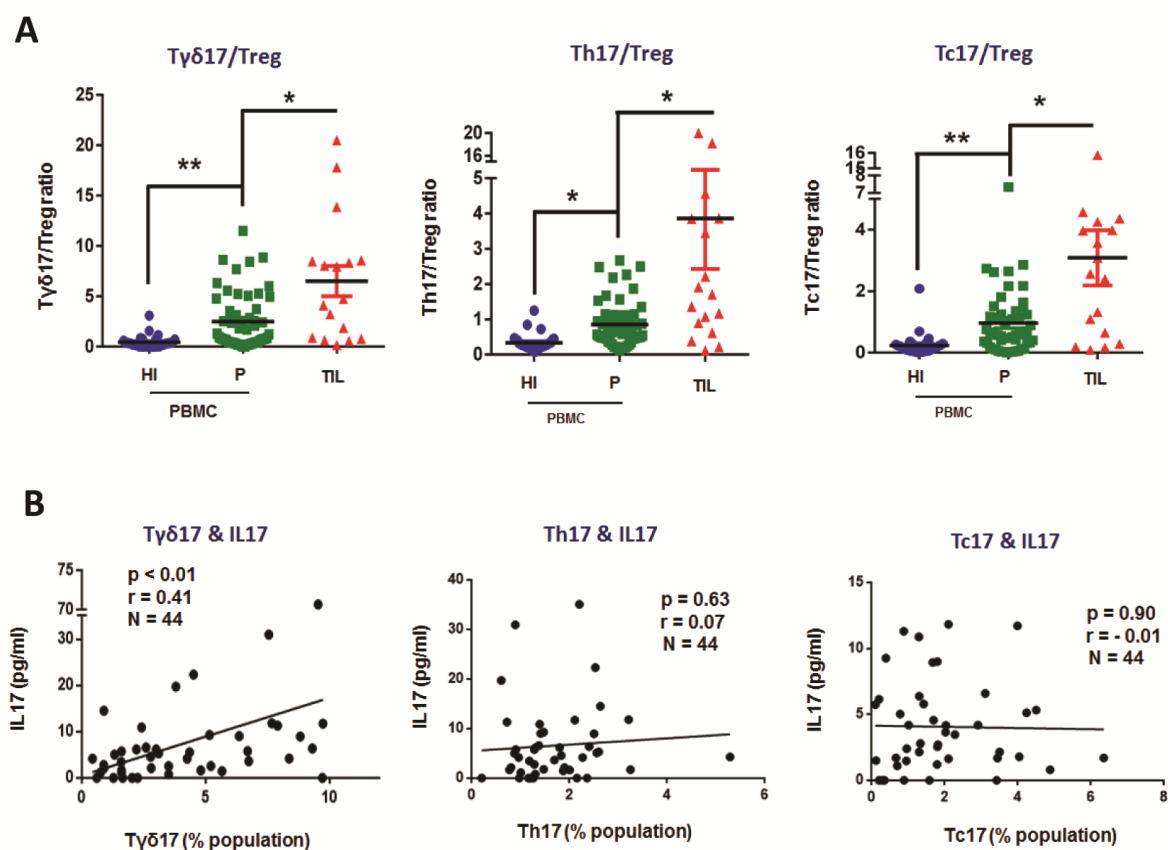


C



**Figure 5.8 : Suppressive potential of Treg cells in GBC patients.** (A) The representative dot plot analysis show purity of Treg cells before and after immunomagnetic separation from peripheral blood of GBC patients and HI. The histograms show percent expression of Foxp3 by  $CD4^+CD25^+CD127^{low/-}$  cells presented as numbers. The horizontal boxes in the histograms indicate median fluorescence intensity of Foxp3 expression (blank histogram) in compared with isocontrol (shaded histogram). (B) Representative figure of three independent experiments depicting suppressive potential of Tregs ( $CD4^+CD25^+$ ) on CFSE labelled autologous responder cells ( $CD4^+CD25^-$ ) from GBC patients ( $n=3$ ) and HI ( $n=3$ ). First peak from right indicates mother population. Figures in the plot indicate division index at respective ratio. (C) Bar diagram summarizes the percent dividing responder T cells at respective Treg:Tres ratio.

HI, healthy individuals; P, GBC patients; CFSE, carboxyfluorescein succinimidyl ester. Data was analysed by student's *t* test and presented as mean  $\pm$  SEM with \*\* $p < 0.01$ .



**Figure 5.9 : Dynamics of Tyδ17, Th17, Tc17 and Treg in peripheral blood of GBC patients.** (A) Scatter plot showing the ratios of Tyδ17/Treg (left), Th17/Treg (middle) and Tc17/Treg (right) in PBMCs ( $n=52$ ) and TIL ( $n=17$ ) of GBC patients and HI ( $n=30$ ). (B) The correlations of Tyδ17 (left), Th17 (middle) and Tc17 (right) with serum IL17 levels

were evaluated respectively. “*r*” indicates Pearson coefficient of correlation and *N* indicates number of pairs in correlation.

*HI*, healthy individuals; *P*, GBC patients *TIL*, Tumor infiltrating lymphocytes; *PBMCs*, peripheral blood mononuclear cells. Data was analysed by student’s *t* test and presented as mean  $\pm$  SEM with \*  $p < 0.05$ ; \*\*  $p < 0.01$ .

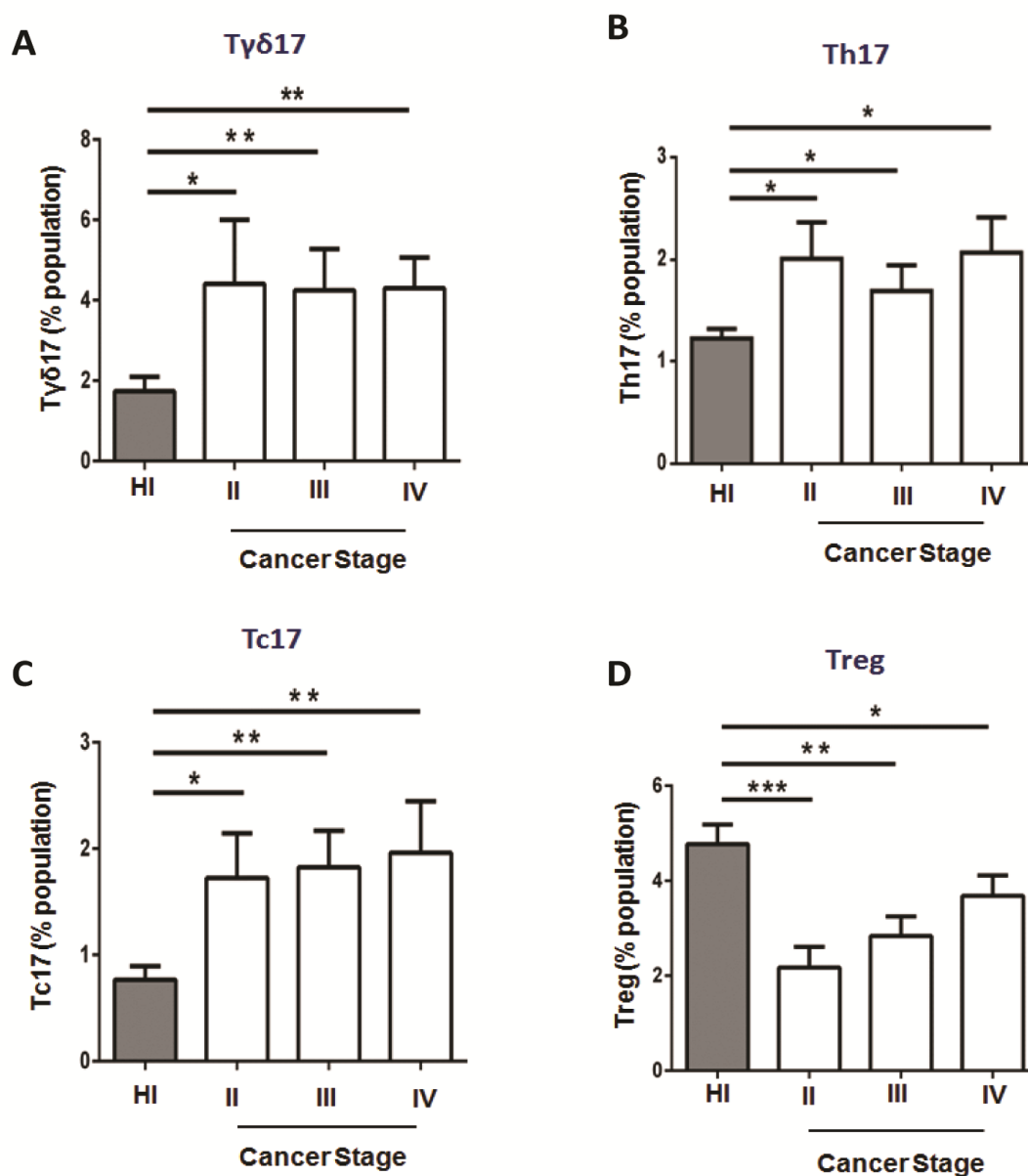
### 5.2.8 $T\gamma\delta 17$ , Th17 and Tc17 cells do not correlate with clinical stage of GBC patients

To investigate the implication of IL17 producing cells on GBC progression, we analyzed the peripheral blood levels of  $T\gamma\delta 17$ , Tc17, Th17 and Treg cells with different stages of GBC patients. The patients were grouped according to the TNM classification as stage II ( $n=5$ ), stage III ( $n=20$ ) and stage IV ( $n=27$ ).  $T\gamma\delta 17$ , Th17 and Tc17 cells showed no correlation with clinical stage (II to IV) of GBC patients. However, their levels remained high in all stages of GBC patients compared to HI (Figure 5.10 A, B and C). In contrast, the levels of Tregs in GBC patients of all stages (II to IV) remained lower than HI (Figure 5.10 D). This clearly indicates that the immune response was skewed towards IL17 producing cells in GBC patients.

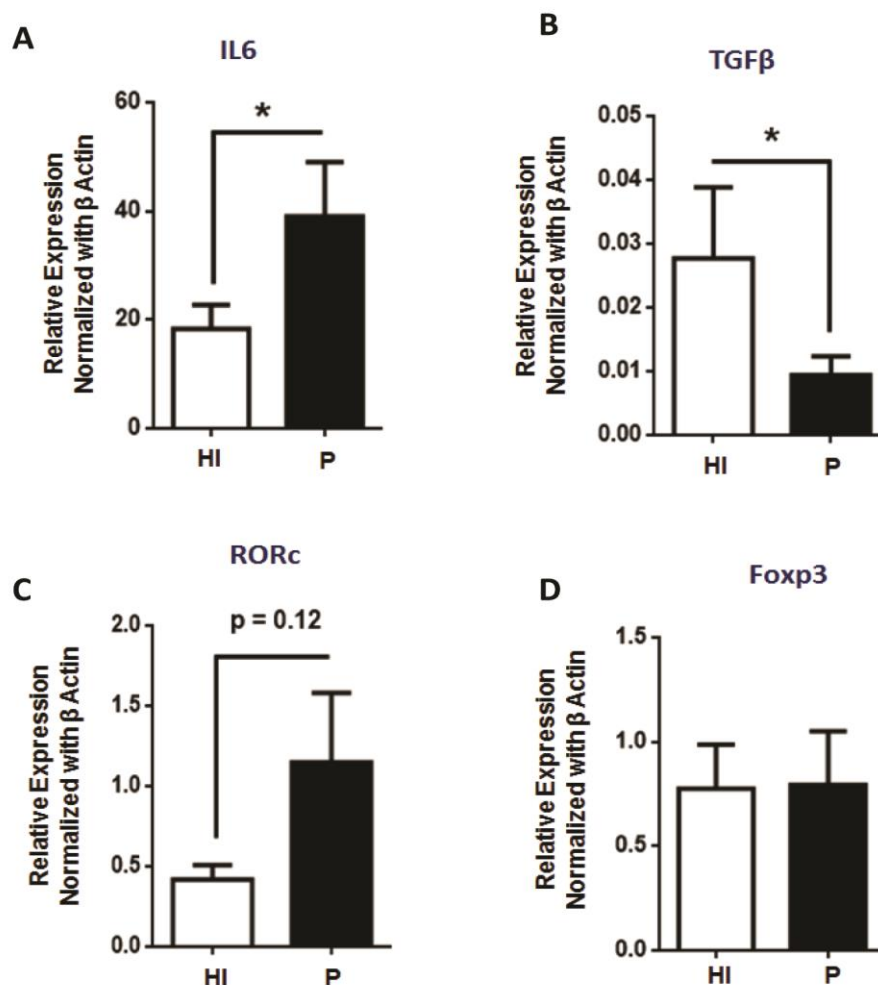
### 5.2.9 mRNA expressions of cytokines and transcription factors regulating $T\gamma\delta 17$ and Treg in PBMCs of GBC patients

It is reported that IL6 regulates the differentiation of  $CD4^+$  T cells towards Th17 or Treg cell lineage. Higher expression of IL6 induces Th17 differentiation and inhibits Treg whereas TGF $\beta$  promotes differentiation and maturation of Tregs [57]. Thus to understand the dynamics of IL6 and TGF $\beta$ , PBMCs from GBC patients ( $n=18$ ) and HI ( $n=18$ ) were analyzed for expression of IL6 and TGF $\beta$  at mRNA level using real time PCR. The expression of IL6 was significantly higher in PBMCs from GBC patients than HI (Figure 5.11 A). However, expression of TGF $\beta$  was decreased in GBC patients compared to HI (Figure 5.11 B). These results corroborate our observation of IL6 and TGF $\beta$  expression at protein level in sera of GBC patients. Moreover, the mRNA expression of RORc, a lineage determining transcription

factor of IL17 producing T cells, was elevated in PBMCs of GBC patients compared to HI (Figure 5.11 C) whereas the mRNA expression of Foxp3 was comparable in GBC patients and HI (Figure 5.11 D). Overall the data showed that the immune response in GBC patients was tilted towards IL17 producing inflammatory T cells.



**Figure 5.10 : Association of T $\gamma\delta$ 17, Th17, Tc17 and Treg cells with clinical stage of GBC patients.** The bar diagram depicts frequencies of T $\gamma\delta$ 17 (A), Th17 (B), Tc17 (C) and Treg (D) were compared with clinical stages of GBC patients. Results are shown as mean  $\pm$  SEM with  $*$ ( $p < 0.05$ );  $**$ ( $p < 0.01$ ).

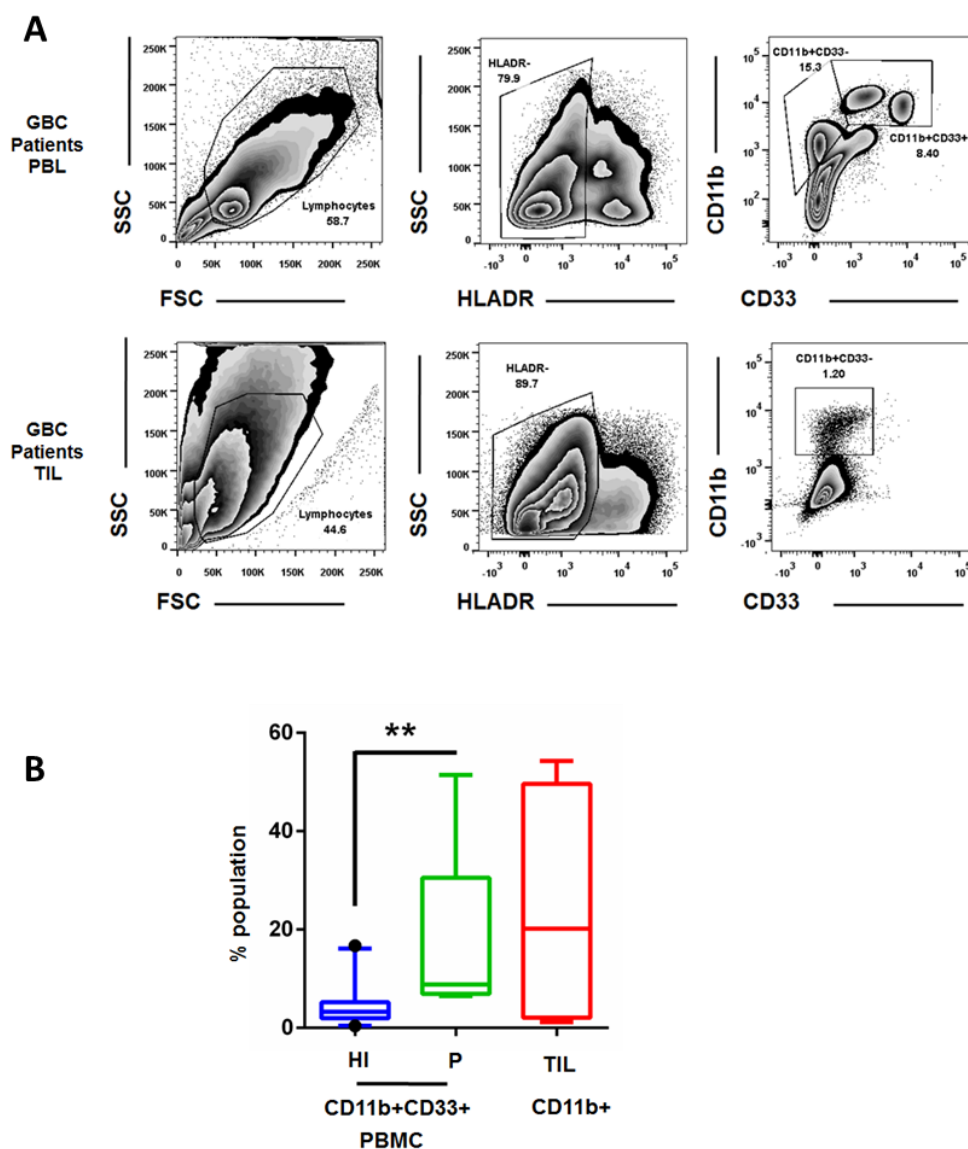


**Figure 5.11 : Expression of  $T\gamma\delta 17$  associated genes in PBMCs of GBC patients.** Total RNA extracted from PBMCs was reversed transcribed to cDNA and expression of IL6 (A), TGF $\beta$  (B), RORc (C) and Foxp3 (D) was evaluated in PBMCs of GBC patients (n=18) and HI (n=16). The expression of genes was normalized to  $\beta$ -actin expression. Results are shown as mean  $\pm$  SEM with \*(p < 0.05).

#### 5.2.10 Myeloid derived suppressor cells are increased in peripheral blood of GBC patients

Recent studies have shown that IL17 is involved in the accumulation of tumor-infiltrating myeloid derived suppressor cells (MDSCs) in mice [316]. Since, IL17 and IL17 producing cells were elevated in GBC; it was hypothesized that MDSCs may be increased in GBC patients. To phenotype MDSCs, PBMCs from GBC patients (n=5) and HI (n=5) and single cells suspension of tumor tissue (n=5) were stained for surface expression of HLADR, CD33

and CD11b. MDSCs were defined as  $CD33^+CD11b^+$  cells gated on  $HLADR^-$  cells [317] (Figure 5.12 A). It was observed that  $CD33^+CD11b^+$  MDSCs were significantly increased in peripheral blood of GBC patients compared to HI (Figure 5.12 B). Interestingly,  $CD33^+CD11b^+HLADR^-$  MDSCs were absent in TILs whereas  $CD11b^+HLADR^-$  phenotype of MDSCs was present in tumor environment of GBC patients (Figure 5.12 B).



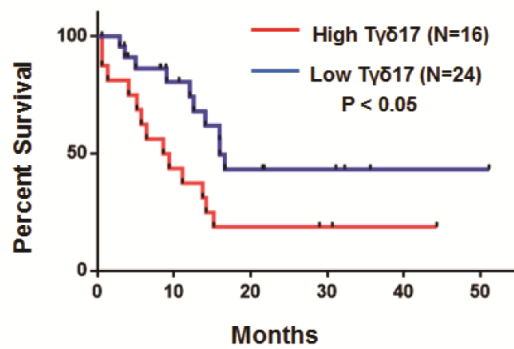
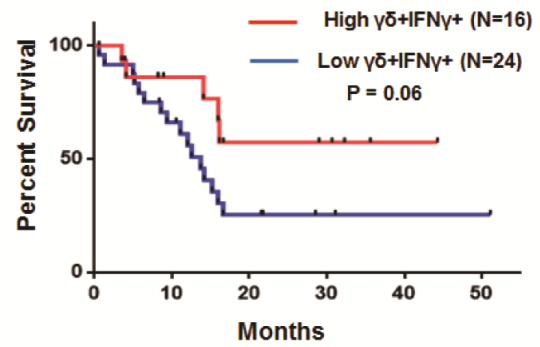
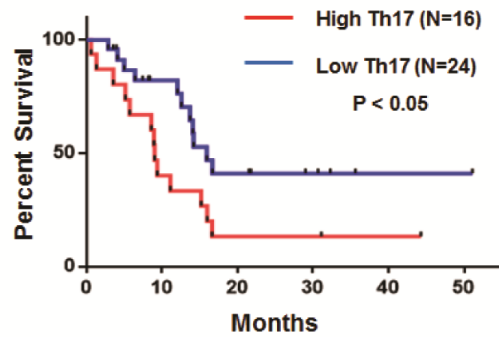
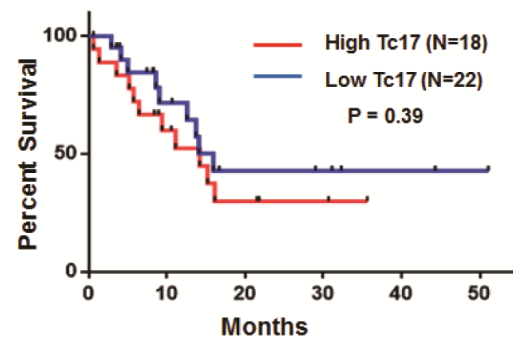
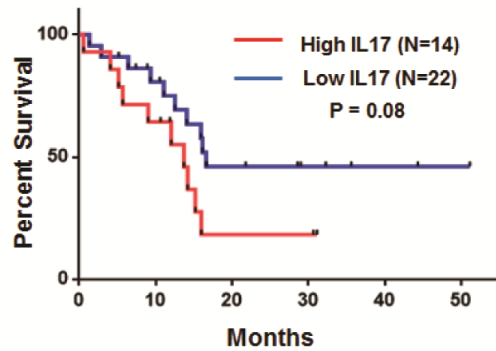
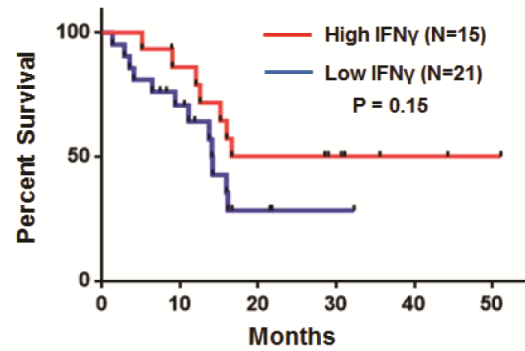
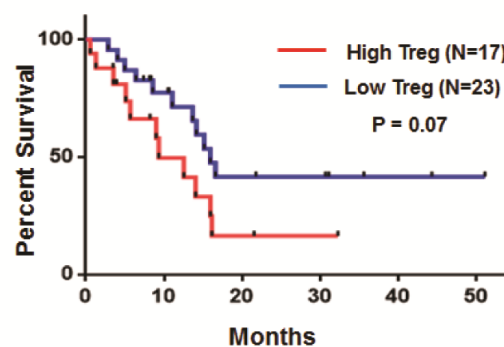
**Figure 5.12 : Prevalence of MDSCs in peripheral blood and TILs of GBC patients.** (A) Representative zebra plot analysis of MDSCs from peripheral blood (n=5) and TILs (n=5) of GBC patients.  $CD33^+CD11b^+$  cells were gated on  $HLADR^-$  population. (B) The levels of MDSCs in PBMCs and TILs of GBC patients compared with HI are

*presented as box whisker plot. HI, healthy individuals; P, GBC patients; TIL, Tumor infiltrating lymphocytes. The box plots show median (middle line), 5<sup>th</sup> and 95<sup>th</sup> percentiles (box), extreme values (whiskers) and outliers (dark circles). Results are analysed by Mann-Whitney test with  $^{**}(p < 0.01)$ .*

### **5.2.11 T $\gamma\delta$ 17, Th17 and Treg cells are associated with poor overall survival of GBC patients**

To investigate the clinical significance of T $\gamma\delta$ 17, Th17, Tc17 and Tregs, the survival time of patients was analyzed with frequency of these cells in peripheral blood of GBC patients (n=40). As there was no clinically defined cut off points for Th17, Tc17, T $\gamma\delta$ 17, Treg cells, the high-expressing or low-expressing groups of GBC patients were defined based on mean values of expression of these lymphocytes (4.7 for T $\gamma\delta$ 17, 1.8 for Th17, 1.8 for Tc17 and 3.2 for Treg). As shown in Figure 5.13 A, cox proportional regression analysis revealed that patients with high levels of T $\gamma\delta$ 17 cells showed poor overall survival (median survival: 8.95 months) than patients with low levels of T $\gamma\delta$ 17 (median survival: 15.97 months). The individuals with high T $\gamma\delta$ 17 levels were at higher risk compared to those with low T $\gamma\delta$ 17 levels (Hazard ratio (HR): 2.4). In contrast, the patients with high levels of  $\gamma\delta^+ \text{IFN}\gamma^+$  had longer overall survival than patients with low levels of  $\gamma\delta^+ \text{IFN}\gamma^+$  cells (HR: 0.4; Figure 5.13 B).

Similarly, GBC patients with high levels of Th17 cells had shorter overall survival compared to patients with low levels (HR: 2.32; Figure 5.13 C). Tc17 were not associated with survival of patients (Figure 5.13 D). However, patients with increased Treg cells had poor overall survival (HR: 2.07; Figure 5.13 G). Next, it was observed that the high levels of serum IL17 were associated with poor survival of patients (HR: 2.12; Figure 5.13 E). In contrast, the patients with high levels of IFN $\gamma$  had survival benefit over patients with low serum levels of

**A****Overall survival (T $\gamma$  $\delta$ 17)****B****Overall survival ( $\gamma$  $\delta$ +IFN $\gamma$ +)** **C****Overall survival (Th17)****D****Overall survival (Tc17)****E****Overall survival (IL17)****F****Overall survival (IFN $\gamma$ )****G****Overall survival (Treg)**

**Figure 5.13 : Increased  $T\gamma\delta 17$  cells in GBC patients associate with poor survival.** Overall survival of GBC patients ( $n=40$ ) was analysed by Kaplan-Meier method for low or high levels of  $T\gamma\delta 17$  cells (A),  $\gamma\delta+IFN\gamma+$  cells (B) Th17 cells (C), Tc17 cells (D), Serum IL17 levels (E), Serum  $IFN\gamma$  levels (F) and Treg cells (G). The curve statistics were compared by log-rank test with  $p < 0.05$ .

$IFN\gamma$  (HR: 0.51; Figure 5.13 F). Altogether, the data suggests that  $T\gamma\delta 17$ , Th17 and Treg cells may serve as predictive biomarkers for prognosis of GBC.

### 5.3 Summary

The immune-phenotyping of peripheral blood lymphocytes and tumor infiltrating lymphocytes revealed elevated levels of IL17 producing T cells in GBC patients irrespective of their clinical stage. Interestingly  $T\gamma\delta 17$  cells emerged as significant contributor of IL17 in tumor tissue and in circulation compared to Th17 and Tc17 cells. In contrast  $\gamma\delta+IFN\gamma+$  and  $CD8+IFN\gamma+$  cells were decreased in tumor compartment of GBC patients. The cytokine profile of sera and tumor environment highlighted the abundance of inflammatory cytokines involved in differentiation and maturation of  $T\gamma\delta 17$  and Th17 cells. Analysis of Treg cells showed that although the peripheral blood levels of Tregs were decreased, their suppressive potential was not compromised. Moreover, Foxp3 expressing Treg cells were elevated in tumor tissue compared to peripheral blood of GBC patients but remained comparable to HI. Study of dynamics of IL17 producing cells and Treg cells showed that immune response was biased towards  $T\gamma\delta 17$ , Th17 and Tc17 cell types in tumor environment. High levels of MDSCs observed in peripheral blood and tumor environment suggest that  $T\gamma\delta 17$  are involved in recruitment of MDSCs towards tumor environment which may further support tumor progression by inducing immunosuppression of antitumor immune response. The survival analysis of GBC patients showed significant association of  $T\gamma\delta 17$  cells with poor prognosis. Thus, the results presented in this chapter unravelled  $T\gamma\delta 17$  cells to be the central player in the pathogenesis of gallbladder cancer.

## **Chapter 6**

# **Exploring the pro-tumor role of *IL17* producing $\gamma\delta T$ (*T $\gamma\delta$ 17*) cells in GBC**

## 6.1 Introduction

IL17 is a potent pro-inflammatory cytokine. It acts through IL17 receptor expressed by epithelial cells and activates MAPK (mitogen-activated protein kinases) and NF- $\kappa$ B (nuclear factor- $\kappa$ B) by TRAF6 (tumour necrosis factor receptor-associated factor-6) and has also been found to physically associate with the NF- $\kappa$ B activator protein (Act1) [135]. IL17A expression has been detected in several human tumours, and is shown to associate with poor prognosis of patients [318]. However, a consensus on the specific role of IL17 in cancer promotion is not achieved which may be specific to cancer type [318]. Our data demonstrated that the IL17 was present in the tumor environment and the levels were elevated in sera of GBC patients. The elevated IL17 in GBC patients was also correlated with poor survival of patients. Thus it was imperative to investigate the mechanism of GBC progression mediated by IL17. The results presented in current chapter highlights the contribution of IL17 in proliferation, migration and invasion of GBC cells.

It was demonstrated in previous chapter that  $\text{T}\gamma\delta 17$  is major contributor of IL17 and was associated with poor prognosis of GBC patients. It is reported that healthy adult human peripheral blood  $\gamma\delta$ T cells distinctively express Th1 signature and 50–80% produce IFN $\gamma$  but < 5% produce IL17 [319]. However,  $\text{T}\gamma\delta 17$  cells have been demonstrated to be involved in the pathogenesis of transplantation rejection [320], autoimmune disease [321], allergy [322], and cancer [246] in humans, suggesting exclusive role of  $\text{T}\gamma\delta 17$  cells in modulating immune response in disease condition and has significant influence on the outcome of the disease. Various infection and autoimmunity models have shown that  $\text{T}\gamma\delta 17$  are distinctly involved in early immune response in the tissue and can modulate the functions of other immune and epithelial cells [251]. However, most of the studies carried out to understand the functions of  $\text{T}\gamma\delta 17$  cells are based on the murine models. Scanty literature is available on functions of  $\text{T}\gamma\delta 17$  cells in human cancers.

T $\gamma$  $\delta$ 17 function influencing the clinical outcome in GBC patients has not been reported. The present chapter is focused on studying the factors involved in the recruitment of T $\gamma$  $\delta$ 17 cells to the tumor bed in GBC patients and understanding the role of T $\gamma$  $\delta$ 17 cells in GBC progression.

## 6.2 Results

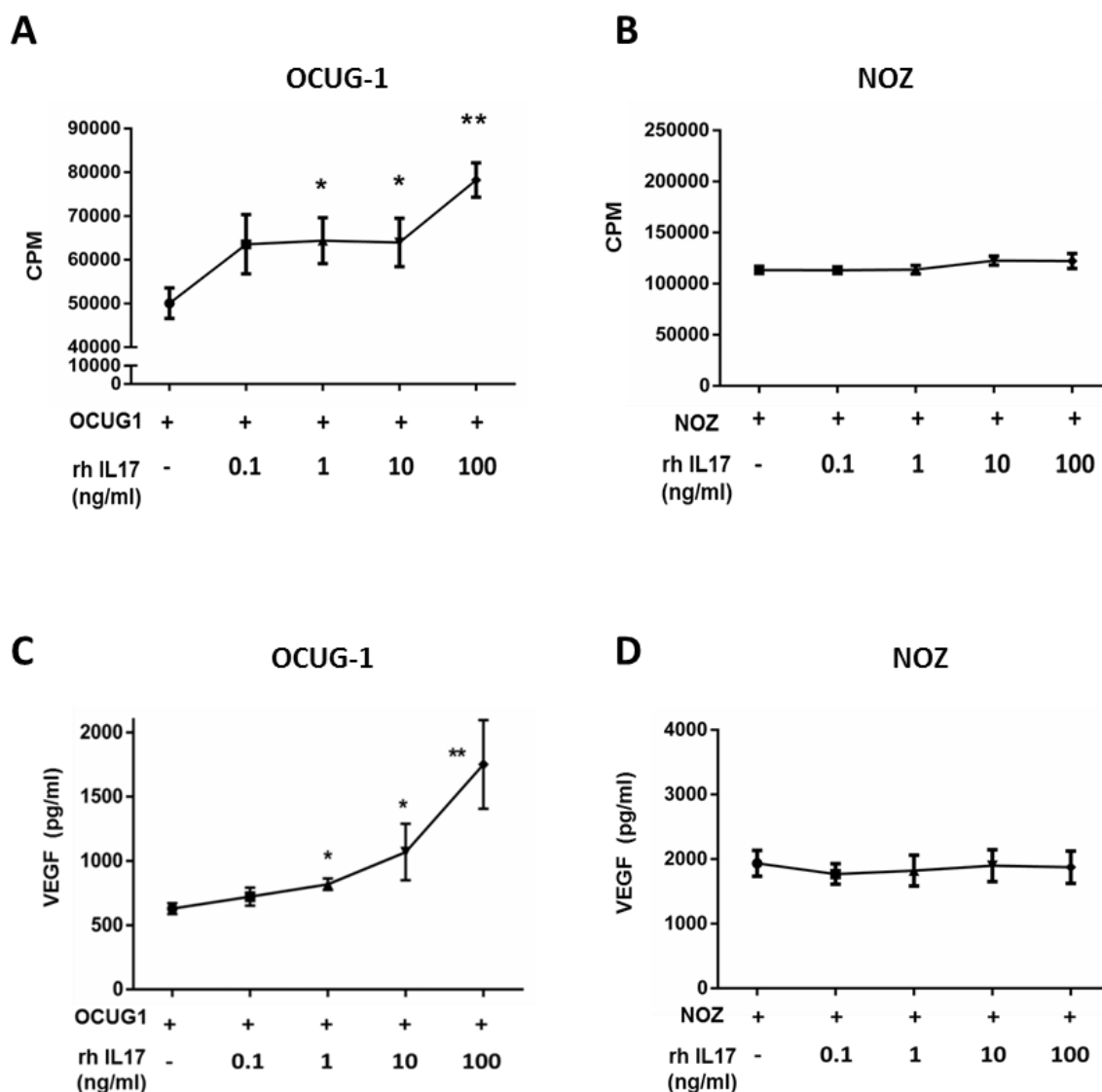
### 6.2.1 rhIL17 induces proliferation of gallbladder tumor cells

To study whether IL17 has direct role in GBC promotion, two GBC cell lines - OCUG-1 (poorly differentiated) and NOZ (moderately differentiated) were cultured with rhIL17. The proliferative response of GBC cells was monitored by  $^3\text{H}$  Thymidine incorporation assay. OCUG-1 and NOZ cells were cultured in flat bottom in 96 well plate for 24 h in William's E medium supplemented with 10% FBS. rhIL17 in different concentration (0.1, 1, 10 and 100 ng/ml) was added to the cells and monitored for another 48 h. It was observed that addition of rhIL17 enhanced the proliferation of OCUG-1 cells in a concentration dependent manner (Figure 6.1 A). Interestingly, rhIL17 did not affect the proliferation of NOZ cells (Figure 6.1 B). Overall the results demonstrated that poorly differentiated GBC cells were more responsive to the tumor promoting effects of IL17.

### 6.2.2 Gallbladder tumor cells produce increased VEGF in presence of rhIL17

VEGF is a key inducer of tumor angiogenesis [323]. To investigate the role of IL17 in VEGF induction in GBC, OCUG-1 and NOZ cells were cultured in presence or absence of rhIL17. Production of VEGF was monitored for 48 h in presence of different concentrations of IL17 (0.1, 1, 10 and 100 ng/ml). It was observed that stimulation of OCUG-1 with rhIL17 resulted into significant increase in the production of VEGF in dose-dependent fashion (Figure 6.1 C). However, secretion of VEGF by NOZ cells did not alter upon stimulation with rhIL17

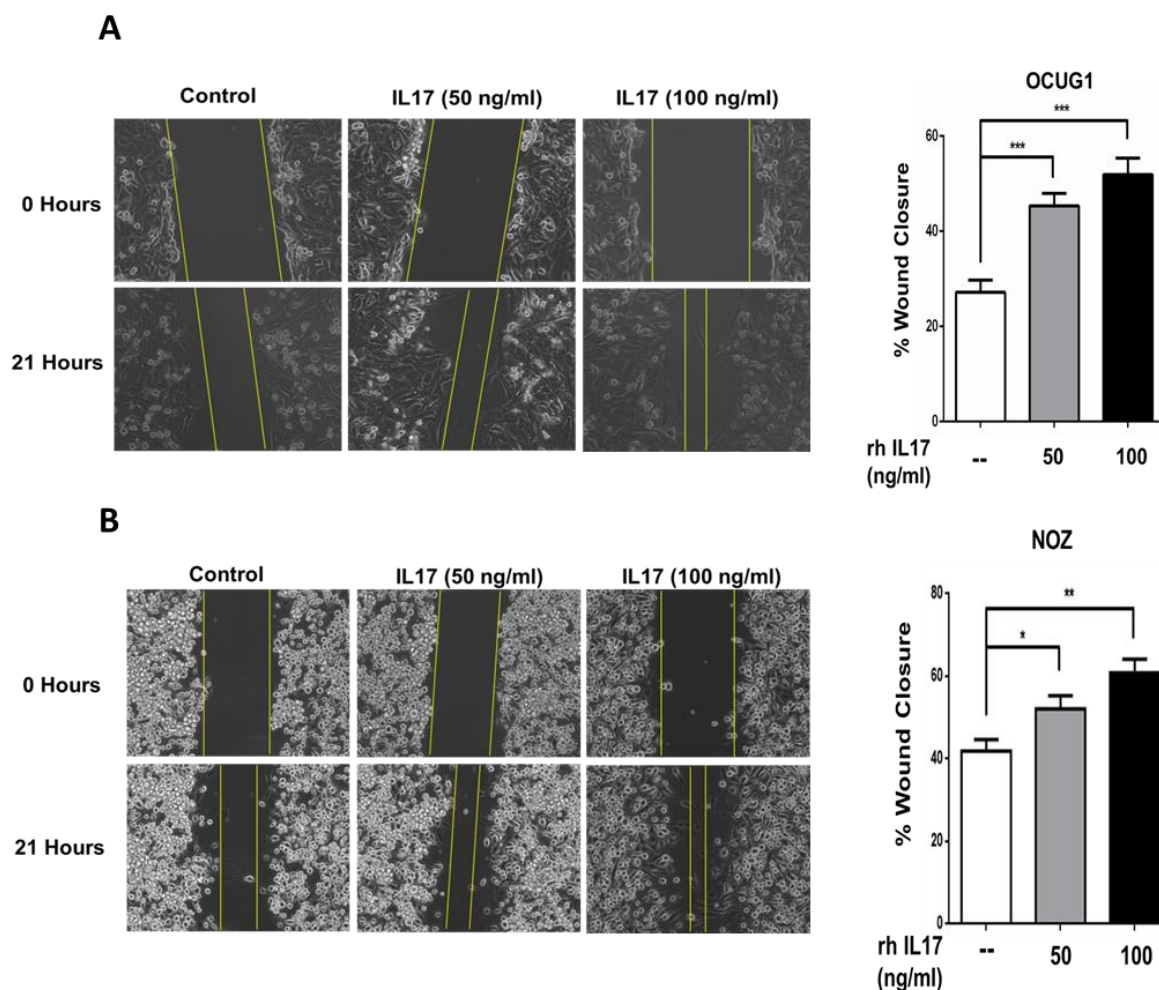
(Figure 6.1 D). Thus the data indicates that IL17 present in the tumor environment induce GBC cells to secrete VEGF which may enhance the GBC angiogenesis.



**Figure 6.1 : Effect of IL17 on proliferation and VEGF production in GBC cell line.** OCUG-1 cells (A) and NOZ cells (B) were cultured in serum free medium and were treated with different concentrations of rhIL17. Proliferation was measured by  $^3\text{H}$ -Thymidine incorporation and represented as counts per minute ( $n=6$ ). OCUG-1 (C) and NOZ (D) cell lines were cultured with different concentrations of rhIL17 in a serum-free medium for 48 h. VEGF was estimated in supernatants by ELISA ( $n=6$ ). Results were statistically analysed using Student's *t* test and shown as mean  $\pm$  SEM with \* $p<0.05$ ; \*\* $p<0.01$ .

### 6.2.3 rhIL17 enhances migration of gallbladder tumor cells

The influence of rhIL17 on migratory potential of gallbladder tumor cells was analysed by wound healing assay. OCUG-1 and NOZ cells were cultured in 6 well plates for 24 h and treated with Mitomycin C (10  $\mu$ g/ml) for 2 h to inhibit the cell proliferation. The scratches were made in monolayers and treated with rhIL17 (50, 100 ng/ml). The closure of the wounds was monitored using time lapse microscope for 21 h. It was observed that the rate of wound closure was high with increase in concentration of rhIL17 compared to GBC cells treated with medium alone (Figure 6.2 A and B). Interestingly, the data revealed that fold increase in wound closure compared to medium alone was higher in OCUG-1 cells (Figure 6.2 A) treated with rhIL17 than that observed with NOZ cells (Figure 6.2 B). Thus the data suggests that pro-migratory effect of rhIL17 was more pronounced in poorly differentiated (OCUG-1) than moderately differentiated GBC cells (NOZ).



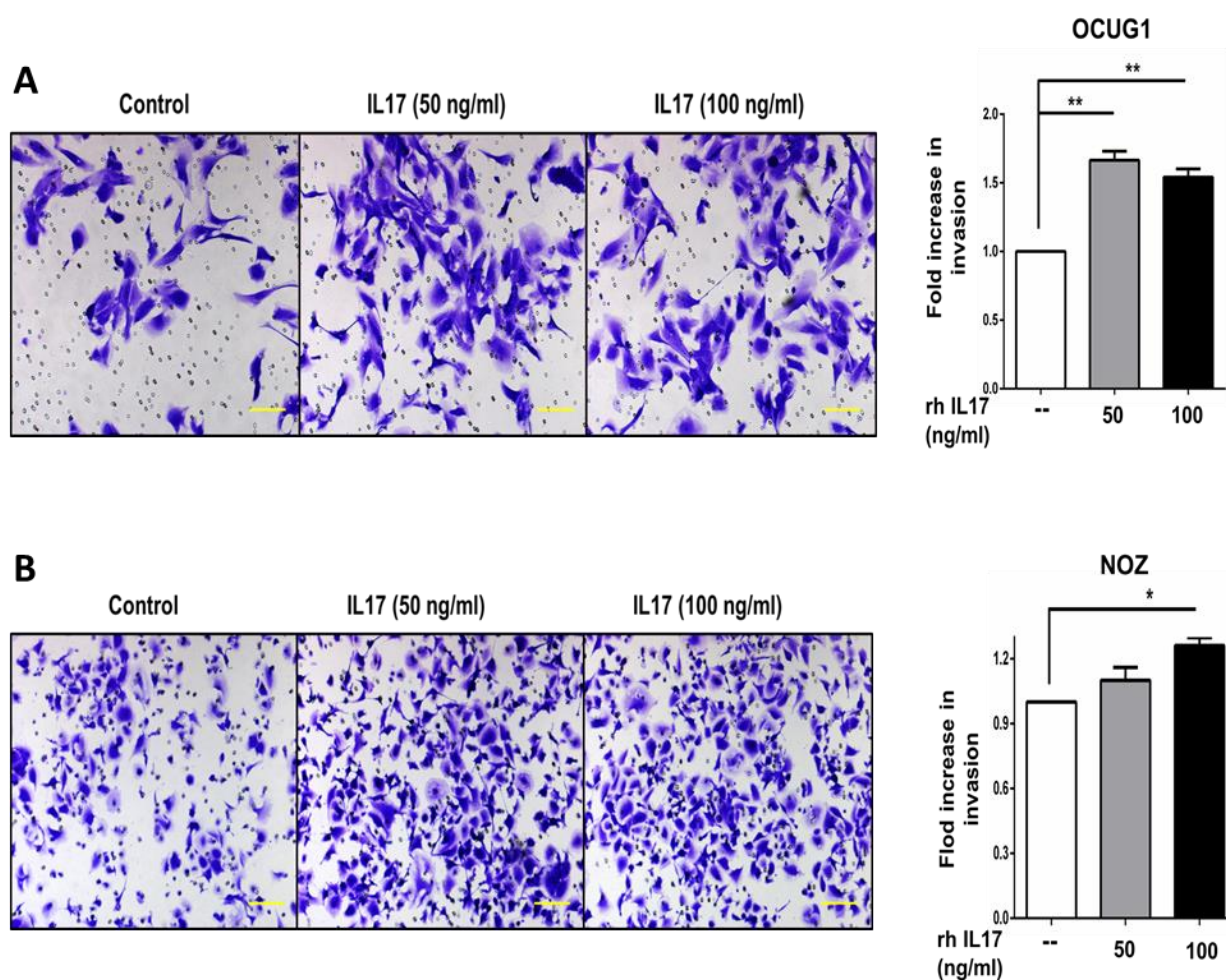
**Figure 6.2 : Effect of IL17 on migratory potential of GBC cells.** OCUG-1 (A) and NOZ (B) cell lines were analysed for migratory potential by wound healing assay in presence of different concentrations of rhIL17 for 21 h. Representative figures of three independent experiments are depicted. Summarized data is presented as percent wound closure and shown as bar diagram. Data was analysed using Student's *t* test and shown as mean  $\pm$  SEM with \*  $p < 0.05$ ; \*\*  $p < 0.01$ .

#### 6.2.4 rhIL17 promotes invasive potential of gallbladder tumor cells

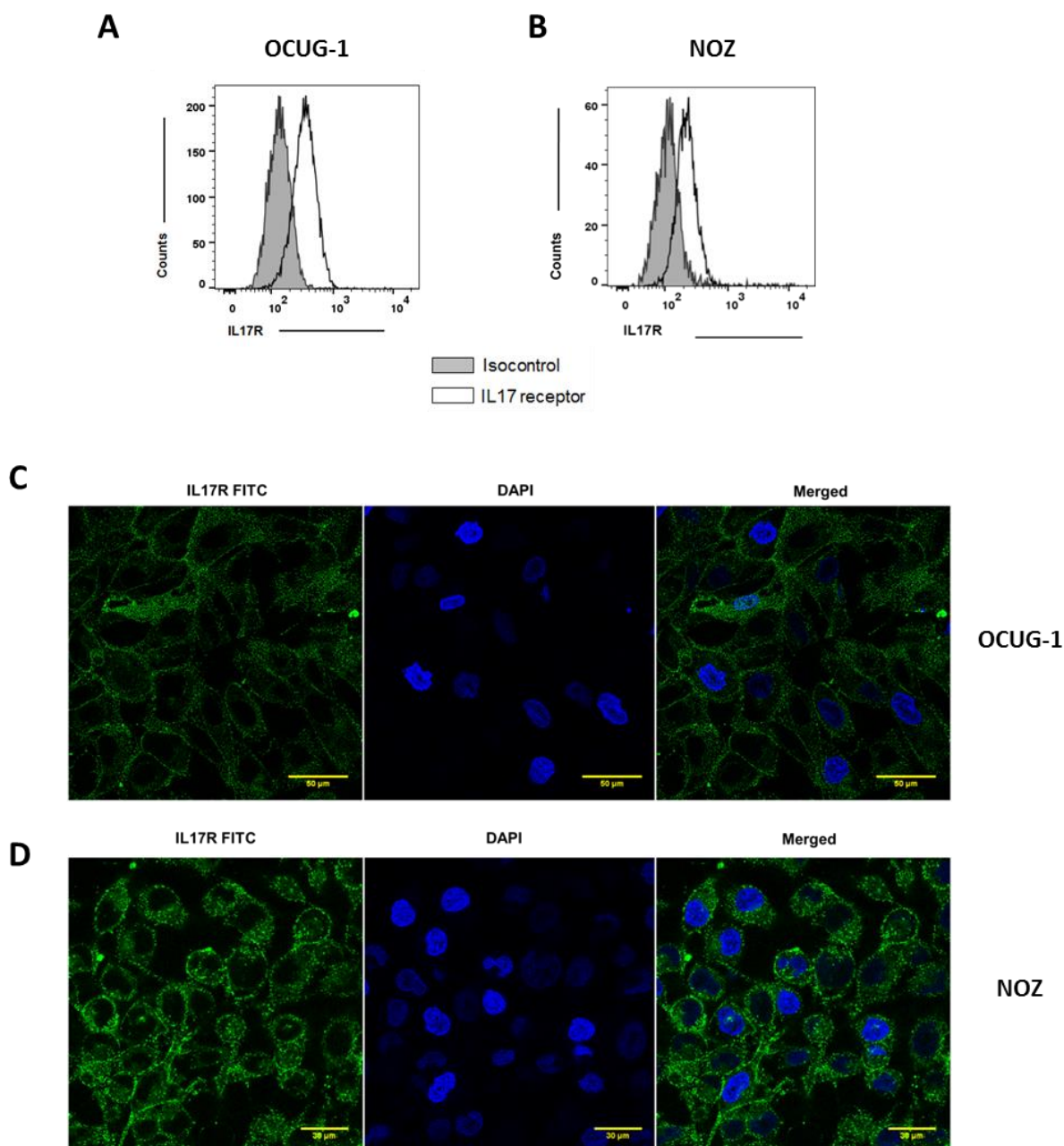
To investigate whether rhIL17 influences the invasive potential of GBC, trans-well migration of GBC cells through matrigel (mimicking basement membrane) was analysed upon treatment with rhIL17. OCUG-1 or NOZ cells treated with rhIL17 (50, 100 ng/ml) were added to the upper chamber (trans-well insert) of 24-well trans-well system pre-coated with matrigel. William's E medium supplemented with 10% FBS was used as chemoattractant in the lower chamber. It was observed that the numbers of OCUG-1 and NOZ cells invaded to the lower side of the trans-well were significantly increased upon treatment of rhIL17 compared to treatment with medium alone (Figure 6.3 A and B). However, the fold increase in invasive potential of OCUG-1 cells (Figure 6.3 A) was higher than NOZ cells (Figure 6.3 B). Thus the data demonstrated that the rhIL17 aids in invasiveness of gallbladder tumor cells and has profound effect on poorly differentiated cells of GBC.

#### 6.2.5 Gallbladder tumor cells express IL17 receptor on the surface

The proinflammatory functions of IL17 are mediated through IL17 receptor. Expression of IL17R on GBC cells was determined on poorly differentiated (OCUG-1) and moderately differentiated (NOZ) GBC cell lines by flow cytometry. It was observed that more than 80% of OCUG-1 and NOZ cells express IL17R (Figure 6.4 A and B). The localization of IL17 receptor was further confirmed by immunofluorescence staining using confocal imaging. As shown in figure 6.4 C and D, IL17 receptor is expressed by both the cell lines (OCUG-1 and NOZ) on the surface. This study clearly indicates that the IL17 receptor present extracellularly on poorly differentiated as well as on moderately differentiated GBC cells.



**Figure 6.3 : Effect of IL17 on invasion potential of gallbladder tumor cells.** The figure depicts invasion potential OCUG-1 (A) and NOZ (B) cell lines depicting in presence of different concentration of rhIL17 using matrigel invasion assay. The Bar graph represents fold increase in invasion. Data was analysed using student's *t* test and shown as mean  $\pm$  SEM with \*  $p < 0.05$ ; \*\*  $p < 0.01$ .



**Figure 6.4 : GBC cells express IL17 receptor.** (A-B) A histogram indicates expression of IL17 receptor on OCUG-1 cells (A) and NOZ cells (B) analysed by flow cytometry. (D-E) Expression of IL17 receptor on OCUG-1 cells (C) and NOZ cells (D) analysed by immunofluorescence staining.

#### 6.2.6 T $\gamma$ $\delta$ 17 cells express CXCR3 chemokine receptor

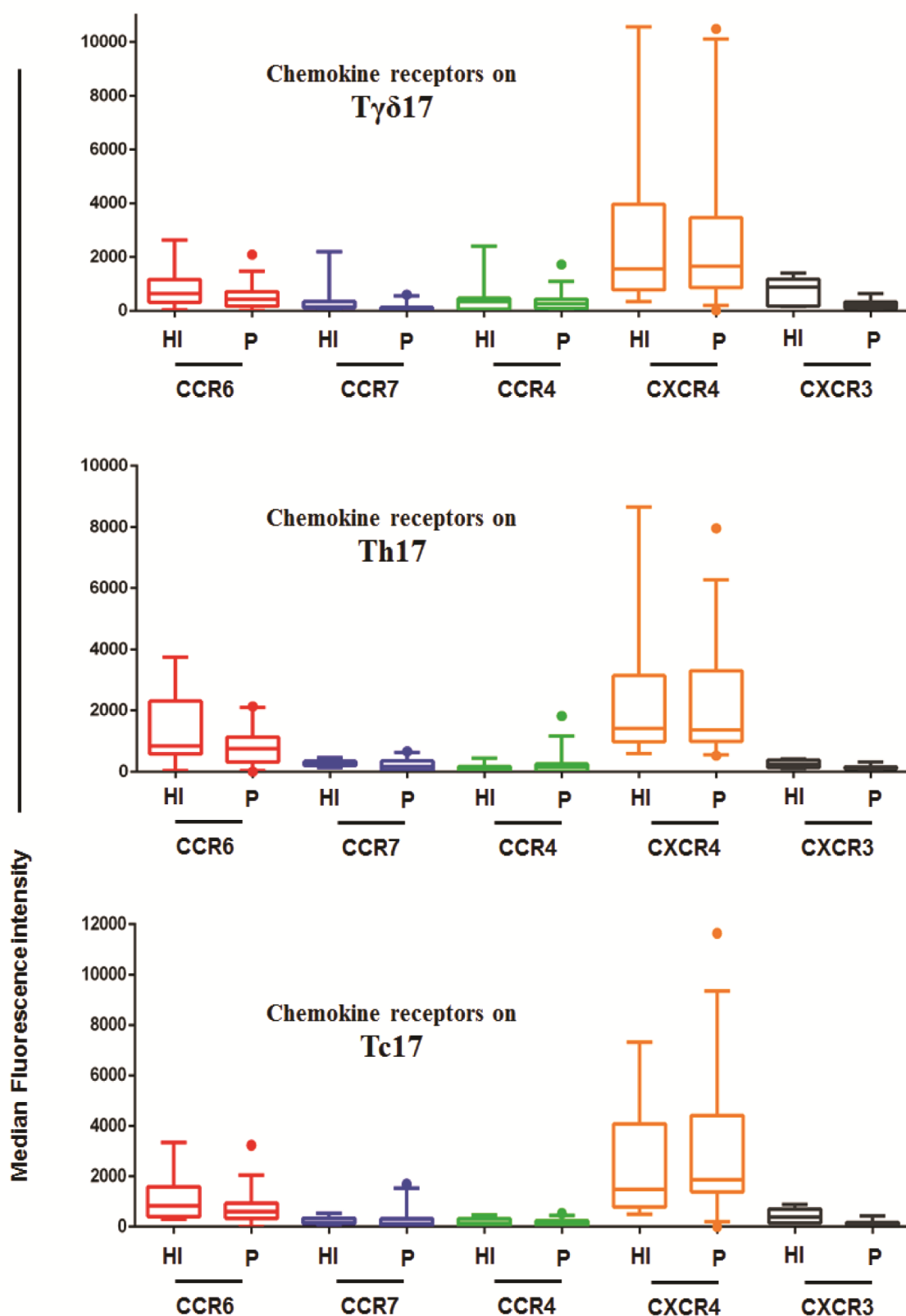
Immunophenotyping of IL17 producing cells in GBC patients revealed that T $\gamma$  $\delta$ 17 cells were elevated in tumor environment. We proposed that T $\gamma$  $\delta$ 17 cells would be migrating to the

tumor tissue from peripheral blood. To test this, the expression of chemokine receptors (CCR6, CCR7, CCR4, CXCR4 and CXCR3) were analysed on Th17, Tc17 and T $\gamma$  $\delta$ 17 cells in peripheral blood of GBC patients (n=35) and HI (n=15) by flow cytometry. It was observed that the expression of these chemokine receptors on T $\gamma$  $\delta$ 17, Th17 and Tc17 cells (measured as median fluorescence intensity) were comparable in GBC patients and HI (Figure 6.5).

Next, the expression of chemokine receptors was compared among Th17, Tc17 and T $\gamma$  $\delta$ 17 cells in peripheral blood of GBC patients (n=35). The data showed that T $\gamma$  $\delta$ 17 expressed elevated levels of CCR4 and CXCR3 expression compared to Th17 or Tc17 (Figure 6.6 C and E). However, CCR6, CCR7 and CXCR4 were expressed at comparable levels by T $\gamma$  $\delta$ 17, Th17 and Tc17 (Figure 6.6 A, B and D). The data suggests that T $\gamma$  $\delta$ 17 cells may be using chemokine axis through CXCR3 and CCR4 receptors.

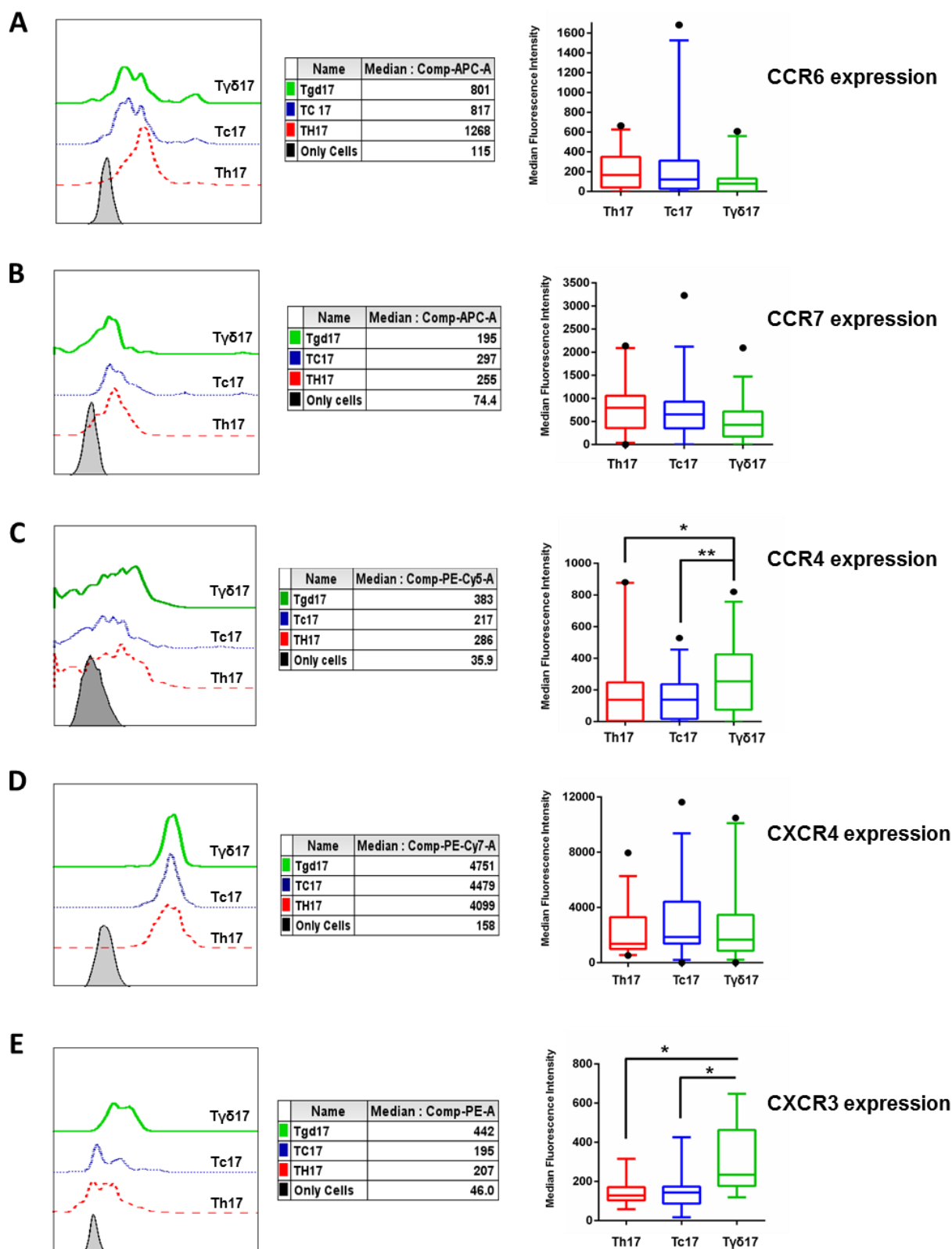
#### **6.2.7 T $\gamma$ $\delta$ 17 cells migrate towards tumor environment through CXCR3/CXCL9 chemokine axis**

It is reported that  $\gamma$  $\delta$ T cells express CCR4 as homing receptor [324-326]. Thus to investigate the contribution by CXCR3 in migration of T $\gamma$  $\delta$ 17 cells to the tumor, T $\gamma$  $\delta$ 17 cells were first purified to > 90% purity using immunomagnetic separation from peripheral blood of HI (Figure 6.7 A). Purified T $\gamma$  $\delta$ 17 cells were cultured with GBC cell line (OCUG-1) or in presence of rhCXCL9 (ligand of CXCR3) or cell-free tumor supernatants of surgically resected gall bladder tumors in trans-well assay. T $\gamma$  $\delta$ 17 cells were pre-incubated in presence or absence of neutralizing anti-CXCR3 antibody. Enhanced migration of T $\gamma$  $\delta$ 17 cells was observed towards OCUG-1 or rhCXCL9 or tumor supernatants compared to medium alone. The migration of T $\gamma$  $\delta$ 17 was significantly curtailed in presence of neutralizing anti-CXCR3 antibody (Figure 6.7 B).



**Figure 6.5 :** Expression of chemokine receptors on T $\gamma$  $\delta$ 17, Th17 and Tc17 in GBC patients and HI. Summarized data presented as box whisker plots shows expression of chemokine receptors (CCR6, CCR7, CCR4, CXCR4 and CXCR3) on T $\gamma$  $\delta$ 17 (A),

Th17 (B) and Tc17 (C) in peripheral blood of GBC patients (n=35) and HI (n=15). The data is presented as median fluorescence intensity. HI, healthy individuals; P, GBC patients. The box plots show median (middle line), 5<sup>th</sup> and 95<sup>th</sup> percentiles (box), extreme values (whiskers) and outliers (dark circles).

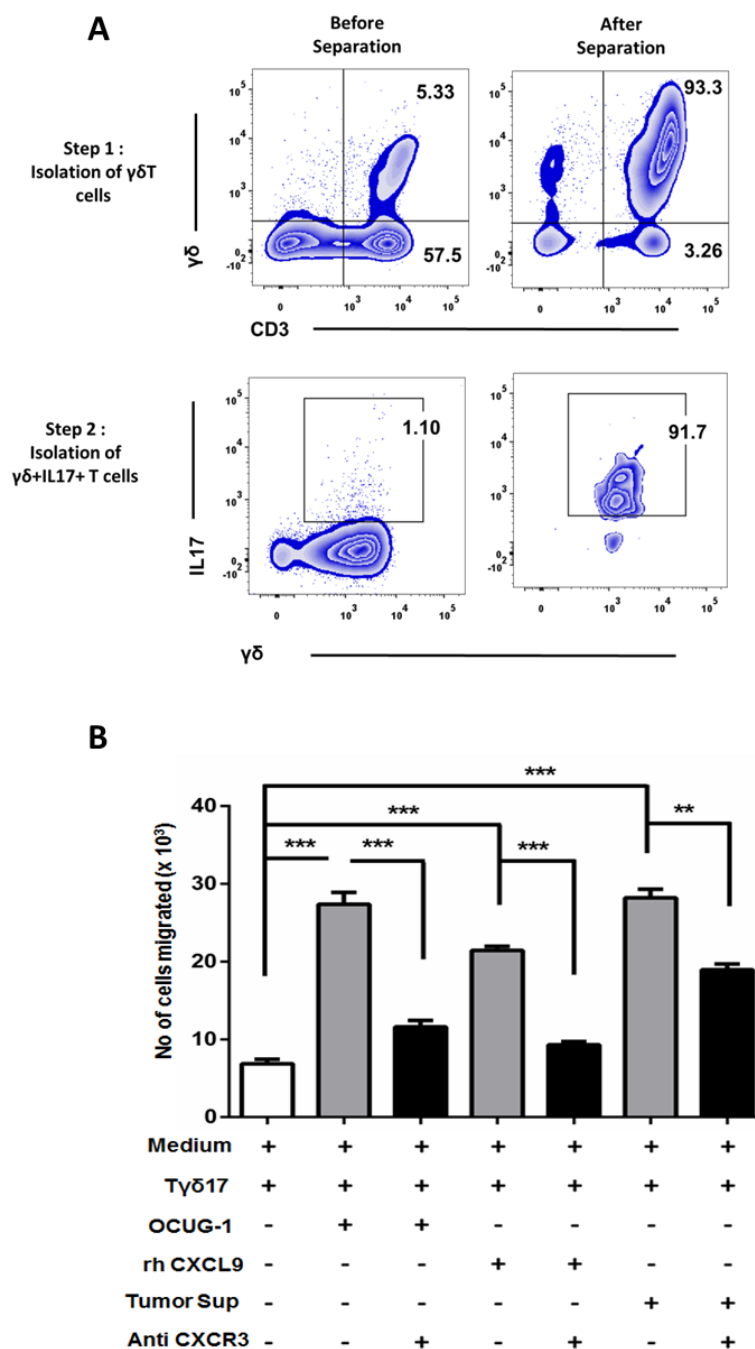


**Figure 6.6 : Comparative analysis of chemokine receptor expression on T $\gamma$  $\delta$ 17, Th17 and Tc17 in GBC patients.** Expression of chemokine receptors on T $\gamma$  $\delta$ 17 (Green), Th17 (Blue) and Tc17 (Red) in peripheral blood of GBC patients (n=35) were analysed by flow cytometry and depicted as representative overlaid histograms. Shaded histogram represents isocontrol of respective fluorochrome. Median expression of respective chemokine receptors on T $\gamma$  $\delta$ 17, Th17 and Tc17 is shown as representative table. A collective data of expression of CCR6 (A), CCR7 (B), CCR4 (C), CXCR4 (D) and CXCR3 (E) is presented as box whisker plots. The box plots show median (middle line), 5<sup>th</sup> and 95<sup>th</sup> percentiles (box), extreme values (whiskers) and outliers (dark circles). Results are analysed by Mann-Whitney test and student's t test with \*(p < 0.05); \*\*(p < 0.01).

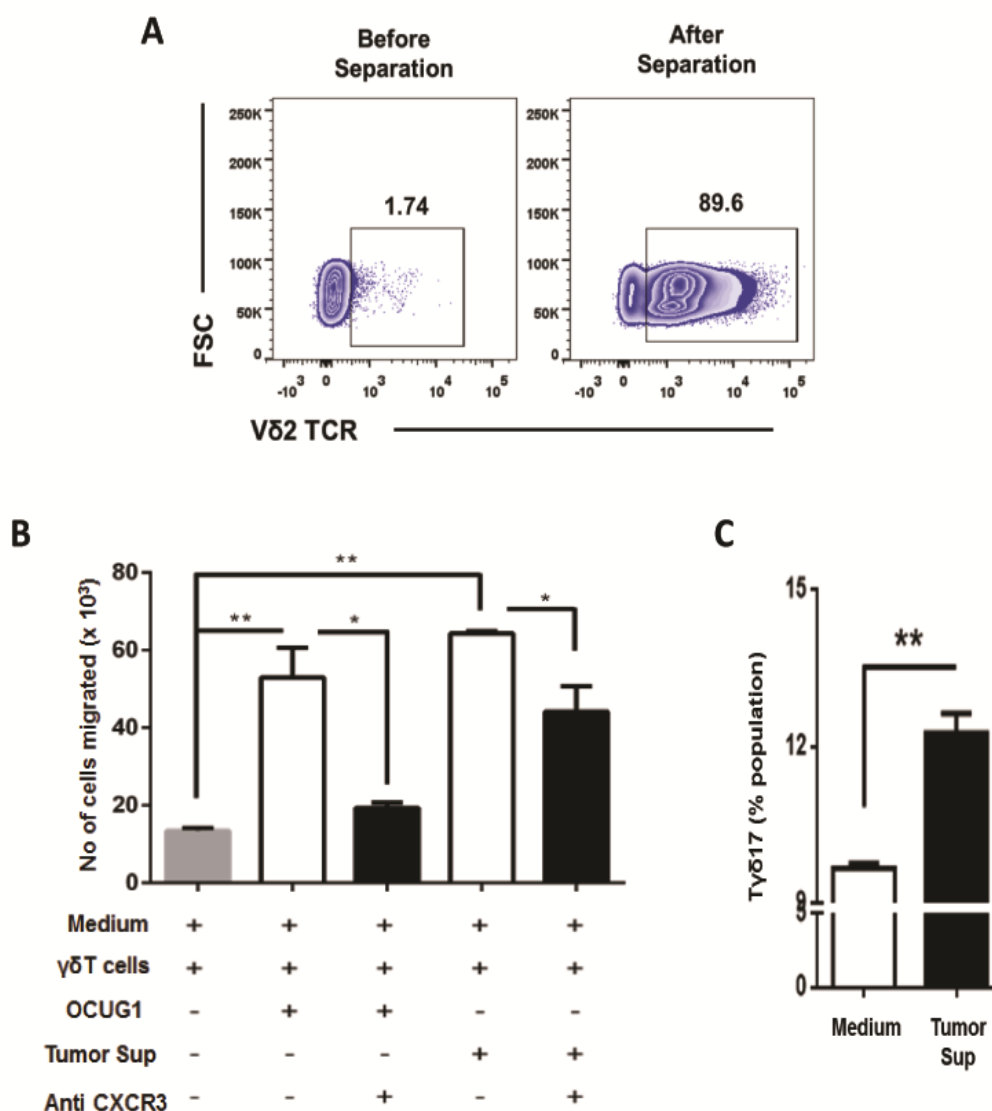
Further to study if total  $\gamma\delta$ T cells can also migrate towards GBC tumor environment, purified  $\gamma\delta$ T cells (Figure 6.8 A) were co-cultured with OCUG1 or cell free tumor supernatant in a trans-well assay in presence or absence of neutralizing anti-CXCR3 antibody. We observed an increased migration of  $\gamma\delta$ T cells towards OCUG-1 cells as well as tumor supernatant compared to medium alone which was significantly abrogated in presence of anti-CXCR3 antibody (Figure 6.8 B). The data suggests that the tumor environment induces recruitment of T $\gamma$  $\delta$ 17 and  $\gamma\delta$ T cells towards tumor bed through CXCL9-CXCR3 axis.

### 6.2.8 GBC tumor environment promotes T $\gamma$ $\delta$ 17 phenotype

As shown in figure 5.6 C, the cytokines (IL6, IL1 $\beta$ , IL23, TGF $\beta$ ) required for differentiation of  $\gamma\delta$ T cells towards T $\gamma$  $\delta$ 17 phenotype were present in GBC tumor environment. Thus to study the immunomodulatory effect of GBC tumor environment, isolated  $\gamma\delta$ T cells were cultured in presence or absence of tumor supernatant of freshly resected gallbladder tumor tissue in the presence of anti-CD3/anti-CD28 for 48 h. The levels of T $\gamma$  $\delta$ 17 cells were analysed in the cultures by flowcytometry.  $\gamma\delta$ T cells cultured in the presence of tumor supernatant showed increased levels of T $\gamma$  $\delta$ 17 cells compared to cells cultured with medium alone (Figure 6.8 C). Thus the data suggests that the GBC tumor environment support the differentiation of  $\gamma\delta$ T cells towards IL17 producing phenotype.



**Figure 6.7 : Migration of Purified T $\gamma\delta$ 17 cells towards GBC tumor tissue.** (A) Representative figure of purity of sorted T $\gamma\delta$ 17 cells from peripheral blood of HI. Upper panel shows purity of  $\gamma\delta$ T cells. IL17 producing  $\gamma\delta$ T cells were sorted to more than 90% purity as shown in lower panel. (B) Isolated T $\gamma\delta$ 17 cells were cultured with OCUG-1 cells or rhCXCL9 or tumor supernatants in a trans-well assay in presence or absence of anti-CXCR3 mAb. Data presented as total number of migrated cells (n=3). Data was analysed by student's *t* test and shown as mean  $\pm$  SEM with \*  $p < 0.05$ ; \*\*  $p < 0.01$ ; \*\*\*  $P < 0.001$ .

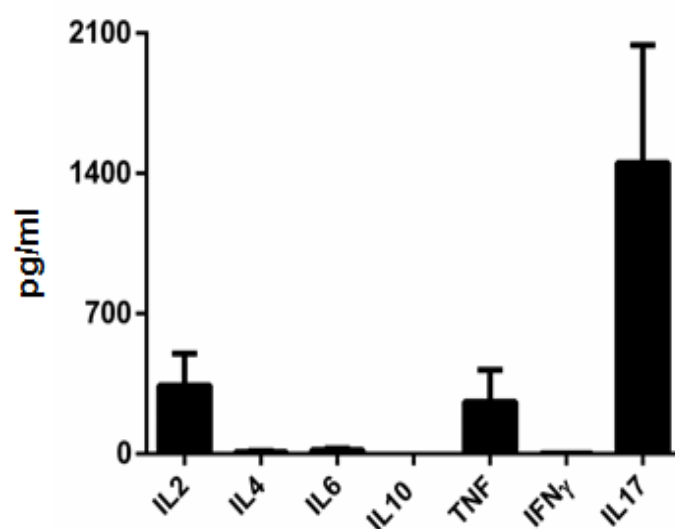


**Figure 6.8 : Recruitment of  $\gamma\delta T$  cells to GBC tumor environment.** (A) Representative zebra plot of purity of  $\gamma\delta T$  cells after immune-magnetic separation from peripheral blood of HI. (B) In a trans-well assay, isolated  $\gamma\delta T$  cells were cultured with OCUG-1 cells or tumor supernatants in presence or absence of anti-CXCR3 mAb. Migration was monitored by counting total number of migrated cells to the lower chamber ( $n=3$ ). (C) Purified  $\gamma\delta T$  cells were cultured with tumor supernatant or medium alone in presence of anti-CD3/anti-CD28 stimulus. IL17 producing  $\gamma\delta T$  cells were determined by flow cytometry ( $n=3$ ). Data was analysed by student's  $t$  test and shown as mean  $\pm$  SEM with \*  $p<0.05$ ; \*\*  $p<0.01$

### 6.2.9 Ty $\delta$ 17 cells predominantly secrete IL17

In order to characterise Ty $\delta$ 17 cells, the cytokine profile of Ty $\delta$ 17 was analysed. Purified Ty $\delta$ 17 cells were stimulated with anti-CD3/anti-CD28 for 24 h in serum free medium. Cytokine estimation in cell free supernatant showed that Ty $\delta$ 17 primarily secrete high levels

of IL17 and low levels of IL2 and TNF $\alpha$  but did not produce other cytokines (IL4, IL6, IL10 and IFN $\gamma$ ) (Figure 6.9 A). Thus the data confirms the purity of T $\gamma$  $\delta$ 17 cells and suggests that IL17 is the signature cytokine of T $\gamma$  $\delta$ 17 cells.

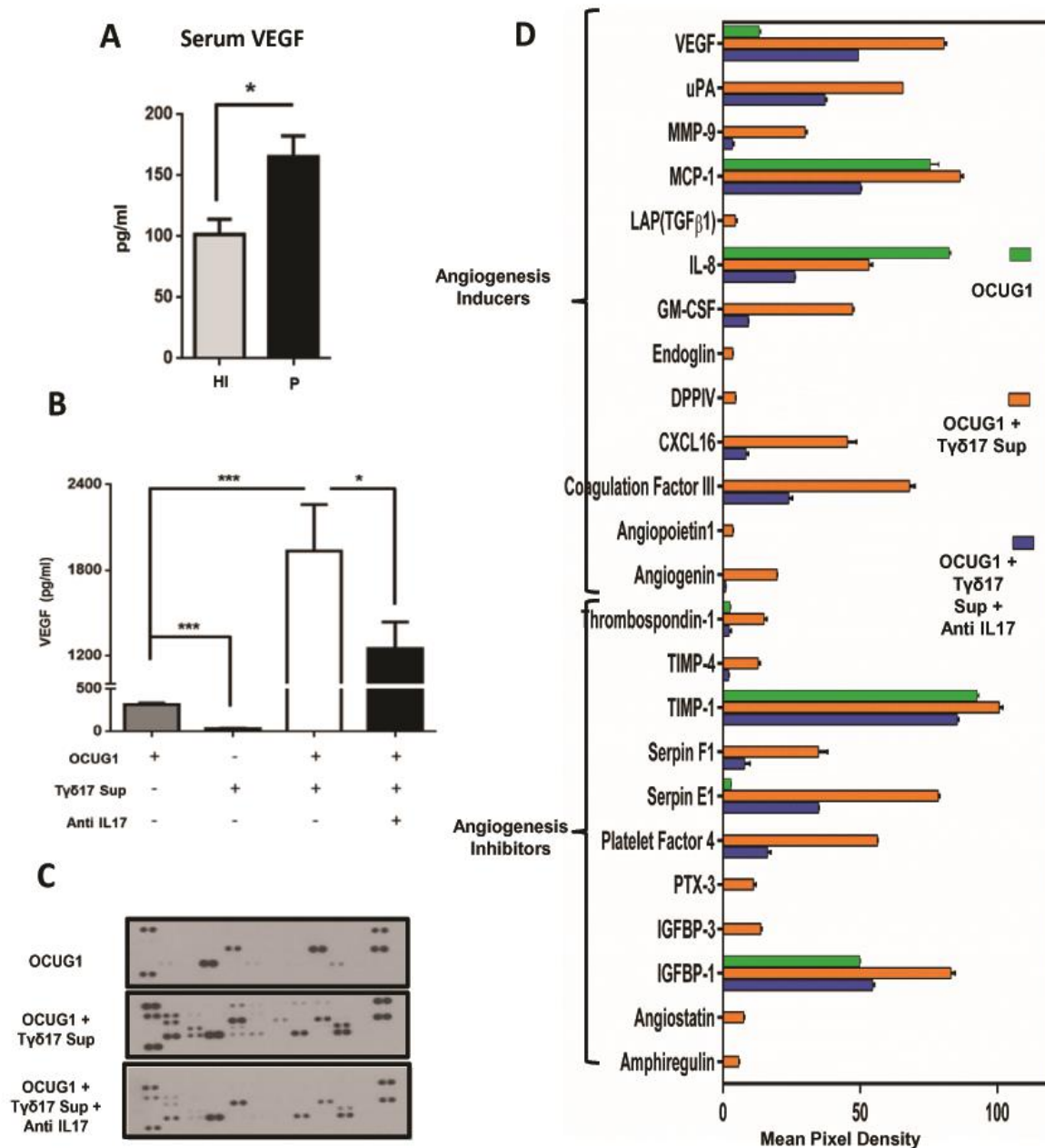


**Figure 6.9 : Characterization of cytokine profile of T $\gamma$  $\delta$ 17 cells.** Isolated T $\gamma$  $\delta$ 17 cell were stimulated with anti-CD3/anti-CD28 for 24 h (n=5). The cytokines were measured in cell-free culture supernatants by cytometric bead array. The data are presented as pg/ml.

#### 6.2.10 T $\gamma$ $\delta$ 17 cells induce angiogenesis related factors in GBC cells

VEGF is a key mediator of tumor angiogenesis and metastasis. As shown in figure 6.10 A, the serum levels of VEGF were significantly increased in GBC patients compared to HI. Thus to investigate whether the elevated levels of T $\gamma$  $\delta$ 17 in GBC patients contribute to VEGF production and tumor progression, the proangiogenic activity of T $\gamma$  $\delta$ 17 cells was studied *in vitro*. The cell-free supernatant of T $\gamma$  $\delta$ 17 cells was cultured with GBC cells (OCUG-1 cell line) for 48 h and the levels of VEGF were estimated in culture supernatants. The data demonstrated that T $\gamma$  $\delta$ 17 cells alone secreted marginal amount of VEGF. However, culture of T $\gamma$  $\delta$ 17 cells with OCUG-1 cells upregulated the secretion of VEGF by OCUG-1 cells compared to OCUG-1 cells cultured with medium alone. Addition of neutralizing anti-IL17

antibody to the T $\gamma$  $\delta$ 17 – supernatant, significantly abrogated VEGF production by OCUG-1 cells (Figure 6.10 B). The data suggests that the VEGF production by the GBC cells is regulated by T $\gamma$  $\delta$ 17 through IL17 secretion.



**Figure 6.10 : T $\gamma$  $\delta$ 17 cells induce angiogenesis related proteins in gallbladder cancer cells.** (A) Serum VEGF levels in GBC patients (n=11) and HI (n=7) were measured by ELISA. VEGF levels are presented as pg/ml. (B) OCUG-1 cells were cultured with cell-

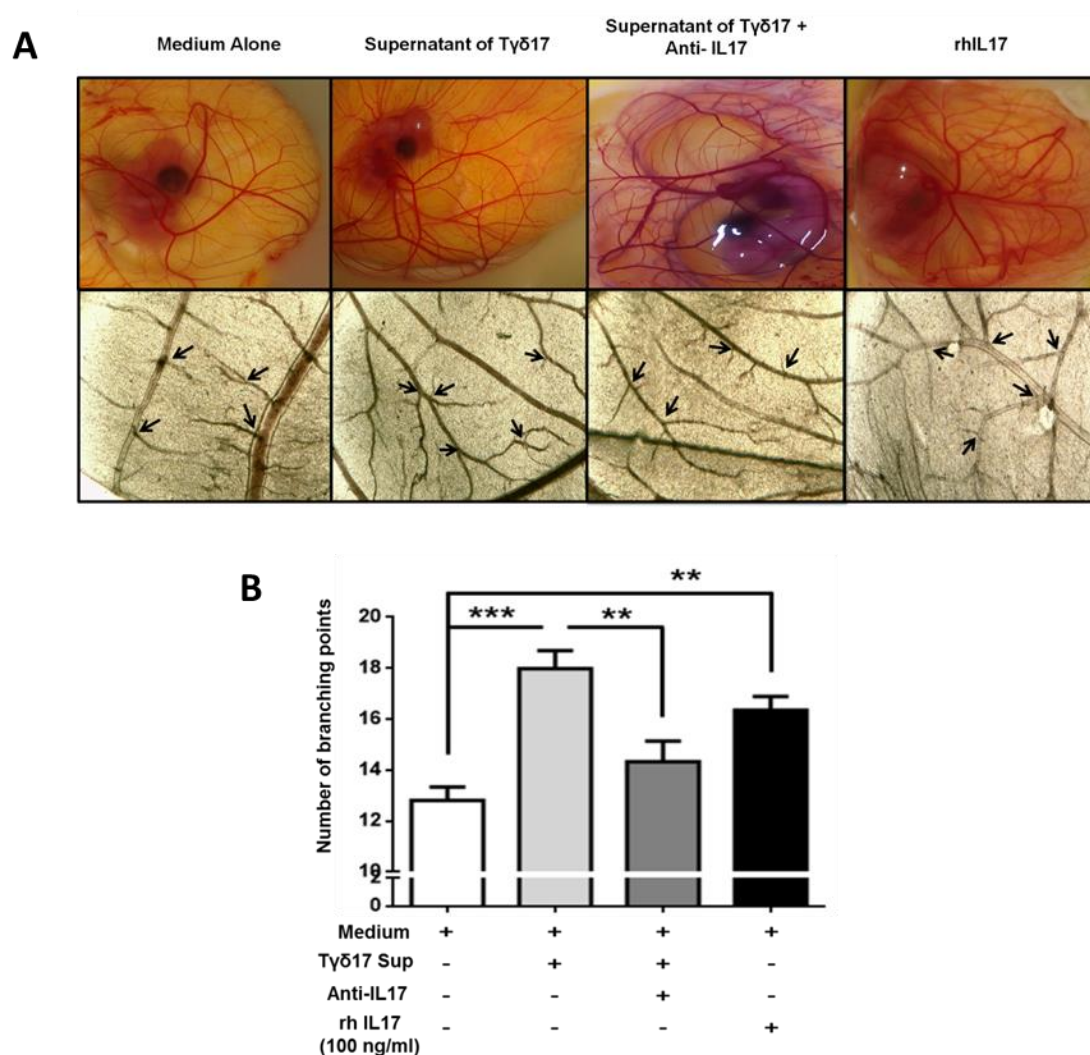
*free supernatants of T $\gamma$  $\delta$ 17 in presence or absence of neutralizing anti-IL17 antibody. VEGF levels in the supernatants were estimated using ELISA (n=6). (C-D) Supernatant of T $\gamma$  $\delta$ 17 was incubated with OCUG-1 cells in presence or absence of anti-IL17. Angiogenesis related proteins in culture supernatants were analysed by human angiogenesis proteome profiler array. (C) Representative membranes showing array blot developed using chemi-luminescence. (D) The bar diagram showing densitometric analysis of angiogenesis array blots represented as mean pixel density (n=2). Data was analysed by student's t test and shown as mean  $\pm$  SEM with \* $p$ <0.05; \*\* $p$ <0.01*

IL17 is reported to regulate many downstream target genes associated with angiogenesis. Thus the effects of T $\gamma$  $\delta$ 17 cells on induction of angiogenesis related genes in GBC cells were studied by human protein profiler angiogenesis array. Cell-free supernatants from T $\gamma$  $\delta$ 17 cells significantly upregulated secretion of angiogenesis promoting factors from OCUG-1 cells such as VEGF, uPA, MMP9, MCP1, GM-CSF, CXCL16, coagulation factor III, angiogenin, etc. compared to OCUG-1 cells cultured with medium alone (Figure 6.10 C and D). This effect was abrogated by neutralizing IL17 in T $\gamma$  $\delta$ 17-supernatant using anti-IL17 mAb. OCUG-1 cells secreted high IL8 and addition of T $\gamma$  $\delta$ 17 supernatant did not further increase its levels. Along with angiogenesis inducers, certain angiogenesis inhibitors like thrombospondin-1, TIMP-1, serpine-1, platelet factor 4, IGFBP-1, etc. were also secreted by OCUG-1 cells in presence of T $\gamma$  $\delta$ 17 supernatant. The levels of angiogenesis inhibitors also decreased in presence of anti-IL17 mAb (Figure 6.6 C and D). Thus the data demonstrated that T $\gamma$  $\delta$ 17 cells induce proangiogenic proteins in GBC cells.

#### **6.2.11 T $\gamma$ $\delta$ 17 cells promote blood vessel formation in chorioallantoic membrane (CAM) of chick embryo**

The proangiogenic effects of T $\gamma$  $\delta$ 17 were further validated by CAM assay. Cell-free supernatants of T $\gamma$  $\delta$ 17 were *ex vivo* inoculated in CAM of 5 days old chick embryos. The number of blood vessels and branching pattern were monitored for 48 h and analysed individually by capturing images. It was observed that treatment of CAM with of T $\gamma$  $\delta$ 17

supernatant significantly enhanced the vascularization (measured as number of branching points emerging from secondary blood vessels) compared to treatment of CAM with medium alone (Figure 6.11 A). Similar pronounced effect of vasculogenesis was observed in presence of rhIL17. The neutralization of IL17 in T $\gamma$  $\delta$ 17 supernatant showed decreased blood vessel formation in the CAM treated with T $\gamma$  $\delta$ 17 supernatant (Figure 6.11 A and B). Further, the blood vessels formed in presence of T $\gamma$  $\delta$ 17 supernatant and rhIL17 showed tree-like branching with increased number of branching points from secondary blood vessels compared to parallel branching observed in presence of medium alone (Figure 6.11 A lower panel). Thus the data suggests that T $\gamma$  $\delta$ 17 cells can modulate the blood vessel formation through IL17.



**Figure 6.11 : Pro-angiogenic effect of T $\gamma$  $\delta$ 17 cells on chorioallantoic membrane of chick embryo** (A) Cell free culture supernatant of T $\gamma$  $\delta$ 17 cells was inoculated to 5 days old CAM of chick embryo in presence or absence of anti-IL17 antibody. Representative images of CAM assay depicting enhanced vasculogenesis in presence of supernatant of T $\gamma$  $\delta$ 17 or rhIL17 compared to medium alone. Addition of anti-IL17 showed decreased blood vessels. The lower panel shows images of CAM recorded using 4X objective. Arrows indicate branching points. (B) Bar diagram showing summarized data of number of branching points in CAM assay (n=3). Data was analysed by student's *t* test and shown as mean  $\pm$  SEM with \*  $p < 0.05$ ; \*\*  $p < 0.01$

### 6.3 Summary

The results presented in current chapter revealed that IL17 induces proliferation, migration and invasion of GBC cells in concentration dependent manner. The pro-tumor functions of IL17 may be mediated through IL17 receptor expressed by GBC cells. It was observed that T $\gamma$  $\delta$ 17 cells expressed elevated levels of CXCR3 receptor than Th17 and Tc17 cells. T $\gamma$  $\delta$ 17 utilize novel CXCR3-CXCL9 chemokine axis to migrate towards GBC cells. Culture of  $\gamma$  $\delta$ T cells with cell free tumor supernatants of gallbladder tumor showed increased T $\gamma$  $\delta$ 17 phenotype. The T $\gamma$  $\delta$ 17 cells were successfully isolated from peripheral blood of HI and the cytokine characterization showed that T $\gamma$  $\delta$ 17 cells predominantly secretes IL17. Culture of T $\gamma$  $\delta$ 17 cells with GBC cells induced VEGF and other angiogenesis related proteins. It was further confirmed by CAM assay that T $\gamma$  $\delta$ 17 cells aid in blood vessel formation through IL17 production. Overall the data demonstrated that T $\gamma$  $\delta$ 17 is a pro-tumorigenic subtype of  $\gamma$  $\delta$ T cells.

## **Chapter 7**

# **Discussion**

## Discussion

GBC is highly malignant cancer known for its aggressive biological nature and poor clinical presentation. The poor prognosis is due to lack of sensitive screening tests for early detection resulting in delayed diagnosis [11]. Although surgical resection of gallbladder is a curative treatment, less than 10% of GBC patients present with early stage disease and can be considered for surgery [12]. As of today, prognostic biomarkers and effective adjuvant immunotherapy for GBC are unavailable. Use of monoclonal antibodies targeting antigens expressed on tumor cells have shown therapeutic efficacy in cancer patients [327]. Antibodies such as rituximab targeting CD20 in non-Hodgkin B cell lymphoma, trastuzumab targeting HER2 in breast cancer, and cetuximab targeting EGFR in colorectal cancer are introduced in clinical practice [327]. These antibodies induce tumor cell death by blocking ligand-receptor growth and survival pathways [327]. The clinical trials using antibodies targeting tumor antigens in biliary tract cancer patients have shown unfavourable outcome [113]. Erlotinib, a small-molecule inhibiting the EGFR tyrosine kinase domain was evaluated in biliary tract cancer patients in phase II study. The study showed that overall survival of patients was 7.5 months with 52% of patients alive after 6 months [328]. Similarly Lapatinib, a dual EGFR1 and ErbB2 inhibitor, when tested in a phase II trial in biliary tract cancer patients showed progression free survival of 1.8 months and overall survival of 5.2 months [329]. The combination therapies using antibodies specific for tumor antigens and chemotherapeutic drugs showed dismal long term survival of patients with biliary tract [113]. These reports suggest that it is necessary to distinguish biliary tract cancer from other hepato-pancreatic malignancies in view of treatment modalities [113]. Therefore, there is a need for developing novel approaches for successful management of GBC.

The emerging evidences in recent past have highlighted the importance of antibody-based strategies focussing on enhancing antitumor immune responses by targeting immune cells,

irrespective of tumor antigens [330, 331]. Promising results are obtained in patients with advanced melanoma, non-small cell lung cancer, prostate cancer, renal cell cancer, colorectal cancer, etc. [332, 333]. The antibodies used in these studies were targeted against immune cells expressing inhibitory molecules CTLA-4, PD-1 and PD-L1 (immune checkpoints) [333]. Cytotoxic T-lymphocyte antigen-4, CTLA-4 (CD152), is a type I transmembrane glycoprotein that presents homology to CD28. It down-regulates T cell activation by inhibiting co-stimulation by CD28, playing a key role in the regulation of immune homeostasis [332]. CTLA-4 is predominantly expressed on activated CD4<sup>+</sup> helper T cells and not on CD8<sup>+</sup> cytotoxic T cells. Therefore, heightened CD8 responses is observed in anti-CTLA-4-treated patients [334].

Similarly PD-1 (CD279) is another inhibitory receptor expressed by activated T cells. TCR engagement with MHC-antigen complex induces PD-1 expression, and PD-1/ PD-L1 binding leads to the inhibition of T cell activation and effector functions [335]. PD-L1 is highly expressed on human tumors and it has been suggested that PD-L1 has a role in attenuating anti-tumor immune responses of CD4<sup>+</sup> and CD8<sup>+</sup> T cells expressing PD-1 [336]. The anti-CTLA-4 monoclonal antibody ipilimumab, a fully human IgG1, and anti-PD-1 antibody nivolumab were the first immune checkpoint-blocking drugs to enter clinical practice for treatment of melanoma, colorectal and prostate cancer patients [334]. Another approach in the treatment of cancer is the use of engineered T cells expressing chimeric antigen receptor (CAR-T cell therapy). T cells are engineered to express TCR derived from the variable region of an antigen-specific antibody and is linked to signalling components of costimulatory signals leading to T cell activation. The treatment protocols for this therapy are under development [337]. Monoclonal antibodies specific for regulatory T cells have also showed improved patient outcome. Treg cells suppress antitumor immune response through CTLA-4 mediated downregulation of costimulatory molecules on APCs [51]. Thus targeting CTLA-4

or CD25 on Treg cells leads to decrease in Treg cells and improved antitumor immune response [51].

The current available modalities of cancer treatment have transformed from non-specific chemotherapeutic drugs to more specific targeted therapy providing long-term clinical benefit in some advanced cancer patients [337]. The understanding of the immune evasion strategies of tumor at molecular level has led to the emergence of novel molecular targets. To extrapolate the advent of targeted therapies to gallbladder cancer treatment, it is necessary to understand the role of immune response which is not investigated in GBC patients.

The GBC patients are predisposed with chronic inflammatory condition of cholelithiasis. The studies in the murine model of cholesterol gallstone disease, presence of cholesterol crystals led to increased mucus layer thickness, interleukin-1 and myeloperoxidase activity in the wall of the gallbladder [91]. These changes were accompanied by inflammatory infiltrate composed of eosinophils, macrophages, neutrophils and lymphocytes within the lamina propria [92]. Another study reported that Rag2<sup>-/-</sup> mice, (deficient for B- and T-cells), were resistant to cholesterol gallstone formation suggesting that functional T cells are crucial in the development of gallstones [93]. Although these studies indicate the significance of inflammatory immune response in gallstone disease, the role of inflammatory factors contributed by immune cells is not investigated in GBC patients.

Thus the present study aimed at understanding the immune scenario in GBC patients and identify the proinflammatory (IL17 producing T cells) and immunosuppressive (Treg) subsets that may contribute to pathogenesis of GBC.

The important hallmark of malignant progression of cancer is an escape from immunosurveillance [121]. The immune escape of cancer is accompanied by profound immune destruction [338]. Immunophenotyping of PBMCs in GBC patients revealed that the

cells contributing to adaptive immunity ( $CD4^+$  T cells,  $CD8^+$  T cells, B cells and NKT cells) were significantly decreased in peripheral blood of GBC patients. However, the ratio of  $CD4^+/CD8^+$  T cells did not alter in GBC patients compared to HI, suggesting that the decline in the percentage of T lymphocytes observed in GBC patients is not subset specific. The PBMCs of GBC patients stimulated with anti-CD3 (TCR agonist) or PHA (mitogen) showed poor proliferative response and secreted decreased levels of effector cytokines ( $IFN\gamma$ , IL6, IL10, IL17, IL8, IL12p70 and IL1 $\beta$ ). The results suggest that the PBMCs in GBC patients are unable to show optimum response to TCR or mitogenic stimulatory signal. The activation of T cells is determined by the engagement of TCR with MHC-antigen complex and efficient signal transduction. The intracellular expression of CD3- $\zeta$  chain associated with TCR is involved in transduction of stimulatory signal and thus plays an important role in T cell activation [339]. Investigation of CD3- $\zeta$  chain in T cells of GBC patients showed that the expression of CD3- $\zeta$  chain was downregulated in T lymphocytes present in peripheral blood and tumor tissue. Moreover, the decrease in CD3- $\zeta$  chain expression was correlated with clinical stage of GBC patients. Our earlier studies in oral cancer patients have demonstrated that CD3- $\zeta$  chain in T lymphocytes of cancer patients undergoes ubiquitination and is subsequently targeted for degradation in the lysosome [340]. However, in tumor compartment, the reduced expression of ELF1, a transcription factor for CD3- $\zeta$  chain expression, resulted into decreased transcription of TCR  $\zeta$  gene [339, 340].

The decreased CD3- $\zeta$  chain expression, poor proliferative response and reduced production of effector cytokines by PBMCs suggest that the immune response in GBC patients is dysfunctional. The alterations observed in immune response in GBC patients and the predisposition of GBC to chronic inflammatory condition of cholelithiasis suggests the significant role of coexistence of poor immunosurveillance and chronic inflammation in GBC. Immunosuppressive cells such as regulatory T cells (Treg) also play significant role in

cancer progression by suppressing antitumor CD4<sup>+</sup> and CD8<sup>+</sup> T cells [51]. The balance of proinflammatory Th17 and immunosuppressive Treg cells is crucial in determining immune response in cancer patients. It is reported that in squamous cell carcinoma the levels of Treg cells were increased and that of Th17 cells decreased with cancer progression [258]. Similar trend was observed in salivary gland tumors [259]. The impaired balance of the Th17 and Treg was also reported in lung cancer, prostate cancer, and cervical cancer [58-60].

Immunophenotyping of GBC patients in the current study revealed that the levels of IL17 producing CD4, CD8 and  $\gamma\delta$ T cells were significantly elevated in peripheral blood and tumor tissue compared to the levels observed in HI. Interestingly, the data highlighted the emergence of recently discovered IL17 producing phenotype of  $\gamma\delta$ T cells. Conventionally  $\gamma\delta$ T cells secrete high levels of IFN $\gamma$  and contribute to antiviral, anti-bacterial, and anti-tumor immunity in humans [212, 234, 341, 342].  $\gamma\delta$ T cells do not require APCs and recognition of antigen is MHC unrestricted, resembling B cells [343]. They can kill infected, activated, stressed, and transformed cells using various strategies such as engagement of death-inducing receptors, such as FAS and TNF-related apoptosis-inducing ligand receptors (TRAILR) and the release of cytotoxic effector molecules such as perforin and granzyme [232, 233]. Human  $\gamma\delta$ T cells recognize HSP (HSP60/70) expressed on tumor cells and enhance its cytolytic activity against the tumors [220, 226]. Similar to Natural killer (NK) cells, human  $\gamma\delta$ T cells also recognise the stress-induced MHC class I-related molecules MICA, MICB and the UL16-binding proteins that are upregulated on malignant or stressed cells [218, 344]. The stress related molecules are ligands for NKG2D expressed by  $\gamma\delta$ T cells and this engagement also enhances  $\gamma\delta$ T cells' response to non-peptide antigens [345].

Studies in recent years have shown the importance of cytotoxic behavior of  $\gamma\delta$ T cells in cell based therapies against cancer [214, 234]. Studies from our lab and others have reported that

$\gamma\delta$ T cells exhibit potent cytotoxicity against tumors [233, 346]. Various clinical trials have been launched in breast, prostate, hepatocellular and renal cell carcinoma patients using *in vivo* activation of  $\gamma\delta$ T cells or by adoptive transfer of activated  $\gamma\delta$ T cells [234]. In contrast,  $\gamma\delta$ T cells isolated from breast tumor biopsies were shown to mediate immunosuppression by inducing senescence in dendritic cells and  $CD4^+$  T cells to suppress their antitumor response [347]. In a murine model of hepatocellular carcinoma,  $\gamma\delta$ T cells were shown as major source of IL17. These cells inhibit  $CD8^+$  T cell response and recruit myeloid derived suppressor cells (MDSCs) thereby promoting development of tumor [255]. Nitric oxide synthase (NOS2) has been shown to polarize  $\gamma\delta$ T cells to produce IL17 and promote metastasis formation in transgenic model of melanoma [348]. In a breast cancer metastasis model,  $T\gamma\delta17$  cells were shown to induce expansion and polarization of neutrophils which suppress cytotoxic antitumor response [349]. Recently, it is shown that  $\gamma\delta$ T cells infiltrating pancreatic ductal adenocarcinoma express elevated levels of T cells exhaustion ligand (PD-L1) and suppress the activity of CD4 and CD8 T cells [235]. Thus, for successful application of  $\gamma\delta$ T cell based immunotherapies in clinics, it is necessary to have a deeper insight into pro-tumor role of  $\gamma\delta$ T cells where data in humans is lacking.

In the present study, we report that  $T\gamma\delta17$  cells are increased in tumor environment and peripheral blood of GBC patients irrespective of clinical stage.  $Th17$  and  $Tc17$  cells were also elevated but  $CD8^+IFN\gamma^+$  and  $\gamma\delta^+IFN\gamma^+$  cells were decreased in GB tumor environment. This supports the existence of chronic inflammation in GBC contributed by immune cells. A murine study in hepatocellular carcinoma has shown that the depletion of  $V\gamma4^+$   $\gamma\delta$  T cells (major source of IL17) resulted in significant reduction in tumor volumes in comparison with wild type mice [255]. Moreover, the infiltrations of effector  $CD8^+IFN\gamma^+$  cells in tumors were significantly increased in  $V\gamma4^+$   $\gamma\delta$ T cell-depleted mice [255]. This suggests that  $T\gamma\delta17$  cells

exhibit pro-tumor functions by dampening anti-tumor immune response. In GBC patients, we observed that T $\gamma\delta$ 17 and Th17 cells were associated with poor survival. On the contrary, GBC patients with increased  $\gamma\delta^+ \text{IFN}\gamma^+$  experienced longer survival. These results strongly suggest that IL17 producing cells play a critical role in immune pathogenesis of human GBC. Moreover, it appears that GBC tumor environment selectively promotes IL17 producing cells as CD8 $^+ \text{IFN}\gamma^+$  and  $\gamma\delta^+ \text{IFN}\gamma^+$  cells were decreased in TILs. Collectively, these results highlight the pathogenic role of T $\gamma\delta$ 17 cells in GBC.

Previously, it was reported that Th17 cells infiltrate the tumor environment and significantly influence the tumor growth through secretion of IL17 [350]. However, the emerging evidences in murine models of hepatocellular carcinoma, breast cancer, skin cancer have shown that major source of IL17 are  $\gamma\delta$ T cells [253, 255, 349]. In GBC patients, it was observed that the propensity of IL17 secretion by  $\gamma\delta$ T cells was increased in tumor compartment than peripheral blood and it was higher compared to Th17 cells. In human colorectal cancer, tumor infiltrating  $\gamma\delta$ T cells were the major contributors of IL17 production and were associated with poor prognosis of patients [246]. It is reported that  $\gamma\delta$ T cells produce IL17 in response to the stimulation by innate cytokines (IL23 and IL1 $\beta$ ) in MHC unrestricted manner [351]. IL17 and IL21 derived from  $\gamma\delta$ T cells promote IL17 production from Th17 cells [351]. Thus the inherent property of  $\gamma\delta$ T cells to respond to early inflammatory signals through innate cytokines may lead to the activation and polarization of  $\gamma\delta$ T cells towards IL17 producing phenotype which can modulate the immune response in the tumor environment.

As increased levels of T $\gamma\delta$ 17 were observed in GBC patients, we reasoned that the cytokine milieu promoting T $\gamma\delta$ 17 differentiation should be present in sera and tumor environment. It was documented that like Th17 cells, T $\gamma\delta$ 17 also differentiate from naïve  $\gamma\delta$ T cells in the

presence of IL6, IL1 $\beta$ , IL23 and TGF $\beta$  upon antigenic stimulation [243]. Serum cytokine profile of GBC patients revealed that the levels of IL6, IL1 $\beta$  and IL23 were elevated in GBC patients than HI. The estimation of cytokines in tumor supernatants of freshly resected tumor tissue showed that these cytokines were also present in tumor compartment and may be responsible for intra-tumoral differentiation and maintenance of T $\gamma$  $\delta$ 17 cells.

In GBC patients, the total percentage and memory phenotype of  $\gamma$  $\delta$ T cells were comparable to that observed in HI. However, the levels of T $\gamma$  $\delta$ 17 were increased and that of  $\gamma$  $\delta$ <sup>+</sup>IFN $\gamma$ <sup>+</sup> were decreased in peripheral blood and tumor environment. T $\gamma$  $\delta$ 17 cells negatively correlated with  $\gamma$  $\delta$ <sup>+</sup>IFN $\gamma$ <sup>+</sup> cells. Moreover, incubation of isolated  $\gamma$  $\delta$ T cells in presence of cell free supernatant of cultured gallbladder tumor cells showed increased percentages of T $\gamma$  $\delta$ 17 cells after 48 h of culture compared to incubation with medium alone. Thus the data suggests that the cytokine milieu present in the GBC tumor environment is conducive for differentiation of  $\gamma$  $\delta$ T cells towards T $\gamma$  $\delta$ 17 phenotype. It is reported that  $\gamma$  $\delta$ T cells producing IFN $\gamma$ , express TNFR superfamily member CD27 and IL17 producing  $\gamma$  $\delta$ T cells are restricted to the CD27<sup>-</sup> subset [249]. In GBC patients, it was observed that the CD27<sup>-</sup>  $\gamma$  $\delta$ T cells were elevated in peripheral blood and tumor tissue than CD27<sup>+</sup>  $\gamma$  $\delta$ T cells.

The analysis of TGF $\beta$  showed decreased mRNA expression in PBMCs and low levels in sera of GBC patients. TGF $\beta$  is required for Treg differentiation and maturation [314]. We observed that compared to HI, Tregs were decreased in peripheral blood of GBC patients at all clinical stages of disease. However, as observed by CFSE dye dilution assay, the suppressive potential of Tregs in GBC patients was not compromised as compared to HI. In addition, the levels of Foxp3 expression (at mRNA and protein level) were comparable to HI, suggesting that the Tregs in GBC patients are functionally normal. Low levels of TGF $\beta$  observed in serum may be responsible for reduced levels of Tregs in peripheral blood of these

patients. Similar observations were reported in patients with multiple myeloma and pancreatic ductal adenocarcinoma [352, 353]. It is reported that the Th17 cells differentiate from Foxp3 expressing CD4<sup>+</sup> T cells [354] and there exists plasticity in the CD4<sup>+</sup> T cells in inflammatory environment [355]. Low concentration of TGFβ and presence of proinflammatory cytokines (IL23, IL21, and IL6) upregulate RORγt expression and inhibit Foxp3 in CD4<sup>+</sup> T cells [356]. Thus the decreased levels of Treg cells in peripheral blood of GBC patients would be because of CD4<sup>+</sup> T cell polarization towards Th17 phenotype in response to the presence of an inflammatory cytokine milieu.

After categorizing the GBC patients having high or low levels of Tregs, we observed that patients with high peripheral blood Treg cells have decreased survival compared to those with low levels (hazard ratio: 2.07). We also noted that Tregs were increased in tumor compartment and express elevated levels of Foxp3 compared to peripheral blood of GBC patients. Given that the suppressive activity of Tregs is determined by Foxp3 expression [357], the Tregs in TILs of GBC patients appear to be more immunosuppressive. A recent study in colorectal cancer patients demonstrated that Tγδ17 cells promote migration and survival of MDSCs which enhanced immunosuppression in these patients [246]. In GBC patients it was observed that the HLADR<sup>+</sup>CD33<sup>+</sup>CD11b<sup>+</sup> MDSCs were elevated in the peripheral blood and tumor environment. MDSCs are known to induce Treg cells in cancer patients [358] Thus, the increased levels of Tregs in tumor environment of GBC may be attributed to the Tγδ17 driven inflammation leading to accumulation of MDSCs and subsequent upregulation of Tregs. However, the mechanism regulating accumulation and suppressive functions of MDSCs mediated by Tγδ17 cells in GBC warrants further investigation. It is reported that Th17 and Treg frequently co-localize at the same anatomic compartments and mutually promote each other's generation and function [359]. We observed the infiltration of Tregs and IL17 producing cells in the tumor environment of GBC

patients which corroborate the earlier observations in GBC patients reported by Zhang et al [360]. This suggests that although the ratios of T $\gamma$  $\delta$ 17/Treg, Th17/Treg and Tc17/Treg were increased in GBC patients, IL17 producing cells and Tregs may act cooperatively and eventually contribute to the poor survival observed in GBC patients.

Next we addressed the functional role of T $\gamma$  $\delta$ 17 cells on GBC tumor progression. The migration of T $\gamma$  $\delta$ 17 cells mediated by chemokines was studied in GBC patients. Murine T $\gamma$  $\delta$ 17 cells have been reported to express various chemokine receptors including CCR6, CCR1, CCR2, CCR4, CCR5, CCR7, CCR9, CXCR1, CXCR3, CXCR4, CXCR5 and CXCR6 [251]. Murine T $\gamma$  $\delta$ 17 cells expressing CCR9 show selective migration towards allergic inflamed tissue in response to CCL25 [361]. The recruitment of T $\gamma$  $\delta$ 17 cells towards inflammatory environment is poorly investigated in human. In GBC patients, it was observed that T $\gamma$  $\delta$ 17 cells showed elevated expression of CXCR3 than Th17 and Tc17. Expression of CCR6, CCR7 and CXCR4 was comparable in T $\gamma$  $\delta$ 17, Th17 and Tc17 cells. We demonstrated that T $\gamma$  $\delta$ 17 cells migrate towards tumor milieu through CXCL9-CXCR3 axis. The increased levels of CXCL9 and CXCL10 observed in sera of GBC patients, further supports the elevated levels of T $\gamma$  $\delta$ 17 cells observed in the tumor environment. Earlier it was reported that Th17 utilized this axis to migrate towards inflamed liver [362]. This is the first report demonstrating migration of T $\gamma$  $\delta$ 17 cells to the tumor environment using CXCL9-CXCR3 axis.

Angiogenesis is a critical step in the progression of solid tumors providing nutrients, growth factors and oxygen for growth of malignant cells. Th17 cells are shown to be proangiogenic in human head and neck squamous cell carcinoma [42]. Proangiogenic functions of T $\gamma$  $\delta$ 17 in human cancer are not yet reported. Our data showed that human T $\gamma$  $\delta$ 17 cells induce blood vessel formation through secretion of IL17 as observed in *ex vivo* chick embryo CAM assay.

T $\gamma\delta$ 17 induced GBC cells to produce proangiogenic factors such as VEGF, uPA, MMP9, MCP1, GM-CSF, CXCL16, coagulation factor III, angiogenin, etc. through secretion of IL17. Interestingly, we observed that T $\gamma\delta$ 17 also induced anti-angiogenic factors (Thrombospondin-1, TIMP1, Serpine1, Platelet factor-4, IGFBP1, etc.). However, TIMP-1 and serpine-1 are also reported as markers of poor prognosis in cancer [363, 364]. A recent study in glioblastoma showed that IGFBP1 secretion by microglial cells induced by MCSF is essential for angiogenesis [365]. A study in IL17<sup>-/-</sup> CMS-G4 fibrosarcoma murine model has shown that  $\gamma\delta$ T cells were the major source of IL17 and depletion of IL17 resulted in decreased vascular density and tumor growth [253]. In the ID8 ovarian cancer model, tumors grown in IL17<sup>-/-</sup> and TCR $\delta$ <sup>-/-</sup> mice express lower levels of *ang-2* and *vegf* compared with tumors grown in wild-type animals [254]. T $\gamma\delta$ 17 also mobilizes the proangiogenic *Tie2*-expressing macrophages into the peritoneal cavity [254]. Thus T $\gamma\delta$ 17 is a major contributor to the tumor angiogenesis. To the best of our knowledge, our data for the first time provides evidence that T $\gamma\delta$ 17 promote angiogenesis in gallbladder cancer and is a pro-tumor subtype of  $\gamma\delta$ T cells in human.

IL17 is a key cytokine in the proangiogenic function of T $\gamma\delta$ 17 cells in GBC. Inhibition of IL17 showed reduced production of angiogenic factors and decreased blood vessel formation in CAM assay. The levels of IL17 were increased in sera of GBC patients than HI. GBC patients with elevated levels of IL17 in sera were associated with poor survival whereas GBC patients with higher levels of IFN $\gamma$  showed better clinical outcome. The data from study in murine model of melanoma showed that the growth of tumor was reduced in double knockout IL17<sup>-/-</sup>IFN $\gamma$ <sup>-/-</sup> mice as observed in IL17<sup>-/-</sup> mice. However, the fast tumor growth was observed in IFN $\gamma$ <sup>-/-</sup> mice [366]. These results suggest importance of IL17 in tumor progression.

IL17 is reported to contribute to neoangiogenesis, activation of matrix metalloproteinases, carcinogenesis, tumor metastasis and resistance to chemotherapy in diverse solid tumors [30, 31, 318]. IL17 induces IL6 production which activates STAT3 upregulating pro-survival and proangiogenic genes [154, 366]. In a 4T-1 metastatic breast cancer model IL17 participates in tumor progression by recruiting neutrophils to the tumor which produce CXCL1, MMP9, VEGF and TNF $\alpha$ . IL17 also induces production of IL6 and CCL20 favouring the migration and differentiation of IL17 producing cells and correlate with poor prognosis of patients with invasive ductal carcinoma [367]. In the present study, it was observed that IL17 enhanced the neoplastic transformation of GBC cells. Addition of IL17 enhanced the proliferation of poorly differentiated GBC cells in a dose dependent manner. IL17 acts through IL17 receptor and activates Tumor progression locus 2 (TPL2) which induces protein kinase/extracellular signal-regulated kinase kinases, c-jun N-terminal kinases and STAT3 signaling pathways [368]. Knockdown of IL17 and/or inhibition of TPL2 attenuated tumorigenicity of human breast cancer MCF7 cells [368]. It was observed that the proliferative effect of IL17 was absent in moderately differentiated NOZ cells although, both cell lines expressed IL17 receptor on the surface. It is reported that IL17 induce phosphorylation of ERK 1/2 and stimulated proliferation of breast cancer cell line T47D. MCF-7, another breast cancer cell line was less sensitive to ERK recruitment and failed to respond to IL17 [31]. Thus it needs to be further investigated whether the differential activation of signalling molecules in two GBC cell lines is responsible for non-responsiveness of NOZ cells to IL17 treatment.

Since, angiogenesis plays a crucial role in local invasion and metastasis of tumor cells, the role of IL17 in angiogenesis of GBC was explored. VEGF is a key mediator of tumor angiogenesis and metastasis [323]. VEGF is reported as an independent prognostic marker and associates with poor survival of GBC patients [369, 370]. Treatment of gallbladder tumor cells (OCUG-1 cells line) with rhIL17 showed dose dependent increase in VEGF production.

The serum levels of VEGF were elevated in GBC patients compared to HI. Moreover, IL17 induced migration and invasion potential of GBC cells in a dose dependent manner. In colorectal cancer, the high expression of IL17 in tumor tissue was correlated with high expression of VEGF, increased micro-vessel density and poor survival of patients [29]. IL17 directly promotes the invasion of non-small cell lung cancer (NSCLC) cells *in vitro* and *in vivo* and the metastasis of NSCLC was impaired in IL17<sup>-/-</sup> mice [371]. IL17 activates JAK2/STAT3 signalling through AKT mediated IL6 production. This signalling subsequently upregulates the downstream targets IL8, MMP2, and VEGF and promote migration and invasion in hepatocellular carcinoma [153]. High expression of molecules involved in JAK2/STAT3 signalling pathway are reported to be associated with high expression of VEGF, increased micro-vessel density and poor survival of patients with NSCLC [372]. The accumulating evidences have suggested the pathogenic role of IL17 in cancer scenario. Thus the role of IL17 to promote angiogenesis and invasiveness of gallbladder tumor cells may explain the pro-tumor effect of  $\gamma\delta$ T cells when IL17 is produced as primary cytokine.

The present study has identified a key role of IL17 and its producer cells (T $\gamma\delta$ 17, Th17 and Tc17) in pathogenesis of GBC. Therapeutic interventions to the IL17 – inflammatory axis exhibits great clinical potential. Recently, Secukinumab, a fully human IL17A specific monoclonal antibody and Ixekizumab a humanized IL17A specific antibody that neutralizes human IL17A have been approved for treatment of psoriasis [373, 374]. Both these antibodies showed superior results than etanercept (fusion protein inhibiting TNF $\alpha$ ) [373, 374]. There are more drug candidates specific for IL17 that include CNTO 6785, ABT-122, COVA322 are under clinical trials [375]. Drugs targeting IL17F (CJM112, ALX-0761 and bimekizumab) are also under clinical trial for patients with inflammatory disease [375]. Although IL17 and TNF $\alpha$  work synergistically to induce a pro-inflammatory signaling cascade [155], patients who are unresponsive to anti-TNF agents may respond to therapies

that target IL17. Other approaches to target IL17 inflammatory axis including monoclonal antibody targeting IL17 receptor (brodalumab), IL23p40 subunit (ustekinumab), IL23p19 subunit and small molecules with inverse agonist activity against ROR $\gamma$ t (Digoxin, SR 1001, Ursolic acid) are under phase II/III clinical trials for inflammatory diseases [26, 376, 377]. However, inhibitors of IL17 may offer superior and more specific response as IL12 and IL23 sit upstream of both T<sub>H</sub>1 and T<sub>H</sub>17 pathways and targeting IL17 do not affect functions of Th1 lineage [375].

Chemotherapeutic drugs like oxaliplatin, doxorubicin, gemcitabine, 5-fluorouracil trigger cancer cell death which activate antitumor immune response. Gemcitabine (gem) and 5-fluorouracil (5-fu) were shown to induce apoptosis in MDSCs and release of IL1 $\beta$  which activates Th17 cells. Release of IL17 further compromised the antitumor effect of gem and 5-fu [378]. However, in a murine study, T $\gamma$  $\delta$ 17 cells improved the anti-tumor efficacy of anthracycline doxorubicin [257]. The studies suggest that the chemotherapeutic drugs should be combined with immunomodulatory agents for increasing efficacy of anticancer therapy. Bevacizumab which target VEGF, when combined with chemotherapy has shown direct antitumor effect and improved patient survival [379]. The present study provides insights into pathogenic role of T $\gamma$  $\delta$ 17 in GBC through IL17 production and inducing angiogenesis. Targeting IL17 - T $\gamma$  $\delta$ 17 axis could be a promising approach for the management of GBC.

The Tregs observed in GBC tumor could also be targeted using various immunotherapeutic strategies. Use of antibodies specific for CD25 (daclizumab), CTLA4 (ipilimumab), GITR, OX-40, PD-L1 or PD-1 (nivolumab) subvert the immunosuppression mediated by Treg cells and have demonstrated efficacy in clinical trials [51, 380]. Implication of combination immunotherapy, targeting both co-inhibitory and co-stimulatory molecules, is advantageous over monotherapy and capable of overcoming tumor immune tolerance ultimately leading to

tumor regression. Combination therapy using anti-OX40/anti-CTLA-4 mAb, Anti-PD1/anti-PDL-1 mAb, anti-OX40/anti-PD-1 have shown improved survival and effector functions of CD4 and CD8 T cells along with depletion of Treg cells [381]. Disrupting tumor homing of Tregs by blocking CCR4 mediated migration is advantageous as it transiently inhibit Treg cells only during priming phase and avoid potential autoimmune complications caused by long term depletion of Treg cells by mAbs [53, 380].

The present study has explored the relationship of IL17 pathway, specifically T $\gamma$  $\delta$ 17 and GBC development and progression. We report for the first time T $\gamma$  $\delta$ 17 and Th17 as predictive markers in GBC and provide evidence for the proangiogenic role of human T $\gamma$  $\delta$ 17. The coexistence of T $\gamma$  $\delta$ 17, Th17 and Treg as well as cytokines other than IL17 present in the tumor microenvironment may have modulated the immune response and tilted the balance towards GBC immune evasion. Our data strongly suggests that T $\gamma$  $\delta$ 17 mediated angiogenesis and Treg cells mediated immunosuppression may contribute to the negative clinical outcome of GBC patients. It may be possible to manipulate  $\gamma\delta$ T cell polarization *in situ* by targeting cytokines such as IL1 $\beta$ , IL6, IL23, and TGF $\beta$ . Thus, future immunotherapeutic treatment modality for GBC may use a combined approach to block the trafficking of T $\gamma$  $\delta$ 17 cells to the tumor, inhibit functions of IL17 and reverse the immunosuppression mediated by Treg cells.

## **Chapter 8**

# **Summary and Conclusion**

## Summary and Conclusion

Gallbladder Cancer (GBC) is a relatively uncommon but lethal biliary tract related cancer. The highly aggressive nature of tumor renders dismal prognosis of patients diagnosed with GBC and show median survival of 3 to 6 months irrespective of treatment. Anatomical location of gallbladder in the abdomen and elusive early symptoms, leads to diagnosis of these patients at an advanced stage. As of today, prognostic biomarkers and effective adjuvant immunotherapy for GBC are unavailable. Targeting tumor associated antigens has not shown promising outcome in GBC. Thus novel approach is necessary for successful management of GBC. The application of immunotherapies targeting immune cells requires deeper insights of the crosstalk of immune cells with tumor cells which is lacking in GBC.

Cholelithiasis is a major risk factor of GBC which predisposes gall bladder wall to persistent inflammation. Chronic inflammation leads to dysplastic changes in gallbladder resulting into high grade premalignant carcinoma *in situ*. The murine models of gallstone disease have reported the role of eosinophils, macrophages, neutrophils and lymphocytes in gallbladder associated inflammation. The inflammatory markers such as COX-2, iNOS, inflammatory cytokines (IL1, TNF) are elevated in the gallbladder wall. In cancer associated inflammation the immune repose by innate and adaptive immunity in response to injury is subverted by tumor cells for their advantage. Thus the investigation of immune scenario (inflammatory and immunosuppressive) in GBC patients is essential to understand the pathogenesis of GBC.

With this background, the present prospective study aimed at investigating how the dynamics of proinflammatory (IL17 producing T cells) and immunosuppressive (Treg) cells contributes to inflammation and thereby progression of GBC. The key questions we asked were:

1. What is the frequency of proinflammatory (Th17, Tc17 and T $\gamma$  $\delta$ 17) and immunosuppressive (Treg) cells in peripheral blood and tumor tissue of GBC patients?

2. Which cytokines are involved in the regulation of these phenotypes?
3. How pro- and anti-inflammatory subtypes contribute to pathogenesis of GBC?

The immunophenotyping of peripheral blood lymphocytes in GBC patients and HI showed that the percentages of cells contributing to adaptive immunity were decreased in peripheral blood of GBC patients. PBMCs of GBC patients also showed poor proliferative response to TCR agonist and mitogen with reduced production of effector cytokines. Investigations of TCR signalling pathway in GBC patients showed downregulated expression of CD3- $\xi$  chain in T cells compared to HI. The compromised signalling through TCR resulted in low lymphocyte proliferative response and decreased secretion of effector cytokines upon stimulation with anti-CD3 mAb and mitogen. Overall the data suggests that the immune response in GBC patients is dysfunctional.

The dysfunctional immune response and predisposition to chronic cholecystitis suggest significant role of impaired immunity and inflammation in GBC. The multicolor flowcytometry analysis of inflammatory T cells subtypes in peripheral blood and tumor tissue of GBC patients, showed that IL17 producing TCR $\gamma\delta^+$  (T $\gamma\delta$ 17), CD4 $^+$  (Th17), CD8 $^+$  (Tc17) cells were significantly increased in PBMCs of GBC patients compared to HI. The increase in the levels of T $\gamma\delta$ 17, Th17 and Tc17 cells were irrespective of clinical stages of GBC patients. Levels of these cells were further elevated in tumor compartment than the peripheral blood of GBC patients. Thus the data highlights the significance of IL17 producing T cells in GBC patients. Interestingly T $\gamma\delta$ 17 cells emerged as an important phenotype in GBC patients. Further it was noted that, the relative percentages and propensity to secrete IL17 were higher in T $\gamma\delta$ 17 cells compared to Th17 and Tc17 in TILs. In contrast,  $\gamma\delta^+$ IFN $\gamma^+$  cells were significantly decreased in TILs compared to PBMCs of GBC patients and HI. Survival analysis of GBC patients showed that T $\gamma\delta$ 17 and Th17 cells in peripheral blood were

associated with poor survival of GBC patients. In contrast, the patients with high levels of  $\gamma\delta^+ \text{IFN}\gamma^+$  had longer overall survival than patients with low levels of  $\gamma\delta^+ \text{IFN}\gamma^+$  cells. Thus the data showed that IL17 is majorly contributed by  $\gamma\delta\text{T}$  cells in GBC patients. It also underscored the clinical significance of  $\text{T}\gamma\delta 17$  cells in GBC patients.

Since, the levels of  $\text{T}\gamma\delta 17$  cells were increased in GBC patients, we investigated the cytokine milieu promoting  $\text{T}\gamma\delta 17$  differentiation in sera and tumor environment. The cytokine profile of GBC patients showed that the cytokines (IL6, IL23, IL1 $\beta$ ) involved in the polarization and/or stabilization of  $\text{T}\gamma\delta 17$  cells were elevated in sera and were present in the tumor environment. We observed that, the levels of TGF $\beta$  were decreased in sera of GBC patients. Since, TGF $\beta$  is required for differentiation of Treg cells, the levels of Treg cells were investigated in peripheral blood and tumor tissue of GBC patients. The analysis of  $\text{CD4}^+ \text{CD25}^+ \text{CD127}^{\text{low/-}}$  regulatory T cells revealed that the levels of Tregs were decreased in peripheral blood but increased in TILs of GBC patients from all clinical stages (II to IV). The expression of Foxp3 was elevated in Tregs present in tumor environment. However, the suppressive potential of Tregs in peripheral blood was comparable to HI. This indicated that although Tregs were decreased in PBMCs of GBC patients, their suppressive potential was not compromised. Moreover, the GBC patients with high peripheral blood levels of Treg were associated with poor survival. The data suggests that although the ratios of Th17/Treg,  $\text{T}\gamma\delta 17/\text{Treg}$  and Tc17/Treg were increased in TILs, IL17 producing cells and Treg cells coexist in GBC tumor environment and may contribute to poor clinical outcome of GBC patients.

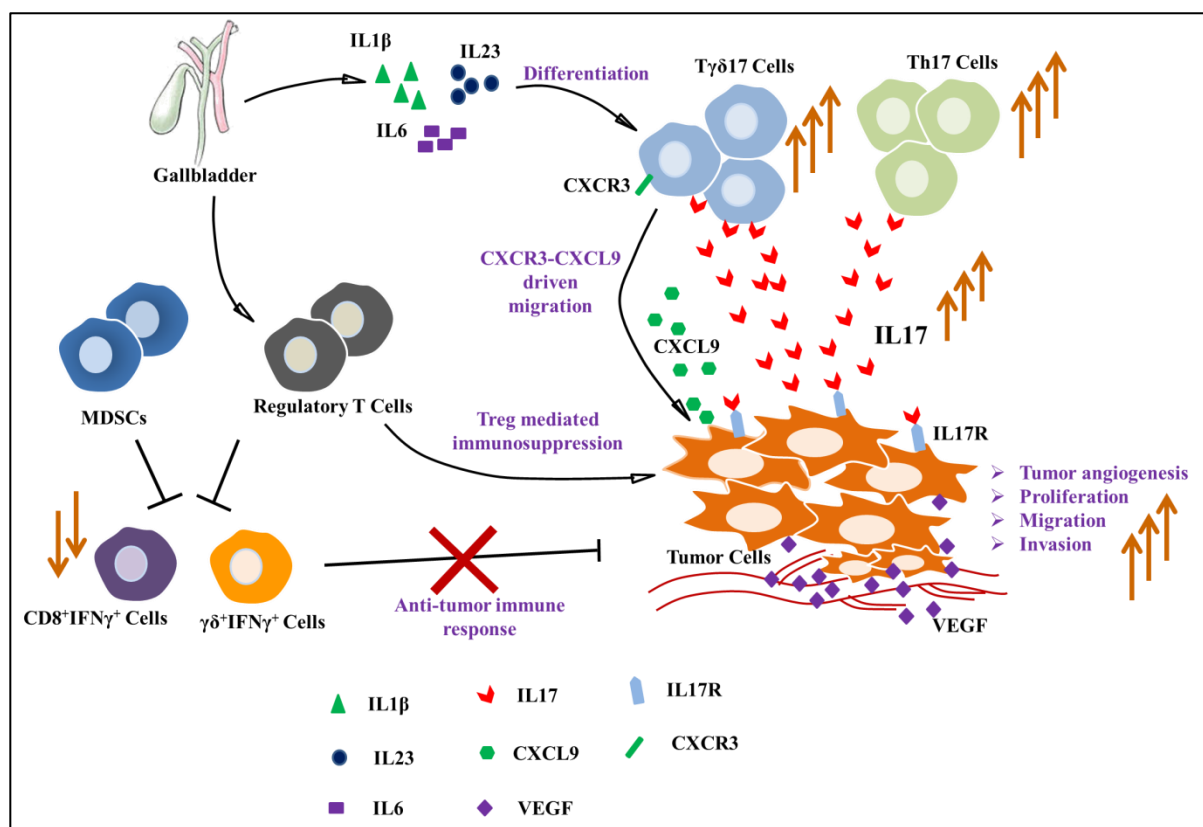
The association of  $\text{T}\gamma\delta 17$  cells with poor prognosis of GBC patients highlighted their importance in pathogenesis of GBC. To further address the functional role of  $\text{T}\gamma\delta 17$ , the expression of chemokine receptors (CCR6, CCR7, CXCR4 and CXCR3) on Th17, Tc17 and

T $\gamma\delta$ 17 cells was analysed in peripheral blood of GBC patients. It was observed that T $\gamma\delta$ 17 expressed elevated levels of CXCR3 than Th17 or Tc17. However, CCR6, CCR7 and CXCR4 were expressed at comparable levels by T $\gamma\delta$ 17, Th17 and Tc17. Using neutralizing antibody for CXCR3 in a trans-well assay, it was shown that T $\gamma\delta$ 17 cells use novel chemokine axis (CXCL9/CXCL10-CXCR3) to migrate towards GBC tumor bed.

In order to investigate the mechanism of T $\gamma\delta$ 17 cells contributing to tumor progression in GBC patients, the cytokine profile of T $\gamma\delta$ 17 was analysed. It was observed that T $\gamma\delta$ 17 primarily secretes high levels of IL17 and low levels of IL2 and TNF $\alpha$  but did not produce other cytokines like IL4, IL6, IL10 and IFN $\gamma$ . In addition, the inherent property of  $\gamma\delta$ T cells to respond to innate cytokines like IL23 and IL1 $\beta$  may explain the current observation that T $\gamma\delta$ 17 are major producers of IL17 than Th17. The analysis of gallbladder tumor cells (OCUG-1 and NOZ cell lines) by flow cytometry and immunofluorescence staining showed that more than 80% of gallbladder tumor cells (OCUG-1 and NOZ cell lines) expressed IL17 receptor on the surface. Thus IL17 secreted by T $\gamma\delta$ 17 cells may act through IL17 receptor to show its effects on gallbladder tumor cells.

Next, the proangiogenic action of T $\gamma\delta$ 17 cells on GBC was studied by human protein profiler angiogenesis array. Cell-free supernatants from T $\gamma\delta$ 17 cells significantly upregulated secretion of angiogenesis promoting factors from OCUG-1 cells such as VEGF, uPA, MMP9, MCP1, GM-CSF, CXCL16, coagulation factor III, angiogenin, etc. This effect was abrogated by addition of anti-IL17 mAb. The proangiogenic effects of T $\gamma\delta$ 17 were validated by chorioallantoic membrane (CAM) assay. Cell-free supernatants of T $\gamma\delta$ 17 enhanced vascularization of CAM and the effect was mediated through secretion of IL17. Next to study whether IL17 has direct role in GBC promotion, GBC cells were treated with rhIL17 and analysed for their proliferation, migration and invasion potential. It was observed that

addition of rhIL17 to gallbladder tumor cells (OCUG-1) induced proliferation, migration, matrigel invasion and VEGF production in concentration dependent manner. Thus the results highlighted that  $T\gamma\delta 17$  is a proangiogenic subtype of  $\gamma\delta T$  cells and explains the correlation of this subset with poor prognosis of GBC patients.



**Figure 8.1 : Role of pro-inflammatory ( $T\gamma\delta 17$ ,  $Th17$  and  $Tc17$ ) cells and immunosuppressive (Treg) cells in progression of GBC.** The proinflammatory cytokines ( $IL1\beta$ ,  $IL6$ ,  $IL23$ ) released by gallbladder tissue promotes differentiation of  $T\gamma\delta 17$  cells.  $CXCL9$  secreted by gallbladder tumor cells induces migration of  $T\gamma\delta 17$  cells to the tumor bed through  $CXCR3$ - $CXCL9$  chemokine axis. The  $IL17$  secreted by  $T\gamma\delta 17$  cells induce proangiogenic factor such as VEGF in gallbladder tumor cells and promotes angiogenesis, migration and invasion of tumour cells. The Treg cells and MDSCs present in the tumor environment suppress the  $IFN\gamma$  producing CD8 and  $\gamma\delta T$  cells thereby inhibit antitumor immune responses. Overall proinflammatory and immunosuppressive cells contribute to gallbladder tumor progression

In conclusion, the inflammatory tumor environment fosters the development and recruitment of T $\gamma\delta$ 17 and Th17 cells to the tumor bed (Figure 8.1). Increased levels of Treg cells and reduced levels of CD8<sup>+</sup>IFN $\gamma$ <sup>+</sup> and  $\gamma\delta$ <sup>+</sup>IFN $\gamma$ <sup>+</sup> cells in the tumor environment suggests the immunosuppression of antitumor immune response. IL17 secreted by T $\gamma\delta$ 17 cells induce proangiogenic factors in GBC tumor cells through IL17 receptor and may promote the migration and invasion of GBC. Thus our data unravelled T $\gamma\delta$ 17 as a “druggable immune target” that plays an important role in GBC progression.

$\gamma\delta$ T cells have been conventionally shown to exhibit broad anti-tumor effects thus it is important to expand our understanding to exploit them for successful immunotherapy of cancer.  $\gamma\delta$ T cells based immunotherapy, although has shown safety and efficacy, IL17 producing  $\gamma\delta$  cells associate with poor prognosis of patients. Our studies suggest that T $\gamma\delta$ 17 can be viewed as opposite of  $\gamma\delta$ T cells. The pro-tumor functions of T $\gamma\delta$ 17 cells suggest that it will be important to evaluate the stable functional polarization of effector  $\gamma\delta$ T cells during adoptive transfer of  $\gamma\delta$ T cells. Targeting T $\gamma\delta$ 17 cells and IL17 inflammatory axis holds significance in future immunotherapeutic interventions. For favourable results of  $\gamma\delta$ T cells based immunotherapy, clinical protocols should maximize IFN $\gamma$  production and minimize IL17 secretion. Combination of  $\gamma\delta$ T cells with immunomodulatory antibodies targeting inflammatory cytokines may also be a promising approach. In this context the data presented in the thesis adds a new dimension to the understanding of GBC pathogenesis and effectively using  $\gamma\delta$ T cells for cancer immunotherapy.

## **Chapter 9**

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# ***Publications***

# IL17 producing $\gamma\delta$ T cells induce angiogenesis and are associated with poor survival in gallbladder cancer patients

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Despite conventional treatment modalities, gallbladder cancer (GBC) remains a highly lethal malignancy. Prognostic biomarkers and effective adjuvant immunotherapy for GBC are not available. In the recent past, immunotherapeutic approaches targeting tumor associated inflammation have gained importance but the mediators of inflammatory circuit remain unexplored in GBC patients. In the current prospective study, we investigated the role of IL17 producing TCR $\gamma\delta^+$  (T $\gamma\delta$ 17), CD4 $^+$  (Th17), CD8 $^+$  (Tc17) and regulatory T cells (Tregs) in pathogenesis of GBC. Analysis by multi-color flow cytometry revealed that compared to healthy individuals (HI), T $\gamma\delta$ 17, Th17 and Tc17 cells were increased in peripheral blood mononuclear cells (PBMCs) and tumor infiltrating lymphocytes (TIL) of GBC patients. Tregs were decreased in PBMCs but increased in TILs of GBC patients. The suppressive potential of Tregs from GBC patients and HI were comparable. Serum cytokines profile of GBC patients showed elevated levels of cytokines (IL6, IL23 and IL1 $\beta$ ) required for polarization and/or stabilization of IL17 producing cells. We demonstrated that T $\gamma\delta$ 17 cells migrate toward tumor bed using CXCL9-CXCR3 axis. IL17 secreted by T $\gamma\delta$ 17 induced productions of vascular endothelial growth factor and other angiogenesis related factors in GBC cells. T $\gamma\delta$ 17 cells promote vasculogenesis as studied by chick chorioallantoic membrane assay. Survival analysis showed that T $\gamma\delta$ 17, Th17 and Treg cells in peripheral blood were associated with poor survival of GBC patients. Our findings suggest that T $\gamma\delta$ 17 is a protumorigenic subtype of  $\gamma\delta$ T cells which induces angiogenesis. T $\gamma\delta$ 17 may be considered as a predictive biomarker in GBC thus opening avenues for targeted therapies.

**Key words:** T $\gamma\delta$ 17, Th17, Treg, vascular endothelial growth factor

**Abbreviations:** CFSE: carboxyfluorescein succinimidyl ester; Foxp3: forkhead box p3; GBC: gallbladder cancer; HI: healthy individuals; IL: interleukin; IFN $\gamma$ : interferon  $\gamma$ ; PBMC: peripheral blood mononuclear cells; PMA: phorbol 12-myristate 13-acetate; RANTES: regulated on activation normal T cell expressed and secreted; Treg: regulatory T cells; Tres: responder T cells; TIL: tumor infiltrating lymphocytes; TCR: T cell receptor; TGF: transforming growth factor; VEGF: vascular endothelial growth factor  
Additional Supporting Information may be found in the online version of this article.

The authors have no conflicts of interest to declare

Study concept and design: SVC. Acquisition of data: RSP and SUS. Analysis and interpretation of data: RSP and SVC. Drafting of the manuscript: RSP and SVC. Critical revision of the manuscript for important intellectual content: SVC. Statistical analysis: RSP. Obtained funding: SVC and RD. Study supervision: SVC. Providing patient samples: SVS, MG and RD

**DOI:** 10.1002/ijc.30134

**History:** Received 2 Dec 2015; Accepted 31 Mar 2016; Online 8 Apr 2016

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## Introduction

Gallbladder cancer (GBC) is a relatively uncommon but lethal biliary tract related cancer. Its occurrence shows ethnic and geographical variations and is prevalent in Peru, Ecuador, Poland, Chile, Pakistan, Japan and northern India.<sup>1</sup> GBC is two to three times common in women than men and highest incidences are reported in north Indian women.<sup>2</sup> Cholelithiasis is a major risk factor for GBC which induces chronic inflammation leading to dysplastic changes and high grade premalignant carcinoma *in situ*.<sup>3,4</sup> Anatomic location, elusive symptoms and diagnosis at advanced stage reduces 5-year survival of GBC patients to <5%.<sup>1</sup> Complete surgical resection is the only curative option available, but >90% GBC patients are with un-resectable or metastatic disease.<sup>5</sup> Despite improved results of chemotherapy and surgery, the long-term outcome remains disappointing.<sup>6</sup> Thus, the need is to identify other etiological factors which would provide better insights into the process of carcinogenesis in GBC patients.

The inflammatory microenvironment is an essential component of a tumor and plays a decisive role at different stages of tumor development. It modulates host immune response to facilitate tumor growth.<sup>7</sup> Interleukin-17 (IL17) is a potent proinflammatory cytokine and its elevated levels have been found to be detrimental in autoimmune diseases and cancers.<sup>8</sup> It increases the immigration of neutrophils, macrophages and

**What's new?**

Human T cells expressing  $\gamma\delta$ -TCR exhibit potent anti-tumor activity and are potential candidates for cell-based therapies. Evidence however also exists of the ability of  $\gamma\delta$ -TCR cells to suppress anti-tumor responses, making deeper insight necessary for the successful clinical application of  $\gamma\delta$ T cell-based immunotherapies. This study identified IL17-producing  $\gamma\delta$ T cells (T $\gamma$  $\delta$ 17) as a pro-tumorigenic subtype of  $\gamma\delta$ T cells associated with poor survival in gallbladder cancer (GBC) patients. T $\gamma$  $\delta$ 17 cells infiltrate the tumor bed via CXCL9-CXCR3 axis and IL17 induces pro-angiogenic factors in GBC cells. T $\gamma$  $\delta$ 17 may be considered as a predictive biomarker in GBC, opening up new avenues for targeted therapies.

monocytes to inflamed tissues. IL17 induces tumor necrosis factor, IL-1, IL-6, colony stimulating factors, chemokines, matrix metalloproteinases, *etc.* which further augment tumor progression.<sup>8</sup> However, the protumor role of IL17 in the progression of GBC remains unexplored. Additionally, the cellular source of IL17 and its clinical relevance in GBC is not well investigated.

CD4<sup>+</sup> IL17<sup>+</sup> (Th17) cells and its related cytokines are reported to be present in tumor environment of various malignancies.<sup>9</sup> Recently,  $\gamma\delta$ T cells have been shown as major innate source of IL17. IL17 producing  $\gamma\delta$ T cells (T $\gamma$  $\delta$ 17) are protective in host defense against extracellular fungi and bacteria but exacerbate autoimmune and inflammatory diseases.<sup>10</sup> However, the role of T $\gamma$  $\delta$ 17 cells in pathogenesis of human malignancies is not well understood. In contrast, regulatory T cells (Treg), are anti-inflammatory and play a critical role in immune tolerance and autoimmunity.<sup>11</sup> They inhibit activation of CD4 and CD8 T cells and impair antitumor immune response.<sup>12</sup> Elevated proportions of Tregs have been identified in peripheral blood as well as in tumor environment and are associated with poor prognosis in several human cancers.<sup>11</sup>

The tumor infiltrating immune cells are engaged in extensive crosstalk with cancer cells, affecting immune surveillance and response to therapy.<sup>7</sup> An expanding body of literature has implicated the dynamics of Th17 and Tregs to play a major role in pathogenesis of several malignancies.<sup>13</sup> Thus, the present study aims at understanding how a specific subset of  $\gamma\delta$ T cells, namely, T $\gamma$  $\delta$ 17, contributes to inflammation and thereby progression of GBC.

**Material and Methods****Patient samples**

Newly diagnosed GBC patients ( $n = 52$ ) were recruited from Tata Memorial Hospital, Mumbai. There were 22 males (mean age =  $54 \pm 2$  years) and 30 females (mean age =  $51 \pm 2$  years) in the study group. Peripheral blood of GBC patients was collected prior to chemotherapy/radiotherapy or surgery after obtaining written informed consent. The study protocol was approved by ACTREC-TMC Institutional review board for human studies. The patients were grouped according to the TNM classification as stage II ( $n = 5$ ), stage III ( $n = 20$ ) and stage IV ( $n = 27$ ). Tumor tissues ( $n = 17$ ) were obtained from GBC patients undergoing cholecystectomy without radiotherapy or chemotherapy. Peripheral blood was obtained from age and sex matched healthy individuals ( $n = 30$ ) who participated voluntarily and written informed consent was obtained.

**Cell isolation and culture**

Peripheral blood mononuclear cells (PBMCs) were isolated from heparinized blood of GBC patients and healthy individuals using Ficoll Hypaque (Sigma-Aldrich, St. Louis, MO). Surgically resected gallbladder tumors were minced finely and incubated in RPMI medium containing enzyme mixture (0.05% collagenase, 0.02% DNase and 5U/ml hyaluronidase [Sigma-Aldrich]), at 37°C for 2 hr with intermittent shaking. The tissue was passed through wire mesh and washed with saline to obtain single cell suspension. Cells were cultured in serum-free medium and tumor supernatants were collected after 24 hr.

T $\gamma$  $\delta$ 17 cells were isolated using IL17 secretion assay-cell enrichment and detection kit (Miltenyi Biotec, Germany) according to manufacturer's instructions. Briefly,  $\gamma\delta$ T cells were purified by positive selection from PBMCs of healthy individuals using anti TCR- $\gamma\delta$  microbeads (Miltenyi Biotec, Germany) and stimulated with PMA (phorbol 12-myristate 13-acetate) and Ionomycin for 5 hr. Cells were then labelled with IL17 catch reagent for 5 min on ice followed by secretion phase of 45 min at 37°C with constant mixing in RPMI containing human AB serum. After labelling with anti-IL17 detection antibody, cells were sorted for IL17-PE positive cells. Purity (>90%) was determined by flow cytometry.

GBC cell line (OCUG-1; JCRB-0191)<sup>14</sup> was purchased from Japan Health Science Research Resources Bank (Osaka, Japan). Cells were cultured in William's E medium (Sigma-Aldrich) supplemented with 10% heat-inactivated FBS under standard culture conditions (37°C, 5%CO<sub>2</sub>).

**Flow cytometry**

Flow cytometric analysis was performed using FACS Aria flow cytometer (Becton Dickinson, CA) and analyzed by FlowJo software (Tree Star, Ashland, OR). Fluorescence minus one control was used in all experiments to determine background fluorescence. For intracellular cytokines staining, PBMCs were stimulated with PMA (50 ng/ml) and ionomycin (1  $\mu$ g/ml) for 5 hr in presence of Brefeldin A (5  $\mu$ g/ml; all from Sigma-Aldrich). Cells were washed with PBS and cold fixed with 1% paraformaldehyde (Sigma-Aldrich) for 15 min at 4°C, followed by permeabilization for 5 min with 0.1% saponin. Cells were incubated with antibodies for 30 min at room temperature. Minimum 50,000 events were acquired on FACS Aria flow cytometer. Antibodies used for flow cytometry staining are provided as Supporting Information Table 1.

### Regulatory T cells suppression assay

Tregs were isolated from PBMCs using BD IMag regulatory T lymphocyte separation set-DM (BD Biosciences). Briefly, CD4<sup>+</sup> T cells were negatively selected from PBMCs followed by positive selection of CD25<sup>+</sup> T cells. CD4<sup>+</sup> CD25<sup>+</sup> T cells were used as responder T cells (Tres) and labelled with carboxyfluorescein succinimidyl ester (CFSE; 5  $\mu$ M; CellTrace proliferation kit, Life technologies) for 10 min at room temperature. Tres cells ( $1 \times 10^4$ ) were cocultured with Tregs for 5 days at different ratios (Tres:Treg = 1:2, 1:1, 1:0.5 and 1:0). Cocultures were stimulated with anti-CD3/anti-CD28 coated beads (1bead:1cell; Treg suppression inspector, Miltenyi biotech). Cells were acquired on FACS Aria and analyzed by FlowJo software.

### Cytokines measurement

Serum samples were obtained from GBC patients and healthy individuals and stored at  $-80^{\circ}\text{C}$  until used. Cytokines and chemokines in sera samples and culture supernatants were measured by Th1/Th2/Th17 cytometric bead array kit and flex sets for IL8, IL1 $\beta$ , IL12p70, CXCL9, CCL5, CXCL10 and CCL2 (BD Biosciences) as per manufacturer's instructions. Samples were acquired on FACS Aria and analyzed using BD FCAP Array (BD Biosciences). TGF $\beta$  (BD Biosciences) and IL23 (eBiosciences, CA) were determined by ELISA.

### Cell migration assay

Migration of T $\gamma$  $\delta$ 17 cells was studied by trans-well assay using Millicell cell-culture inserts (Merck Millipore, MA) with pore size 8.0  $\mu$ m. OCU-1 cells ( $5 \times 10^4$ ), cultured in 24 well plate were washed and 600  $\mu$ l serum-free William's E medium was added to the lower chamber. In some experiments, rhCXCL9 (100 ng/ml; PeproTech, NJ) or tumor supernatants were added to the lower chamber. Isolated T $\gamma$  $\delta$ 17 cells ( $5 \times 10^4$ /100  $\mu$ l medium) were added onto the trans-well filter. Migrated cells from lower chamber were counted using hemocytometer after 7 hr. For blocking experiments, T $\gamma$  $\delta$ 17 cells were incubated with anti-CXCR3 antibody (10  $\mu$ g/ml; R&D Systems, MN), 30 min before transwell coculture.

### Angiogenesis array

T $\gamma$  $\delta$ 17 cells were cultured in serum-free RPMI medium for 24 hr in the presence of anti-CD3/anti-CD28 coated beads. Cell-free supernatant of T $\gamma$  $\delta$ 17 was incubated with OCU-1 cells ( $2 \times 10^4$ /well) in presence or absence of neutralizing anti-IL17 antibody (10  $\mu$ g/ml; R&D Systems). After 48 hr, supernatants were collected and analyzed for VEGF by ELISA (R&D Systems) or angiogenesis related proteins by human proteome profiler angiogenesis antibody array (R&D Systems). Briefly, equal amounts of cell-free supernatants were diluted (1: 3) and mixed with a cocktail of biotinylated detection antibodies specific for angiogenesis related proteins and incubated with the membranes coated with array of antibodies for overnight at  $4^{\circ}\text{C}$ . Membranes were washed to remove unbound material followed by incubation with HRP-conjugated streptavidin. Chemiluminescence was used for sig-

nal detection. The data were evaluated using Image J 1.48V software (NIH) and expressed as mean pixel density.

### Chorioallantoic membrane assay

Fertilized chicken eggs were incubated in humidified incubator at  $37^{\circ}\text{C}$ . On embryonic Day 5, a small window was made in the shell and 200  $\mu$ l medium/T $\gamma$  $\delta$ 17 supernatant/rhIL17 (100 ng/ml, R&D Systems) was added onto the chorioallantoic membrane (CAM) of growing embryo. After 48 hr, eggs were cracked open and embryos were carefully transferred to 100 mm petri dish and images were captured. CAM was cut and transferred to a glass slide to observe under the microscope. Angiogenesis was quantitatively evaluated by scoring number of branching points in control and treated CAMs.

### OCUG-1 cell proliferation assay

Proliferative response of OCU-1 cells was analyzed by tritiated thymidine ( $^3\text{H}$ -Thymidine) incorporation assay. OCU-1 cells ( $1 \times 10^4$ ) were cultured in flat bottom 96 well plates (Nunc, Denmark) in medium containing serum. After 24 hr, cells were washed with serum-free medium and rhIL17 (R&D Systems) was added in different concentrations. 0.5 $\mu$ Ci/10  $\mu$ l/well  $^3\text{H}$ -Thymidine (specific activity 240 GBq/mmol; Radiation and Isotope Technology, India) was added during last 18 hr of the assay. After 72 hr, cells were harvested on glass-fibre filter paper (Titer-tek, Norway) using cell harvester (Titer-tek, Norway). The filter paper was dried at  $60^{\circ}\text{C}$  and each disc corresponding to single well was placed in 3 ml liquid scintillation fluid [0.7% 2,5 diphenyloxazole + 0.05% 1,4 bis(5-phenyloxazole)]. Radioactivity was measured on liquid  $\beta$ -scintillation counter (Packard USA) as counts per minute (CPM).

### Statistical analysis

Statistical analysis was performed using GraphPad Prism software (Prism Software, Lake Forest, CA). Statistical significances were calculated by two-tailed Student's *t* test or Mann-Whitney test. As there was no clinically defined cut off points for Th17, Tc17, T $\gamma$  $\delta$ 17, Treg cells, the high-expressing or low-expressing groups of GBC patients were defined based on mean values of expression of these lymphocytes (4.7 for T $\gamma$  $\delta$ 17, 1.8 for Th17, 1.8 for Tc17 and 3.2 for Treg). Overall patient survival was calculated by Kaplan-Meier curve and compared by Log-rank test. Survival time was defined as the interval between date of diagnosis and date of death or last follow-up, whichever occurred earlier. Data were censored for patients who were alive at the time of last follow-up.  $p < 0.05$  was considered statistically significant.

### Results

#### T $\gamma$ $\delta$ 17 cells are increased in peripheral blood and tumor infiltrating lymphocytes (TILs) of GBC patients

In order to study the prevalence of circulating IL17 producing cells, peripheral blood mononuclear cells (PBMCs) were isolated from GBC patients ( $n = 52$ ) and healthy individuals (HI;  $n = 30$ ). The single cell suspension of tumor tissue ( $n = 17$ ) was prepared by enzyme digestion. Cells were stimulated with PMA and Ionomycin in the presence of Brefeldin A followed by

immunophenotyping. Figure 1a describes representative gating strategy to define Th17, Tc17 and T $\gamma$  $\delta$ 17 cells. IL17<sup>+</sup> cells were gated on CD3<sup>+</sup> CD4<sup>+</sup>, CD3<sup>+</sup> CD8<sup>+</sup> and CD3<sup>+</sup> V $\delta$ 2TCR<sup>+</sup> cells. A similar strategy was used to define CD4<sup>+</sup> IFN $\gamma$ <sup>+</sup>, CD8<sup>+</sup> IFN $\gamma$ <sup>+</sup> and  $\gamma$  $\delta$ <sup>+</sup>IFN $\gamma$ <sup>+</sup> cells.

Th17, Tc17 and T $\gamma$  $\delta$ 17 cells were significantly increased in PBMCs of GBC patients compared to HI. Levels of these cells were further elevated in tumor compartment than the peripheral blood of GBC patients. Interestingly, the relative percentages of T $\gamma$  $\delta$ 17 were higher in TILs compared to Th17 and Tc17 (Fig. 1b). In contrast,  $\gamma$  $\delta$ <sup>+</sup>IFN $\gamma$ <sup>+</sup> cells were significantly decreased in TILs compared to PBMCs of GBC patients and HI. A significant decrease was also observed in CD8<sup>+</sup> IFN $\gamma$ <sup>+</sup> cells in TILs compared to PBMCs of GBC patients. However, no change was observed in CD4<sup>+</sup> IFN $\gamma$ <sup>+</sup> in GBC patients compared to HI (Fig. 1c). Collectively, the data indicate that T $\gamma$  $\delta$ 17 cells are emerging as an important phenotype in GBC patients.

#### CD4<sup>+</sup> CD25<sup>+</sup> CD127<sup>low/-</sup> Foxp3<sup>+</sup> Tregs are decreased in peripheral blood of GBC patients

The frequency of Tregs in PBMCs of GBC patients ( $n = 52$ ) and HI ( $n = 30$ ) were analyzed by surface staining for CD4, CD25 and CD127 followed by intracellular staining for Foxp3. Figure 2a describes the gating strategy of Tregs where Tregs were defined as CD25<sup>+</sup> CD127<sup>low/-</sup> cells within CD4<sup>+</sup> cells with Foxp3 expression of  $\geq 80\%$ .

Tregs were significantly decreased in PBMCs of GBC patients compared to HI. However, the percentages of Tregs in TILs were higher than PBMCs of GBC patients but comparable to HI (Fig. 2b). The median fluorescence intensity (MFI) of Foxp3 expression on Tregs was significantly increased in TILs than PBMCs of GBC patients (Fig. 2c). In order to investigate functional potential of Tregs in GBC patients, Tregs from peripheral blood were cocultured with autologous responder T cells (Tres; CD4<sup>+</sup> CD25<sup>-</sup>) stimulated with anti-CD3/anti-CD28. It was observed that culture of Tres with Treg in 1:2 ratio significantly inhibited proliferation of Tres. However, the suppressive potential of Tregs in GBC patients was comparable to HI (Figs. 2d and 2e). Thus, the results indicate that although Tregs were decreased in PBMCs of GBC patients, their suppressive potential was not compromised.

#### Dynamics of T $\gamma$ $\delta$ 17, Th17, Tc17 and Tregs in GBC patients

The ratios of T $\gamma$  $\delta$ 17/Treg, Th17/Treg and Tc17/Treg were significantly increased in PBMCs as well as in TILs of GBC patients indicating an inverse correlation of IL17 producing cells and Tregs (Fig. 2f). T $\gamma$  $\delta$ 17, Th17 and Tc17 cells showed no correlation with clinical stage (II to IV) of GBC patients. However, their levels remained high in all stages of GBC patients compared to HI. In contrast, the levels of Tregs in GBC patients of all stages (II to IV) remained lower than HI (Fig. 2g). This clearly indicates that the immune response is skewed toward IL17 producing cells in GBC patients.

#### T $\gamma$ $\delta$ 17 polarizing cytokines are present in sera and tumor of GBC patients

Studies have shown that the differentiation of T $\gamma$  $\delta$ 17 and Th17 from naive T cells is facilitated by combinations of IL6, TGF $\beta$ , IL1 $\beta$  and IL23.<sup>15,16</sup> The serum levels of these and related cytokines/chemokines were evaluated in GBC patients ( $n = 49$ ) and HI ( $n = 25$ ). As shown in Figure 3a, levels of IL6, IL1 $\beta$  and IL23 were high in GBC patients whereas TGF $\beta$  was low compared to HI. IL17 was significantly elevated in GBC patients. However, IFN $\gamma$  was decreased and IL12 remained unaltered compared to HI. Levels of IL10 also did not alter among HI and GBC patients. Analysis of chemokines revealed that monokine induced by gamma interferon (MIG; CXCL9), interferon induced protein 10 (IP-10; CXCL10) and IL8 were increased in sera of GBC patients. Levels of Monocyte chemo-attractant protein-1 (MCP-1; CCL2) and RANTES (CCL5) in GBC patients were comparable to HI (Fig. 3b).

Further to evaluate the cytokine profile in tumor environment, single cell suspension of tumor tissue was prepared and cytokines were measured in cell-free culture supernatant collected after 24 hr. It was observed that cytokines involved in polarization of IL17 producing cells (IL6, TGF $\beta$ , IL1 $\beta$  and IL23) were present in the tumor environment. Levels of IL12, IFN $\gamma$ , IL2 and IL4 were low whereas chemokines such as IL8, CXCL9, CXCL10 and CCL2 were remarkably high (Fig. 3c). Taken together, these results suggest that cytokines involved in the polarization of T $\gamma$  $\delta$ 17 are elevated in sera and tumor environment of GBC patients.

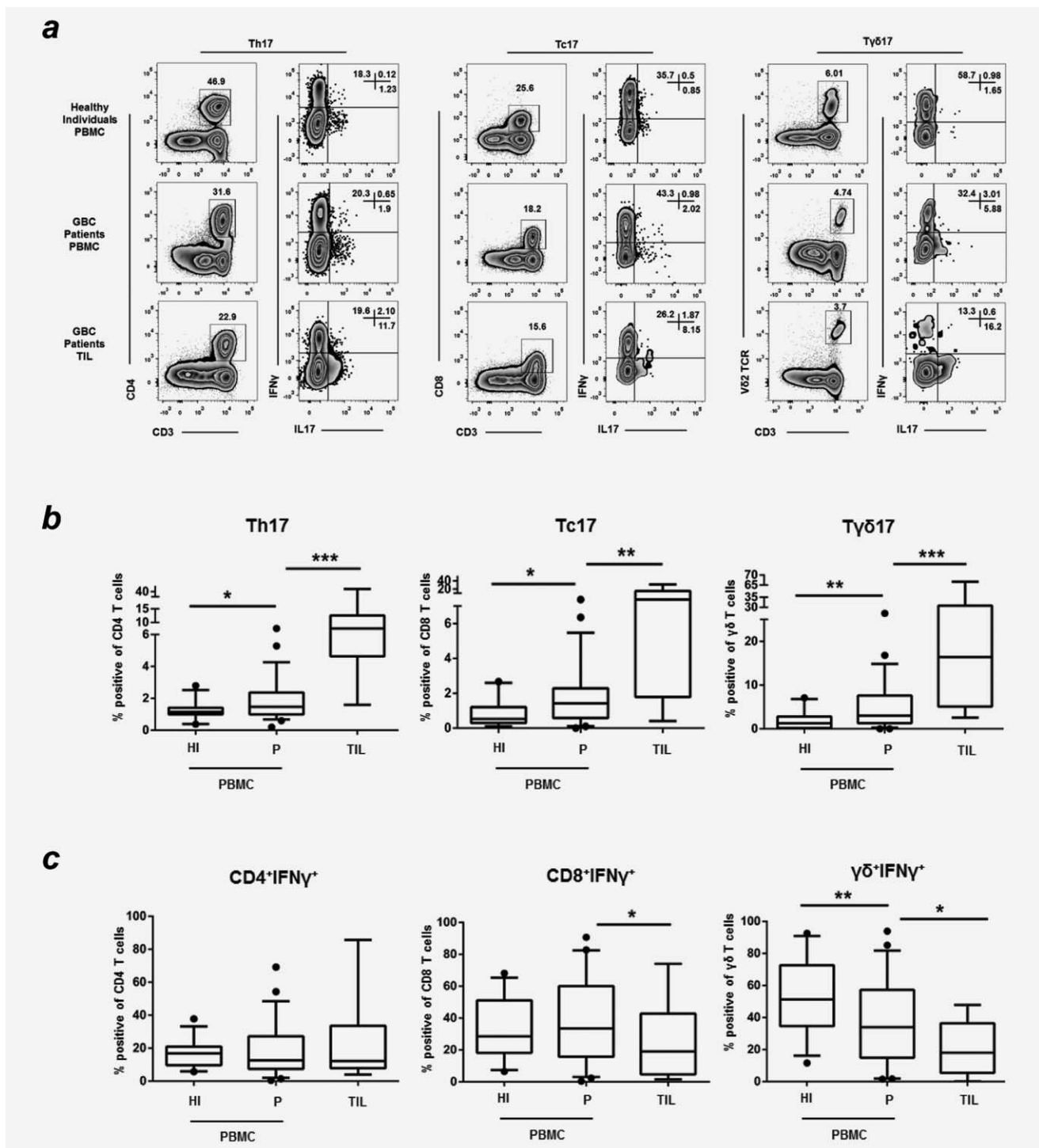
#### T $\gamma$ $\delta$ 17 cells are recruited to the tumor environment of GBC

The increased levels of T $\gamma$  $\delta$ 17 cells observed in tumor environment of GBC patients suggest that they would be migrating to the tumor. To test this hypothesis, expression of chemokine receptors (CCR6, CCR7, CXCR4 and CXCR3) on Th17, Tc17 and T $\gamma$  $\delta$ 17 cells was analyzed in peripheral blood of GBC patients ( $n = 35$ ). It was observed that T $\gamma$  $\delta$ 17 expressed elevated levels of CXCR3 than Th17 or Tc17 (Fig. 4a). However, CCR6, CCR7 and CXCR4 were expressed at comparable levels by T $\gamma$  $\delta$ 17, Th17 and Tc17 (Supporting Information Fig. 1).

Next, to investigate migration of T $\gamma$  $\delta$ 17 cells to the tumor, purified T $\gamma$  $\delta$ 17 cells (Fig. 4b) were cultured with GBC cell line (OCUG-1) or in presence of rhCXCL9 or cell-free tumor supernatants of surgically resected tumors in trans-well assay. Enhanced migration of T $\gamma$  $\delta$ 17 cells was observed toward OCUG-1 or rhCXCL9 or tumor supernatants compared to medium alone. The migration of T $\gamma$  $\delta$ 17 was significantly curtailed in presence of neutralizing anti-CXCR3 antibody (Fig. 4c). The data suggest that tumor environment induces infiltration of T $\gamma$  $\delta$ 17 cells toward tumor bed through CXCL9-CXCR3 axis.

#### T $\gamma$ $\delta$ 17 cells promote angiogenesis in GBC

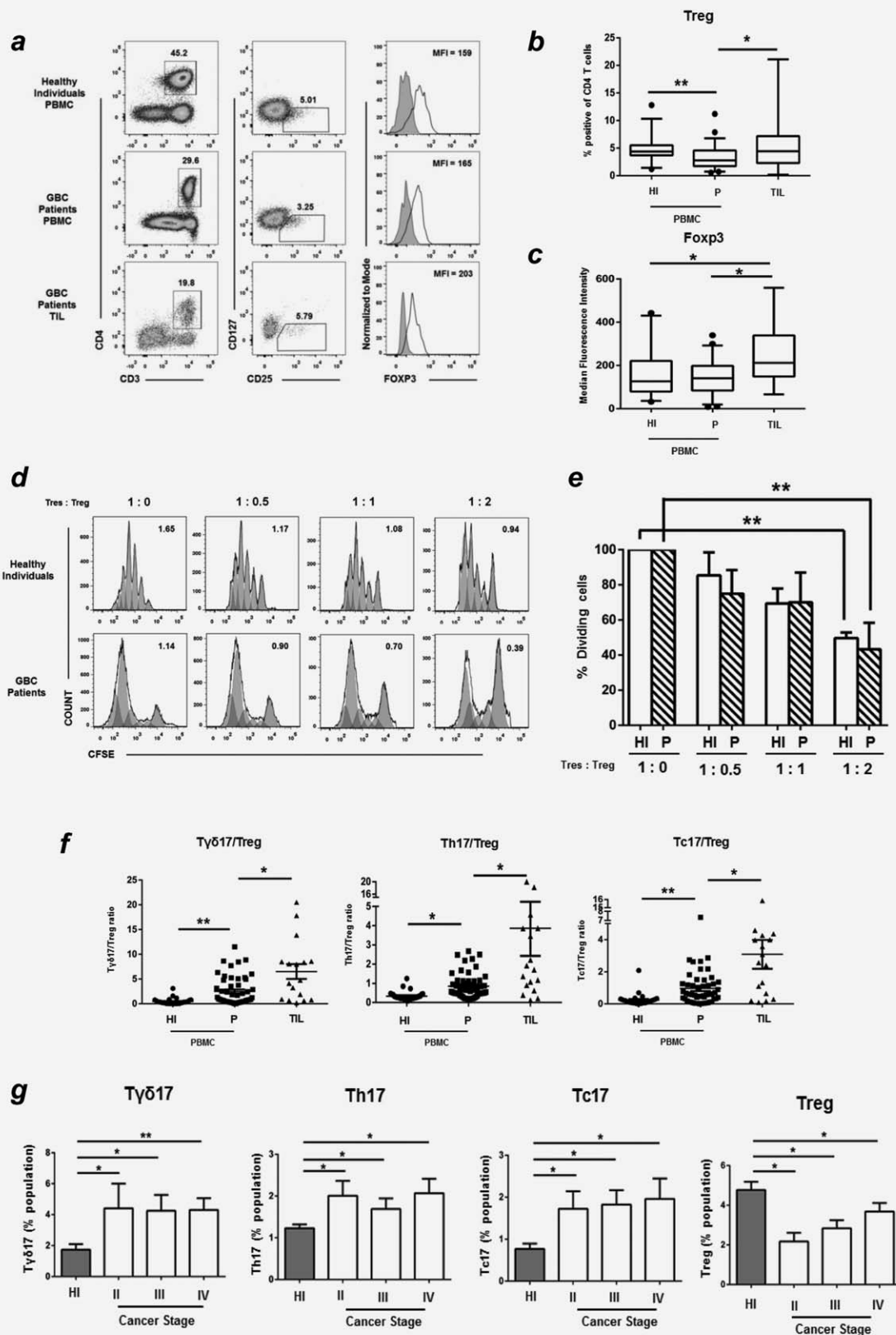
In order to investigate whether the elevated levels of T $\gamma$  $\delta$ 17 in GBC patients, contribute to tumor progression, the cytokine profile of T $\gamma$  $\delta$ 17 was analyzed. It was observed that



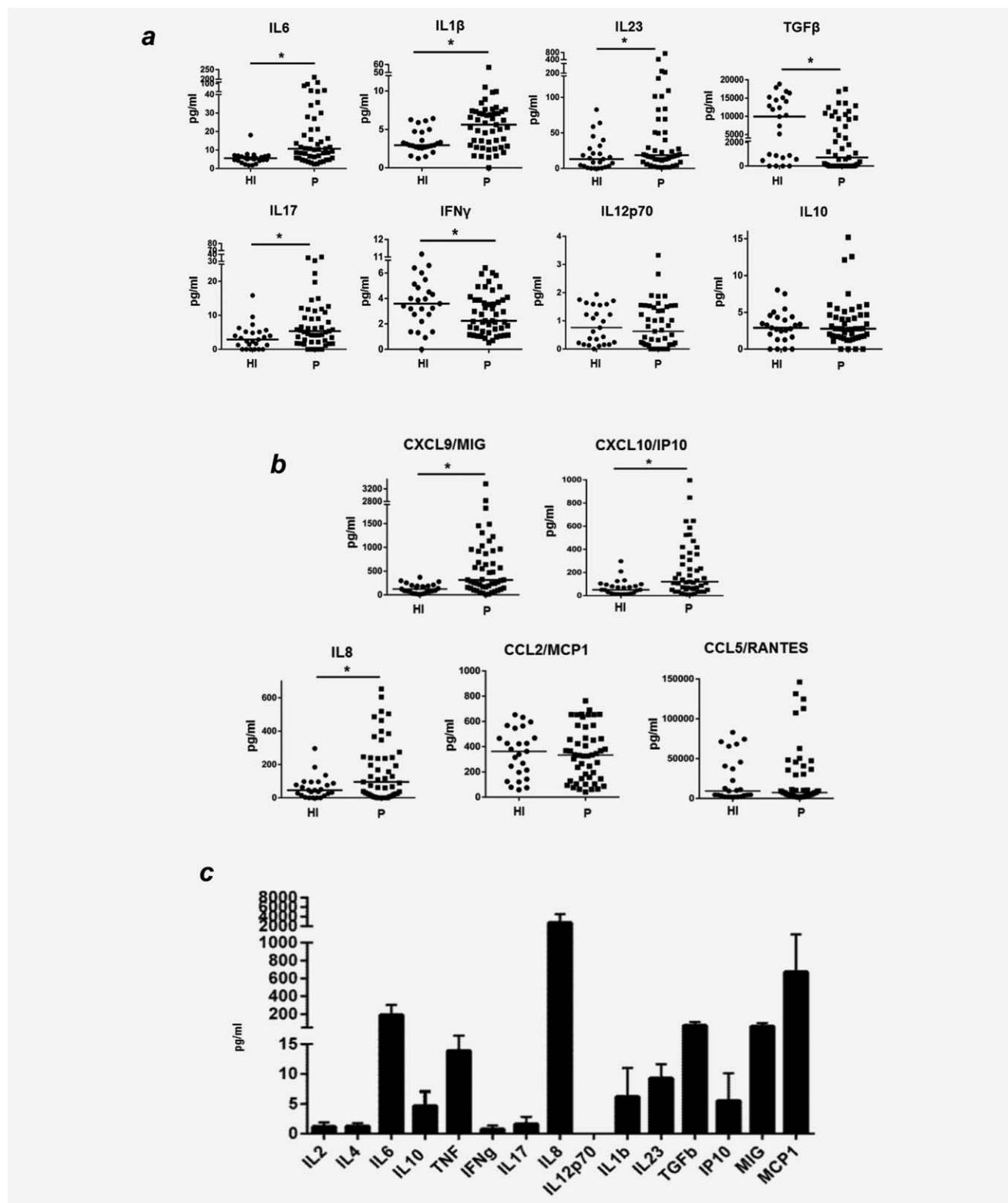
**Figure 1.** Prevalence of Th17, Tc17 and Tγδ17 cells in GBC patients. (a) Representative zebra plot analysis of Th17 (left), Tc17 (middle) and Tγδ17 (right) from PBMCs ( $n = 52$ ) and TILs ( $n = 17$ ) of GBC patients and HI ( $n = 30$ ). Cells were gated as  $CD3^{+} CD4^{+}$ ,  $CD3^{+} CD8^{+}$  and  $CD3^{+} Vδ2TCR^{+}$  population, respectively. Numbers in the plot indicate percent positive cells. (b) A summarized data show percentages of Th17 (left), Tc17 (middle) and Tγδ17 (right) in PBMCs and TILs of GBC patients compared with HI. (c) Frequency of  $CD4^{+} IFNγ^{+}$  (left),  $CD8^{+} IFNγ^{+}$  (middle) and  $γδ^{+} IFNγ^{+}$  (right) cells in PBMCs and TILs of GBC patients compared with HI. The box plots (b, c) show median (middle line), 5th and 95th percentiles (box), extreme values (whiskers) and outliers (dark circles). Results are analyzed by Mann-Whitney test with  $*p < 0.05$ ;  $**p < 0.01$ .

Tγδ17 primarily secrete high levels of IL17 and low levels of IL2 and TNFα but did not produce other cytokines (IL4, IL6, IL10 and IFNγ; Fig. 4d). Interestingly, GBC cells (OCUG-1

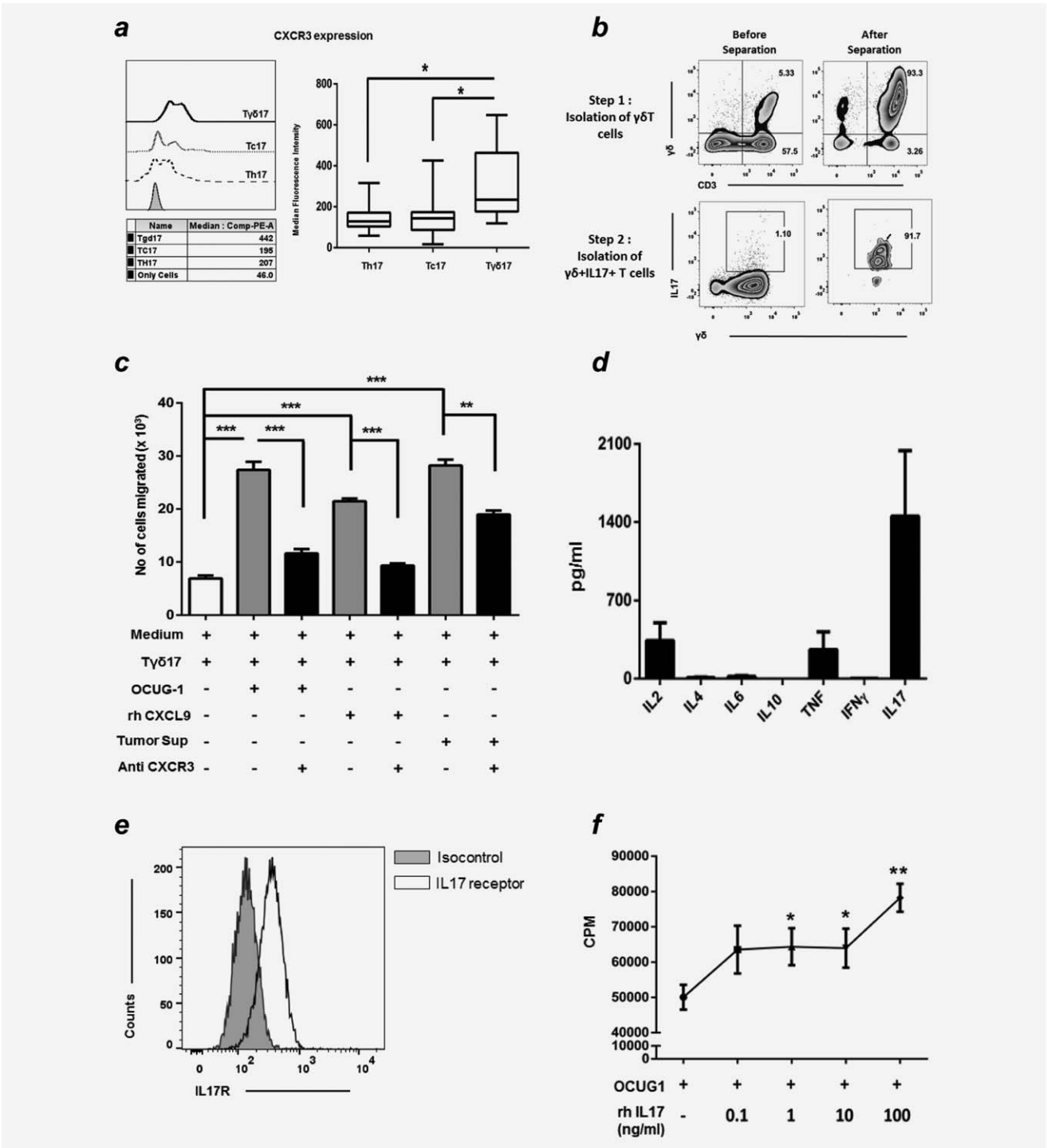
express IL17 receptor as observed by flow cytometry (Fig. 4e). Next, to investigate the effect of IL17 on proliferation of GBC, OCUG-1 cells were cultured with rhIL17. It



**Figure 2.** Frequency of regulatory T cells in GBC patients. (a) A representative dot plot describing Tregs, characterized as CD25<sup>+</sup> CD127<sup>low/-</sup> within CD4<sup>+</sup> T cells. Histograms indicate expression of Foxp3 within CD25<sup>+</sup> CD127<sup>low/-</sup> population. Figures in the histogram indicate median fluorescence intensity of Foxp3 expression (blank histogram) corrected with isocontrol (shaded histogram). (b) Box plots showing composite results of Tregs in PBMCs ( $n = 52$ ) and TILs ( $n = 17$ ) of GBC patients compared with HI ( $n = 30$ ). (c) Comparison of median fluorescence intensity of Foxp3 expression within Tregs in GBC patients and HI. Results are analyzed by Mann-Whitney test with  $*p < 0.05$ . (d) Representative figure depicting suppressive potential of Tregs (CD4<sup>+</sup> CD25<sup>+</sup>) on CFSE labelled autologous responder cells (CD4<sup>+</sup> CD25<sup>-</sup>) from GBC patients and HI ( $n = 3$ ). First peak from right indicates mother population. Figures in the plot indicate division index at respective ratio. (e) Bar diagram summarizes the percent dividing responder T cells. (f) Scatter plot showing the ratios of Ty $\delta$ 17/Treg (left), Th17/Treg (middle) and Tc17/Treg (right) in PBMCs ( $n = 52$ ) and TIL ( $n = 17$ ) of GBC patients and HI ( $n = 30$ ). (g) Frequencies of Ty $\delta$ 17, Th17, Tc17 and Treg were compared with clinical stages of GBC patients. Results are shown as mean  $\pm$  SEM with  $*p < 0.05$ ;  $**p < 0.01$ .



**Figure 3.** Cytokine profile in serum and tumor environment of GBC patients. (a and b) Scatter plots depict concentration of various cytokines (A) and chemokines (B) in sera of GBC patients ( $n = 49$ ) and HI ( $n = 25$ ) analyzed by cytometric bead array. Horizontal lines indicate median values. Data were analyzed by Mann–Whitney test with  $*p < 0.05$ . (c) Cytokines and chemokines were measured in cell-free tumor supernatants ( $n = 15$ ) by cytometric bead array. Data presented as concentration in pg/ml.



**Figure 4.** T $\gamma$  $\delta$ 17 cells migrate toward GBC tumor environment. (a) CXCR3 expression was analyzed on Th17, Tc17 and T $\gamma$  $\delta$ 17 cells by flow cytometry and depicted in a representative overlaid histogram. Data are presented as median fluorescence intensity ( $n = 35$ ). (b) Representative figure of purity of sorted T $\gamma$  $\delta$ 17 cells. Upper panel shows purity of  $\gamma\delta$ T cells. IL17 producing  $\gamma\delta$ T cells were sorted to >90% purity as shown in lower panel. (c) T $\gamma$  $\delta$ 17 cells were cultured with OCUG-1 cells or rhCXCL9 or tumor supernatants in a trans-well assay in presence or absence of anti-CXCR3 mAb. Data presented as total number of migrated cells ( $n = 3$ ). (d) Cytokines measured in culture supernatants of T $\gamma$  $\delta$ 17 cells stimulated with anti-CD3/anti-CD28 for 24 hr ( $n = 5$ ). (e) A histogram indicates expression of IL17 receptor on OCUG-1 cells analyzed by flow cytometry. (f) rhIL17 induces proliferation of OCUG-1 cells measured by  $^3$ H-Thymidine incorporation and represented as counts per minute ( $n = 6$ ). Results are shown as mean  $\pm$  SEM with \* $p < 0.05$ ; \*\* $p < 0.01$ ; \*\*\* $p < 0.001$ .

was observed that IL17 stimulated their proliferation in a dose-dependent manner indicating protumor role of IL17 (Fig. 4f).

Next to investigate whether T $\gamma\delta$ 17 induces angiogenesis, OCU-1 cells were cultured with cell-free supernatant of T $\gamma\delta$ 17 and levels of VEGF were estimated in culture supernatants. As shown in Figure 5a, T $\gamma\delta$ 17 cells secreted marginal amount of VEGF but upregulated secretion of VEGF by OCU-1 cells compared to OCU-1 cultured with medium alone. Addition of neutralizing anti-IL17 antibody significantly abrogated VEGF production by OCU-1 cells. Further, the addition of rhIL17 to OCU-1 cells induced VEGF production in a concentration-dependent manner (Fig. 5b).

Since, IL17 is known to regulate many downstream target genes associated with angiogenesis, proangiogenic action of T $\gamma\delta$ 17 cells on GBC was studied by human protein profiler angiogenesis array. Cell-free supernatants from T $\gamma\delta$ 17 cells significantly upregulated secretion of angiogenesis promoting factors from OCU-1 cells such as VEGF, uPA, MMP9, MCP1, GM-CSF, CXCL16, coagulation factor III, angiogenin, etc. compared to OCU-1 cells cultured with medium alone (Figs. 5c and 5d). This effect was abrogated by addition of anti-IL17 mAb. OCU-1 cells secreted high IL8 and addition of T $\gamma\delta$ 17 supernatant did not further increase its levels. Along with angiogenesis inducers, certain angiogenesis inhibitors like thrombospondin-1, TIMP-1, serpine-1, platelet factor 4, IGFBP-1, etc. were also secreted by OCU-1 cells in presence of T $\gamma\delta$ 17 supernatant.

Further to validate proangiogenic effects of T $\gamma\delta$ 17, cell-free supernatants of T $\gamma\delta$ 17 were *ex vivo* inoculated in CAM of 5-day-old chick embryos. It was observed that vascularization of CAM was enhanced in presence of T $\gamma\delta$ 17 supernatant compared to medium alone. Similar pronounced effect of vasculogenesis was observed in presence of rhIL17. The blood vessels formed in presence of T $\gamma\delta$ 17 supernatant showed tree-like branching with increased number of branching points from secondary blood vessels compared to parallel branching observed in presence of medium alone (Figs. 5e and 5f). Collectively, these results indicate that T $\gamma\delta$ 17 cells are proangiogenic and may contribute to carcinogenesis of GBC.

#### Increased T $\gamma\delta$ 17 cells associate with poor survival of GBC patients

To investigate the clinical significance of T $\gamma\delta$ 17, Th17, Tc17 and Tregs, the survival time of patients was analyzed with frequency of these cells in peripheral blood of GBC patients ( $n = 40$ ). Patients were divided into two groups based on mean percent values of respective cells (T $\gamma\delta$ 17, Th17, Tc17 or Tregs). As shown in Figure 6a, cox proportional regression analysis revealed that patients with high T $\gamma\delta$ 17 showed poor overall survival (median survival: 8.95 months) than patients with low levels of T $\gamma\delta$ 17 (median survival: 15.97 months). The individuals with high T $\gamma\delta$ 17 levels were at higher risk compared to those with low T $\gamma\delta$ 17 levels (Hazard ratio (HR): 2.4). In contrast, the patients with high levels of

$\gamma\delta^+ \text{IFN}\gamma^+$  had longer overall survival than patients with low levels of  $\gamma\delta^+ \text{IFN}\gamma^+$  cells (HR: 0.4; Fig. 6e).

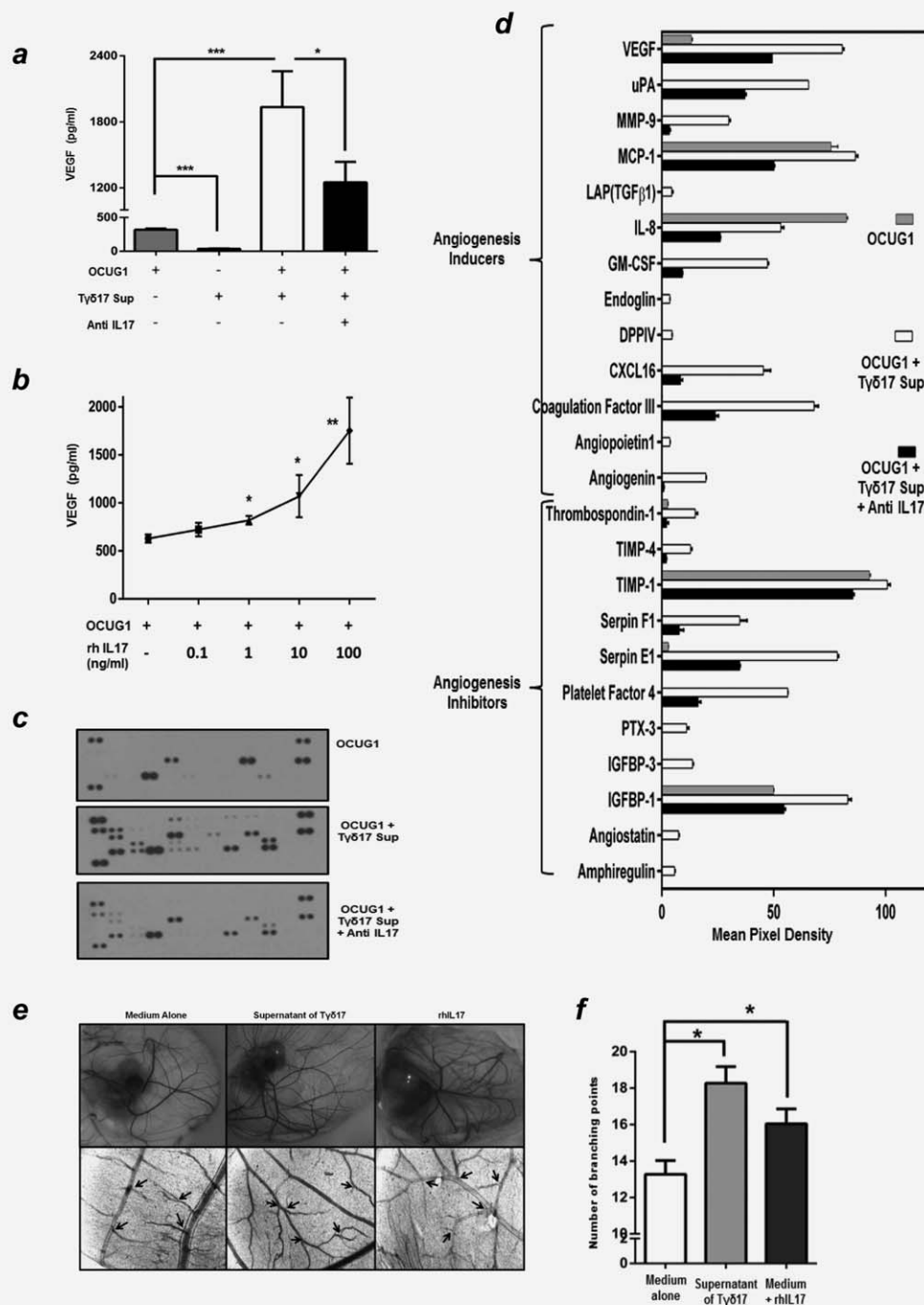
Similarly, GBC patients with high levels of Th17 cells had shorter overall survival compared to patients with low levels (HR: 2.32; Fig. 6b). Tc17 were not associated with survival of patients (Fig. 6c). However, patients with increased Treg cells had poor overall survival (HR: 2.07; Fig. 6d). Altogether, the data suggest that T $\gamma\delta$ 17, Th17 and Treg cells might serve as valuable factor for prediction of risk and prognosis of GBC.

#### Discussion

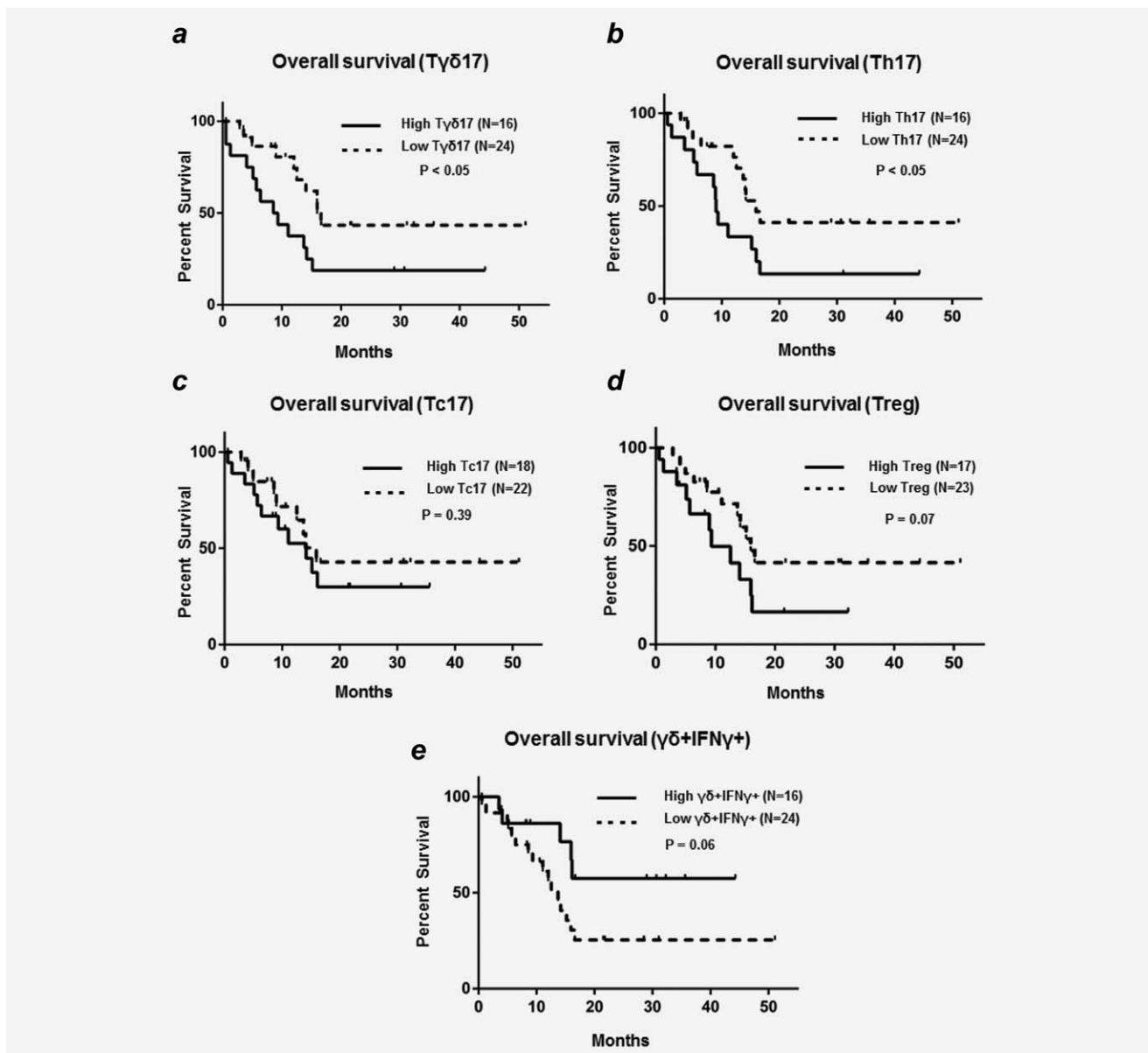
GBC is highly malignant cancer known for its aggressive biological nature and poor clinical presentation. As of today, prognostic biomarkers and effective adjuvant immunotherapy for GBC are unavailable. Therefore, efforts are needed to identify factors contributing to pathogenesis of GBC. Dissecting the complex network of immune cells in peripheral blood and inflammatory tumor environment is vital to design successful immunotherapeutic strategies. Studies in recent years have shown the importance of  $\gamma\delta$ T cells in cell based therapies against cancer.<sup>17,18</sup> Studies from our lab and others have reported that  $\gamma\delta$ T cells exhibit potent cytotoxicity against tumors.<sup>19,20</sup> Various clinical trials have been launched in breast, prostate, hepatocellular and renal cell carcinoma patients using *in vivo* activation of  $\gamma\delta$ T cells or by adoptive transfer of activated  $\gamma\delta$ T cells.<sup>17</sup> In contrast,  $\gamma\delta$ T cells isolated from breast tumor biopsies were shown to mediate immunosuppression by inducing senescence in dendritic cells and CD4<sup>+</sup> T cells to suppress their antitumor response.<sup>21</sup> In a murine model,  $\gamma\delta$ T cells are shown as major source of IL17. These cells inhibit CD8<sup>+</sup> T cell response and recruit myeloid-derived suppressor cells (MDSCs) thereby promoting development of hepatocellular carcinoma.<sup>22</sup> In a mouse model of breast cancer metastasis, T $\gamma\delta$ 17 cells are shown to induce expansion and polarization of neutrophils which suppress cytotoxic antitumor response.<sup>23</sup> Thus, for successful application of  $\gamma\delta$ T cell based immunotherapies in clinics, it is necessary to have a deeper insight into protumor role of  $\gamma\delta$ T cells where data in humans are lacking.

In the present study, we report that T $\gamma\delta$ 17 cells are increased in tumor environment and peripheral blood of GBC patients irrespective of clinical stage. Th17 and Tc17 cells were also elevated but CD8<sup>+</sup> IFN $\gamma^+$  and  $\gamma\delta^+ \text{IFN}\gamma^+$  cells were decreased in GB tumor environment. This supports the existence of chronic inflammation in GBC contributed by immune cells. A murine study in hepatocellular carcinoma has shown that the depletion of V $\gamma$ 4<sup>+</sup>  $\gamma\delta$  T cells (major source of IL17) resulted in significant reduction in tumor volumes in comparison with wild-type mice. Moreover, the infiltrations of effector CD8<sup>+</sup> IFN $\gamma^+$  cells in tumors were significantly increased in V $\gamma$ 4<sup>+</sup>  $\gamma\delta$ T cell-depleted mice.<sup>22</sup> This suggests that T $\gamma\delta$ 17 cells exhibit protumor functions by subsiding anti-tumor immune response.

As increased levels of T $\gamma\delta$ 17 were observed in GBC patients, we reasoned that the cytokine milieu promoting T $\gamma\delta$ 17 differentiation should be present in sera and tumor



**Figure 5.** T $\gamma$  $\delta$ 17 cells induce angiogenesis in gallbladder cancer cells. (a) OCU1 cells were cultured with cell-free supernatants of T $\gamma$  $\delta$ 17 in presence or absence of neutralizing anti-IL17 antibody. VEGF levels in the supernatants were estimated using ELISA ( $n = 6$ ). (b) OCU1 cells were cultured with rhIL17 in a serum-free medium for 48 hr. VEGF was estimated in supernatants by ELISA ( $n = 6$ ). (c and d) Supernatant of T $\gamma$  $\delta$ 17 was incubated with OCU1 cells in presence or absence of anti-IL17. Angiogenesis related proteins in culture supernatants were analyzed by human angiogenesis proteome profiler array. (c) Representative membranes showing array blot developed using chemiluminescence. (d) The bar diagram showing densitometric analysis of angiogenesis array blots represented as mean pixel density ( $n = 2$ ). (e) Representative images of CAM assay depicting enhanced vasculogenesis in presence of supernatant of T $\gamma$  $\delta$ 17 (middle) or rhIL17 (right) compared to medium alone (left). The lower panel shows images of CAM recorded using 4 $\times$  objective. Arrows indicate branching points. (f) Bar diagram showing summarized data of number of branching points in CAM assay ( $n = 3$ ). Results are shown as mean  $\pm$  SEM with  $*p < 0.05$ ;  $**p < 0.01$ ;  $***p < 0.001$ .



**Figure 6.** Increased T $\gamma\delta$ 17 cells in GBC patients associate with poor survival. Overall survival of GBC patients ( $n = 40$ ) was analyzed by Kaplan-Meier method for low or high levels of T $\gamma\delta$ 17 cells (a), Th17 cells (b), Tc17 cells (c), Treg cells (d) and  $\gamma\delta^+$ IFN $\gamma^+$  cells (e). The curve statistics were compared by log-rank test with  $p < 0.05$ .

environment. It was documented that like Th17 cells, T $\gamma\delta$ 17 also differentiate from naïve  $\gamma\delta$ T cells in the presence of IL6, IL1 $\beta$ , IL23 and TGF $\beta$  upon antigenic stimulation.<sup>16</sup> Serum cytokine profile of GBC patients revealed that the levels of IL6, IL1 $\beta$  and IL23 were elevated and are also present in tumor compartment thus making the environment conducive for differentiation of T $\gamma\delta$ 17 cells.

In the present study, we showed that IL17 enhanced proliferation of GBC cells highlighting its protumor role. IL17 is known to induce, chemoresistance, neoangiogenesis and activation of matrix metalloproteinases which in turn enhances tumor progression.<sup>24,25</sup> In GBC patients, we observed T $\gamma\delta$ 17 and Th17 cells to be associated with poor survival. On the contrary, GBC patients with

increased  $\gamma\delta^+$ IFN $\gamma^+$  experienced longer survival. These results strongly suggest that IL17 producing cells play a critical role in immune pathogenesis of human GBC. It appears that tumor environment selectively promotes IL17 producing cells as CD8 $^+$ IFN $\gamma^+$  and  $\gamma\delta^+$ IFN $\gamma^+$  cells were decreased in TILs. Collectively, these results highlight the pathogenic role of T $\gamma\delta$ 17 in GBC.

Serum cytokine analysis revealed decreased levels of TGF $\beta$  in GBC patients. TGF $\beta$  is required for Treg differentiation and maturation.<sup>26</sup> We observed that compared to HI, Tregs were decreased in peripheral blood of GBC patients at all stages of disease. However, their suppressive potential was not compromised suggesting that Tregs in GBC patients are functionally normal. Low levels of TGF $\beta$  observed in serum may be

responsible for reduced levels of Tregs in peripheral blood of these patients. Similar observations were reported in multiple myeloma and pancreatic ductal adenocarcinoma patients which showed that Treg cells were significantly reduced in peripheral blood of patients compared to HL.<sup>27,28</sup> It is reported that the Th17 cells differentiate from FOXP3 expressing CD4<sup>+</sup> T cells<sup>29</sup> and there exists plasticity in the CD4<sup>+</sup> T cells in inflammatory environment.<sup>30</sup> Thus the decreased levels of Treg cells in peripheral blood of GBC patients would be because of skewing of CD4<sup>+</sup> T cell polarization toward Th17 phenotype in response to inflammatory cytokine milieu.

After categorizing the GBC patients having high or low levels of Tregs, we observed that patients with high peripheral blood Treg cells have decreased survival compared to those with low levels. We also noted that Tregs were increased in tumor compartment and express elevated levels of Foxp3 compared to peripheral blood of GBC patients. Given that the suppressive activity of Tregs is determined by Foxp3 expression,<sup>31</sup> the Tregs in TILs of GBC patients appear to be more immunosuppressive. A recent study in colorectal cancer patients demonstrated that T $\gamma$  $\delta$ 17 cells promote migration and survival of MDSCs which enhanced immunosuppression.<sup>32</sup> MDSCs are also known to induce Treg cells in cancer patients.<sup>33</sup> Thus, the increased levels of Tregs in tumor environment of GBC may be attributed to the T $\gamma$  $\delta$ 17 driven inflammation leading to accumulation of MDSCs and subsequent upregulation of Tregs which warrants further investigation. Moreover, it is reported that Th17 and Treg frequently colocalize at the same anatomic compartments and mutually promote each other's generation and function.<sup>13</sup> We observed the infiltration of Treg and IL17 producing cells in the tumor environment of GBC patients which corroborate the earlier observations in GBC patients reported by Zhang *et al.*<sup>34</sup> This suggests that although the ratios of T $\gamma$  $\delta$ 17/Treg, Th17/Treg and Tc17/Treg were increased in GBC patients, IL17 producing cells and Tregs may act cooperatively and eventually contribute to the poor survival observed in GBC patients.

Next we addressed the functional role of T $\gamma$  $\delta$ 17 cells on GBC tumor progression. We showed that T $\gamma$  $\delta$ 17 cells migrate toward tumor milieu through CXCL9-CXCR3 axis. The increased levels of CXCL9 and CXCL10 observed in sera of GBC patients, further supports the elevated levels of T $\gamma$  $\delta$ 17 cells observed in the tumor environment. Earlier it was reported that Th17 utilized this axis to migrate toward inflamed liver.<sup>35</sup> This is the first report demonstrating migration of T $\gamma$  $\delta$ 17 cells to the tumor environment using CXCL9-CXCR3 axis.

Angiogenesis is a critical step in the progression of solid tumors providing nutrients, growth factors and oxygen for growth of malignant cells. Th17 cells have been shown to be proangiogenic in human head and neck squamous cell carcinoma.<sup>36</sup> Proangiogenic functions of T $\gamma$  $\delta$ 17 in human cancer are not yet reported. Our data have shown that human T $\gamma$  $\delta$ 17 cells are proangiogenic and induce blood vessel formation as observed in *ex vivo* chick embryo CAM assay. T $\gamma$  $\delta$ 17 induced GBC cells to produce proangiogenic factors such as VEGF, uPA, MMP9, MCP1, GM-CSF, CXCL16, Coagulation factor

III, angiogenin, etc. through secretion of IL17. A study in IL17<sup>-/-</sup> murine model has shown that  $\gamma$  $\delta$ T cells were the major source of IL17 and depletion of IL17 resulted in decreased vascular density and tumor growth.<sup>37</sup> Interestingly, we observed that T $\gamma$  $\delta$ 17 also induced anti-angiogenic factors (Thrombospondin-1, TIMP1, Serpine1, Platelet factor-4, IGFBP1, *etc.*). However, TIMP-1 and serpine-1 are also reported as markers of poor prognosis in cancer.<sup>38,39</sup> A recent study in glioblastoma showed that IGFBP1 secretion by microglial cells induced by MCSF is essential for angiogenesis.<sup>40</sup>

VEGF is a key mediator of tumor angiogenesis and metastasis. VEGF is reported as an independent prognostic marker and associates with poor survival of GBC patients.<sup>41,42</sup> Bevacizumab which targets VEGF, when combined with chemotherapy has shown direct antitumor effect and improved patient survival.<sup>43</sup> Chemotherapeutic drugs like oxaliplatin, doxorubicin, gemcitabine, 5-fluorouracil trigger cancer cell death which activate anti-tumor immune response. Gemcitabine (gem) and 5-fluorouracil (5-fu) were shown to induce apoptosis in MDSCs and release of IL1 $\beta$  which activates Th17 cells. Release of IL17 further compromised the antitumor effect of gem and 5-fu.<sup>44</sup> However, in a murine study, T $\gamma$  $\delta$ 17 cells improved the anti-tumor efficacy of anthracycline doxorubicin.<sup>45</sup> The studies suggest that the chemotherapeutic drugs should be combined with immunomodulatory agents for increasing efficacy of anticancer therapy. Recently, Secukinumab, monoclonal antibody that binds to human IL17A has been approved for treatment of psoriasis.<sup>46</sup> Other approaches to target IL17 inflammatory axis including monoclonal antibody targeting IL17 receptor (brodalumab), IL23 p40 subunit (ustekinumab), IL23 p19 subunit and small molecules with inverse agonist activity against ROR $\gamma$ t are under Phase II/III clinical trials for inflammatory diseases.<sup>47,48</sup> Our data provide insights into proangiogenic role of T $\gamma$  $\delta$ 17 through IL17 production which could be a promising candidate for targeted therapy for treatment of GBC. Moreover, the increased levels of Tregs observed in GBC tumor could also be targeted using various immunotherapeutic strategies. Use of antibodies specific for CD25 (daclizumab), CTLA4 (ipilimumab), GITR, OX-40, PD-L1 or PD-1 (nivolumab) subvert the immunosuppression mediated by Treg cells and have demonstrated efficacy in clinical trials.<sup>11,49</sup> Disrupting tumor homing of Tregs by blocking CCR4 mediated migration is advantageous as it transiently inhibit Treg cells only during priming phase and avoid potential autoimmune complications caused by long-term depletion of Treg cells by mAbs.<sup>49,50</sup>

In conclusion, we report for the first time T $\gamma$  $\delta$ 17 and Th17 as predictive markers in GBC and provide evidence for the proangiogenic role of human T $\gamma$  $\delta$ 17. Our data strongly suggest that T $\gamma$  $\delta$ 17 mediated angiogenesis and Treg cells mediated immunosuppression may contribute to the negative clinical outcome of GBC patients. Thus, future immunotherapeutic treatment modality for GBC may use a combined approach to block the trafficking of T $\gamma$  $\delta$ 17 cells to the tumor, inhibit functions of IL17 and reverse the immunosuppression mediated by Treg cells.

## Acknowledgements

The work is supported by Department of Biotechnology, Government of India, under Centre of Excellence grant (BT/01/CEIB/09/V/06). We

acknowledge Department of Atomic Energy for providing research fellowship to R.S.P. We thank Prof. M. Indap (Ruparel College, Mumbai, India) for the help extended toward the chick chorioallantoic membrane assay.

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# The Jekyll and Hyde story of IL17-producing $\gamma\delta$ T cells

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In comparison to conventional  $\alpha\beta$ T cells,  $\gamma\delta$ T cells are considered as specialized T cells based on their contributions in regulating immune response.  $\gamma\delta$ T cells sense early environmental signals and initiate local immune-surveillance. The development of functional subtypes of  $\gamma\delta$ T cells takes place in the thymus but they also exhibit plasticity in response to the activating signals and cytokines encountered in the extrathymic region. Thymic development of T $\gamma\delta$ 1 requires strong TCR, CD27, and Skint-1 signals. However, differentiation of IL17-producing  $\gamma\delta$ T cells (T $\gamma\delta$ 17) is independent of Skint-1 or CD27 but requires notch signaling along with IL6 and TGF $\beta$  cytokines in the presence of weak TCR signal. In response to cytokines like IL23, IL6, and IL1 $\beta$ , T $\gamma\delta$ 17 outshine Th17 cells for early activation and IL17 secretion. Despite expressing similar repertoire of lineage transcriptional factors, cytokines, and chemokine receptors, T $\gamma\delta$ 17 cells differ from Th17 in spatial and temporal fashion. There are compelling reasons to consider significant role of T $\gamma\delta$ 17 cells in regulating inflammation and thereby disease outcome. T $\gamma\delta$ 17 cells regulate mobilization of innate immune cells and induce keratinocytes to secrete anti-microbial peptides thus exhibiting protective functions in anti-microbial immunity. In contrast, dysregulated T $\gamma\delta$ 17 cells inhibit Treg cells, exacerbate autoimmunity, and are also known to support carcinogenesis by enhancing angiogenesis. The mechanism associated with this dual behavior of T $\gamma\delta$ 17 is not clear. To exploit, T $\gamma\delta$ 17 cells for beneficial use requires comprehensive analysis of their biology. Here, we summarize the current understanding on the characteristics, development, and functions of T $\gamma\delta$ 17 cells in various pathological scenarios.

**Keywords:**  $\gamma\delta$ T cell, IL17, T $\gamma\delta$ 17, infection, inflammation, cancer

## INTRODUCTION

Decades have passed since the accidental discovery of T cells expressing  $\gamma$  and  $\delta$  chains (1), yet it is hard to define  $\gamma\delta$ T cells like  $\alpha\beta$ T cells. Ambiguity in understanding the functions of  $\gamma\delta$ T cells is attributed to their unparalleled characteristics as compared to  $\alpha\beta$ T cells. Current understanding of T cell biology has emerged extensively from studies on  $\alpha\beta$ T cells; however, recent findings have underlined the crucial role of  $\gamma\delta$ T cells in shaping the immune response in infections, inflammatory diseases, and cancer. They are involved in early immune response like innate cells, produce proinflammatory cytokines (IFN $\gamma$ , IL17, and TNF $\alpha$ ), and activate adaptive immune cells. The cytokines secreted by  $\gamma\delta$ T cells determine their effector functions. In humans, the major cytokine produced by  $\gamma\delta$ T cells is IFN $\gamma$ , contributing to its role in anti-viral, anti-bacterial, and anti-tumor immunity (2–4). However, upon activation  $\gamma\delta$ T cells can be skewed toward IL17, IL4, or TGF $\beta$  producing phenotype governed by the polarizing cytokines present in the surrounding milieu (5). Recent investigations in mice and human have highlighted the role of IL17-producing  $\gamma\delta$ T cells (hereafter referred as T $\gamma\delta$ 17) in bacterial infection, inflammatory disease, and cancer (6–8). They are the primary source of IL17 in early disease condition and are pivotal in progression and disease outcome (9, 10). To understand the functional significance of T $\gamma\delta$ 17 in pathological conditions, many efforts have made in mouse models but there is scanty literature available on human T $\gamma\delta$ 17 cells. In this review, we will discuss the recent findings of

T $\gamma\delta$ 17 differentiation, mechanisms regulating IL17 production, and their relevance in pathological conditions.

## $\gamma\delta$ T CELLS: UNIQUE BUT VERSATILE

Survival of  $\gamma\delta$ T cells over strong evolutionary selection pressure highlights their exclusive importance and disparate properties from conventional  $\alpha\beta$ T cells. Initially,  $\gamma\delta$ T cells were considered as cells of innate immunity owing to their ability to recognize conserved non-peptide antigens expressed by stressed cells. In addition to this, they recognize pathogen-associated molecular pattern (PAMP) or danger-associated molecular pattern (DAMP) through pattern recognition receptors (PRR) expressed by them (11). Like adaptive immune cells, human  $\gamma\delta$ T cells undergo clonal expansion and exhibit antigen-specific memory (12). Thus,  $\gamma\delta$ T cells link innate and adaptive immunity thereby enhancing the immune response against invading pathogen or danger signal posed by “self” cells. Antigen recognition by murine or human  $\gamma\delta$ T cells does not require antigen presentation by major histocompatibility complex (MHC) class I or class II (13) and the crystal structure of  $\gamma\delta$ TCR has revealed its close homology with immunoglobulins suggesting that antigen recognition by  $\gamma\delta$ T cells is similar to antigen–antibody interaction (14). However, diversity of antigens recognized by  $\gamma\delta$ T cells brands it different from B cells. The antigens exclusively recognized by  $\gamma\delta$ T cells are not peptides of protein antigens rather are small mono- and pyrophosphates of linear C5 isoprenoids called as phosphoantigens (13). These

prenyl pyrophosphates are metabolites of cholesterol biosynthesis and are recognized through complementarity determining regions (CDRs) of  $\gamma\delta$ T cells (15). In humans, during cholesterol biosynthesis, phosphorylated precursors such as isopentenyl pyrophosphate (IPP) and DMAPP (dimethylallyl pyrophosphate) are synthesized by mevalonate pathway (16). However, microbial pathogens use non-mevalonate pathway to produce these phosphorylated precursors (17).  $\gamma\delta$ T cells respond to these natural or synthetic stimulators with varying degree. Based on this, stimulators are classified either as weak or potent stimulators. HMBPP [(E)-4-hydroxy-3-methyl-but-2-enyl pyrophosphate], a metabolite of non-mevalonate pathway of bacteria *Mycobacterium tuberculosis* is  $10^4$  times more potent stimulator of human  $\gamma\delta$ T cells than IPP (18). The exclusive response of  $\gamma\delta$ T cells to these phospho-antigens has a potential therapeutic significance and synthetic pyrophosphates can be used to harness the cytotoxic potential of  $\gamma\delta$ T cells.

Murine and human  $\gamma\delta$ T cells also recognize phycoerythrin (PE) – fluorescent molecule of cyanobacteria and red algae. PE is directly recognized by  $\gamma\delta$ T cells but there is no sequence similarity between PE-specific murine and human  $\gamma\delta$  TCR (19). Naturally occurring primary alkyl amines activate human V $\gamma$ 2V $\delta$ 2 T cells and enhance immunity against certain microbes and plant-derived antigens (20, 21). Similar to natural killer (NK) cells, human  $\gamma\delta$ T cells also recognize the stress-induced MHC class I-related molecules MICA, MICB, and the UL16-binding proteins that are upregulated on malignant or stressed cells (22, 23). The stress-related molecules are ligands for NKG2D expressed by  $\gamma\delta$ T cells and this engagement also enhances  $\gamma\delta$ T cells' response to non-peptide antigens (24). Human and murine  $\gamma\delta$ T cells recognize lipid antigens presented by CD1 molecules, a classical ligand for NK T cell suggesting the phenomenon similar to MHC-restricted antigen recognition by  $\alpha\beta$ T cells (25–27). The murine  $\gamma\delta$ T cells also recognize non-classical MHC class I molecules like T10 and T22 ( $\beta$ 2 microglobulin-associated molecules lacking peptide binding groove) (28, 29). In addition to non-protein and MHC related antigens, murine and human  $\gamma\delta$ T cells also recognize small peptides such as heat shock proteins (HSPs) (30–32). However, they do not require antigen-presenting cells (APCs) and recognition of antigen is MHC unrestricted, resembling B cells (33). Thus, the broad spectrum antigen responsiveness of  $\gamma\delta$ T cells helps them to mount faster immune response.

Like  $\alpha\beta$ T cells,  $\gamma\delta$ T cells develop in the thymus from CD4<sup>−</sup>CD8<sup>−</sup> (double negative, DN) thymocytes (34); however, they precede  $\alpha\beta$ T cells in T cells ontogeny.  $\gamma\delta$  TCR rearrangements can be traced in early embryonic stages in mice as well as in humans (35, 36). This highlights their role in neonatal protection as conventional T cells are functionally impaired and APCs are immature in newborns (37). During thymic development, the decision of  $\gamma\delta$  versus  $\alpha\beta$  T cell commitment is determined by TCR signal strength or notch signaling (38). In mice, the strong TCR signaling in absence of notch signal induces  $\gamma\delta$ T cells lineage commitment whereas low TCR signal strength in presence of strong notch signaling promotes  $\alpha\beta$  T cell lineage (39–41). However, notch signaling alone is insufficient to decide  $\gamma\delta/\alpha\beta$  T cell commitment. The intrinsic signals from T cell receptor complex and trans-conditioning by different subsets of thymocytes also

determine thymic development of  $\gamma\delta$ T cells (42). In humans, notch has opposite role in  $\alpha\beta$  versus  $\gamma\delta$ T cell lineage decision, sustained notch signaling is required for the development of  $\gamma\delta$ T cells (43) which is determined by differential notch receptor–ligand interaction importantly Jagged2/Notch3 signaling (44). In human,  $\gamma\delta$ T cells differentiate along two pathways, a notch-independent DN pathway, generating mature DN and CD8 $\alpha\alpha^+$  SP (single positive) TCR $\gamma\delta^+$  cells. In the notch-dependent DP (double positive) pathway, immature CD4<sup>+</sup> SP, and subsequently DP TCR $\gamma\delta^+$  cells are generated. Human postnatal thymus thus exhibits a scenario of DN, DP, and SP TCR $\gamma\delta^+$  population, which highlights heterogeneity in human  $\gamma\delta$ T cell development (45). The activated extrathymic  $\gamma\delta$ T cells, in humans, express notch receptors, which regulate their effector functions. Inhibiting notch signaling in  $\gamma\delta$ T cells dampened their anti-tumor cytotoxic potential (46). Thus, validates the requirement of notch signaling in both thymic development and functions of human  $\gamma\delta$ T cells. The diversity of human  $\gamma\delta$  T cell repertoire at birth (majorly contributed by V $\delta$ 1<sup>+</sup> subset of  $\gamma\delta$ T cells in cord blood) is restricted in adulthood especially to V $\gamma$ 9V $\delta$ 2, a circulating subset of  $\gamma\delta$ T cells. The absolute numbers of V $\gamma$ 9V $\delta$ 2 T cells increase from minor population at birth to more than 75% of  $\gamma\delta$ T cells pool in peripheral blood (35), which constitute around 1–10% of total T cells in humans. The  $\gamma\delta$ T cells exit the thymus as mature T cells and express markers that are associated with antigen-experienced T cells (47).

The other important feature of  $\gamma\delta$ T cells apart from antigen recognition is their tissue tropism. In humans, the first  $\gamma\delta$ T cells to arise from thymus are V $\delta$ 1<sup>+</sup> (paired with various V $\gamma$  chains), which preferentially populate in epithelial tissue and constitute larger proportion of intraepithelial lymphocytes (IELs) (48). They rapidly and innately recognize stressed cells found to be enriched in various tumor tissues (4). The V $\gamma$ 9V $\delta$ 2 is a lymphoid homing subset of  $\gamma\delta$ T cells, which continually expand in response to microbial antigen in circulation and exhibit characteristics of adaptive immune system (49). These cells recognize, expand, and secrete cytokines in response to non-peptide antigens associated with microbes in circulation. In mouse, a substantial proportion of  $\gamma\delta$ T cells reside as the IEL in the skin, intestine, and genitourinary tract. In response to the chemokine signals, V $\gamma$ 5V $\delta$ 1<sup>+</sup> T cells leave the fetal thymus, reside in the epidermis, and form dendritic-like network similar to Langerhans cells. These cells are called as dendritic epidermal T cells (DETCs) and constitute more than 90% of epidermal T cells (50). V $\gamma$ 6<sup>+</sup> T cells home to tongue and reproductive tract whereas V $\gamma$ 7<sup>+</sup> T cells home to intestinal tract suggesting that distinct TCR repertoire are present at different anatomical site and respond to antigens unique to their resident tissues (51–53). However, the functions of IELs are determined by the environment at the anatomical site (54) and hence specific  $\gamma\delta$  T cell subset could be used in tissue repair and generation of effective immune response at different epithelial sites.

$\gamma\delta$ T cells perform diverse effector functions determined by the TCR expressed, tissue localization, and activation status. Apart from these, MHC-independent recognition of antigens, production of IFN $\gamma$ , and expression of cytotoxic granules classify  $\gamma\delta$ T cells as potential cytotoxic cells (55). They can kill activated, infected, stressed, and transformed cells using various strategies such as engagement of death-inducing receptors, such as FAS

and TNF-related apoptosis-inducing ligand receptors (TRAILR) and the release of cytotoxic effector molecules such as perforin and granzyme (56, 57). Human  $\gamma\delta$ T cells also recognize HSP (HSP60/70) expressed on tumor cells and enhance its cytolytic activity against the tumors (31, 58).  $\gamma\delta$ T cells support the maturation and activation of other lymphocytes, NK cells, and macrophages with the help of secreted chemokines (CCL3, CCL4, CXCL10) (55). Another chemokine CXC–chemokine ligand 13 (CXCL13) produced by V $\gamma$ 9V $\delta$ 2 cells can regulate B cell organization within lymphoid tissues and help B cells to produce antibodies (59). Human  $\gamma\delta$ T cells can also crosstalk with dendritic cells (DCs) influencing each other functions like the antigen presentation by DCs, activation, and secretion of IL12 and IFN $\gamma$  by  $\gamma\delta$ T cells, which result in DC maturation (11, 60). These properties of  $\gamma\delta$ T cells aid in generation of the effective immune response in the appropriate condition. Not only this, activated V $\gamma$ 9V $\delta$ 2 cells can take up and process the soluble antigens, opsonize target cells, and can migrate to lymph nodes through CC-chemokine receptor 7 (CCR7) where they upregulate expression of MHCs and co-stimulatory receptors CD80 and CD86 (61, 62). Activated V $\gamma$ 9V $\delta$ 2 cells has also been licensed to act as APC and activate CD4 and CD8 T cells (63). Collectively, these observations highlight the multi-talented role of  $\gamma\delta$ T cells, having both Th- and Tc-like properties along with acting as APC. The special trait of  $\gamma\delta$ T cells is their ability to recognize phosphorylated non-protein antigens and mediate its effector function in spatial and temporal manner making them a robust cell type, which can be manipulated to develop a promising tool for novel immunotherapies against certain types of diseases. However, care should be adapted while designing such immunotherapies because these cells have capacity to secrete various cytokines under different conditions.

### T $\gamma$ $\delta$ 17: A SUBTYPE OF $\gamma\delta$ T CELLS

Unlike  $\alpha\beta$  T cells, in mice, which leave thymus as naïve cells and are primed in the peripheral compartment,  $\gamma\delta$ T cells undergo subset commitment in the thymus itself. However, in humans, upon activation with different cytokines, V $\gamma$ 9V $\delta$ 2 cells can be polarized toward different effector subtypes like  $\gamma\delta$ 1,  $\gamma\delta$ 2 (64),  $\gamma\delta$ 17 (65, 66), and  $\gamma\delta$ Treg (67, 68). This functional plasticity of  $\gamma\delta$ T cells assists them to tackle the distinct disease conditions and play important role in the early responses to invasive pathogens. The recent findings have stated that  $\gamma\delta$ T cells are major IL17 producers and have shown their involvement in early onset of immune activation (69). Similar to Th17 cells, T $\gamma$  $\delta$ 17 cell express ROR $\gamma$ t as a lineage determination transcriptional factor (70). Healthy adult human peripheral blood V $\gamma$ 9V $\delta$ 2 T cells distinctively express Th1 signature and 50–80% produce IFN $\gamma$  but <5% produce IL17 (6). However, T $\gamma$  $\delta$ 17 cells have been demonstrated to be involved in the pathogenesis of transplantation rejection (71), autoimmune disease (72), allergy (73), and cancer (74) in humans. The biology of T $\gamma$  $\delta$ 17 is so naïve that it compels us to cross-examine its genesis, functions, and clinical relevance to understand its therapeutic potential.

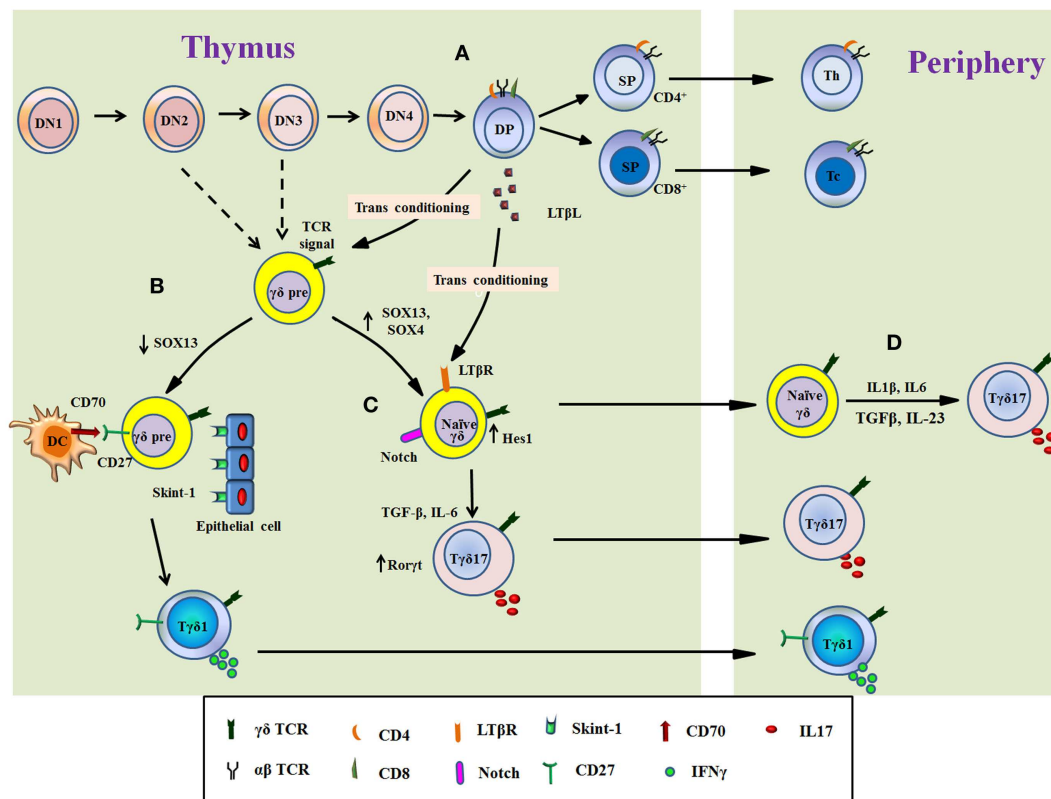
### MOLECULAR EVIDENCES OF T $\gamma$ $\delta$ 17 GENESIS

The molecular mechanism of IL17-producing  $\gamma\delta$ T cells remains an enigma. Most of the studies carried out to understand the

differentiation mechanisms of T $\gamma$  $\delta$ 17 cells are based on the murine models.  $\gamma\delta$ T cells preferentially localized to barrier tissues are the initial source of IL17 and are likely to originate from the fetal thymus. These are called as the natural IL17-secreting  $\gamma\delta$ T cells.  $\gamma\delta$ T cells that make IL17 within 24 h fall in this category (75).  $\gamma\delta$ T cells acquire IL17-secreting phenotype in secondary lymphoid tissues after antigen exposure, which is referred to as induced T $\gamma$  $\delta$ 17 cells (76, 77).

During development of T cells in thymus, murine  $\gamma\delta$ T cells branch off at the transition of thymocytes from DN3 stage to DN4 stage (34). It is also reported that  $\gamma\delta$ T cells develop from DN2 stage and specifically produce IL17 whereas IFN $\gamma$ -producing  $\gamma\delta$ T cells can develop from both DN2 and DN3 precursors (78) (**Figure 1**). This suggests that  $\gamma\delta$ T cells do not develop like  $\alpha\beta$ T cells and follow evolutionary ancient path of T cell development. However, the precise DN stage from which  $\gamma\delta$ T cells develop is elusive (79). Fetal thymic  $\gamma\delta$  T-cell development occurs in successive waves by using the different V $\gamma$  and V $\delta$  segments during the embryonic development (34, 80). Successful gene rearrangement of  $\gamma\delta$  T cells from early thymic precursors (CD44<sup>hi</sup>) lead to the development of naïve  $\gamma\delta$  T cell characterized by CD44<sup>lo</sup> CD27<sup>+</sup> CD62L<sup>+</sup> phenotype. This phenotype can either leave the thymus to populate in secondary lymphoid organs or it can undergo further intrathymic differentiation that results in the development of multiple  $\gamma\delta$  T cell subtypes such as dendritic epidermal  $\gamma\delta$ T cell (DETCs), T $\gamma$  $\delta$ 17, or NK 1.1<sup>+</sup>  $\gamma\delta$  cell ( $\gamma\delta$ NKT cells) (80, 81). Recently, it was described that when thymic lobes of mice at E14 were colonized with DN1a cells from mice at E13 and E18, respectively. It was observed that although both populations (E13 DN1a cells and E18 DN1a cells) generated similar number of  $\gamma\delta$ T cells, only E13 DN1a cells generated V $\gamma$ 3<sup>+</sup> DETCs. These observations indicate that precursor lineage of DETCs may be different and needs further investigation (82). DETCs develop at embryonic day 13 (E13) to approximately E17 and readily secrete IFN $\gamma$  when activated. After the development of DETCs, the next functional developmental wave consists of T $\gamma$  $\delta$ 17 cells. T $\gamma$  $\delta$ 17 cells are heterogeneous in using TCR chains that mainly include V $\gamma$ 6<sup>+</sup> and V $\gamma$ 4<sup>+</sup> but also use V $\gamma$ 1<sup>+</sup> chain. V $\gamma$ 6<sup>+</sup> cells develop by E14 to around birth and finally V $\gamma$ 1 and V $\gamma$ 4 cells develop E16 onward (81). The other subtypes of  $\gamma\delta$  T cells, which develop in thymus, are  $\gamma\delta$  NKT cells, which are similar to invariant TCR $\alpha\beta$ <sup>+</sup> NKT cells (83, 84).

There are different thymic signaling processes, which determine functional phenotype of  $\gamma\delta$ T cells in thymus before migration to periphery and contribute to the balance between IFN $\gamma$  committed versus IL17-committed subtypes (85). This biasness toward IL17 or IFN $\gamma$  depends on the antigen experience in thymus. The  $\gamma\delta$  T cells that have encountered the cognate antigen interaction in thymus, gain the potential to differentiate into the IFN $\gamma$ -producing functional phenotype while antigen naïve  $\gamma\delta$  T cells develop into IL17-producing  $\gamma\delta$ T cells (86). This skewedness also reflects in their distribution outside the thymus. Most of T $\gamma$  $\delta$ 17 cells reside in lymph nodes whereas IFN $\gamma$ -producing  $\gamma\delta$ T cells are mainly found in the spleen and the mechanism for this distribution is not clear (86). Similar distribution is also found in  $\alpha\beta$ T cells and it seems to be logical as the lymph nodes serve as the site of initial exposure to foreign antigens and propagate the wave of inflammation, thus are suited for the earliest source of the IL17 secretion (87).



**FIGURE 1 | Overview of T $\gamma\delta$ 17 cells development.** The figure illustrates the differentiation of T $\gamma\delta$ 17 cells from T cell progenitors in the murine thymus (A–C) and from naïve  $\gamma\delta$  T cells in periphery in human (D). Progenitor T cells differentiate through double negative stage 1 (DN1) to DN stage 4 (A). The decision of  $\alpha\beta$  or  $\gamma\delta$  TCR expression takes place at early T cells precursor (from DN2 or DN3 stage) as showed by dashed line. The thymocytes expressing  $\alpha\beta$  TCR develop into double-positive thymocytes, which support differentiation of functional subtypes of  $\gamma\delta$  T cells called as transconditioning. DP thymocytes secrete LT $\beta$ L, which support differentiation of T $\gamma\delta$ 17. The DP  $\alpha\beta$  thymocytes then exit the thymus as mature single positive T cells (either CD4 $^{+}$  or CD8 $^{+}$  T cells) (A). The functional programming of  $\gamma\delta$  T cells is

determined by TCR signal and/or other related signals. TCR signal, interaction with Skint-1 from epithelial cells, downregulation of SOX13, and signaling through CD27/CD70 divert  $\gamma\delta$  thymocytes toward IFN $\gamma$ -producing phenotype (T $\gamma\delta$ 1), which migrate to periphery (B). Conversely, signaling through Notch receptor maintain Sox13 levels with increase in Hes1 and ROR $\gamma$ t expression induce  $\gamma\delta$  thymocytes to produce IL17. Progression of  $\gamma\delta$  thymocytes to T $\gamma\delta$ 17 cells is independent of signaling through Skint-1 and/or CD27 but require inputs from IL6 and TGF $\beta$ . The natural T $\gamma\delta$ 17 cells developed in thymus migrate to tissue or periphery (C). In human, naïve  $\gamma\delta$  T cells, which exit thymus, can also differentiate into T $\gamma\delta$ 17 cells in presence of TCR signal and cytokines such as IL6, IL1 $\beta$ , IL23, and TGF $\beta$  (D).

Besides the  $\gamma\delta$  TCR signaling (86), expression of tumor necrosis factor receptor family member, CD27, determines the IL17 versus IFN $\gamma$  production by  $\gamma\delta$  T cells (88). CD27 $^{+}$   $\gamma\delta$  T cells differentiate into IFN $\gamma$  producing cells whereas IL17 production was restricted to CD27 $^{-}$  T cells (89) (Figure 1). Thus thymic “imprinting” of the  $\gamma\delta$  T cells as CD27 $^{+}$  or CD27 $^{-}$  regulates effector functions of  $\gamma\delta$  T cells and is preserved in the periphery (89). CD27 is not only associated with IFN $\gamma$  production but also aids  $\gamma\delta$  T cells to interact with its ligand CD70 expressed on DCs, thymic epithelial cells, and double-positive thymocytes thus acting as a costimulatory receptor (89). Therefore, CD27 conveys an intrathymic message that licenses the CD27 $^{+}$   $\gamma\delta$  T cells for the production of IFN $\gamma$  (47). Another signaling pathway that influences the differentiation of T $\gamma\delta$ 17 is the signaling through lymphotoxin- $\beta$  receptor (LT $\beta$ R), a member of the tumor necrosis factor receptor family (90). Signaling through LT $\beta$ R leads to the activation of the alternative nuclear factor (NF)- $\kappa$ B pathway via RelB. Ligands for LT $\beta$ R regulating this developmental process are produced by CD4 $^{+}$ CD8 $^{+}$  thymocytes

(91). The homeostasis of this functional phenotypic differentiation, influenced by other thymic progenitors is known as transconditioning (91), which highlights coordination between different signaling pathways in thymus that occur in physically separate thymic niche (92). LT $\beta$ R signaling pathway controls T $\gamma\delta$ 17 development by regulating transcription factors ROR $\gamma$ t and ROR $\alpha$ 4, required for IL17 expression in  $\gamma\delta$  thymocytes (93). The role of LT $\beta$ R signaling, however, remains controversial as LT $\beta$ R is present downstream to CD27 signaling, which is associated with the IFN- $\gamma$  production (89).

The maturation of T $\gamma\delta$ 17 cells from its precursors requires TCR signaling as mice with reduced ZAP70 show decreased number of T $\gamma\delta$ 17 cells (94). However, TCR signaling alone is not sufficient as it also requires other signals (95). An src family kinase, Blk (B lymphoid kinase), is required for T $\gamma\delta$ 17 cells development in thymus as Blk-deficient mice was reported to have less number of IL17-producing  $\gamma\delta$  T cells (96). Similarly, high-mobility group (HMG) box transcription factors, SOX4 and SOX13 are

positive regulators of T $\gamma$  $\delta$ 17 development (95, 97). These transcription factors expressed in immature T cells (98) highlight that the development of T $\gamma$  $\delta$ 17 is from early precursors (DN2) (78, 95). Other thymic determinant, which is responsible for the functional dichotomy in T $\gamma$  $\delta$ 17 and T $\gamma$  $\delta$ 1, is Skint-1, a thymic epithelial cell determinant. The interaction between Skint-1<sup>+</sup> cells and  $\gamma$  $\delta$  thymocytes (V $\gamma$ 5<sup>+</sup>V $\delta$ 1<sup>+</sup>) induce an Egr3-mediated pathway, leading to differentiation toward IFN $\gamma$ -producing  $\gamma$  $\delta$  T cells. Further, it suppresses Sox13 and an ROR $\gamma$ t transcription factor-associated T $\gamma$  $\delta$ 17 cells lineage differentiation suggesting that the functions of the earliest T cells are substantially preprogrammed in the thymus (99). Notch signaling is known to be involved in thymic determination and development of T $\gamma$  $\delta$ 17 cells. Hes1, one of the basic helix–loop–helix (bHLH) proteins induced by Notch signaling is critical for the IL17 expression by  $\gamma$  $\delta$  T cells and its thymic development (100–102). Further, the specific expression of Hes1 in CD25<sup>+</sup> and CD27<sup>+</sup>  $\gamma$  $\delta$  T cells and decreased levels of T $\gamma$  $\delta$ 17 in Hes1-deficient mice highlights the critical role of Notch–Hes1 pathway in T $\gamma$  $\delta$ 17 development in thymus as well as in periphery (101). The thymic development of T $\gamma$  $\delta$ 17 is independent of STAT3 but partly dependent on ROR $\gamma$ t (101) and most peripheral IL17-producing  $\gamma$  $\delta$  cells express ROR $\gamma$ t and respond rapidly to IL23 (103).

Developmental process of T $\gamma$  $\delta$ 17 also requires signaling through different cytokines. TGF $\beta$  signaling is necessary for T $\gamma$  $\delta$ 17 development (104). It has been shown that in absence of TGF $\beta$ 1 or Smad3 (a component of the TGF $\beta$  signaling), the number of T $\gamma$  $\delta$ 17 thymocytes reduced drastically relative to that of wild-type mice (104). As compared to TGF $\beta$ , requirement of IL6 for T $\gamma$  $\delta$ 17 development is not well understood as there are contrasting reports on its role (72, 105). It is also reported that IL6 does not act directly on uncommitted  $\gamma$  $\delta$  thymocytes but instead it acts indirectly by regulating the expression of Delta-like ligand 4, a ligand for notch receptor, expressed by thymic epithelial cells that promote the differentiation of T $\gamma$  $\delta$ 17 (101, 106). Moreover, IL23 and IL1 produced by DCs are crucial for IL17 production by  $\gamma$  $\delta$  T cells. IL23<sup>−/−</sup> and IL23R<sup>−/−</sup> mice showed the significant reduction in T $\gamma$  $\delta$ 17 cells after *L. monocytogenes* infection supporting earlier observation (107–110).

Thymic development of human T $\gamma$  $\delta$ 17 cells is poorly investigated. Around 80% circulating human V $\gamma$ 9V $\delta$ 2 T cells are IFN- $\gamma$  producers and express CD27 whereas CD27 negative cells are IL17-producing  $\gamma$  $\delta$  T cells are <5% (65). Interaction of CD70 with CD27 promotes the expansion of Th1-biased V $\gamma$ 9V $\delta$ 2 T cells in periphery (111). However, such role in their thymic development is unknown. Human V $\gamma$ 9V $\delta$ 2 T cells can be polarized to T $\gamma$  $\delta$ 17 cells in periphery upon IPP activation and in the presence of cytokines like TGF $\beta$ , IL1 $\beta$ , IL6, and IL23, followed by a week of culture in differentiation medium supplemented with IL2 can induce IL17 in these cells (65, 66). In humans, there are contrasting reports on role of IL6 and IL23 in differentiation of T $\gamma$  $\delta$ 17. It has been shown that IL6 is required for differentiation of neonatal T $\gamma$  $\delta$ 17, and IL23 is required for the generation of adult IL17-producing  $\gamma$  $\delta$  T cells (65). In another study, it is reported that in the presence of TCR signaling, IL23 promotes the induction of IL17 in neonatal (but not adult)  $\gamma$  $\delta$  T cells (112). However, it appears that IL23 induces  $\gamma$  $\delta$  T cells to coproduce IL17 and IFN $\gamma$  in adults but

support development of T $\gamma$  $\delta$ 17 cells in neonates. In addition to the above-mentioned cytokines, IL7 selectively promotes the mouse and human IL17-producing  $\gamma$  $\delta$  T cells. IL7 activates STAT3 preferentially in  $\gamma$  $\delta$  T cells competent to produce IL17 (113). However, the increased IL17 production by  $\gamma$  $\delta$  T cells upon TCR stimulation in presence of IL7 is observed only in case of cord blood cells but not with peripheral lymphocytes. Thus, it is important to note that the antigen naïve  $\gamma$  $\delta$  T cells only can be reprogrammed *in vitro* toward T $\gamma$  $\delta$ 17 phenotype (66, 113).

The kinetic study of IL17 production by  $\gamma$  $\delta$  T cells has shown that murine  $\gamma$  $\delta$  T cells secrete IL17 within few hours after stimulation (70). This phenomenon can be reasoned by the thymic development of murine T $\gamma$  $\delta$ 17 cells and constitutive presence of transcriptional regulators for IL17 production. However, human  $\gamma$  $\delta$  T cells in thymus are functionally immature and can attain their functional differentiation in periphery in presence of cytokines (114). This supports the kinetics of IL17 production by human  $\gamma$  $\delta$  T cells that mRNA expression of IL17 and ROR $\gamma$ t peaks by day 3–6 and decrease by day 9 onward, after stimulation. The expression of cytokine receptors (IL1 $\beta$ R, IL6R, TGF $\beta$ R, and IL23R) on V $\gamma$ 9V $\delta$ 2 T cells peaks on day 3 and decrease by day 6 (66). Thus, coordinated combination of TCR and cytokine stimulation could be necessary for the sustained secretion of IL17 by  $\gamma$  $\delta$  T cells, which highlights the difference in kinetics of IL17 secretion by murine and human T $\gamma$  $\delta$ 17 cells. This underscores that human  $\gamma$  $\delta$  T cells can be “reprogrammed” in the periphery into different functional lineages.

Upon antigenic challenge, T cells differentiate to memory phenotype; either central memory (TCM) or effector memory (TEM) (115). Human T $\gamma$  $\delta$ 17 cells present in non-lymphoid environment belong to CD27<sup>−</sup> CD45RA<sup>±</sup> effector (74) or terminally differentiated (TEMRA) (66) memory phenotype. Similarly, murine T $\gamma$  $\delta$ 17 cells also show effector memory phenotype with CD44<sup>high</sup>, CD45RB<sup>low</sup>, and CD62L<sup>low</sup> (116). Thus, T $\gamma$  $\delta$ 17 cells differentiated either in thymus or in periphery, belong to memory phenotype, and licensed to patrol the blood, lymphoid organs, and peripheral tissues.

### T $\gamma$ $\delta$ 17 IN MICROBIAL INFECTIONS

T $\gamma$  $\delta$ 17 cells can rapidly produce IL17 upon Toll-like receptors (TLR) or cytokine stimulation alone even in absence of antigen presentation. The general proinflammatory functions of IL17 [reviewed in Ref. (117, 118)] could be associated with  $\gamma$  $\delta$  T cells as they are major producers of IL17. Studies carried out in various infection models showed that T $\gamma$  $\delta$ 17 cells are protective against infection. During mycobacterial infection, IL17 produced by V $\gamma$ 4<sup>+</sup> and V $\gamma$ 6<sup>+</sup> cells induce pulmonary granuloma formation by recruitment of granulocytes and monocytes. The IL17 participates in maturation of granuloma by promoting tight cell to cell binding via ICAM1 and LFA1 induction (119). Mycobacteria-infected DCs secrete IL23, which regulate IL17 production by  $\gamma$  $\delta$  T cells emphasizing that the early activation of T $\gamma$  $\delta$ 17 cells is important for initiating inflammation and recruiting innate immune cells to the site of infection thereby enhancing bacterial clearance from host (120, 121). T $\gamma$  $\delta$ 17 cells also support cell-mediated immunity by inducing Th1 cells against pulmonary mycobacterial infection (122).

In *Escherichia coli* infection model also,  $\gamma\delta$ T cells were reported to be the major producers of IL17, which enhanced neutrophil infiltration to the peritoneum. The infiltration of cells diminished after antibody depletion of resident V $\delta$ 1<sup>+</sup> subtype of  $\gamma\delta$ T cells highlighting its involvement in IL17 secretion in response to IL23 (9). Thus, IL23 and T $\gamma$  $\delta$ 17 cells play a dominant role as first line of defense in infection before CD4 T cell activation. In case of *L. monocytogenes* infection, a large number of  $\gamma\delta$  T cells accumulate in the lymph organs shortly after infection and begin to produce IL17A, signifying the role of T $\gamma$  $\delta$ 17 cells in the *Listeria* infection (123). IL17 was also shown to promote proliferation of CD8<sup>+</sup> cytotoxic T lymphocytes by enhancing DC cross-presentation *in vitro*. DCs stimulated with IL17 showed upregulation of MHC-I molecule H2Kb and enhanced secretion of cytokines (IL12, IL6, and IL1 $\beta$ ). CD8 $\alpha$ <sup>+</sup> DCs from *Il17a*<sup>-/-</sup> mice also produced less IL12 and are less potent in activating naive CD8<sup>+</sup> T cells (123). This indicate that T $\gamma$  $\delta$ 17 cells not only induce innate response but also critical for optimal adaptive cytotoxic response against intracellular bacterial infection. The alliance of IL23 and T $\gamma$  $\delta$ 17 is also demonstrated to have a protective role during infections such as *Klebsiella pneumonia* (124), *Citrobacter rodentium* (125, 126), *Salmonella enterica* (127, 128), and *Toxoplasma gondii* (129). The T $\gamma$  $\delta$ 17 cells also play a vital role in clearing fungal infections. The rapid production of IL17A was reported in the lungs at a very early stage after intravenous infection with *C. albicans*. Lung resident  $\gamma\delta$  T cells were the major source of early IL17A production regulated by IL23 and TLR2/MyD88-dependent pathway (130). Presence of T $\gamma$  $\delta$ 17 cells were also reported in the lungs of neutropenic mice during *C. neoformans* infection. These T $\gamma$  $\delta$ 17 cells played an important role in the chemotaxis of leukocytes and induction of protective immune response (131). T $\gamma$  $\delta$ 17 cells thus orchestrate the protective immunity by acting at the early onset in infection models (108).

Relatively few studies have evaluated the role of T $\gamma$  $\delta$ 17 cells in human microbial immunity. In patients with tuberculosis (TB), elevated levels of T $\gamma$  $\delta$ 17 cells were found in peripheral blood and were major producers of IL17 (6). As a protective role, in response to bacterial antigens, IL17-producing V $\gamma$ 9V $\delta$ 2 T cells induce neutrophil migration through secretion of CXCL8 and promote their phagocytic activity (66). T $\gamma$  $\delta$ 17 cells also induce epithelial cells to secrete anti-microbial peptides like  $\beta$ -defensins in response to bacterial antigens (66). This signifies the modulatory effects of T $\gamma$  $\delta$ 17 cells on keratinocytes and other immune cells in anti-microbial defense. In children with bacterial meningitis, the population of IL17<sup>+</sup> V $\gamma$ 9V $\delta$ 2 T cells significantly increase in peripheral blood and at the site of infection (cerebrospinal fluid). The reversal of this pattern after successful anti-bacterial therapy clearly suggests the anti-microbial role of T $\gamma$  $\delta$ 17 cells (66). Collectively, these studies provide new insight into the functions of  $\gamma\delta$  T cells as the first line of host defense against bacterial and fungal infection in human and may pave a path in designing newer treatment modalities.

### TOLL-LIKE RECEPTORS REGULATE IL17 PRODUCTION IN T $\gamma$ $\delta$ 17 CELLS

$\gamma\delta$ T cells express various chemokine receptors, cytokine receptors, and PRRs, which regulate IL17 production. TLRs are the well-studied PRRs expressed by DCs, macrophages, and  $\gamma\delta$ T cells. The

unique microbial molecules called as PAMP are recognized by TLRs, which orchestrate the anti-microbial response in  $\gamma\delta$ T cells (11). In malarial infection, MyD88 deficiency results in severe impairment of IL17A producing  $\gamma\delta$ T cells levels, but not IFN $\gamma$  producing  $\gamma\delta$ T cells highlighting differential control by innate signaling through TLRs in infections (132). Murine T $\gamma$  $\delta$ 17 cells specifically express TLR1 and TLR2 but not TLR4. High number of T $\gamma$  $\delta$ 17 cells were induced upon *in vivo* stimulation with Pam3CSK4 (ligand for TLR2) but not with LPS (TLR4 ligand) or CpG (TLR9 ligand) (70). Interestingly, it has been shown that TLR4 indirectly controls IL17 generation by  $\gamma\delta$ T cells through IL23 secreted by TLR4 expressing macrophages in response to HMG Box 1 (HMGB1, a damage-associated protein and TLR4 ligand) (133). Moreover, T $\gamma$  $\delta$ 17 cells promote experimental intraocular neovascularization (134) as well as early acute allograft rejection (135) in response to HMGB1. Signaling through TLR2 is indispensable for T $\gamma$  $\delta$ 17 in anti-microbial functions. Absence of TLR2 or MyD88 in cutaneous *Staphylococcus aureus* infection, or in *Candida albicans* infection, caused an impaired IL17 production and poor microbial clearance in the skin infiltrated with V $\gamma$ 5<sup>+</sup>  $\gamma\delta$ T cells (130, 136). T $\gamma$  $\delta$ 17 cells also express DC-associated C-type lectin 1 (dectin 1) and intraperitoneal injection of curdlan (dectin 1 ligand), induced IL17 production by  $\gamma\delta$ T cells (70). In imiquimod (IMQ)-induced psoriasis-like model, dermal  $\gamma\delta$ T cells spontaneously secreted a large amount of IL17 in IMQ-treated skin cells. Thus, it appears that TLR7/8 (receptor of IMQ) may regulate the IL17 production by  $\gamma\delta$ T cells. It is important to note that the modulatory effects of TLRs on  $\gamma\delta$ T cells as showed in *in vivo* murine models are mediated through IL23 and/or IL1 $\beta$  cytokines. The direct stimulation of CD27<sup>+</sup>  $\gamma\delta$ T cells by TLR ligands (LPS or PAM) show no effect on IL17 production (132). This suggests that TLR signaling indirectly modulates T $\gamma$  $\delta$ 17 function.

### RECEPTOR REPERTOIRE EXPRESSED BY T $\gamma$ $\delta$ 17 CELLS

The receptor profile of T $\gamma$  $\delta$ 17 cells is similar to Th17 cells. In mice, the majority of IL17-producing CD4 cells belong to CCR6<sup>+</sup> compartment compared to CCR6<sup>-</sup> (137). Sorted CCR6<sup>+</sup>  $\gamma\delta$ T cells showed increased mRNA expression of IL17, IL22, IL23R, Ror $\gamma$ t, and aryl hydrocarbon receptor (AhR) compared to CCR6<sup>-</sup>  $\gamma\delta$ T cells (70, 138). This suggests that CCR6 can be a phenotypic surface marker of T $\gamma$  $\delta$ 17 cells. Besides CCR6, T $\gamma$  $\delta$ 17 cells express various chemokine receptors including CCR1, CCR2, CCR4, CCR5, CCR7, CCR9, CXCR1, CXCR3, CXCR4, CXCR5, and CXCR6 (7). The early onset recruitment of T $\gamma$  $\delta$ 17 to the site of inflammation is determined by the type of chemokine receptor on them. T $\gamma$  $\delta$ 17 cells expressing CCR6 and CCR9 show selective migration toward allergic inflamed tissue in response to CCL25 (ligand for CCR9).  $\alpha$ 4 $\beta$ 7 integrin expression is indispensable for this migration and transendothelial crossing of T $\gamma$  $\delta$ 17 cells. (139). Since migration through CCL2/CCR2 axis is determinant for total  $\gamma\delta$ T cells, CCL25/CCR9-mediated migration seems to be specific for T $\gamma$  $\delta$ 17 subtype (140, 141).

In humans, T $\gamma$  $\delta$ 17 cells express CCR6 but not CXCR3, CXCR5, CCR3, CCR4, or CCR5. However, they express granzyme B, FASL, and TRAIL but not perforin (66). The lack of granzyme B and perforin coexpression may be responsible for absence of cytolytic activity of T $\gamma$  $\delta$ 17 cells. On the contrary, it has been shown that the

human colorectal tumor-infiltrating T $\gamma$  $\delta$ 17 cells do not express FASL or TRAIL but express CD161 and CCR6 (74). The inconsistency in expression of cytolytic markers and their relevance on T $\gamma$  $\delta$ 17 cells needs to be understood in detail. The AhR is indispensable for T $\gamma$  $\delta$ 17 cells as it promotes differentiation of naïve V $\gamma$ 9V $\delta$ 2 T cells toward T $\gamma$  $\delta$ 17 phenotype (66).

In mouse model, it has been shown that Ahr<sup>-/-</sup> T $\gamma$  $\delta$ 17 cells express IL17 but fail to produce IL22 (70). Moreover, in mouse model of *Bacillus subtilis* induced pneumonitis, deficiency of Ahr resulted into low IL22 production but IL17 levels were maintained (142). Thus, although Ahr promotes IL17, it is indispensable for IL22 production by T $\gamma$  $\delta$ 17 cells.

### INFLAMMATORY DISORDERS AND MANIA OF T $\gamma$ $\delta$ 17

Th17 cells and T $\gamma$  $\delta$ 17 cells are essential in disease progression and are pathogenic in autoimmune disease. Dysregulated levels and sustained secretion of proinflammatory cytokines by  $\gamma\delta$  and/or CD4 T cells have devastating effects on autoimmune disease progression. In a collagen-induced arthritis (CIA) model (resembling human rheumatoid arthritis), IL17-producing V $\gamma$ 4/V $\delta$ 4<sup>+</sup> T cells selectively increase in joints and lymph nodes. Depletion of  $\gamma\delta$  T cells by anti V $\gamma$ 4 antibody, markedly reduced the disease severity score revealing its pathogenic nature (143). Interestingly, both Th17 and T $\gamma$  $\delta$ 17 are present in the joints but Th17 cells localize proximal to the bone, which facilitates its interaction with osteoclast. Selective depletion of Th17 cells abrogated the bone resorption suggesting that Th17 but not T $\gamma$  $\delta$ 17 cells are responsible for bone destruction. Thus, T $\gamma$  $\delta$ 17 cells may be responsible for enhancing joint inflammation and exacerbate CIA (144). In contrast, absence of T $\gamma$  $\delta$ 17 was reported in patients with rheumatoid arthritis and in murine model of autoimmune arthritis (SKG model) (145). The SKG mouse model has defects in the differentiation of T $\gamma$  $\delta$ 17 cells (94), which might result into low T $\gamma$  $\delta$ 17 cells in the inflamed joints. Thus, the role of T $\gamma$  $\delta$ 17 cells in autoimmune arthritis need to be evaluated comprehensively.

T $\gamma$  $\delta$ 17 also enhanced experimental autoimmune encephalomyelitis (EAE) (mouse model for human multiple sclerosis). Upon immunization of mice with myelin oligodendrocyte glycoprotein (MOG) peptide in complete Freund's adjuvant (CFA), V $\gamma$ 4<sup>+</sup>CCR6<sup>+</sup>IL23<sup>+</sup>  $\gamma\delta$ T cells accumulate in the central nervous system (CNS), which expand by 20-fold in absolute number during development of clinical signs of the disease (72). In contrast, IFN $\gamma$ -producing  $\gamma\delta$ T cells are low in CNS and marginally increase during course of EAE (103). The mechanism behind aggravation of EAE could be attributed to restraining the development of Foxp3<sup>+</sup> regulatory T cells (Tregs) functions by T $\gamma$  $\delta$ 17 cells. Supernatants from IL23-activated  $\gamma\delta$ T cells inhibited the TGF $\beta$  driven conversion of naïve Foxp3<sup>-</sup>  $\alpha\beta$  T cells into Foxp3 expressing T cells and also reversed the suppressive effect of Treg cells (72). Similar function of T $\gamma$  $\delta$ 17 was reported in cardiac transplantation in mice. IL17, majorly produced by  $\gamma\delta$ T cells, accelerates acute rejection of transplanted heart but IL17 deficiency enhanced Treg expansion and prolonged allograft survival (71). In ischemic brain injury, T $\gamma$  $\delta$ 17 were reported to be present at the infarct areas (146). T $\gamma$  $\delta$ 17 rather than Th17 was the major source of IL17 whereas IFN $\gamma$  was majorly produced by Th1 cells. In mice, genetically deficient for IL17 or IL23, the infarct areas were reduced suggesting a role of

T $\gamma$  $\delta$ 17 as a key contributor of neuroinflammation (146). Overall, this suggests that in chronic inflammatory condition, innate cytokines IL23 and IL1 $\beta$  promote infiltration and generation of IL17-producing  $\gamma\delta$ T cells, which aggravate the disease.

Experimental silicosis is a useful model for depicting chronic lung inflammation, tissue damage, and fibrosis. T $\gamma$  $\delta$ 17 along with Th17 accumulated in the lung in response to IL23 expressing macrophages by third day after silica treatment but interestingly did not induce lung fibrosis (73). On the contrary, in allergic lung inflammation, T $\gamma$  $\delta$ 17 cells are known to be protective (147, 148). Functional blockage of both IL17 and  $\gamma\delta$ T cells impaired the resolution of airway lung inflammation (148). It is claimed that this protective role is mediated by prostaglandins (PGs), which are abundant at the site of inflammation. PGI2 analog iloprost enhanced IL17 production by  $\gamma\delta$ T cells in the thymus, spleen, and lungs, reducing airway inflammation (147). This highlights the role of PGI2 analogs that can be exploited in the development of immune response in immunotherapeutic approaches. Age-related macular degeneration (AMD) is another chronic inflammation associated disease, characterized by choroidal neovascularization (CNV). In an experimental model, T $\gamma$  $\delta$ 17 cells along with Thy-1<sup>+</sup> ILCs (innate lymphoid cells) infiltrate the eye after laser treatment and promote neovascularization. This recruitment is in response to IL1 $\beta$  but not IL23 produced by macrophages (134).

### T $\gamma$ $\delta$ 17 CELLS AS HEROES OR VILLAINS IN CANCER

The unmatched characteristics of human  $\gamma\delta$ T cells to have MHC unrestricted tumor directed cytotoxicity, release of copious amounts of IFN $\gamma$ , and recognition of cancer cells through variety of mechanisms render them as potential candidate for cancer immunotherapy (4, 149). Upon activation,  $\gamma\delta$ T cells show cytotoxicity against myeloma (150), lymphoma (151), leukemia (152, 153), and other epithelial carcinomas (57, 154, 155) *in vitro*. Several clinical trials have been launched using  $\gamma\delta$ T cells based therapies in cancer patients. The hallmark characteristic of  $\gamma\delta$ T cells to be used for therapy is their ability to infiltrate tumors (156). *In vivo* activation by phosphoantigens or adaptive transfer of preactivated autologous  $\gamma\delta$ T cells have proved successful in cancer treatment (157). However, the role of T $\gamma$  $\delta$ 17 cells as anticancer effector cells is not well defined.

In a chemotherapeutic approach, T $\gamma$  $\delta$ 17 cells are reported to play decisive role in several transplantable tumor models (EG7 thymoma, MCA205 sarcoma, CT26 colon cancer, and TS/A mammary carcinomas). T $\gamma$  $\delta$ 17 (V $\gamma$ 4<sup>+</sup>/V $\gamma$ 6<sup>+</sup>) cells were shown to invade the tumor bed early in response after drug treatment. This was followed by infiltration and induction of IFN $\gamma$ -producing CD8 (Tc1) cells to the tumor bed. This infiltration of T $\gamma$  $\delta$ 17 and Tc1 cells was correlated and associated with tumor regression post radio or chemotherapy (158). Thus, IL17-producing V $\gamma$ 4<sup>+</sup>/V $\gamma$ 6<sup>+</sup> cells are critical for the induction of Tc1 response in tumor tissue in response to drug treatment or radiation. Another study in bladder cancer supports the helper function of T $\gamma$  $\delta$ 17 cells in cancer treatment. T $\gamma$  $\delta$ 17 cells induce neutrophil infiltration to the tumor site and show anti-tumor effect upon *Mycobacterium bovis* BCG treatment (159).

In contrast to anti-tumor role of T $\gamma$  $\delta$ 17 cells, they also promote tumor development. With the notion that IL17 is a proangiogenic

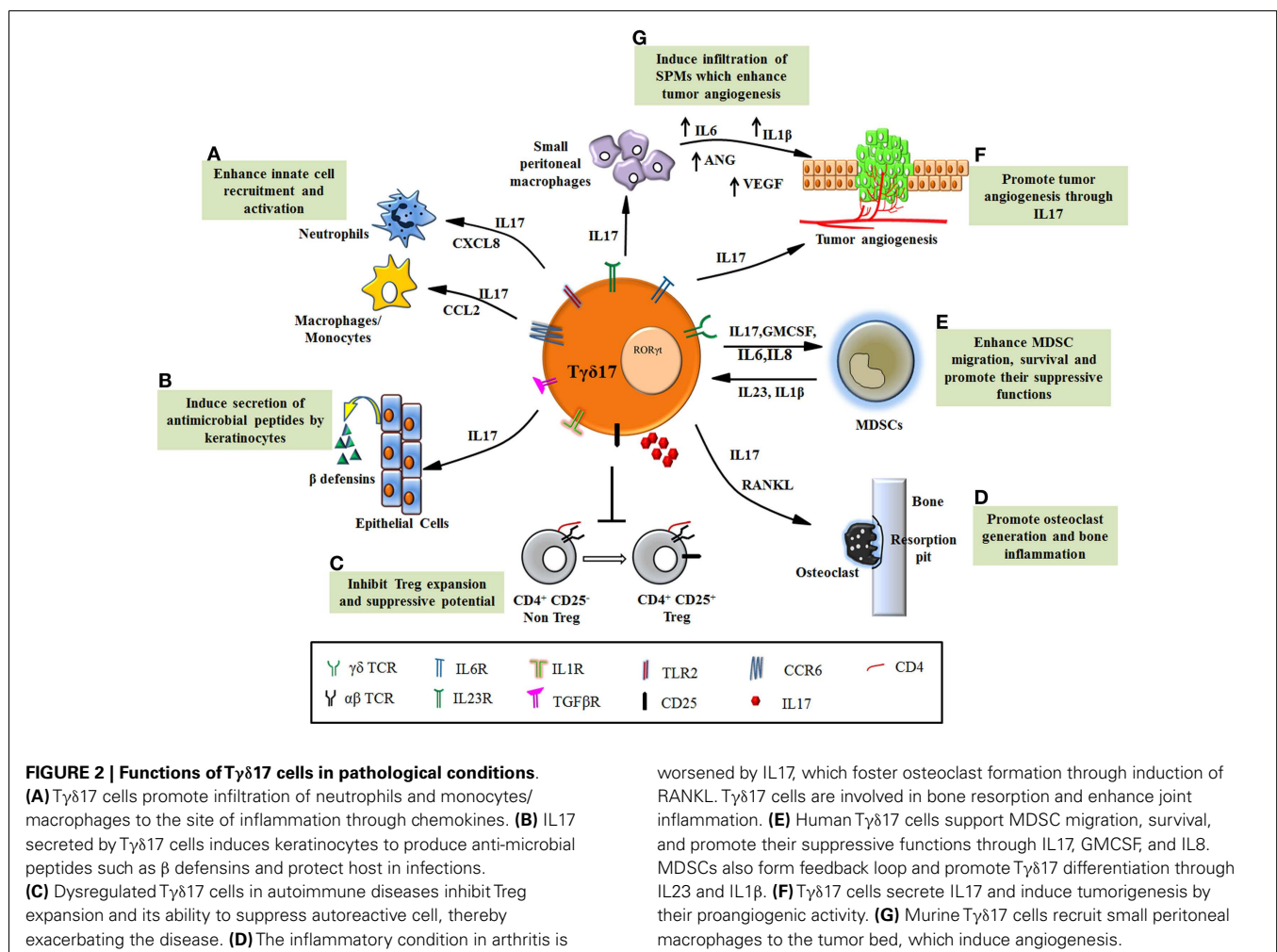
cytokine (160), T $\gamma$  $\delta$ 17 cells promote angiogenesis in tumor model. In IL17<sup>-/-</sup> tumor bearing mice, the blood vessel density was markedly decreased compared to wild type. In addition, IL17 induced the expression of Ang-2 (angiopoietin) and VEGF (vascular endothelial growth factor) in tumor cells (8). In ovarian cancer model, it has been reported that CD27<sup>-</sup> V $\gamma$ 6<sup>+</sup> cells produced higher IL17 and induce VEGF and Ang-2 in peritoneal exudates of tumor bearing mice after 6 weeks of post-tumor inoculation (161). Additionally, T $\gamma$  $\delta$ 17 cells induce mobilization of protumor small peritoneal macrophages (SPM) to the tumor bed, which express IL17-dependent proangiogenic profile (*Il1b*, *Il6*, *vegfa*, *tgfb*, *mif*, *cxcl1*, *cxcl8*, and *tie2*). SPMs also enhance ovarian cancer growth by stimulating tumor cell proliferation (161). In hepatocellular carcinoma mouse model, it was reported that IL17, majorly produced by V $\gamma$ 4<sup>+</sup> $\gamma$  $\delta$ T cells, induced CXCL5 production by tumor cells, which enhance migration of MDSCs (myeloid-derived suppressor cells) expressing CXCR2 to the tumor site. In addition, IL17 also enhanced suppressive functions of MDSCs by inhibition of T cells proliferation and cytokine (IFN $\gamma$  and TNF $\alpha$ ) production (162). In return, MDSCs induced  $\gamma$  $\delta$ T cells to produce IL17 through IL23 and IL1 $\beta$  secretion forming positive feedback loop for T $\gamma$  $\delta$ 17 activation (162). Thus, T $\gamma$  $\delta$ 17 cells interact with myeloid cells and counteract tumor immune-surveillance.

In human colorectal cancer, IL8 and GM-CSF secreted by T $\gamma$  $\delta$ 17 promote migration of MDSCs while IL17 and GM-CSF enhanced their proliferation. T $\gamma$  $\delta$ 17 cells also support survival of MDSCs through IL17, IL8, and TNF $\alpha$  (74). Thus, it is possible to speculate that T $\gamma$  $\delta$ 17 cells might be responsible for gradual shift from initial inflammatory to immunosuppressive tumor environment in advanced stage cancer (163). In human colorectal carcinoma, T $\gamma$  $\delta$ 17 cells were positively correlated with advancing tumor stages as well as with clinicopathological features including tumor size, tumor invasion, lymphatic and vascular invasion, lymph node metastasis, and serum CEA (Carcinoembryonic antigen) levels suggesting their pathogenic role (74).

Collectively, these findings highlight the apparently opposite roles of T $\gamma$  $\delta$ 17 cells in cancer immunity. It seems that during tumor development, inflammatory environment (IL1 $\beta$  and IL23) modulate the cytokine profile of  $\gamma$  $\delta$ T cells from primary IFN $\gamma$  toward proinflammatory IL17, which support tumor progression.

## CONCLUDING REMARKS

Despite the small percentage in total T cell population,  $\gamma$  $\delta$ T cells have emerged as an important modulator of early immune responses. The development of functional subtypes of  $\gamma$  $\delta$ T cells require polarizing cues including molecular and cellular



interaction and combination of multiple cytokines and chemokine receptors that regulate their distribution. This suggests that the functional determination of  $\gamma\delta$ T cell subtypes is dictated by the local environment (thymus or peripheral blood or the inflamed tissue) in which they are present. T $\gamma$  $\delta$ 17 is a special  $\gamma\delta$ T cell subset, distinctly present at early immune response in the tissue and can modulate the functions of other immune and epithelial cells but their relevance in disease outcome remains controversial. In response to microbial antigens, T $\gamma$  $\delta$ 17 cells promote infiltration of neutrophils and macrophages and induce production of anti-microbial peptides resulting in clearance of microbial load. Such protective behavior of T $\gamma$  $\delta$ 17 cells in infections can be exploited to develop newer approaches to tackle the microbial pathology (Figure 2).

The opposite side of T $\gamma$  $\delta$ 17 functions has revealed its detrimental role in enhancing inflammation in autoimmunity and cancer (Figure 2). The mechanism, which regulates such dual personality of T $\gamma$  $\delta$ 17 cells is unknown. It appears that the obvious common role executed by these cells is enhancement of inflammation but due to functional heterogeneity and their complex interdependency on other cells (innate and adaptive); the emerging scenario of their biology is far from complete. This provokes us to consider contextual behavior of T $\gamma$  $\delta$ 17 cells in disease pathology. Current progress in understanding the significance of T $\gamma$  $\delta$ 17 cells in inflammatory diseases has revealed their novel but debilitating functions such as suppression of Tregs in autoimmunity, induction of angiogenesis, and recruitment and activation of MDSCs in various malignancies. Thus, in inflammatory disorders, T $\gamma$  $\delta$ 17 cells can be targeted using various immunotherapeutic approaches. However, need of hour is to expand the understandings of T $\gamma$  $\delta$ 17 in humans and develop a protocol for their propagation and activation. The future therapies will rely on regulating the key transcription factor ROR $\gamma$ t by designing suitable antagonists that will help in fine tuning T $\gamma$  $\delta$ 17 differentiation and eventually their function in chronic inflammation and infection.

## ACKNOWLEDGMENTS

Department of Atomic Energy-Tata Memorial Centre (DAE-TMC), Council for Scientific and Industrial research (CSIR), and University Grants Commission (UGC) for providing the fellowships to Rushikesh S. Patil, Asif A. Dar, and Sajad A. Bhat, respectively. This work is supported by Department of Biotechnology Centre of Excellence grant, Govt. of India (DBT-COE) to Shubhada V. Chiplunkar (Grant No: BT/01/CEIB/09/V/06).

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**Conflict of Interest Statement:** The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Received: 27 October 2014; accepted: 20 January 2015; published online: 04 February 2015.

Citation: Patil RS, Bhat SA, Dar AA and Chiplunkar SV (2015) The Jekyll and Hyde story of IL17-producing  $\gamma\delta$ T cells. *Front. Immunol.* **6**:37. doi: 10.3389/fimmu.2015.00037

This article was submitted to T Cell Biology, a section of the journal *Frontiers in Immunology*.

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# Insights into the relationship between toll like receptors and gamma delta T cell responses

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The tumor microenvironment is an important aspect of cancer biology that contributes to tumor initiation, tumor progression and responses to therapy. The composition and characteristics of the tumor microenvironment vary widely and are important in determining the anti-tumor immune response. Successful immunization requires activation of both innate and adaptive immunity. Generally, immune system is compromised in patients with cancer due to immune suppression, loss of tumor antigen expression and dysfunction of antigen presenting cells (APC). Thus, therapeutic immunization leading to cancer regression remains a significant challenge. Certain cells of the immune system, including dendritic cells (DCs) and gamma delta ( $\gamma\delta$ ) T cells are capable of driving potent anti-tumor responses. The property of MHC-unrestricted cytotoxicity, high potential of cytokine release, tissue tropism and early activation in infections and malignant disease makes  $\gamma\delta$  T cells as an emerging candidate for immunotherapy. Various strategies are being developed to enhance anti-tumor immune responses of  $\gamma\delta$  T cells and DCs one of them is the use of novel adjuvants like toll like receptors (TLR) agonists, which enhance  $\gamma\delta$  T cell function directly or through DC activation, which has ability to prime  $\gamma\delta$  T cells. TLR agonists are being used clinically either alone or in combination with tumor antigens and has shown initial success in both enhancing immune responses and eliciting anti-tumor activity. TLR activated  $\gamma\delta$  T cells and DCs nurture each other's activation. This provides a potent base for first line of defense and manipulation of the adaptive response against pathogens and cancer. The available data provides a strong rationale for initiating combinatorial therapy for the treatment of diseases and this review will summarize the application of adjuvants (TLRs) for boosting immune response of  $\gamma\delta$  T cells to treat cancer and infectious diseases and their use in combinatorial therapy.

**Keywords:** immunotherapy,  $\gamma\delta$  T cells, toll like receptors, tumors, dendritic cells

## INTRODUCTION

Innate and adaptive immune responses are sentinels of host against the diverse repertoire of infectious agents (viruses and bacteria) and cancer. Both components of immune system identify invading microorganisms or damaged tissues as non-self and activate immune responses to eliminate them. Efficient immune responses depend upon how close an interaction is between the innate and adaptive immune system.  $\gamma\delta$  T cells and toll like receptors (TLR) serve as an important link between the innate and adaptive immune responses (1–3). Extensive studies have suggested that  $\gamma\delta$  T cells play important roles in host defense against microbial infections, tumorigenesis, immunoregulation and development of autoimmunity.  $\gamma\delta$  T cells also have several innate cell-like characters that allow their early and rapid activation following recognition of cellular stress and infection (4, 5). However to accomplish these functions,  $\gamma\delta$  T cells use both the T cell receptor (TCR) and additional activating receptors (notably NKG2D, NOTCH, and TLR) to respond to stress-induced ligands and infection.  $\gamma\delta$  T cells express TLRs and modulate early immune responses against different pathogens (6). In this review, we summarize and discuss some of the recent advances of the  $\gamma\delta$  T cell biology and how direct control of  $\gamma\delta$  T lymphocyte function

and activation is monitored by TLR receptors and ligands. The review highlights involvement of TLR signaling in  $\gamma\delta$  T cell functions and their implications in harnessing  $\gamma\delta$  T cells for cancer immunotherapy.

## $\gamma\delta$ T CELLS, ANATOMICAL DISTRIBUTION AND ANTIGENIC DIVERSITY

Based on the type of TCR they express, T lymphocytes can be divided into two major subsets,  $\alpha\beta$  and  $\gamma\delta$  T cells.  $\gamma\delta$  T cell represents a small subset of T lymphocytes (1–10%) in peripheral blood. While in anatomical locations like small intestine,  $\gamma\delta$  T cells comprise a major bulk of T cells (25–60% in human gut) (7).  $\gamma\delta$  T cells are the first T cells to appear in thymus during T cell ontogeny in every vertebrate (8), which suggests that their primary contribution could be neonatal protection because at this point conventional  $\alpha\beta$  T cell responses are severely functionally impaired and DCs are immature (9). In neonates, the V $\delta$ 2<sup>+</sup> cells derived from human cord blood showed early signs of activation. These cells secrete IFN- $\gamma$  and express perforin after short-term *in vitro* stimulation (10). In comparison to the neonate derived  $\alpha\beta$  T cells of peripheral blood,  $\gamma\delta$  T cell subset produces copious amount of IFN- $\gamma$  and are precociously active (11). Hence,  $\gamma\delta$

T cells are well engaged in newborns to contribute to immune-protection, immune-regulation and compensate for impaired  $\alpha\beta$  T cell compartment.

$\gamma\delta$  T cells are unconventional CD3<sup>+</sup> T cells and differ from the conventional  $\alpha\beta$  T cells in their biology and function (Table 1). Although a sizeable fraction of  $\gamma\delta$  T cells in the intraepithelial lymphocyte compartments of human and mice are CD8 $\alpha\alpha$ <sup>+</sup> but the peripheral blood  $\gamma\delta$  T cells are predominantly double negative (CD4<sup>−</sup>CD8<sup>−</sup>) T cells. The absence of CD4 or CD8 expression on majority of the circulating  $\gamma\delta$  T cells is well in line with the fact that antigen recognition is not MHC restricted (12, 13). Crystal structure analysis of the  $\gamma\delta$  TCR revealed that  $\gamma\delta$  TCR is highly variable in length resembling immuno-globulins (Ig) more than the  $\alpha\beta$  TCR. The antigen recognition property of  $\gamma\delta$  T cells is fundamentally different from  $\alpha\beta$  T cells but similar to antigen-antibody binding, which is more likely to occur independent of MHC cross presentation (14). However, recently butyrophilin BTN3A1, a non-polymorphic ubiquitously expressed molecule was identified as an antigen presenting molecule of V $\gamma$ 9V $\delta$ 2 T cells. Soluble BTN3A1 binds (Isopentenyl diphosphate) IPP and (E)-4-hydroxy-3-methyl-but-2-enyl diphosphate (HMBPP) with different affinities in 1:1 ratio to stimulate  $\gamma\delta$  T cells (15).

The important feature of  $\gamma\delta$  T cells is their tropism to epithelial tissues. With respect to anatomical localization,  $\gamma\delta$  T cell population can be divided into two groups: lymphoid-homing  $\gamma\delta$  T cells that can be primed in the circulation and clonally expand in a conventional “adaptive” manner; and innate-like cells that respond rapidly and at a relatively high frequency in many tissue sites. Migration and anatomical localization of T lymphocytes is crucial for their antigen specificity and maintaining homeostasis in the mammalian immune system. Although  $\gamma\delta$  T cells are well represented among peripheral blood mononuclear cells (PBMC) and in afferent and efferent lymph, they are rarely found in lymph node parenchyma, spleen, Peyer’s patches and thymus. Moreover, unlike  $\alpha\beta$  T cells, splenic  $\gamma\delta$  T cells, if present, are not confined to the lymphoid areas (the white pulp) but are also found throughout the red pulp of spleen and marginal zones of cell trafficking (16).  $\gamma\delta$  T cells are abundantly present in the epithelia of skin, genital and intestinal tract (17). In the small intestines of humans, mice, chickens and cattle,  $\gamma\delta$  T cells comprise a substantial fraction of intestinal intraepithelial lymphocytes (IELs); in mice  $\gamma\delta$ <sup>+</sup>

IELs constitute 50–60% of the IEL pool (18–20). The epidermal  $\gamma\delta$ <sup>+</sup> IELs of mice and cattle (but not humans) have a marked dendritic morphology and are hence known as dendritic epidermal T cells (DETCs) (21). DETCs are maintained at steady state in normal adult murine skin but on activation execute specialized functions like tissue repair (22). DETCs also maintain keratinocyte homeostasis, which along with Langerhan cells forms its neighborhood (23). Under pathological conditions,  $\gamma\delta$  T cells quickly expand and infiltrate into lymphoid compartments and other tissues.

Another striking difference between  $\alpha\beta$  and  $\gamma\delta$  T cells is the range of antigens or ligands that are recognized by the respective TCRs. Unlike  $\alpha\beta$  T cells, which recognize protein antigen processed inside the cell and presented by MHC molecules,  $\gamma\delta$  T cells recognize antigens like B cells as revealed by structural and functional studies (24).  $\gamma\delta$  T cells can respond to a variety of stimuli irrespective of their molecular or genetic nature. In mice, the non-classical MHC class I molecules T10 and T22 are recognized by  $\gamma\delta$  T cells (25–28). Similar to T10 and T20, murine class II MHC (IA) antigens IE and IA are identified to act as ligands for  $\gamma\delta$  T cell clones (29, 30). In addition, herpes glycoprotein GI-reactive  $\gamma\delta$  T cell clones protect mice from herpes simplex virus (HSV) induced lethal encephalitis (31, 32).  $\gamma\delta$  TCRs can also bind to an algal molecule, phycoerythrin inducing upregulation of CD44 and downregulation of CD62L in  $\gamma\delta$  T cells (33). B6 murine splenic and hepatic  $\gamma\delta$  T cells respond to cardiolipin (bacterial cell-wall phospholipid and endogenous component of mitochondria) presented by CD1d molecules (34). Insulin derived peptide B:9–23 is also recognized by the  $\gamma\delta$  T cell clones derived from non-obese diabetic mice (NOD mice) (35). SKINT1, a mouse immunoglobulin superfamily member, bears structural similarity to human CD277 (butyrophilin 3A1) and is expressed by medullary thymic epithelial cells (mTECs) and keratinocytes that is crucial for the development of V $\gamma$ 5V $\delta$ 1<sup>+</sup> DETCs (36).

In humans, majority of  $\gamma\delta$  T cells express a rearranged T cell receptor (TCR) composed of V $\gamma$ 9 and V $\delta$ 2 domains; thus, this population is referred to as V $\gamma$ 9V $\delta$ 2. The V $\gamma$ 9V $\delta$ 2 T cells recognize self and microbial phosphorylated metabolites generated in eukaryotic mevalonate pathway and in the microbial 2-C-methyl-derythritol 4-phosphate (MEP) pathway (37). Initially, it was reported that the non-peptidic ligands isolated from mycobacterial cell lysates were

**Table 1 | Comparison between  $\alpha\beta$  and  $\gamma\delta$  T cells.**

S.No.	$\alpha\beta$ T cells	$\gamma\delta$ T cells
1	Constitutes about 65–70% of total PBMCs	Constitutes about 1–10% of total PBMCs
2	Recognize the processed peptide antigen with the help antigen presenting molecule MHC1 and MHC II	Do not show MHC restriction but may require the antigen presenting molecule Butyrophilin 3A1 molecule
3	Express either CD8 <sup>+</sup> or CD4 <sup>+</sup>	Mostly double negative, murine intestinal IELs may be CD8 $\alpha\alpha$ <sup>+</sup>
4	TCR junctional diversity is very diverse	TCR junctional diversity is small
5	Do not show tissue tropism	Show tissue tropism
6	$\alpha\beta$ T Cells response is late	$\gamma\delta$ T cells respond earlier
7	Regulatory phenotype is attributed to CD4 <sup>+</sup> CD25 <sup>+</sup> T cells	Regulatory phenotype is attributable to various subsets, including murine V $\gamma$ 5 <sup>+</sup> DETCs and human V $\gamma$ 1 <sup>+</sup> peripheral cells

stimulatory for V $\gamma$ 9V $\delta$ 2 T cell clones. Later, IPP, an intermediate metabolite of the mevalonate pathway, was isolated and identified as a stimulatory molecule. Characterization of the microbial antigens recognized by human  $\gamma\delta$  T cells predicted that these are non-proteinaceous in nature and have critical phosphate residues (37, 38). Subsequent studies, conducted with *M. tuberculosis*, identified HMBPP, an intermediate metabolite of the MEP pathway, as a strong agonist of  $\gamma\delta$  TCR. The measured potencies of IPP and HMBPP show an enormous difference. The ED50 of IPP is  $\sim 20$   $\mu$ M, whereas that of HMBPP is  $\sim 70$  pM, i.e., more than 105 times lower (38).

Another stimulatory molecule is *Staphylococcus aureus* enterotoxin A (SEA) that directly interacts with the TCR V $\gamma$ 9 chain independently of the paired V $\delta$  chain. The mechanism of recognition of this superantigen is different from that of phosphorylated metabolites and requires the interaction with MHC class II molecules.  $\gamma\delta$  T cells kill target cells and release cytokines upon interaction with SEA but do not proliferate (39).

Recently, the TCR from a  $\gamma\delta$  T cell clone derived from a cytomegalovirus (CMV)-infected transplant patient was shown to directly bind to endothelial protein C receptor (EPCR), which is a lipid carrier with a similar structure to CD1, showing again that  $\gamma\delta$  TCR engagement is cargo independent (40). ATP F1 synthase has been identified as stimulatory ligand of the TCR V $\gamma$ 9V $\delta$ 2. ATP F1 synthase is an intracellular protein complex involved in ATP generation. However, optimal responses of V $\gamma$ 9V $\delta$ 2 T cells by tumor target cell lines expressing F1-ATPase requires apolipoprotein A1. A monoclonal antibody interacting with apolipoprotein A1 was shown to inhibit TCR  $\gamma\delta$  activation as it disrupted the trimolecular complex of ApoA1, ATP F1 synthase, and  $\gamma\delta$  TCR required for optimal response (41).

The second major population of human  $\gamma\delta$  T cells utilizes the V $\delta$ 1 chain, which pairs with a variety of V $\gamma$  chains. This subset of V $\delta$ 1<sup>+</sup> T cells is mainly found in tissues and is activated by CD1c and CD1d-expressing cells. The group 1 CD1 molecules have ability to present lipid A to human  $\gamma\delta$  T cells. The human  $\gamma\delta$  T cells also recognize the related group 2 CD1 molecule as CD1d/lipid complex. Phosphatidyl ethanol amine (PE), a phospholipid, activates  $\gamma\delta$  T cells in a CD1d manner dependent suggesting its CD1d restricted recognition (42). In addition, some populations of  $\gamma\delta$  T cells in normal human PBMCs also recognize lipid molecules such as cardiolipin (a marker of damaged mitochondria), sulfatide (a myelin glycosphingolipid), or  $\alpha$ -galactosylceramide ( $\alpha$ -GalCer) in association with CD1d, which are noted ligands of natural killer T (NKT) cells (34, 43–45). Human  $\gamma\delta$  T cells also recognize the stress-induced MHC class I-related MICA/MICB molecules and the UL16-binding proteins that are upregulated on malignant or stressed cells (46–48). Heat shock proteins (HSPs) expressed on the cell membrane play an important role in cancer immunity. Hsp60 expressed on oral tumors act as ligand for V $\gamma$ 9V $\delta$ 2 T cells (49, 50). Hsp60 and Hsp70 expressing human oral and esophageal tumors are lysed by V $\gamma$ 9V $\delta$ 2 T cells (49–51). Hsp72 expressing neutrophils were rapidly killed by  $\gamma\delta$  T cells through direct cell to cell contact, indicating that hsp72 expression on cell surface pre-disposes inflamed neutrophils to killing by  $\gamma\delta$  T cells (52). In Another study, hsp90 expression on EBV infected B cells rapidly promoted  $\gamma\delta$  T cell proliferation (53). This confirms that  $\gamma\delta$  T cells recognize

qualitatively distinct antigens, which are profoundly regulated by their anatomical localization.

## CO-RECEPTORS AND $\gamma\delta$ T CELL ACTIVATION

Most  $\gamma\delta$  T cells respond to non-peptidic antigens even in the absence of antigen presenting cells (APCs). However, the presence of APCs can greatly enhance the  $\gamma\delta$  T cell response (54). This suggests that accessory molecules/receptors may be involved in effector functions of these cells. Some of important co-receptors used by  $\gamma\delta$  T cells include NOTCH, NKG2D, and TLR (55).

Our study has identified Notch as an additional signal contributing to antigen specific effector functions of  $\gamma\delta$  T cells. We have shown that  $\gamma\delta$  T cells express Notch1 and Notch2 at both mRNA and protein level. Inhibition of Notch signaling in anti-CD3 MAb stimulated  $\gamma\delta$  T cells resulted in marked decrease in proliferation, cytotoxic potential, and cytokine production by  $\gamma\delta$  T cells confirming the involvement of Notch signaling in regulating antigen specific responses of  $\gamma\delta$  T cells (55).

$\gamma\delta$  T cells express NKG2D on their cell surface resulting in their activation. Treatment of PBMC with immobilized NKG2D-specific mAb or NKG2D ligand MHC class I related protein A (MICA) resulted in the up-regulation of CD69 and CD25 on V $\gamma$ 9V $\delta$ 2. Furthermore, NKG2D increased the production of TNF- $\alpha$  and release of cytolytic granules by V $\gamma$ 9V $\delta$ 2 T cells (56). Later, it was shown that the protein kinase C transduction pathway as a main regulator of the NKG2D-mediated costimulation of anti-tumor V $\gamma$ 9V $\delta$ 2 T cell cytolytic response (57).

TLR agonists are also known to trigger the early activation and the IFN- $\gamma$  secretion by V $\gamma$ 9V $\delta$ 2 T cells (58). TLR ligands indirectly increase the anti-tumoricidal activity of V $\gamma$ 9V $\delta$ 2 T cells (59). In this review, we will focus on TLR as an additional co-receptor modulating the function of immune cells with special focus on  $\gamma\delta$  T cells.

## TOLL LIKE RECEPTOR AND IMMUNE CELLS

The immune system functions in anti-microbial defense by recognizing groups of molecules unique to microorganisms (60). These unique microbial molecules are called pathogen-associated molecular patterns (PAMPs) and are recognized by a family of cellular receptors called pattern recognition receptors (PRRs) (61). TLRs along with retinoic acid-inducible gene (RIG)-I-like receptors (RLRs) and nucleotide-binding oligomerization domain (NOD)-like receptor (NLRs) are prototype PRRs, which recognize pathogen-associated molecular patterns (PAMPs) from microorganisms or danger-associated molecular patterns (DAMPs) from damaged tissues (62). Recognition of PAMPs by TLRs trigger release of inflammatory cytokines and type 1 interferon's (IFN) for host defense (60, 63–65). The adaptive immune system, on the other hand, is responsible for elimination of pathogens in the late phase of infection and in the generation of immunological memory mediated by B and T cells (66).

TLRs derived their name from *Drosophila melanogaster* Toll protein based on their homology (67). In mammals, till date 13 members of TLR family has been identified (63, 68–71). TLR1-9 is conserved in humans and mice while TLR10 is non-functional in mice because of a retroviral insertion while TLR11-13 is lost from the human genome. The first TLR identified was TLR4

and recognizes bacterial lipopolysaccharide (LPS) from Gram-negative bacteria (67, 72, 73). TLRs are classified into several groups based on the types of PAMPs they recognize. TLR1, 2, 4 and 6 recognize lipids whereas the highly related TLR7, TLR8 and TLR9 recognize nucleic acids. Murine TLR11 recognizes a protozoan derived profilin-like protein while TLR13 recognizes *Vesicular stomatitis virus* (63). TLRs are localized in the distinct cellular compartments, for example; TLR1, TLR2, TLR4, TLR5, TLR6, and TLR11 are expressed on the cell surface whereas TLR3, TLR7, TLR8, TLR9, TLR11, TLR12 and TLR13 are expressed in intracellular vesicles such as the endosome and ER. The intracellular TLRs are transported to the intracellular vesicles via UNC93B1, a trans-membrane protein, which is localized in the ER of the cell (70, 71, 74–77). TLR family receptors have a common structural architecture. TLRs are type I integral membrane glycoproteins characterized by multiple extracellular leucine-rich repeats (LRRs) and a single intracellular Toll/interleukin-1 (IL-1) receptor (TIR). TLRs mostly form homo-dimers with a few exceptions, which form heterodimers to trigger a signal. For example, TLR2 forms heterodimers with TLR1 or TLR6 enabling differential recognition of lipopeptides. The TIR domain of TLRs is required for the interaction and recruitment of various adaptor molecules to activate downstream signaling pathway. After recognizing PAMPs, TLRs activate intracellular signaling pathways that lead to the induction of inflammatory cytokine genes such as TNF- $\alpha$ , IL-6, IL-1 $\beta$  and IL-12 through the recruitment of adaptors such as MyD88, TRIF, TRAM, TIRAP and SARM1 (78). MyD88 is a universal adaptor used by all TLRs, except TLR3, to induce inflammatory pathways through activation of MAP Kinases (ERK, JNK, p38) and transcriptional factor NF- $\kappa$ B (63, 79). TLR3 and TLR4 use TRIF to bring activation of alternative pathway (TRIF-dependent pathway) through transcription factors IRF3 and NF- $\kappa$ B to induce type 1 IFN and inflammatory cytokines (80–82). TRAM selectively participates in the activation of the TRIF-dependent pathway downstream of TLR4, but not TLR3 (83, 84). TIRAP functions to recruit MyD88 leading to activation of MyD88-dependent pathway downstream of TLR2 and TLR4 (85, 86). Sterile- $\alpha$ - and armadillo-motif-containing protein 1 (SARM1), was shown to inhibit TRIF and is also critical for TLR-independent innate immunity (87). Thus, signaling pathways can be broadly classified as either MyD88-dependent pathway or TRIF-dependent pathway.

Hornung et al. have showed differential expression of TLR1–10 on human APCs and lymphocytes including T cells and their functional discrepancy in recognition of specific TLR ligands (88). CD4<sup>+</sup> T cells express almost all TLRs at mRNA levels but may not express all as functional protein (89, 90). Moreover, they do not respond to all TLR ligands. Stimulation with TLR5, 7, or 8 agonists combined with TCR activation of CD4<sup>+</sup> T cells resulted in increased proliferation and production of IL-2, IL-8, IL-10, IFN- $\gamma$  and TNF $\alpha$  (91). There are other reports as well suggesting the functional modulation of subtypes of CD4<sup>+</sup> T cells by TLR ligands. The mouse Th1 but not Th2 cells responded to TLR2 agonist and resulted in enhanced proliferation and IFN- $\gamma$  production independent of TCR stimulation (92). This work validated that the TLR can regulate function of CD4<sup>+</sup> T cells even in absence of TCR engagement. CD4<sup>+</sup>CD25<sup>+</sup> regulatory T cells (Tregs) express

majority of TLRs with selectively higher expression of TLR2, 4, 5, 7/8, and 10 compared to CD4<sup>+</sup>CD25<sup>−</sup> conventional T cells (93). Liu et al. showed that CD4<sup>+</sup>CD25<sup>+</sup> regulatory T cells and CD4<sup>+</sup>CD25<sup>−</sup> conventional T cells express TLR2 and proliferated upon stimulation with its agonist. TLR2 stimulation also led to transient loss of Treg suppressive potential through suppression of FOXP3 (94, 95). However, Tregs also express TLR5 but upon stimulation with flagellin (ligand of TLR5), do not proliferate rather showed increased suppressive capacity and enhanced expression of FOXP3 (96). These reports suggest that the suppressive function of Treg can be either enhanced or dampened by the type of TLR ligand engaged. TLR2 stimulation not only abrogates suppressive functions of CD4<sup>+</sup> Tregs but also drives naïve as well as effector Treg population toward IL17 producing Th17 phenotype (97). Th17 cells express TLR2 along with TLR6 compared to Th1 and Th2 subsets and promote Th17 differentiation upon Pam3Cys stimulation and accelerates experimental autoimmune encephalomyelitis (98). Like TLR2, TLR4 also regulate the functions of CD4<sup>+</sup> T cells. In a mouse model of arthritis, mice lacking TLR2 showed enhanced histopathological scores of arthritis by a shift in T cell balance from Th2 and T regulatory cells toward pathogenic Th1 cells. TLR4, in contrast, contributes to more severe disease by modulating the Th17 cell population and IL-17 production (99, 100). Recently, Li et al. showed that high-mobility group box 1 (HMGB1) proteins decrease Treg/Th17 ratio by inhibiting FOXP3 and enhancing ROR $\gamma$ t in CD4<sup>+</sup> T cells via TLR4–IL6 axis in patients with chronic hepatitis B infections (101). This shows that HMGB1 (TLR4 ligand) act as a modulator of CD4<sup>+</sup> T cells responses in chronic viral inflammation. CD4<sup>+</sup> T cells also express intracellular TLRs such as TLR9 and TLR3. Both these TLRs promote T cell survival via activation of NF- $\kappa$ B and MAPK signaling (102). Although the effector functions of CD4<sup>+</sup> T cells are regulated by TLRs but the molecular pathway involved in skewing of CD4<sup>+</sup> T cell function is poorly understood.

Like CD4<sup>+</sup> T cells, CD8<sup>+</sup> T cells also show differential expression of TLRs with high expression of TLR3 but lower expression of TLR1, 2, 5, 9, 10 compared to CD4<sup>+</sup> T cells at mRNA level. It is important to note that the expression of TLR2, TLR3 and TLR5 increases on CD8 T cells in infected tonsils compared to controls (89) indicating immune activating role of TLRs in infections. Stimulation of CD8<sup>+</sup> T cells through TLR2 agonists enhances their proliferation and IFN- $\gamma$  production (103, 104). It also promotes cytolytic activity of CD8<sup>+</sup> T cells and enhances anti-tumor response mediated through MyD88-dependent TLR1/2 pathway (105). Recently, Mercier et al. showed that TLR2 cooperate with NOD-containing protein 1 (NOD1) to enhance TCR mediated activation and can serve as alternative co-stimulatory receptor in CD8<sup>+</sup> T cells (106). CD8<sup>+</sup> T cells also express intracellular TLRs such as TLR3, TLR9 which are more potent in inducing CD8<sup>+</sup> T cell activation *in vivo* (107).

Natural killer (NK) cell is a vital player in innate immune system. They recognize infected and transformed cells with down-regulated major histocompatibility complex (MHC) class I molecules. They are the primary producers of IFN- $\gamma$  and are protective against infections. Unlike CD4 and CD8 T cells NK cells as well as CD56<sup>+</sup>CD3<sup>+</sup> NKT cells constitutively express TLR 1–8 with high expression of TLR2 and 3 at mRNA level. They recognize

bacterial PAMPs and respond by producing  $\alpha$ -defensins (108–111). Human NK cells can also directly recognize *Mycobacterium bovis* via TLR2 and enhance their cytolytic activity against tumor cells (112). Tumor-associated macrophages induce NK cell IFN- $\gamma$  production and cytolytic activity upon TLR engagement (113). TLRs modulate NK cell function directly or indirectly to promote antibody dependent cell mediated cytotoxicity and cross presentation of viral antigens to T lymphocytes (114, 115). This highlights that the cells of adaptive immune system do express TLRs and their function can be directly or indirectly modulated by TLR ligands.

### ACTIVATION OF $\gamma\delta$ T CELLS BY TLR LIGANDS

In 1997, the first human homolog of *Drosophila* Toll protein was cloned and characterized. It was also established that  $\gamma\delta$  T cells also express hToll mRNA (67). Purified  $\gamma\delta$  T cells were found to respond to the *E. coli* native lipid A in a TCR-independent fashion and the LPS/lipid A-reactive  $\gamma\delta$  T cells strongly expressed TLR2 mRNA. TLR2 antisense oligonucleotide inhibited the proliferation of  $\gamma\delta$  T cells in response to the native lipid A as well as the TLR2-deficient mice showed an impaired response of the  $\gamma\delta$  T cells following injection of native lipid A. These results suggest that TLR2 is involved in the activation of canonical V $\gamma$ 6/V $\delta$ 1 T cells by native lipid A (116). Again, functional presence of TLR2 on V $\gamma$ 2V $\delta$ 2 T cells (also known as V $\gamma$ 9V $\delta$ 2 T cells) was reported when the dual stimulation of V $\gamma$ 2V $\delta$ 2 T cells with anti-TCR antibody and Pam<sub>3</sub>Cys increased synthesis and secretion of IFN- $\gamma$  and elevated the levels of CD107a expression. IFN- $\gamma$  secretion and cell surface CD107a levels are markers of increased effector function in V $\gamma$ 2V $\delta$ 2 T cells (117). Similarly, Bruno et al. reported that IL-23 and TLR2 co-stimulation induces IL17 expression in  $\gamma\delta$  T cells. However, TLR1 and TLR2 expression was found only on CCR6<sup>+</sup> IL-17 producing murine peritoneal  $\gamma\delta$  T cells but not others. Thus,  $\gamma\delta$  T cells with innate receptor expression coupled with IL-17 production establishes them as first line of defense that can orchestrate an inflammatory response to pathogen-derived and environmental signals long before Th17 can sense the bacterial invasion (118). Pam3CSK4, TLR2 agonist was able to stimulate only splenic  $\gamma\delta$  T cell proliferation but not the dermal  $\gamma\delta$  T cells demonstrating that TLR2 signaling shows tissue tropism. (19). Furthermore, a profound change in the circulating  $\gamma\delta$  T-cell population was observed in early burn injury (24 h). These  $\gamma\delta$  T-cells showed TLR2 and TLR4 expression, priming them for TLR reactivity, However TLR expression was specific to circulatory  $\gamma\delta$  T cell subset and was transient, since it was not observed after post-injury (7 days). Transient nature of the post-burn increase in  $\gamma\delta$  T-cell TLR expression is likely to be protective to the host, most likely via regulation of inflammation and initiation of healing processes (119). Mitochondrial danger-associated molecular patterns (MTDs) induce TLR2 and TLR4 expression on  $\gamma\delta$  T cells in dose dependent manner. MTDs also induced the production of IL-1 $\beta$ , IL-6, IL-10, RANTES, and vascular endothelial growth factor by  $\gamma\delta$  T-cells thereby resulting in initiation of sterile inflammation leading to tissue/cellular repair (120).

Different studies have reported that  $\gamma\delta$  T cells express TLR3 (121, 122). TLR3 recognizes viral dsRNA, synthetic analogs of dsRNA, polyinosinic-polycytidylic acid [poly (I:C)] and small interfering (si) RNA. The direct stimulation of freshly isolated  $\gamma\delta$

T cells via TCR and surrogate TLR3 ligand poly (I:C) dramatically increased IFN- $\gamma$  production. Addition of neutralizing anti-TLR3 mAb inhibited the co-stimulatory effect of poly (I:C), presumably by antagonizing the TLR3 signaling (122). Thus, the integrated signals of TLR3 and TCR induce a strong antiviral effector function in  $\gamma\delta$  T cells supporting the decisive role of  $\gamma\delta$  T cells in early defense against viral infection. In other study, it has been reported that  $\gamma\delta$  cells of term babies and of adults express TLR3 and TLR7 while the preterm babies have reduced levels. The greater levels of IFN- $\gamma$  protein was observed in adult and cord blood cells co-stimulated with anti-CD3 and poly(I:C) whereas this was not seen in  $\gamma\delta$  T cell clones of preterm babies. Thus, reduced level of TLR3 expression by preterm-derived clones had an overt functional consequence on IFN- $\gamma$  levels (11). Interestingly, a primary role of TLR3 in humans appears to mediate resistance to HSV-induced encephalitis (123). Hence, premature babies are particularly susceptible to HSV infection because of reduced levels of TLR3 on  $\gamma\delta$  T cells.

TLR4 was reported to be absent in the  $\gamma\delta$  T cells but can become functional in  $\gamma\delta$  T cells depending on localization, environmental signals, or  $\gamma\delta$  TCR usage (19, 118, 124). However, our own data has shown that TLR4 is expressed on human  $\gamma\delta$  T cells. Stimulation of  $\gamma\delta$  T cells with LPS (TLR4 ligand) increased their proliferation, IFN- $\gamma$  release, and cytotoxic potential (125). DETCs lack cell surface expression of TLR4–MD2. MD-2 physically associates with TLR4 on the cell surface and is required for LPS signaling. However, TLR4–MD2 expression was upregulated when DETCs emigrated from the epidermis during cutaneous inflammation. The migration signals of DETCs may promote the TLR4–MD2 expression (126). Cairns et al. showed that late post-burn injury increased expression of TLR-4 on splenic T-cells (127). However, Martin et al. reported transient TLR-4 expression post-burn in the circulation or spleen but were specific for the  $\gamma\delta$  T-cell subset (119). Several evidences suggest that murine  $\gamma\delta$  T cells recognize LPS/LA through TLR2 or TLR4 (128, 129). Importantly activated  $\gamma\delta$  T cells, especially V $\delta$ 2 T cells, in peripheral blood cells recognize LA, a major component of LPS, via TLR4 resulting in extensive proliferation and production of IFN- $\gamma$  and TNF- $\alpha$  *in vitro* (130). The data suggest that  $\gamma\delta$  T cells play an important role in the control of infection induced by gram negative bacteria. Reynolds et al. showed that a heterogeneous population of  $\gamma\delta$  T cells responds to LPS via TLR4 dependent manner and demonstrate the crucial and innate role of TLR4 in promoting the activation of  $\gamma\delta$  T cells, which contributes to the initiation of autoimmune inflammation (100). Another study showed the indirect role of TLR4 in HMGB–TLR4–IL-23–IL17A axis between macrophages and  $\gamma\delta$  T cells, which contribute to the accumulation of neutrophils and liver inflammation. Necrotic hepatocytes release HMGB1, a damage-associated molecule or TLR4 ligand, which increased IL-23 production of macrophages in a TLR4 dependent manner. IL-23 aids  $\gamma\delta$  T cells in liver in the generation of IL-17A, which then recruits hepatic neutrophils (131).

Human  $\gamma\delta$  T cells were found to express appreciable levels of TLR7. Costimulation with poly I:C upregulated the TLR7 expression in TCR-cross linked freshly isolated  $\gamma\delta$  T cells (124). In addition, tumor-infiltrating  $\gamma\delta$  T cells also express TLR7 (132). In case of mouse dermal  $\gamma\delta$  T cells, both TLR7 and

TLR9 signaling promoted IL-17 production, which could be synergistically enhanced with the addition of IL-23 (19).

The identification of dominant  $\gamma\delta$  T cells in the total population of tumor-infiltrating lymphocytes (TILs) in renal, breast, and prostate cancer suggested that these cells might have the potent negative immune regulatory function (132, 133). The breast tumor-derived bulk  $\gamma\delta$  T cell lines and clones efficiently suppressed the proliferation and IL-2 secretion of naïve/effector T cells and inhibited DC maturation and function. Hence, their depletion or the reversal of their suppressive function could enhance anti-tumor immune responses against breast cancer. Indeed as in CD4<sup>+</sup> regulatory T cells (Tregs), the immunosuppressive activity of  $\gamma\delta$  T cells could be reversed by human TLR8 ligands both *in vitro* and *in vivo*. Study revealed that MyD88, TRAF6, IKK $\alpha$ , IKK $\beta$  and p38 $\alpha$  molecules in  $\gamma\delta$ 1 cells were required for these cells to respond to TLR8 ligands (132, 134, 135). **Table 2** shows expression and co-stimulatory effects mediated by TLR activation of  $\gamma\delta$  T cells

### TLRs MODULATE CROSSTALK BETWEEN $\gamma\delta$ T AND DENDRITIC CELLS

The functional fate of effector T cells is governed by antigen presentation and the cytokine milieu in the local environment. Dendritic cells (DCs) being professional APCs, recognize the danger signal, process it, and present it to the T lymphocytes thereby modulate adaptive immune response.  $\gamma\delta$  T cells influence the antigen presenting property of DCs. DCs pre-incubated with activated  $\gamma\delta$  T cells enhance the production of IFN- $\gamma$  by alloreactive T cells in mixed lymphocyte reaction (136). Moreover,  $\gamma\delta$  T cells not only upregulated CD86 and MHC I expression on DC but themselves get activated, leading to up-regulation of CD25, CD69, and cytokine production (137). These studies showed how  $\gamma\delta$  T cell and DCs regulate each other's function. There are reports, which have shown how  $\gamma\delta$  T cells interact with DC or *vice versa* via TLR ligands. Leslie et al. reported that stimulation with TLR ligands in  $\gamma\delta$ /DC cocultures enhanced the maturation and production of IL12p70 by DCs (138). TLR also regulate the  $\gamma\delta$  T cells and DC crosstalk in microbial context. TLR2-stimulated DCs enhanced IFN- $\gamma$  production by V $\delta$ 2 T cells; conversely, phospho-antigen activated V $\delta$ 2 T cells enhanced TLR2-induced DC maturation via IFN- $\gamma$ , which co-stimulated interleukin-12 (IL-12) p70 secretion by DCs (139). Further,  $\gamma\delta$  T cells stimulated with TLR7 (CL097) or TLR3 (poly I:C) agonists produce IFN- $\gamma$ , TNF $\alpha$  and/or IL-6 thereby inducing DC maturation, which prime effector T cells against West Nile Virus (WNV) infection (140). This study

confirmed that the antiviral effector immunity may be regulated by interplay of DCs,  $\gamma\delta$  T cells and TLRs. Similarly, in human's  $\gamma\delta$  T cells and DCs regulate each other's immunostimulatory functions. TLR3 and TLR4 ligands stimulation of human PBMCs induced a rapid and exclusive IFN- $\gamma$  production by V $\gamma$ 9V $\delta$ 2 subset dependent on type 1 IFN secreted by monocytic DC. TLR-induced IFN- $\gamma$  response of V $\gamma$ 9V $\delta$ 2 T cells led to efficient DC polarization into IL-12p70-producing cells (58). In another study, it was reported that V $\delta$ 2 cells are indirectly activated by BCG and IL-12p70 secreted by DCs. IL-12p70 production by DC is modulated by Toll like receptor 2/4 ligands from BCG and IFN- $\gamma$  secreted by memory CD4 T cells (141). This study portrayed the complex interplay between cells of the innate and adaptive immune response in contributing to immunosurveillance against pathogenic infections.

### TLRs COMPLEMENT CYTOTOXIC POTENTIAL OF $\gamma\delta$ T CELLS AGAINST TUMOR CELLS

$\gamma\delta$  T cells have capability to lyse different types of tumors and tumor-derived cell lines (49, 50, 142–145). Circulating as well as tumor-infiltrating  $\gamma\delta$  T cells have the ability to produce abundant proinflammatory cytokines like IFN- $\gamma$  and TNF- $\alpha$ , cytotoxic mediators and MHC-independent recognition of antigens, render them as important players in cancer immunotherapy (143, 145). In addition to TCR,  $\gamma\delta$  T cells use additional stimulatory co-receptors or ligands including TLRs to execute effector functions and TLR agonists are considered as adjuvants in clinical trial of cancer immunotherapy (146). Kalyan et al. even quoted that “TLR signaling may perfectly complement the anti-tumor synergy of aminobisphosphonates and activated  $\gamma\delta$  T cells and this combined innate artillery could provide the necessary ammunition to topple malignancy's stronghold on the immune system” (147). Paradoxically, TLR agonists execute dual role of enhancing immune response (148) as well as increasing invasiveness of tumor cells (149–152). Hence, the tripartite cooperation of tumor cell, TLRs, and  $\gamma\delta$  T cells should be carefully analyzed. In concordance to this, Shojaei et al. reported that Toll like receptor 3 and 7 agonists enhanced the tumor cell lysis by human  $\gamma\delta$  T cells. The enhanced capability of  $\gamma\delta$  T cells to lyse tumor cells was attributed to increased expression of CD54 and downregulation of MHC class 1 on tumor cells. Poly(I:C) treatment of pancreatic adenocarcinomas resulted in overexpression of CD54 and concomitant coculture of tumor cells with  $\gamma\delta$  T cells led to interaction between CD54 and its ligand CD11a/CD18 triggering effector function in  $\gamma\delta$  T cells. However, TLR7 surrogate ligand induced

**Table 2 | Expression and functions mediated by TLRs on  $\gamma\delta$  T cells.**

TLR	Functions	References
TLR 2	Recognize LPS, enhance proliferation, induce IFN $\gamma$ and CD107a expression, enhance IL17 secretion, expression transiently increases after burn injury, mitochondrial danger-associated molecular patterns (MTDs) induce expression and production of IL-1 $\beta$ , IL-6, IL-10, RANTES, and VEGF	(19, 116–120)
TLR3	Induce IFN $\gamma$ production in conjunction with TCR stimulation, resistance to HSV induced encephalitis	(11, 121–123)
TLR4	Increases proliferation, IFN- $\gamma$ release, and cytotoxic potential, activation following burn injury	(100, 125, 127, 130)
TLR7/9	Upregulate upon poly I:C costimulation, promote IL-17 production	(19, 124, 132)
TLR8	Reversal of immunosuppressive activity	(132, 134, 135)

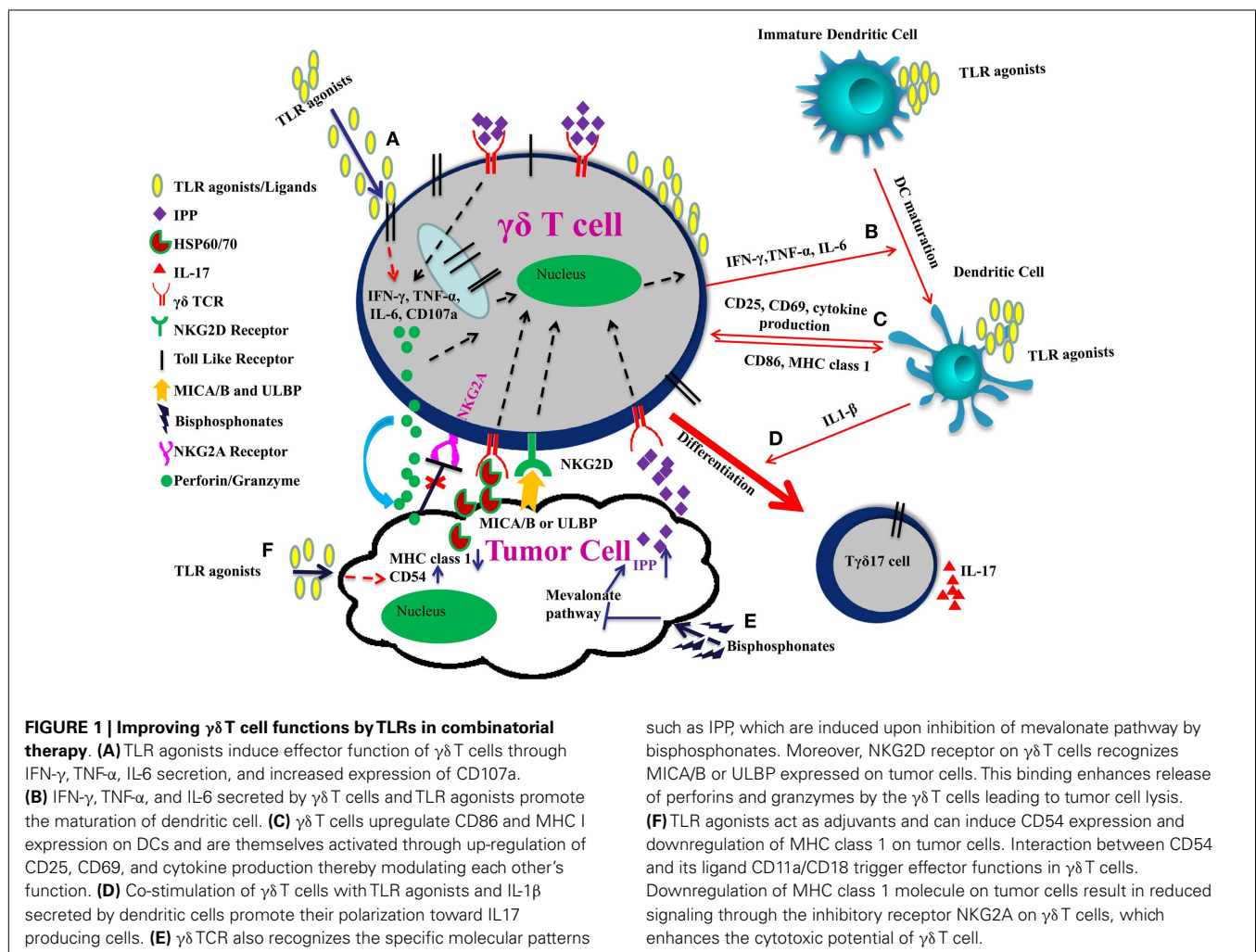
downregulation of MHC class 1 molecule on tumor cells resulting in a reduced affinity for inhibitory receptor NKG2A on  $\gamma\delta$  T cells (59). Manipulation of TLR signaling by using TLR8 agonists reversed the suppressive potential of  $\gamma\delta$  Tregs found elevated in breast cancer (132). Polysaccharide K (PSK) known for its anti-tumor and immuno-modulatory function can also activate TLR2 leading to increased secretion of IFN- $\gamma$  by  $\gamma\delta$  T cells on stimulation. The cell–cell contact between  $\gamma\delta$  T cells and DC was required for optimal activation of  $\gamma\delta$  T cells. However, PSK along with anti-TCR could co-activate  $\gamma\delta$  T cells even in the absence of DC. The study confirmed that the anti-tumor effect of PSK was through activation of  $\gamma\delta$  T cells (153).

Studies from our lab have shown that the TLR signaling in  $\gamma\delta$  T cells derived from the oral cancer (OC) patients may be dysfunctional. We reported that  $\gamma\delta$  T cells from healthy individuals (HI) and OC patients express higher levels of TLR2, TLR3, TLR4, and TLR9 than in  $\alpha\beta$  T cells. Higher TLR expression was observed in HI compared to OC patients. Stimulation with IL2 and TLR agonists (Pam3CSK, Poly I:C, LPS, and CpG ODN) resulted in higher proliferative response of peripheral blood lymphocytes from HI compared to OC patients. However, the role of other immune cells that may influence the TLR ligand stimulation induced activation

status of lymphocytes cannot be ignored (125). Impairment in TLR expression/signaling can be viewed as a strategy employed by tumor cells to avoid immune recognition.

### TLRs AND $\gamma\delta$ T CELLS IN DISEASES

Studies have demonstrated the protective role of  $\gamma\delta$  T cells in infection and inflammation (154–157). Inoue et al. showed that during mycobacterial infection,  $\gamma\delta$  T cells precedes the  $\alpha\beta$  T cells, indicating role of  $\gamma\delta$  T cells as first line of defense against infections (158). The conserved molecular patterns associated with pathogens are directly recognized by  $\gamma\delta$  T cells leading to rapid protective response against the danger signal. Unlike  $\alpha\beta$  TCR,  $\gamma\delta$  TCR acts as pattern recognition receptor providing advantage in anti-infection immunity by directly initiating cytotoxicity against infected cells or through production of cytokine to involve multiple immune system components to combat infection (159, 160). Activated  $\gamma\delta$  T cells through TLR3 and TLR4 ligands rescue the repressed maturation of virus-infected DCs and mount a potent antiviral response (58, 140). Malarial infection in MyD88 deficient mice resulted in impairment in CD27<sup>+</sup>IL-17A-producing  $\gamma\delta$  T cell without affecting the IFN- $\gamma$  producing  $\gamma\delta$  T cells (161). This study specifies the role of TLR in promoting proliferation



of proinflammatory  $\gamma\delta$  T cells. Another study by Martin et al. showed that IL17 producing  $\gamma\delta$  T cells express TLR1 and TLR2 and expand in response to their ligands and mount an adequate response against heat-killed *M. tuberculosis* or *C. albicans* infection (118). However,  $\gamma\delta$  T cell are also known to directly recognize the pathogen-derived molecules and mediate cytotoxic effector function either through secretion of perforin and granzyme B or by secretion of proinflammatory cytokine IL17 (162–164). The involvement of TLRs in regulating anti-microbial  $\gamma\delta$  T cell function should be investigated in depth to exploit it as a cell based therapy for infectious diseases.

## CONCLUDING REMARKS

The characteristic copious IFN- $\gamma$  or IL17 secretion, MHC-independent antigen recognition, tissue tropism, and potent cytotoxicity make  $\gamma\delta$  T cells promising targets for immunotherapy. Similar to  $\alpha\beta$  T cells,  $\gamma\delta$  T cells exhibit functional and phenotypic plasticity, which influences the nature of the downstream adaptive immune response. The adoptive transfer of *ex vivo* expanded V $\gamma$ 9V $\delta$ 2 T cells or *in vivo* activation of V $\gamma$ 9V $\delta$ 2 T cells (phosphoantigens or amino-bisphosphonates) can be utilized as adjuvant to conventional therapies. Clinical trials of V $\gamma$ 9V $\delta$ 2 T cells as immunotherapeutic agents have shown encouraging results that could be attributed to its low toxicity grade. Combinations of cellular immune-based therapies with chemotherapy and other anti-tumor agents may be of clinical benefit in the treatment of malignancies. Combinatorial treatment using, chemotherapeutic agents or bisphosphonate zoledronate (ZOL) sensitizes tumor-derived cell lines to rapid  $\gamma\delta$  T cells killing. V $\gamma$ 9V $\delta$ 2 T cell triggering may be also enhanced by combining TCR stimulation with engagement of TLRs. Various TLR agonists are currently under investigation in clinical trials for their ability to orchestrate anti-tumor immunity. In one study, simultaneous use of both Imiquimod (TLR7 agonist) and CpG-ODN (TLR9 agonist) loaded onto virus like nanoparticles was found to be effective in triggering effector and memory CD8<sup>+</sup> T cell response (165). Similarly, combination of  $\gamma\delta$  T cells and DCs along with nanoparticle loaded TLR agonists can be employed for developing effective immunotherapeutic strategies. The direct or indirect stimulation of  $\gamma\delta$  T cells by TLR agonists could be a strategy to optimize Th1-mediated immune responses as adjuvant in vaccines against infectious or malignant diseases.

Administration of an “immunogenic chemotherapy” (such as oxaliplatin or anthracycline or an X-ray-based regimen) or local delivery of TLR surrogates in the tumor microenvironment (which stimulate local DCs and provides a source of IL-1 $\beta$ ) may be also instrumental in polarization of  $\gamma\delta$  TILs into IL17 producing cells. T $\gamma\delta$ 17 cells play a crucial role in anti-microbial immunity but their role in tumor immunity remains controversial. T $\gamma\delta$ 17 have both pro and anti-tumor properties. TLR use in combinatorial therapy, therefore, could be a double edged sword. Careful use of TLR agonists in combinatorial  $\gamma\delta$  T cell based therapy is needed to strike the balance between pro and anti-tumor effects (Figure 1).

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**Conflict of Interest Statement:** The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Received: 27 May 2014; accepted: 15 July 2014; published online: 31 July 2014.

Citation: Dar AA, Patil RS and Chiplunkar SV (2014) Insights into the relationship between toll like receptors and gamma delta T cell responses. *Front. Immunol.* 5:366. doi: 10.3389/fimmu.2014.00366

This article was submitted to Tumor Immunity, a section of the journal *Frontiers in Immunology*.

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