

博士論文 (要約)

Studies on Functions of Cells Involved in Immune Responses in the Intestinal Lymphoid Tissues

(腸管のリンパ組織における免疫応答に関わる細胞の機能についての研究)

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Contents

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Abbreviations

Ab	antibody
Ag	antigen
AhR	aryl hydrocarbon receptor
AID	activation-induced cytidine deaminase
APRIL	a proliferation-inducing ligand
BAFF	B cell activating factor
BCR	B cell receptor
CaeP	caecal patch
CDR	complementarity-determining region
CFSE	5(6)-Carboxyfluorescein N-hydroxysuccinimidyl ester
CoP	colonic patch
CSR	class-switch recombination
DC	dendritic cell
DMSO	dimethyl sulfoxide
FcεR	Fcε receptor
FCS	fetal calf serum
FDC	follicular dendritic cell
GALT	gut-associated lymphoid tissue
GC	germinal center
GF	germ-free
GLT	germ line transcript
GM-CSF	granulocyte macrophage colony-stimulating factor
IDO	indoleamine 2,3-dioxygenase
IFN	interferon
Ig	immunoglobulin
IL	interleukin
ILC	innate lymphoid cell
ILCN	group <i>N</i> innate lymphoid cell (<i>N</i> : a natural number)
Int.	intermediate
Lin.	lineage markers
LN	lymph node
LP	lamina propria
LTi cell	lymphoid tissue inducer cell
MHC	major histocompatibility complex
MHC <i>X</i>	major histocompatibility complex class <i>X</i> (<i>X</i> = I, II)

Abbreviations

MLN	mesenteric lymph node
NK cell	natural killer cell
OVA	ovalbumin
OVAp	ovalbumin peptide
PP	Peyer's patch
PST	post-switch transcript
pT _{reg} cell	peripherally derived regulatory T cell
RA	retinoic acid
RALDH	retinal dehydrogenase
SFB	segmented filamentous bacteria
SHM	somatic hyper-mutation
SPF	specific pathogen-free
SPL	spleen
TCR	T cell receptor
T _{FH} cell	T follicular helper cell
T _{FR} cell	follicular regulatory T cell
TGF	transforming growth factor
T _H <i>N</i> cell	T helper <i>N</i> cells (<i>N</i> : a natural number)
TLR	Toll-like receptor
TNF	tumor necrosis factor
T _{reg} cell	regulatory T cell
TSLP	thymic stromal lymphopoietin
tT _{reg} cell	thymus-derived regulatory T cell

Chapter 1

General Introduction

§1.1 Preface

The present studies focused on cells in the intestinal immune system (**Fig. 1-1**). The intestine is an important immune organ because it is exposed to many pathogens invading orally with food intake every day. The intestinal immune system should eliminate these pathogens. At the same time, the intestine needs to efficiently acquire nutrients from the foods. Further, the intestine harbors trillions of commensal microbes, which have beneficial functions to the host, e.g. digesting foods, eliminating pathogens, and even preventing diseases (1, 2). The intestinal immune system should be regulated not to attack these beneficial substances and organisms. Deficiency in the regulation probably lead to detrimental abnormalities, such as food allergy and inflammatory bowel diseases. Thus, the intestinal immune system has to induce the opposite responses to different targets at the same place. Huge numbers of studies have intensely investigated into the intestinal immune system. However, we have not obtained the whole picture of the complex system.

The immune system is a complex and ingenious multi-cellular system. Various immune cells in the system function in a complex cell-cell network to satisfy the requirements for the system. In subsequent sections, the author will discuss about regulation of the immune responses and characteristics of the intestinal immune system. Such discussion is expected to present an overview of a cellular network in the immune regulation revealed by previous studies.

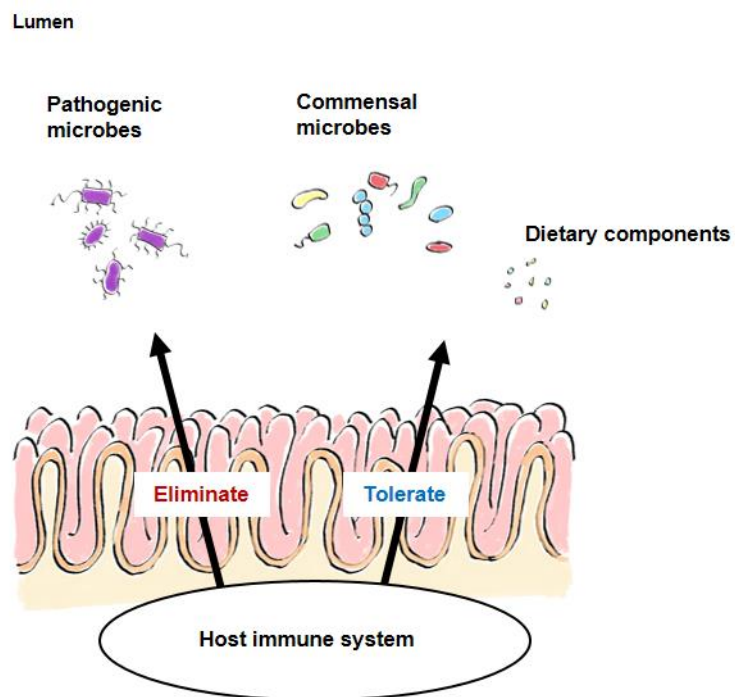


Fig. 1-1 The intestinal immune system

§1.2 Immune Responses to Various Agents

§1.2.1 The immune system distinguishes self and non-self.

We, living individuals, are separated physically from the external environment by epithelium at the skin and mucosal sites, which functions as a primary barrier to exogenous pathogens, such as bacteria and viruses. However, some pathogens could pass through this primal barrier taking advantage of physical injury or developing their own strategy to break down the barrier function. Such invading pathogens should be eliminated. For the elimination, mammals have evolved their immune system, which attacks the pathogens. To efficiently eliminate pathogens, the immune system should attack the pathogens specifically. Such specific elimination requires recognition of the exogenous pathogens. To accomplish this, the immune system utilizes self components to distinguish non-self pathogens, i.e. the system attacks non-self agents as pathogens.

§1.2.2 T cells play a pivotal role in recognizing specificity.

To distinguish self and non-self, the immune systems should be equipped with a mechanism to recognize specificity of various substances and organisms including exogenous non-self components and endogenous self components. This is accomplished by T cells. T cells express T cell receptors (TCRs) which recognize a specific sequence of peptides presented on major histocompatibility complex (MHC) molecules (**Fig. 1-2A**). Proteins which include such TCR-recognizable peptide sequences (epitopes) are called antigens (Ags). There are innumerable Ags derived from self and non-self.

T cells experience genomic diversification of genes encoding TCR α - and TCR β -chains, called V(D)J recombination (3, 4). This process produces diverse T cell clones, each of which express different TCRs recognizing different epitopes (**Fig. 1-2B**). Thus, T cells could distinguish diverse Ag-specificity as a whole. Theoretical study has estimated that the VDJ recombination process in a TCR β gene can produce about 10^{14} different nucleotide sequences (5). In combination with TCR α , a diversity of TCR $\alpha\beta$ repertoire is estimated to be about 10^{20} (6). Namely, each individual could contain 10^{20} different T cell clones potentially. The diversified T cells subsequently experience positive and negative selection in the thymus (7, 8). Here, the author briefly describes a conceptual overview of the processes below (**Fig. 1-3A**).

The selection process is largely dependent on a reactivity of expressed TCRs on T cell precursors to self-peptide-MHC complex on Ag-presenting cells in the thymus. Each TCR chain contains three variable domains called complementarity-determining regions (CDRs), which are different among different T cell clones. The CDRs are involved in interaction of TCRs with not only Ag epitopes but also MHC molecules which have genetic polymorphism (9). Therefore, individuals require T cells expressing TCRs which can interact with their self MHC molecules. Such self-MHC-recognizing T cells are selected by positive selection. T cells require interaction of their TCRs with peptide-MHC for survival, and TCRs without any signals from peptide-MHC complex in the thymus lead the T cells to undergo apoptotic processes.

To prevent detrimental auto-immune responses, a negative selection process deletes T cell clones which

have TCRs strongly recognizing self-peptide on MHCs. This process is also known as clonal deletion. Among T cells having lower affinity to self-peptide-MHC complex, those with intermediate affinity to self-peptide-MHC probably undergo differentiation to immunosuppressive regulatory T (T_{reg}) cells. Indeed, it has been reported that TCR affinity strength correlates with T_{reg} cell generation in the thymus (10). The remaining T cells with low affinity to self-peptide-MHCs differentiated into naïve T cells, which survey all through the body to find invading foreign Ags. These T cells are composed of MHC class I (MHC I) - restricted $CD8^+$ cytotoxic T cells and MHC class II (MHC II) - restricted $CD4^+$ helper T cells. Cytotoxic T cells eliminate pathogens by induce death of infected cells whereas helper T cells help other immune cells, mainly through cytokine secretion, to eliminate pathogens.

Naïve T cells in individuals include various clones with diverse specificity. These T cells go through clonal selection in immune responses (11)(**Fig. 1-3B**). When foreign substances and organisms invade, naïve T cell clones expressing reactive TCRs to the Ags of the foreign agents are selected to respond to and eliminate the Ags.

Activated naïve T cells differentiate into effector T cells or long-lived memory T cells. Effector cytotoxic T cells secrete interferon (IFN) $-\gamma$, tumor necrosis factor (TNF) $-\alpha$, perforin, and granzyme to kill infected cells (12). Although these effector cytotoxic T cells exhibit some heterogeneity in functional property and phenotype, such effector cells are principally directed to kill other cells (13). In contrast, effector helper T cells contain several subsets which have distinct functions. Well-known effector helper T cells include T helper (T_H) 1 cells, T_H2 cells, and T_H17 cells. These T_H cells express and secrete their characteristic transcription factors and cytokines: T_H1 cells express T-bet and secrete IFN- γ ; T_H2 cells express GATA3 and secrete interleukin (IL) -4, IL-5, and IL-13; T_H17 cells express ROR γ t and secrete IL-17A and IL-22. In addition, T_{reg} cells, which express a transcription factor Foxp3, can be induced from naïve T cells in periphery. Such T_{reg} cells are distinguished from thymic T_{reg} cells mentioned above, and these T_{reg} cells are named as peripherally derived T_{reg} (pT_{reg}) cells (also called as induced T_{reg} cells) and thymus-derived T_{reg} (tT_{reg}) cells (also called as naturally occurring T_{reg} cells) (14). Differentiation of naïve $CD4^+$ T cells into these subsets is biased by environmental factors (15, 16). For instance, differentiation into T_H1 cells, T_H2 cells, T_H17 cells, and pT_{reg} cells are induced by IL-12, IL-4, IL-6 with transforming growth factor (TGF) $-\beta$, and TGF- β , respectively. Such environmentally biased regulation enabled helper T cells to enhance a suitable immune response to each infection. In addition, it has been reported that TCR specificity itself could affect helper T cell differentiation fate (17).

§1.2.3 Lymphoid tissues function as a unit for immune responses.

Ag-presentation to naïve T cells mainly occurs in secondary lymphoid tissues, such as lymph nodes (LNs) and a spleen (SPL). The lymphoid tissues function as a site for naïve T cell priming. Naïve T cells, after positive and negative selection in the thymus, migrate blood, lymphoid tissue, and efferent lymph, and then recirculate into blood through thoracic duct (18, 19)(**Fig. 1-4A**). LNs drain Ag-presenting cells from periphery (**Fig. 1-4B**). One peripheral region has its specific draining LN, i.e. Ags in the region is always carried to the region-specific LN (18–20). Thus, lymphoid tissues probably function as a unit for the immune system. Such region-specific immune unit enable the immune system to induce a suitable response to the region where Ags are derived from, i.e. immune responses to the intestinal Ags and to the skin Ags can be different, even though they are the same Ags.

To induce T cell responses in lymphoid tissues, Ags need to be carried into the lymphoid tissue. This is accomplished by Ag-presenting cells immigrating to the LN from periphery through afferent lymph. An important Ag-presenting cell type is dendritic cells (DCs; discussed later in **§1.5**). DCs take up Ags in periphery, migrate into LNs, and present the Ag to naïve T cells inducing T cell subset differentiation. Lymphoid tissues have different mechanisms of Ag acquisition. In SPL, Ags in blood are obtained by marginal zone DCs and macrophages, i.e. Ag acquisition occurs in the lymphoid tissue (21). Another type of lymphoid tissues is mucosa-associated lymphoid tissues, which is located in mucosal sites. This type of lymphoid tissues has no afferent lymph and directly acquire exogenous Ags through epithelium on the tissues.

In the intestine, there are several lymphoid tissues which survey exogenous Ags (**Fig. 1-5**). These lymphoid tissues include both of LNs and mucosa-associated lymphoid tissue, the latter is called gut-associated lymphoid tissue (GALT) (20, 22, 23). GALTs include Peyer's patches (PPs), caecal patches (CaePs), and colonic patches (CoPs) in the small intestine, the caecum, and the large intestine, respectively. The GALT capture Ags from the intestinal lumen through epithelial cells on it and thus have no afferent lymph (24). The intestinal LNs include mesenteric LNs (MLNs) draining Ags from both of the small and large intestines and caudal LNs draining Ags from the large intestine. Therefore, these lymphoid tissues probably play a pivotal role in regulating Ag-specific immune responses in the intestine.

§1.2.4 Short summary

The immune responses to various Ags are regulated by T cells, which express Ag-specific TCRs. The TCR specificity has broad spectrum, resulted from V(D)J recombination process, and each T cells can respond to specific Ag inducing a suitable response specifically to the Ag. T cells recognize their Ags presented on MHC molecules of Ag-presenting cells in lymphoid tissues, which function as a unit of the immune system. In the intestine, MLNs, caudal LNs, and GALT including PP, CaeP, and CoP are probably important sites for immune regulation.

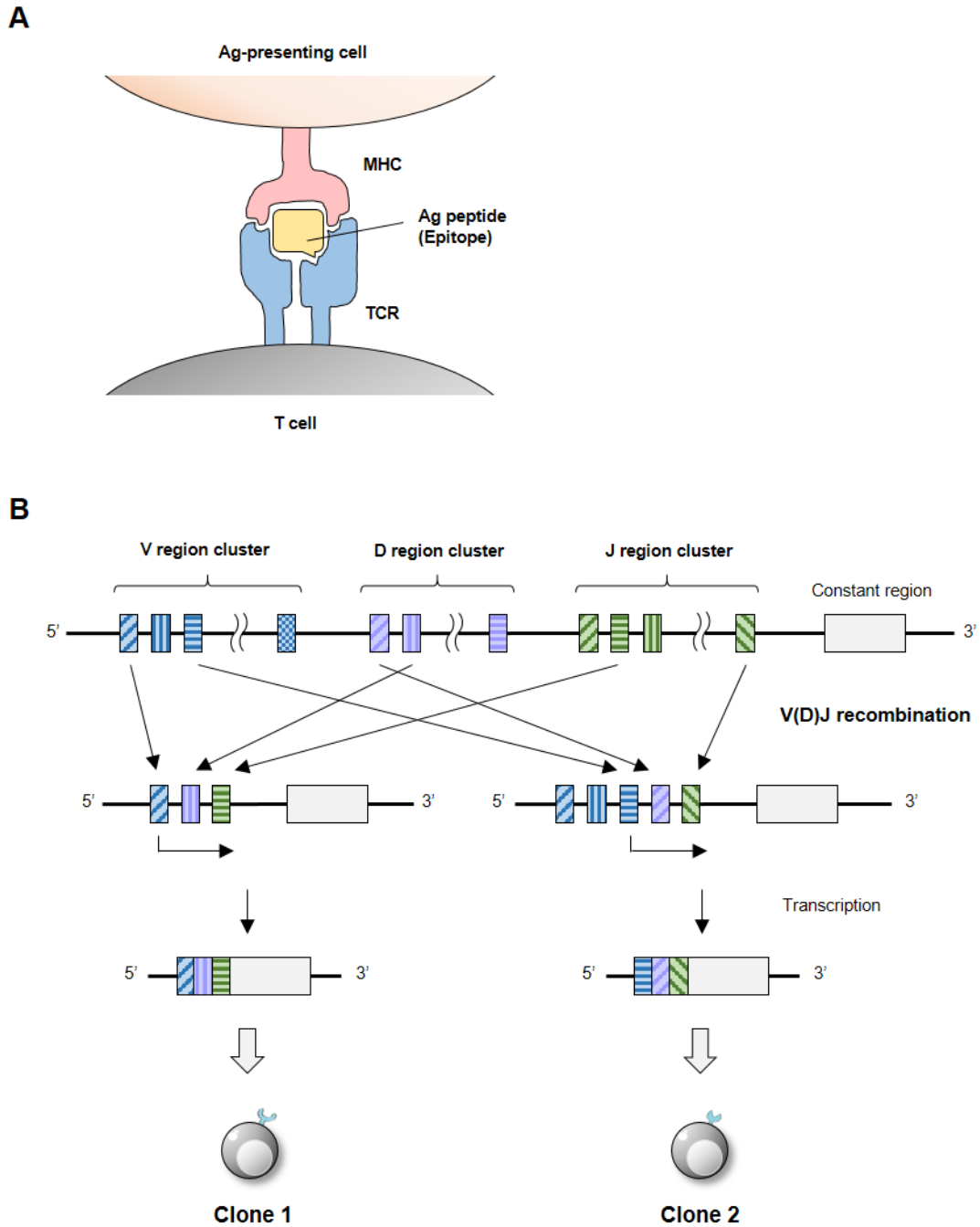


Fig. 1-2 Conceptual description of T cell specificity

A. TCRs recognize peptide-MHC complex.

B. Genes encoding TCRs are diversified by V(D)J recombination process.

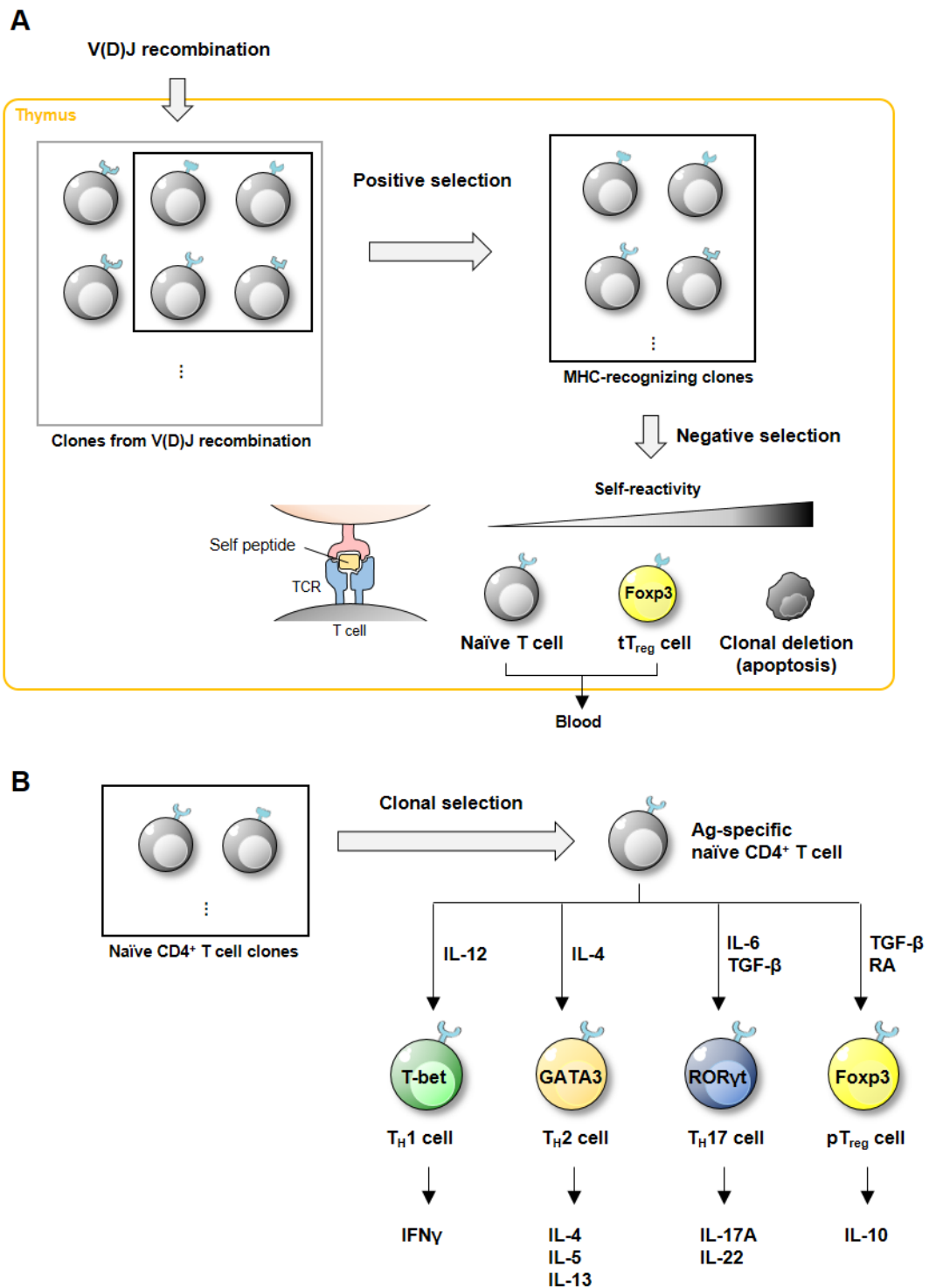


Fig. 1-3 Selection and responses of T cell

A. T cell clones with TCR recognizing self MHC and weakly responding to self peptides are selected in the thymus through positive and negative selection.

B. In response to foreign Ag, Ag-specific T cell clones differentiate into suitable subsets to an environmental cue.

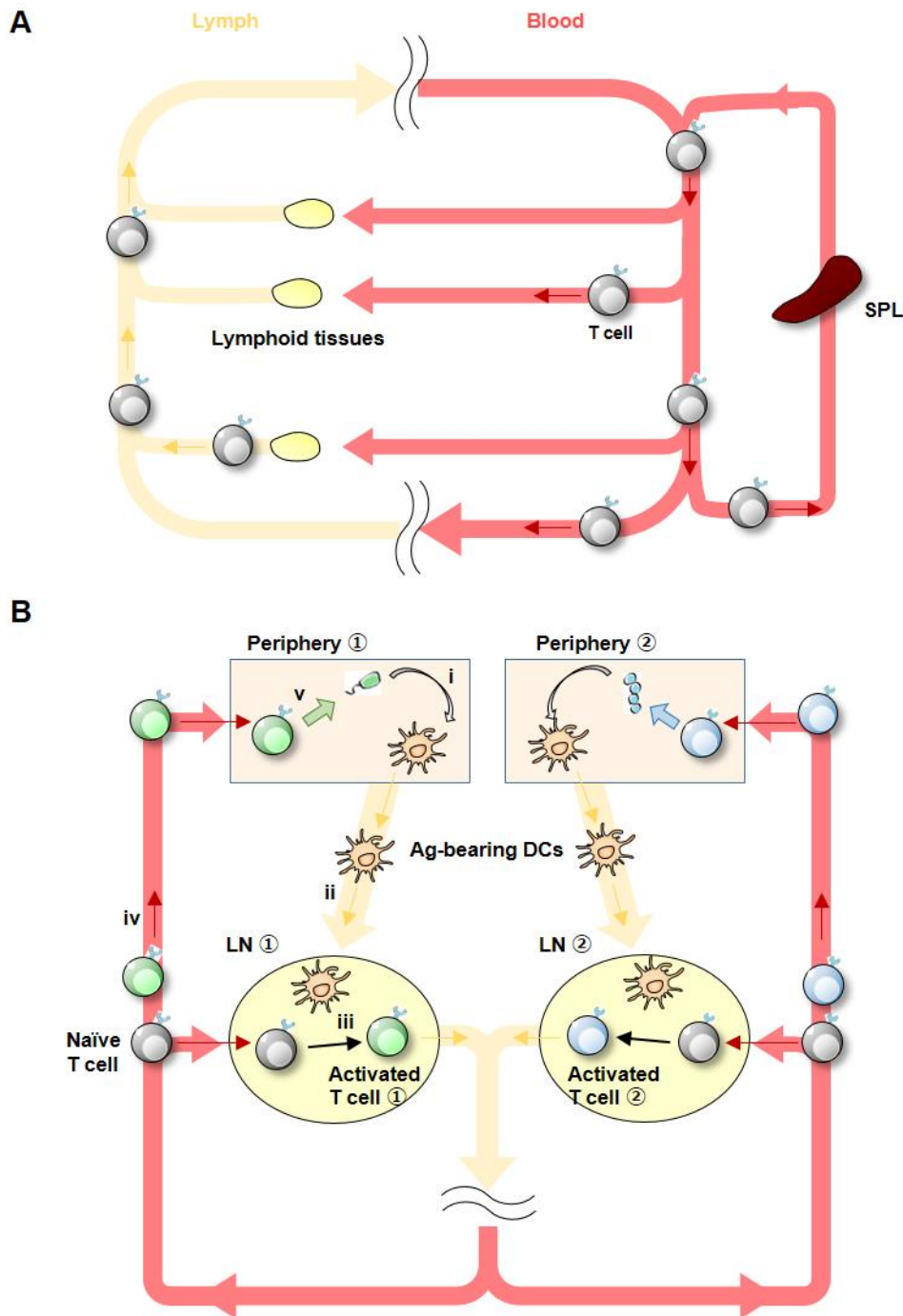


Fig. 1-4 T cell circulation

A. In the steady state, naïve T cells circulate lymphoid tissues through blood and lymph to survey their specific Ags.

B. In invasion of non-self, DCs capture Ags in the invaded periphery (i), migrate to LN (ii), and present the Ags to T cells (iii). Subsequently, activated T cells migrate to the periphery through lymph and blood (iv) and respond to the Ags in the periphery (v). DCs in each periphery (① and ② in the figure) migrate to the specific LNs (LN ① and LN ②, respectively).

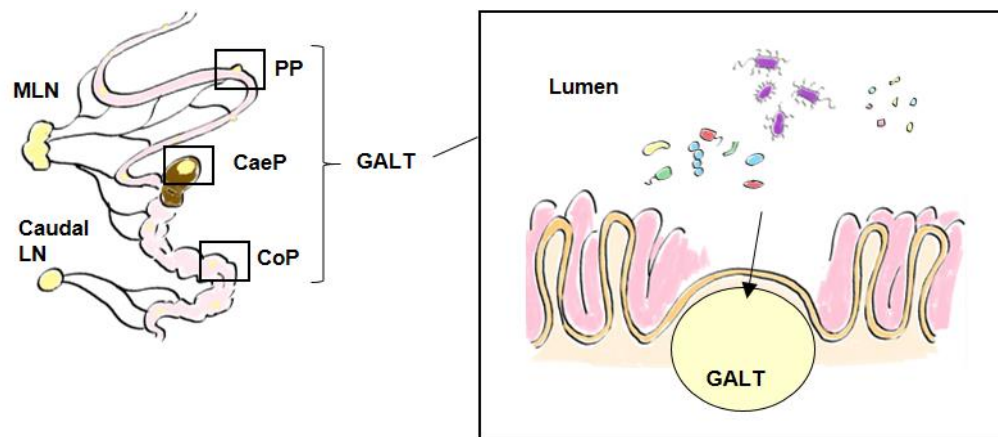


Fig. 1-5 Lymphoid tissues in the intestine

§1.3 Effector Functions of T Cells

§1.3.1 Helper T cell subsets induce various responses.

Naïve CD4⁺ helper T cells are activated by their specific Ag-presenting MHC II and differentiate into several subsets, which have distinct functions as mentioned in §1.2.2. The fate of T cell differentiation is largely dependent on environmental factors at the activation. This enabled T cells to induce a suitable response to the circumstance around the Ag. The differentiated T_H cell subsets, including T_H1, T_H2, and T_H17 cells, secrete their specialized cytokines to induce subset-specific response (25, 26)(Fig. 1-6).

Naïve T cells differentiate into T_H1 cells, which highly produce IFN- γ to eliminate intracellular pathogens. This cytokine activates macrophages and cytotoxic T cells to kill the pathogens and infected cells, respectively. Responses induced by T_H2 cells are toward helminth infection. These responses are mediated by IL-4, IL-5, and IL-13. Secreted IL-4 stimulates B cells to produce immunoglobulin (Ig) G1 and IgE antibodies (Abs; discussed later in §1.4) and macrophages to promote tissue repair (27). Ab secretion is also enhanced by IL-5, which promotes differentiation of Ab-secreting cells from B cells (28). The other T_H2 cytokine, IL-13, promotes mucin production by goblet cells, one of epithelial cells in mucosal sites. T_H17 cells secrete IL-17A, IL-17F, IL-22, granulocyte macrophage colony-stimulating factor (GM-CSF), and TNF- α . This T cell subset induces protective responses to extracellular pathogens through activating neutrophils (29). In addition, IL-17A, IL-17F, and IL-22 can promote antimicrobial peptides secretion from mucosal epithelium (30).

Although these helper T cell subsets promote protective responses to infection, they could have destructive effects on the host by excessive responses (31). Excess T_H1 and T_H17 cell responses could trigger autoimmune diseases whereas excess T_H2 cell responses could induce allergy and asthma. Therefore, the immune system should precisely regulate these responses. Such regulation is partly accomplished by T_{reg} cells, which suppress effector T cell responses (32–36). Suppressive effects of T_{reg} cells work on effector T cells, mediated by cell cycle arrest through suppressor cytokines including IL-10, IL-35, and TGF- β and apoptosis induction through IL-2 consumption and cytolysis, and on Ag-presenting cells, mediated by inhibiting Ag-presentation and co-stimulation molecules on the Ag-presenting cells (37, 38). The immune suppressive ability is acquired by expression of a transcription factor Foxp3, which is considered as a master regulator for T_{reg} cells (39, 40). Similarly, effector T cells are regulated by their master regulator transcription factors, namely T-bet, GATA3, and ROR γ t for T_H1, T_H2, and T_H17 cells, respectively. These transcription factors regulate genes involved in their functions and localization. Thus, T_{reg} cells also express these T_H cell master regulators to localize with the effector subsets and suppress their responses (34, 36).

Effector T cells activated and differentiated in lymphoid tissues should migrate to the periphery where Ags are derived. The directional migration is accomplished by regionally specific homing receptors. The homing receptors expressed on activated T cells are regulated by environmental factors in lymphoid tissues. Homing to the small intestine requires expression of integrin $\alpha_4\beta_7$ and chemokine receptor CCR9 (18, 41). Expression of these homing receptors is induced by retinoic acid (RA) in the intestinal lymphoid tissues (42). RA is a metabolite of vitamin A (retinol) via retinal. This metabolism process is largely dependent on retinal dehydrogenase (RALDH)

enzymes. In the intestinal lymphoid tissues, RALDHs are highly expressed on DCs and non-hematopoietic stromal cells (42, 43).

§1.3.2 Regulation of intestinal T cells is affected by commensal microbiota.

Among T cell subsets, T_H17 cells and T_{reg} cells are abundant in the intestine (44–46). The abundance of these T cells is dependent on specific commensal microbiota. In the case of T_H17 cells, segmented filamentous bacteria (SFB) are required for induction of small intestinal T_H17 cells (47, 48). These bacteria adhere to intestinal epithelial cells, and this adherence is critical for the T_H17 cell induction (49). Ags derived from the SFB are presented to T cells by DCs, and this Ag-presentation is also indispensable for SFB-dependent T_H17 cell induction (50). Indeed, T_H17 cells in the intestine express TCRs specific to SFB-derived Ags (51). In addition to the SFB-dependent mechanisms, T_H17 cells has been reported to be induced by ATP and DNA derived from commensal bacteria (45, 52). Activated T_H17 cells are involved in autoimmune diseases, and SFB colonization has been reported to exacerbate the pathological score of autoimmune disease model of mice (53). Therefore, the intestinal immune regulation by microbiota could have effects on extra-intestinal homeostasis.

In the intestine, T_H17 cell population is regulated in balance with that of T_{reg} cells (45, 54). The intestinal T_{reg} cells, especially in the large intestine, are also dependent on microbiota. A series of outstanding studies has revealed that the large intestinal T_{reg} cells are induced by colonization of *Clostridium* bacteria derived from mice and humans (46, 55). This is mediated by the bacteria-derived butyrate (56, 57). Another bacterial strain involved in T_{reg} cell induction is *Bacteroides fragilis* which express surface polysaccharide A (58). The induced T_{reg} cells suppress T_H17 cell differentiation through IL-10 production (59). Thus, the T_{reg} cells induced by commensal bacteria contribute to preventing excess T_H17 cell responses in the intestine. These T_{reg} cells have been reported to express commensal bacteria-specific TCRs and to be p T_{reg} cells, i.e. they are induced in the intestinal immune system rather than the thymus (60). Such commensal-specific T_{reg} cells probably tolerate immune responses to these commensal bacteria and contribute to their stable colonization.

Collectively, some species in commensal microbiota have a potential to induce T_H17 cells in Ag-specific and non-specific manners, which could be detrimental for the host when excess. Then, other species can induce T_{reg} cells in the intestinal immune system, which in turn induce immune tolerance toward the bacteria. Further, these T_{reg} cells suppress T_H17 cells probably contributing to an appropriate equilibrium between these T cell subsets in the intestine.

§1.3.3 Regulatory T cells are involved in oral tolerance.

In addition to commensal microbiota, the intestinal immune system also should regulate its responses to food components, which may also be beneficial to the host. Most of food-derived proteins are digested into di- or tri-peptides which TCRs cannot recognize (61). But some proteins are actively sampled by the intestinal immune system through several pathways (discussed later in §1.5.4). Immune responses to these Ags are set to be tolerogenic as default in the intestine (61–63). The intestine is rich in immunosuppressive factors, such as TGF- β and RA, which

are involved in T_{reg} cell differentiation. These T_{reg} cells could contribute to suppressing immune responses toward the Ags not only in the intestine but also in the systemic immune system. This phenomenon is called oral tolerance.

Oral tolerance is defined as a systemic hyporesponsiveness toward Ags administrated through the oral route (61, 62, 64). Dysregulation of oral tolerance could cause food allergy. Thus, to establish preventive and therapeutic strategies for food allergy, the mechanism underlying oral tolerance should be revealed. Furthermore, oral tolerance is probably a useful way as prevention or treatment for systemic diseases caused by immunological pathogenesis. Indeed, some studies have reported that autoimmune disease model is ameliorated by oral administration of the model Ag (65, 66). Likewise, oral administration of transgenic rice expressing cedar pollen-derived epitope has been reported to induce tolerance for hay fever in mouse model (67). Further, therapeutic use of oral tolerance for food allergy has been started in clinical studies (68–70).

In oral tolerance, T_{reg} cells play a pivotal role (**Fig. 1-7**). Especially, pT_{reg} cells, but not tT_{reg} cells, are indispensable for oral tolerance (71). These T_{reg} cells are probably induced mainly in MLNs because surgical removal of MLNs abolished oral tolerance induction in mice (72). In contrast, oral tolerance has been induced in PP-depleted mice (73–75). These studies support the idea that a site for inducing oral tolerance is MLNs, although it should be noted that another group has reported that PP-depletion abolishes oral tolerance, which suggests that PPs may contribute to oral tolerance in some condition (76). Oral tolerance also requires expression of gut-homing receptors, CCR9 and $\alpha_4\beta_7$, on T_{reg} cells (77, 78). These studies have suggested that induced T_{reg} cells migrate into the intestinal lamina propria (LP) and further differentiate to tolerogenic IL-10-producing T_{reg} cells in response to IL-10 secreted by LP CX₃CR1⁺ macrophages. Collectively, the intestinal immune system is required to induce CCR9⁺ $\alpha_4\beta_7$ ⁺ T_{reg} cells specific to food-derived Ags, and this induction probably occurs in MLNs.

§1.3.4 T follicular helper cells help B cell responses in germinal center.

As mentioned in §1.3.1, CD4⁺ helper T cells differentiate into several types of effector subsets. Recently, a new subset, T follicular helper (T_{FH}) cells, has been established (79, 80). This helper T cell subset functions in germinal center (GC) responses, which are involved in Ab production of B cells (discussed later in §1.4). Although first studies on T_{FH} cells were reported in early 2000s, it had been barely regarded as an established helper T cell subset due to a lack of a lineage-defining transcription factor (81–83). In 2009, Bcl6 was identified as the transcription factor required for T_{FH} cell commitment, and then T_{FH} cells were broadly accepted as a helper T cell subset (84–86). This transcription factor functions reciprocally to Blimp1, i.e. T_{FH} cell commitment proceeds with Bcl6 up-regulation and Blimp1 down-regulation.

As well as other helper T cell subsets, T_{FH} cells have a signature phenotype. They secrete IL-4 and IL-21, and highly express co-stimulatory receptors, ICOS and PD-1, and a chemokine receptor, CXCR5. The cytokines, IL-4 and IL-21, are involved in class-switch recombination (CSR) and somatic hyper-mutation (SHM) of B cells (discussed later in §1.4). Expression of ICOS on T_{FH} cells is required for development of T_{FH} cells and interaction between T_{FH} cells and B cells in GCs whereas PD-1 represses T_{FH} cell responses probably in order to prevent production of auto-reactive Abs (87–90). CXCR5 is a receptor for chemokine CXCL13, which is produced by GC stromal cells named follicular dendritic cells (FDCs). Thus, CXCR5-CXCL13 axis leads to T_{FH} cell localization

into GCs in corporation with down-regulation of CCR7, which mediates localization to T cell zone in lymphoid tissues (91).

In addition to T_{FH} cells, $Foxp3^+ T_{reg}$ cells are also observed in GCs. These T_{reg} cells express T_{FH} cell-signature surface molecules such as CXCR5, PD-1, and ICOS, but not IL-21, and named as follicular regulatory T (T_{FR}) cells (92, 93). Follicular regulatory T cells suppress T_{FH} cell function and GC reaction probably to prevent auto-reactive Ab production. Indeed, T_{FR} cells differentiate from tT_{reg} cells, which express TCRs specific to self-peptides (92–94).

In the intestine, properties of T_{FH} cells have been studied intensely in PPs (95). A notable characteristic of PP T_{FH} cells is their origin. PP T_{FH} cells could be generated not only from naïve T cells but also from other T cell subsets, $Foxp3^+ T_{reg}$ cells and T_H17 cells (96, 97). Germinal centers in PPs are largely dependent on microbiota, i.e. germ-free (GF) mice have no or very few GCs in PPs (22). Thus, PP GCs are probably important for microbiota-specific Ab production. As mentioned in §1.3.2, intestinal T_{reg} cells and T_H17 cells are induced by some specific bacteria. This raise a possibility that conversion of T_{reg} cells and T_H17 cells into T_{FH} cells in PP GCs helps production of Abs toward such commensal bacteria (95). In addition, it has been reported that T_{FR} cells also function to regulate microbiota (98).

§1.3.5 Short summary

Naïve T cells which recognize their specific Ags differentiate into a suitable subset for the environment. In the intestine, several characteristic subsets are involved in regulation of immune responses to foods and commensal bacteria, namely T_{reg} cells, T_H17 cells, and T_{FH} cells. T_{reg} cells and T_H17 cells are regulated in the host-commensal interaction. Further, T_{reg} cells are mainly induced in MLNs and play a pivotal role in oral tolerance whereas T_{FH} cells are observed in PPs and control microbiota through regulation of Ab-producing GC reaction.

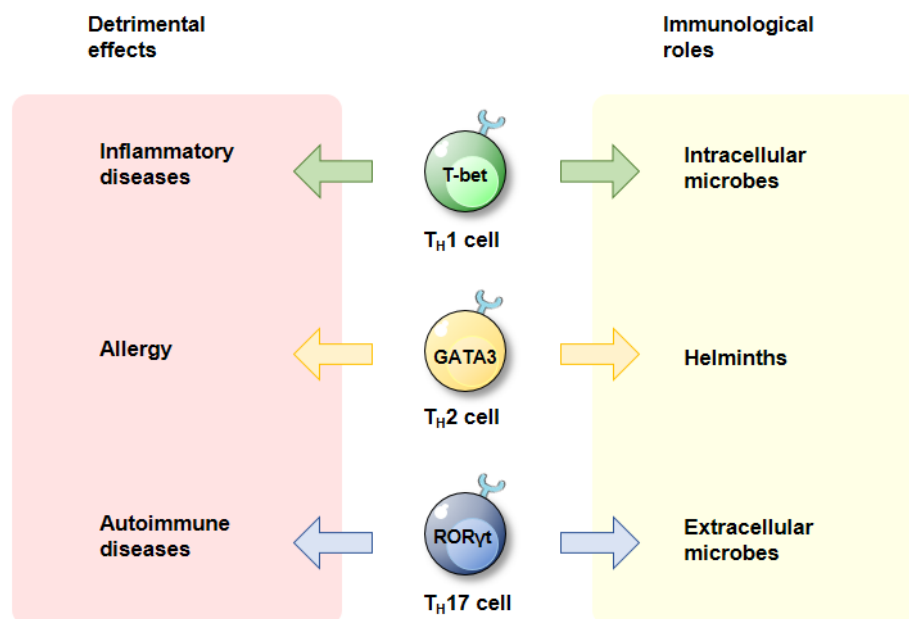


Fig. 1-6 Helper T cell subsets in health and disease

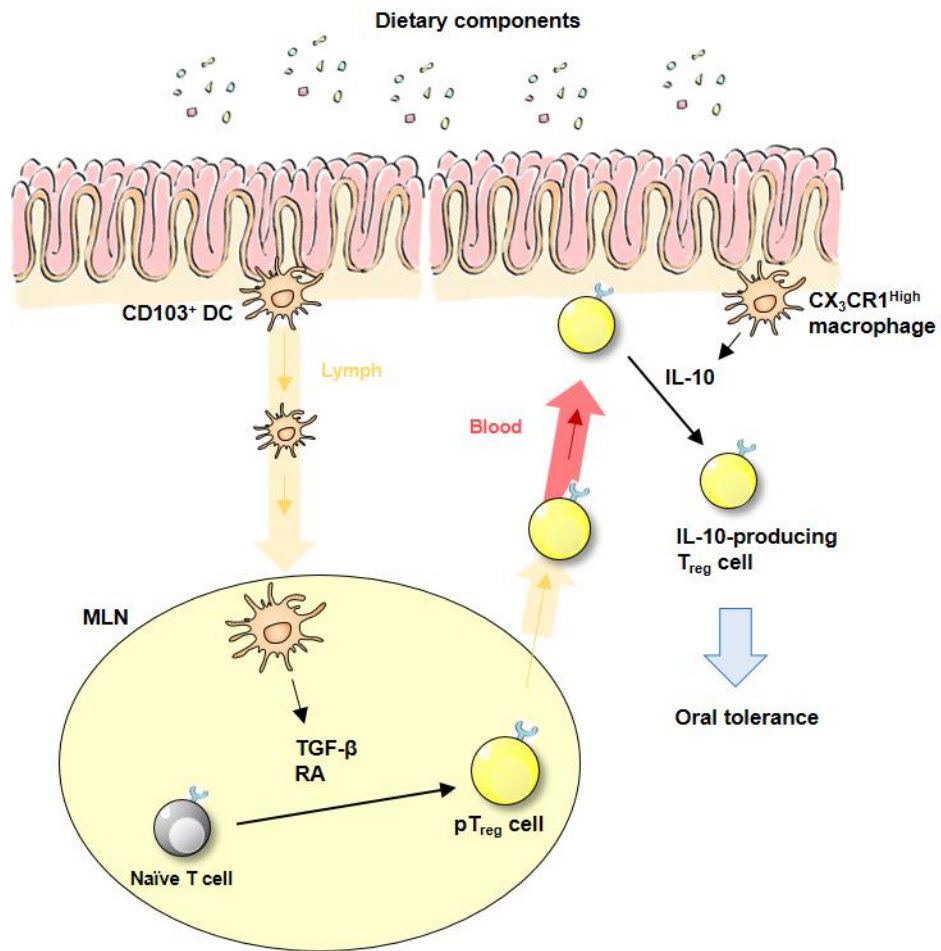


Fig. 1-7 Oral tolerance induction

§1.4 Antibody Production by B Cells

§1.4.1 Antibodies also have antigen-specificity through genetic diversification.

As well as T cells, B cells express Ag-specific receptors which are processed through somatic gene rearrangement, named B cell receptors (BCRs). BCRs are secreted as Abs from terminally differentiated B cells, named plasma cells. Abs are composed of two immunoglobulin (Ig) heavy chains and two Ig light chains connected by disulphide bonds (99, 100). Both chains have variable and constant regions, and the variable regions of two chains recognize Ags. The variable region of the Ig chains are genetically diversified by VDJ recombination like TCRs (101–104). Thus, each Ab binds to its specific Ag. Further, BCR genes are processed by somatic manipulation, CSR and SHM, after the VDJ recombination. CSR occurs in constant regions of heavy chains and leads to a functional switching whereas SHM occurs in variable regions of both chains and increases affinity of the Ab to its Ag. These processes are induced by a common enzyme, activation-induced cytidine deaminase (AID). This enzyme mediates conversion of cytidine to uridine, which in turn leads to DNA repair process resulting in genetic recombination and mutation. Detailed molecular mechanism underlying AID activity is reviewed in elsewhere (105, 106).

§1.4.2 Class-switch recombination results in distinct immunoglobulin-class antibodies with functional difference.

The constant regions of Ig heavy chain has several classes. Available classes are somewhat different between species. Humans have IgA1, IgA2, IgD, IgE, IgG1, IgG2, IgG3, IgG4, and IgM whereas mice have IgA, IgD, IgE, IgG1, IgG2a, IgG2b, IgG3, and IgM (106, 107). These classes are encoded by Ig gene exons, such as C α , C δ , C ϵ , C γ , and C μ . The exons encoding Ig classes are sequentially ordered, starting with C μ to downstream other exons (**Fig. 1-8**). Upstream of C α , C ϵ , C γ , and C μ contains switch regions, namely S α , S ϵ , S γ , and S μ respectively whereas C δ exon exists in immediate downstream of C μ without S region. Such ordered exons play a pivotal role in Ig class expression on B cells. Naïve B cells express IgD and IgM as BCRs, which are encoded by upstream C δ and C μ genes, respectively. These genes of Ig class is switched to other classes through recombination between S μ and one of other S regions by AID-dependent mechanism. The recombination results in replacement of targeted C region to immediate downstream of variable region with depletion of any other upstream C regions including C δ and C μ genes. This leads to transcription of variable region followed by the switched C region, i.e. switched Ig class Ab with the same specificity as pre-CSR IgD and IgM. Target class of CSR is controlled by environmental factors around the B cell.

Class-switched Abs, such as IgA, IgE, and IgGs, have specific effector functions and localization properties (108). For example, IgE constant regions are recognized by Fc ϵ receptors (Fc ϵ Rs) on mast cells leading to secretion of inflammatory mediators in allergic pathology. Meanwhile, constant regions of IgGs highly activate the complementary system, which helps, e.g., phagocytosis of macrophages.

Whereas blood is rich in IgG, mucosal sites, including the intestine, contain large quantity of IgA. These IgA are produced by plasma cells in the LP and are secreted into the lumen across a epithelial layer through

transcytosis (109). Such secretory IgA are mainly in dimeric form. These properties of mucosal IgA are due to constant region property. In dimeric IgA produced by plasma cells, constant regions of two IgA monomers are linked to each other through joining protein called J chain (110). Such IgA-J chain-IgA complex is taken up by epithelial cells through poly Ig receptors expressed on basal side of the epithelial cells (111). The polymeric Ig receptors bind to IgA dimers through the J chain. Subsequently, IgA dimer is secreted into luminal side with an ectodomain fragment of polymeric Ig receptor called secretory component. Secreted IgA functions to neutralize pathogens and regulate commensal bacteria (discussed in §1.4.4).

Many factors in the intestine are involved in CSR to IgA. Early studies have revealed that TGF- β induce IgA production from B cells (112, 113). This factor directly stimulate B cells through TGF- β receptor to express I α -S α -C α mRNA, which is required for CSR to IgA (114–116). The effect of TGF- β is supported by IL-21 (116–119). In addition, TNF superfamily members, B cell activating factor (BAFF) and a proliferation-inducing ligand (APRIL), are involved in IgA CSR (120–124).

The site for IgA CSR in the intestine are probably lymphoid tissues, such as GALT and MLNs, although it is still in controversy (107, 125). Some groups have reported IgA CSR in LP as well as GALT (126–128). In contrast, other groups have reported that IgA CSR is limited in lymphoid tissues including PPs and isolated lymphoid follicles (129–132). This discrepancy may be due to difficulty in isolating LP cells without lymphoid tissue contamination. It has been reported that careful exclusion of lymphoid contamination resulted in no CSR detection in LP (131, 132). Further, B cell proliferation, which is required for CSR, is not detected in the intestinal LP (125).

§1.4.3 Somatic hyper-mutation increase affinity of antibodies.

Whereas CSR occurs in constant regions of Abs, SHM induces mutation in gene loci encoding variable regions, which determine specificity of Abs (**Fig. 1-9A**). Somatic hyper-mutation is induced by AID-dependent conversion of cytidine to uridine and subsequent error-prone DNA repair (105, 106). The gene mutation in variable regions occurs with frequency of 10^{-4} - 10^{-3} per base (133). Accumulation of SHM-induced mutation is involved in improving the affinity of Ab to its Ag, called affinity maturation. This process takes place in GCs in B cell follicles of secondary lymphoid tissues. In the steady state, GC structure is not observed in the systemic immune system. Upon infection, the structure is formed dynamically in an Ag-dependent manner (134, 135).

The process of the GC reaction is a miniature of Darwinian evolution, characterized by random mutation and subsequent selection of high affinity B cells (**Fig. 1-9B**). Structure of GCs includes two regions called light zone and dark zone. B cells in the GCs circulate these two regions in affinity maturation process. In the light zone, high affinity Ab-expressing B cells are selected and SHM is induced whereas the dark zone is a site for proliferation of the selected B cells (136). The proliferated B cells are processed by the selection, and some of the selected cells recirculate into the dark zone and the others emigrate from the GC to differentiate memory B cells or plasma cells.

Light zones contain two characteristic cell types involved in affinity maturation, i.e. T_{FH} cells and FDCs. These cells play critical roles in affinity-dependent B cell selection. B cells in the light zone capture Ags presented on FDCs in an affinity-dependent manner (137, 138). The number of Ags on FDCs is limited, and thus B cells with

low affinity BCRs cannot capture the Ags. Subsequently, the Ag-bearing B cells present the Ags to T_{FH} cells. In response to the Ag-presentation, T_{FH} cells offer help signals to the B cells, such as CD40 ligand, IL-21, and IL-4, which induce SHM in BCR of the B cell. Therefore, B cells with Ags, which is due to their high affinity BCRs, can receive the help signals from T_{FH} cells and proliferate in a dark zone (136). B cells experience this dynamical process repeatedly, which results in generating and selecting B cells producing high affinity Abs.

§1.4.4 Host-microbe interaction through immunoglobulin A in the intestine.

The intestine is frequently exposed to harmful pathogenic microbes invading with foods. To prevent infection of such microbes, the intestinal immune system intensely secretes IgA Abs into the lumen. Indeed, polymeric Ig receptor-deficient mice is more susceptible to *Salmonella* infection in the intestine (139). Further, IgA-deficiency in human may causes gastroenteritis and *Helicobacter* infection (140).

In addition to pathogenic microbes, $>10^{15}$ non-harmful commensal bacteria, including $>10^3$ species, exist in the intestinal lumen (141, 142). Further, some of them inhabit the inside of GALTs (143). Dysregulation of the intestinal microbiota, called dysbiosis, has harmful effects on the host, such as inflammatory bowel diseases and probably extra-intestinal diseases (1, 144). Thus, the intestinal immune system should precisely regulate the microbiota. This regulation is largely dependent on IgA functions (125, 145). Commensal microbes in the intestine are coated with IgA (146, 147). In some case, IgA binding causes changes in gene expression of the bacteria (148). Further, deficiency in AID, which results in defect of CSR and SHM, causes dysbiosis (149, 150). These findings suggest that IgA is required for appropriate regulation of the intestinal microbiota.

The intestinal IgA conceptually contains Ag-specific ‘classical high-affinity IgA’ and poly-reactive ‘natural low-affinity IgA’ (125). In parallel, IgA can be induced by two distinct pathways, namely T cell-dependent and -independent pathways (107). T cell-dependent pathway literally means IgA induction through T cell help, especially from T_{FH} cells in GCs, whereas T cell-independent pathway is IgA induction without T cells and GCs. Sequencing experiments have revealed that most of human intestinal plasma cells have highly mutated variable region gene probably processed by SHM, which means most IgA Abs in the intestine are induced through T cell-dependent pathway in GCs (151, 152). The number of mutation in intestinal plasma cells in mice has been reported to be much lower (153). However, experiments usually use laboratory-reared mice in a strictly-controlled environment with specific pathogen-free (SPF) equipment, controlled and constant diets and drinking water. Such sanitary condition may effect on the homeostasis of intestinal immune system. Indeed, compared with laboratory-reared mice, wild-living mice have larger GCs in GALT, which suggests that, in wild-living mice, GC-dependent highly mutated IgA probably plays more dominant roles in the intestine like humans (107). In addition, AID^{G23S}-mutated mice, which lack SHM but not CSR activity of AID, spontaneously develop dysbiosis (154). Collectively, SHM-dependent highly-mutated IgA is important in regulation of the intestinal microbes.

As mentioned above, IgA is conceptually classified into Ag-specific ‘classical IgA’ and poly-reactive ‘natural IgA’. One plausible explanation for entities of these conceptual IgA groups is that classical IgA is T cell-dependent and natural one is T cell-independent. Considering a dominant role of T cell-dependent pathway as discussed above, classical IgA, recognizing specific Ags, is abundant in the intestine. However, this is against the

observation that most bacteria are coated by IgA even in the human intestine (146, 147). Such discrepancy could be explained by Ag-binding through other than variable region and cross-reactivity of Abs (125). Secretory IgA can bind to many bacteria through secretory components mediated by modulated carbohydrate moiety (155, 156). Meanwhile, the intestinal IgA contains poly-reactive Abs, which can recognize several Ags (157, 158). Poly-reactive Abs probably recognize a common Ag among microbes. Such Abs can be selected and matured through sequential exposure to several microbes in GCs (159). In the intestine, it has been reported that individual B cells circulate into several distinct GCs repeatedly (160). This process may contribute to the poly-reactive IgA through SHM-dependent pathway. These mechanisms enable the intestinal T cell-dependent IgA to recognize broad spectrum of bacteria.

To regulate the intestinal microbes, the immune system should constantly survey microbial contents in the intestine. Therefore, GALT and MLN take up Ags from the lumen and induce IgA (22). Especially, GALT constantly includes GC structure, which is dependent on microbiota (107, 149, 161). The microbial composition is gradually changing along the intestinal parts, i.e. from duodenum to colon, a diversity and the number of bacteria is explosively increasing (162). Further, dominant microbial species also differ among the regions. Corresponding to such microbial difference, the intestine changes some of its properties among regions. One of the differences is in mucus layer (163). The small intestine has thinner mono-layer whereas the large intestine has thick two mucus layers. An inner layer of the large intestinal mucosa excludes bacteria (164). Another difference is in IgA repertoire. The small and large intestines have different IgA repertoire (153). This may reflect the microbial difference. Recently, it has been reported that plasma cells in these sites could have different sources. B cells in PPs migrate to the small intestine, whereas CaEP B cells migrate to the large intestine (165).

§1.4.5 Short summary.

As well as T cells, B cells have a receptor, which is genetically rearranged, with diverse Ag-specificity. This BCR is finally secreted as Abs. B cells pass through specific processes, namely CSR and SHM. CSR manipulates effector function of Abs, and SHM improves Ab affinity to its Ags. These processes are probably located in lymphoid tissues and their GCs depending on help from T_{FH} cells. The intestine is rich in secretory IgA in the lumen, which not only prevents infection but also regulates the commensal microbiota. The intestinal IgA is probably induced by GC reactions located in GALTs.

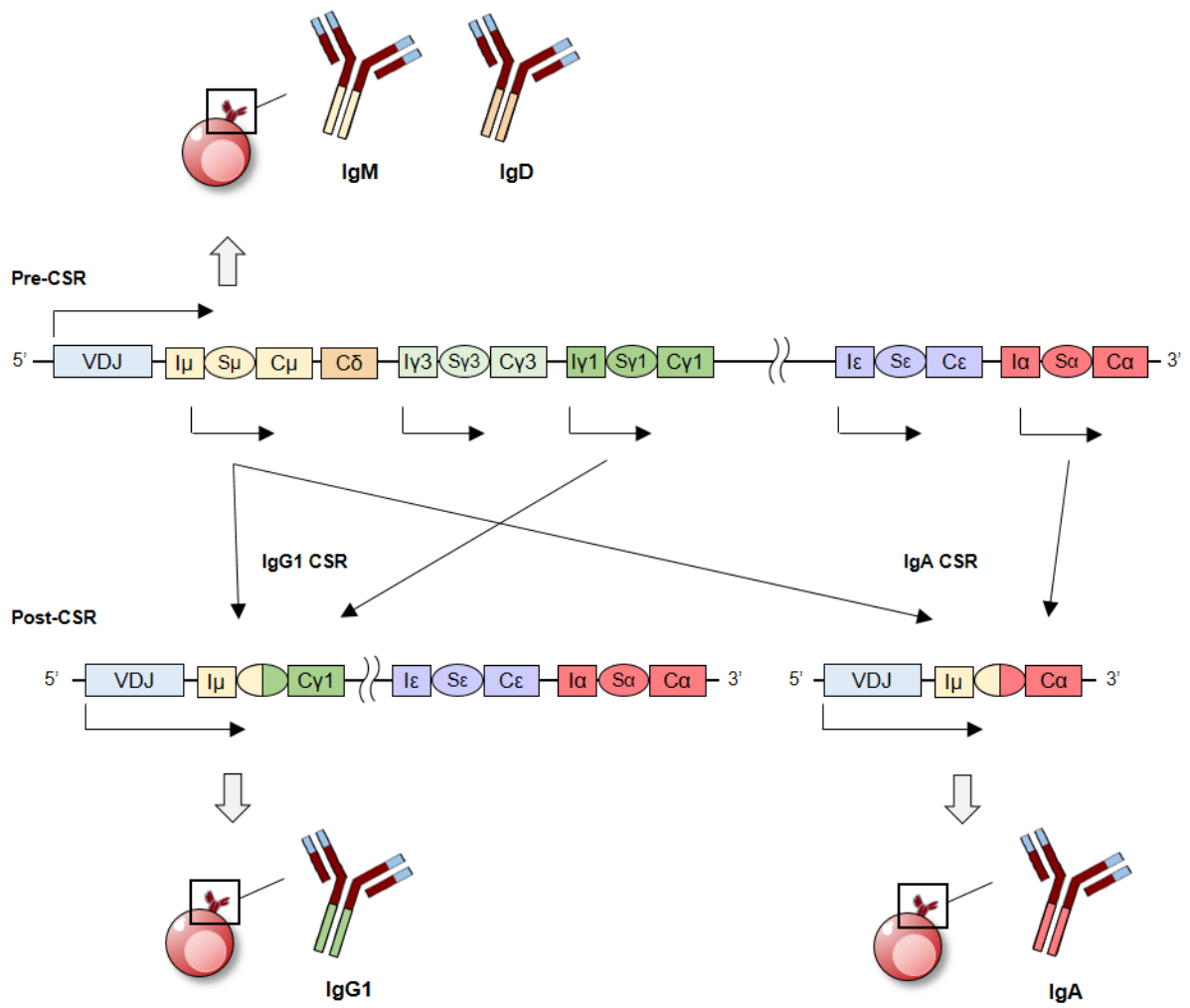


Fig. 1-8 Class-switch recombination

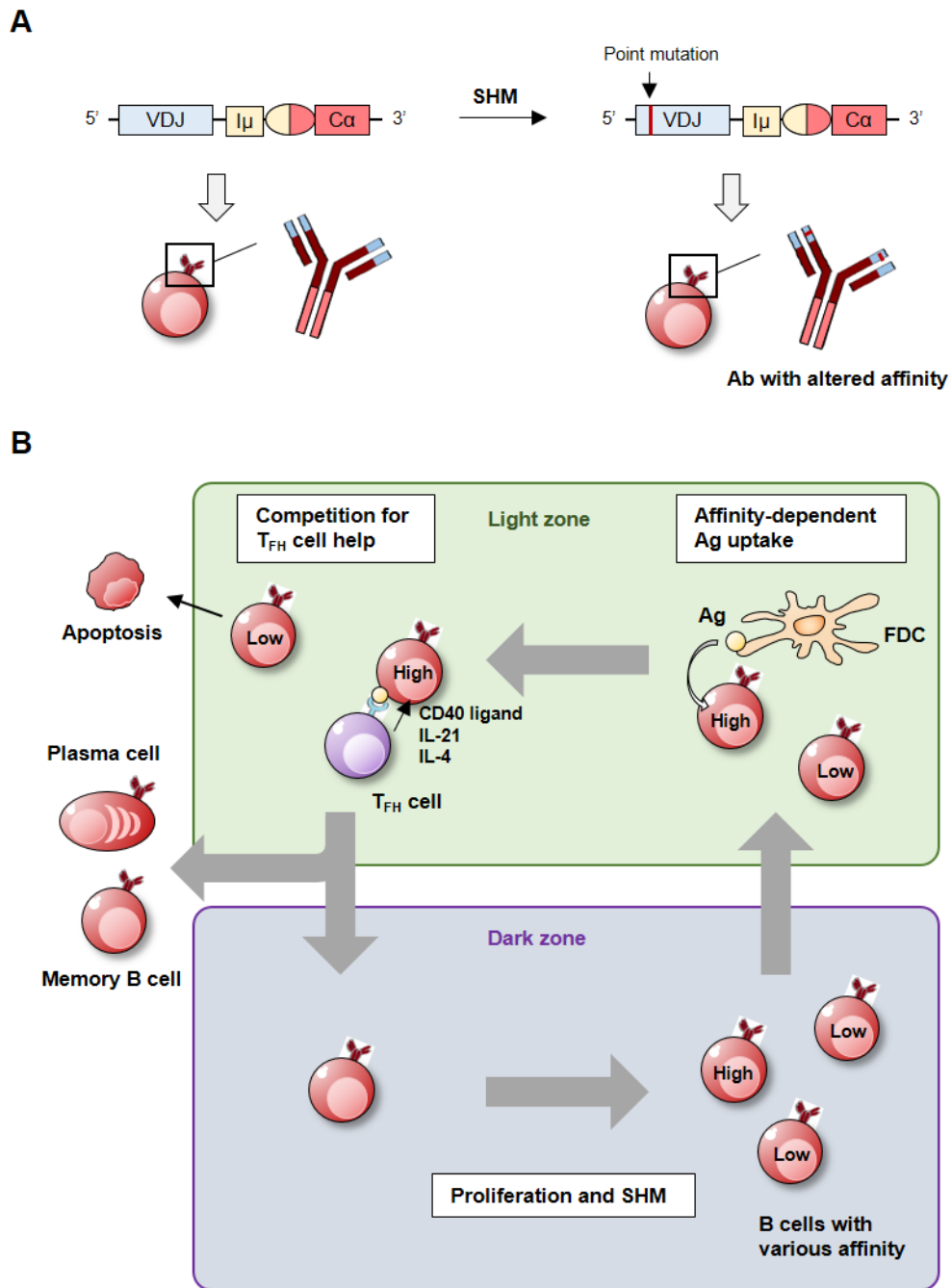


Fig. 1-9 Affinity maturation

A. SHM process induces a point mutation in VDJ region of Ab, leading to alteration of affinity.
 B. Conceptual description of affinity maturation in GCs.

§1.5 Priming Immune Responses by Dendritic Cells

§1.5.1 Dendritic cells initiate antigen-specific immune responses.

As discussed above, T cells and B cells play pivotal roles in Ag-specific immune responses. These cells are activated in lymphoid tissues. Therefore, to prime immune responses, Ags should be carried into lymphoid tissues from periphery and be presented to T cells through peptide-MHC-TCR interaction. Such immune priming is dependent on Ag-presenting cells, especially DCs. A kind of DCs, Langerhans cells in skin, was firstly observed by Paul Langerhans in the 19th century (166). At the time, the cells were considered to have functions in the nerve system. In 1973, Ralph Steinmann identified DCs in lymphoid tissues (167, 168). Later, Steinmann *et al.* have reported that DCs can highly prime immune responses (169). Then, other innumerable studies have revealed that DCs are professional Ag-presenting cells.

Generally, DCs capture Ags in periphery, migrate into LNs, and then present the Ags to T cells in the LNs (**Fig. 1-10**). To prime immune responses efficiently, DCs are equipped with several characteristic features. They highly express MHC II molecules on their surface, which may contribute to high potency to priming T cells. In addition, DCs can retain phagocytosed Ags for a long time because they have proteases of low activity (170). Further, DCs can present exogenous Ags on MHC I to CD8⁺ T cells, called cross-presentation as reviewed in elsewhere (171).

Mononuclear phagocytes includes DCs and macrophages. These cells have marked heterogeneity and are classified into detailed subsets using expression of surface marker molecules (172). Although DCs and macrophages had been historically considered as distinctive cell types, it has been revealed that these cells have some overlaps in phenotypic and functional properties (172–174). There have been proposed a nomenclature based on the ontogeny (174). In the present studies, the author uses the nomenclature as much as possible.

The intestine harbors several types of DCs, usually classified based on expression of CD11b, CD103, CD8 α , and other markers (175, 176). Subset composition of DCs are locally different throughout the intestine. For example, small intestinal LP contains CD11b⁺CD103⁺CX₃CR1⁻ and CD11b⁺CD103⁻CX₃CR1⁺ subsets whereas PPs contain CD11b⁻CD103⁺ and CD11b⁺CD103⁻ subsets (177, 178).

§1.5.2 Dendritic cells can initiate a suitable immune response sensing environmental factors.

To induce a suitable immune response to the environment, DCs can receive the environmental factors. Such environmental sensing is mediated, at least partly, by innate immune receptors, such as Toll-like receptors (TLRs), RIG-I-like receptors, and NOD-like receptors. These receptors recognize ligands conserved among many microbes, called microbe-associate molecular patterns. Among the receptors, TLRs, including several subtypes, are located on membranes and recognize ligands derived from microbes existing in topologically outer of the cells, *i.e.* ligands out of the plasma membrane and in the lysosomes. In contrast, RIG-I-like receptors and NOD-like receptors are in cytoplasm to recognize intracellular bacteria and viruses, and are reviewed in elsewhere (179, 180).

Many studies have focused on TLRs from identification in the late 1990s (181). This type of innate

immune receptors are expressed on various cell types; DCs, macrophages, B cells, T cells, epithelial cells, and so on. As mentioned above, TLRs include several subtypes, TLR1 - TLR11 (182). Especially, TLR1 - TLR9 were identified earlier and thus have been well studied. These receptor molecules form homo- or hetero-dimers to sense their specific ligands (**Table 1-1**). Among TLRs, TLR2/1, 2/6, 4, and 5 are located in plasma membrane and recognize surface molecules of microbes whereas TLR3, 7, 8, and 9 are in endosome membrane and recognize nucleic acids. All subtypes consist of three domains, namely ligand-recognizing extracellular domain, transmembrane domain, and signal-transducing intracellular domain (183). The extracellular domains are different among the subtypes to recognize different ligands as shown in **Table 1-1** (184–190). In contrast to the extracellular domain, the intracellular domains of TLR family are relatively conserved to transduce signals to shared adaptor molecules, MyD88 and/or TRIF (191–198). These signals result in activation of NF- κ B, MAP kinases, and IRFs.

In response to TLR stimulation, DCs are activated to prime T cell responses. Such activated DCs highly express MHC II and co-stimulatory molecules such as CD80 and CD86. Further, TLR stimulation has DCs secrete cytokines, such as IL-6, IL-12, and IL-23, to bias differentiation of T cell subsets (199). To control a suitable T cell differentiation, TLR-induced cytokines should change according to environmental cues. For example, IFN- γ and CD40 stimulation enhance TLR-induced IL-12 whereas IL-10, thymic stromal lymphopoietin (TSLP), and prostaglandin E2 have been reported to suppress TLR-induced IL-12 (200–205). In addition to the environmental factors, TLR subtypes could affect subsequent responses. It has been reported that specific response can be induced by specific TLR subtype, such as TLR2/1, but not other TLRs, induces RALDH2 gene expression whereas TLR9, but not others, induces IL-12 production (206, 207). Collectively, in response to TLR stimulation, DCs efficiently present Ags to Ag-specific T cells under specific cytokine milieu resulting in a suitable T cell responses to the environment.

§1.5.3 The intestinal dendritic cells regulate the intestinal immune system through their characteristic properties.

To regulate the intestinal immune system, the intestinal DCs have several characteristics. Especially in T cell responses, the intestinal CD103⁺ DCs tend to induce T_{reg} cells and T_H17 cells (52, 208–215). This is largely dependent on TGF- β , which are produced and activated by the DCs. In addition, T_{reg} cells are also induced through RA production by DCs. The intestinal DCs, especially CD103⁺ DCs, highly express RALDH2 (208, 216). This also enhances T cell homing to the intestine through induction of CCR9 and $\alpha_4\beta_7$ expression on T cells (208, 212, 217, 218). These properties can be obtained by the environmental factors. For example, stimulation on TLR2/1, which could occur frequently in the intestine from commensal bacteria, induces RALDH2 gene expression in DCs (206). Further, mucus components enhance TGF- β production and RALDH activity in the intestinal DCs (219). The intestinal DCs regulate T cell responses through these characteristic properties.

§1.5.4 The intestinal dendritic cells capture antigens from the lumen.

To prime T cell responses, DCs should take up Ags. At the infection, DCs can contact with invaded pathogens in

the tissue and blood. In contrast, luminal bacteria and foods are separated by epithelial layer in the steady state intestine. Thus, the intestinal DCs have some specialized pathways to obtain the luminal Ags (24).

One characteristic pathway is through GALT (see **Fig. 1-5**). These tissues are more accessible by luminal Ags than other sites in the intestine due to several properties of epithelial cells on them (24, 220). The epithelium has thinner mucus, expresses less polymeric Ig receptors resulting in less secretory IgA around the tissues, secretes less anti-microbial peptides, and contains specialized cells transporting Ags from lumen, named M cells. M cells take up Ags through transcytosis. The transcytosed Ags are internalized by antigen-presenting cells under the M cells. Further, PP DCs have been reported to obtain Ags directly from the lumen extending their dendrites across M cells (221).

As well as in GALT, Ags are obtained by DCs in the intestinal LP through several pathways. Goblet cells, a kind of epithelial cells, hand over Ags to CD103⁺ DCs (222). Further, CD103⁺ DCs can obtain Ags directly from the lumen through their dendrites (223). CX₃CR1⁺ macrophages can also internalize the luminal Ags through trans-epithelial dendrites (224). CX₃CR1⁺ macrophages hand over obtained Ags to CD103⁺ DCs (225). Through these pathways, DCs obtain Ags from the intestinal lumen and present the Ags to T cells in lymphoid tissues.

§1.5.5 Antigen-bearing dendritic cells migrate to lymphoid tissues from periphery.

To present Ags efficiently to naïve T cells, Ag-bearing DCs should migrate to lymphoid tissues. From the small and large intestinal LP, DCs mainly migrate to T cell zone of MLNs (20, 226). Main migratory DCs have CD103⁺ phenotype (217). But migration of CD103⁻ subsets to MLNs are also detected (227, 228). In PPs, DCs migrate to T cell zone in the PP from region under epithelium called sub-epithelium dome (229). In addition, PP DCs also migrate to MLNs (230). In all of these reports, such migration is dependent on CCR7 expression on the DCs. This chemokine receptor induces migration toward chemokines, CCL19 and CCL21, which are secreted from T cell zone stromal cells, fibroblastic reticular cells (231, 232). Naïve T cells also express CCR7 and migrate toward such chemokines (18). Thus, both Ag-bearing DCs and naïve T cells migrate toward the same chemokines. This mediates co-localization of these cells for efficient Ag-presentation from DCs to T cells.

In T cell zone of lymphoid tissues, fibroblastic reticular cells organize a scaffold network, along which DCs and T cells can move (233, 234). In the T cell zone DCs are in close contact with each other (235). In some case, migratory DCs hand over Ags obtained in periphery to LN resident subsets (236). Naïve T cells move to search on DCs for MHC presenting their specific Ags (237). Once T cells contact with the Ag-bearing DCs, they decrease their mobility and contact with the DCs for long time to receive signals. Then, activated T cells re-circulate into blood and migrate to peripheral tissues depending on expression of homing receptors.

§1.5.6 Short summary

Mononuclear phagocytes, including DCs and macrophages, can be classified into several subsets based on surface markers. In the intestine, CD103⁺ DCs play a pivotal role in regulating the intestine-specific immune responses, such as T_{reg} cells and T_H17 cells induction. These properties are largely dependent on TGF- β and RA. The intestinal

DCs capture the luminal Ags through direct or indirect pathways and migrate to T cell zone in lymphoid tissues in a CCR7-dependent manner and present the Ags to naïve T cells there.

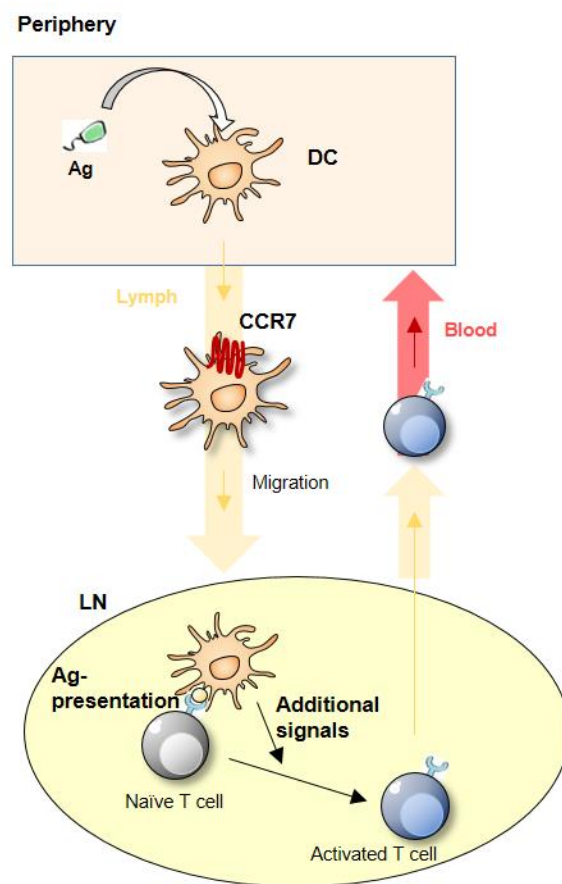


Fig. 1-10 DCs in the immune responses

Table 1-1 Toll-like receptors

TLR	Ligands
TLR2/1, TLR2/6	Lipopeptides
TLR3	Double-stranded RNA
TLR4	Lipopolysaccharides
TLR5	Flagellin
TLR7, TLR8	Single-stranded RNA
TLR9	Non-methylated CpG DNA

§1.6 Innate Lymphoid Cells in Mucosal Immune System

§1.6.1 Innate lymphoid cells are newly established immune cells.

One of the most remarkable current topics in immunology is establishment of a new lymphocyte lineage – innate lymphoid cells (ILCs). This cell type is now defined as lymphoid cells, i.e. derived from a common lymphoid progenitor, expressing no lineage markers of other immune cells including T cells, B cells, DCs, macrophages and so on (238–240)(**Table 1-2**). In 2010, three independent studies have reported that lineage markers[−] (Lin.[−]) lymphoid cells in various tissues secrete T_H2 cytokines such as IL-5 and IL-13 (241–243). These discoveries were followed by many studies which have investigated in properties of Lin.[−] lymphoid cells, such as developmental processes and physiological functions. Then, a concept of ILCs has been generally accepted. In addition to newly identified cells, classically known Lin.[−] cells such as natural killer (NK) cells and lymphoid tissue inducer (LTi) cells are also categorized into ILCs.

ILCs are classified into several subsets based on transcription factor dependency, cytokine production, and effector function (**Fig. 1-11**). As mentioned below, ILCs have many similarities to T cells in transcription factors and cytokines, and classification of ILC subsets mirrors that of T cell subsets resulting in one cytotoxic subset and three groups of helper type subsets (239). The cytotoxic one is NK cells, which is a counterpart of CD8⁺ T cells. The other three groups are named as group 1 ILC, group 2 ILC, and group 3 ILC (ILC1, ILC2, and ILC3). Roughly, ILC1s express T-bet and produce IFN- γ like T_H1 cells, ILC2s express GATA3 and produce IL-5 and IL-13 like T_H2 cells, and ILC3s express ROR γ t and produce IL-22 like T_H17 cells. Although such similarities, ILCs express no Ag-specific receptor like TCRs and BCRs. Instead, ILCs express cytokine receptors, such as receptors for IL-2, IL-7, IL-12, IL-23, IL-25, IL-33 and so on. Distinct ILC groups express different patterns of such receptors and regulate immune responses through cytokine secretion according to the environment. Further, some ILCs express MHC II and could directly regulate T cell responses (50, 244–246).

§1.6.2 Functions of innate lymphoid cells in health and disease.

Although ILCs are very rare population, <1% of whole lymphocytes, they are largely involved in various physiological functions and pathological conditions. In response to viral infection, NK cells protect the host by killing the infected cells through granzyme and perforin and by secreting IFN- γ (247). Protective responses to infection are also regulated by other ILCs. ILC1s highly produce IFN- γ and TNF to provide protection from infection (248, 249). Such ILC1s exist in intraepithelial region and LP in the intestine. ILC3s produce IL-22 in response to inflammatory cytokines such as IL-1 β and IL-23 (250–253). IL-22 from ILC3s is in turn received by intestinal epithelial cells resulting in secretion of antimicrobial peptide and fucosylation of the epithelial cells to prevent infection of pathogens (254–257). Further, a subset of ILC3s can be converted to ILC1-like phenotype such as T-bet⁺ and producing IFN- γ , which contributes to protecting the host from infection (258–260). These ILC1s and ILC3s also exacerbate inflammation in some contexts (248, 252, 258, 260–262).

Whereas ILC1s and ILC3s protect against viral and bacterial infection, ILC2s contribute to expulsion of

helminths through T_H2 cytokines (241–243). ILC2s require GATA3 expression for their maintenance and function although this transcription factor is indispensable for development of all ILC subsets (263–265). Many studies have revealed that ILC2s can highly produce IL-5, IL-9, and IL-13 in response to IL-2, IL-4, IL-25, IL-33, TSLP, and TLA1, a TNF family member (264, 266–272). These cytokines secreted from ILC2s induce mucus production and tissue repair in the lung and intestine, resulting in helminth expulsion. Meanwhile, ILC2s exacerbate allergic pathologies through T_H2 cytokine production in the lung and skin (266, 269, 270, 273–275).

In addition to such immunological functions, ILCs are also involved in regulation of non-immunological homeostasis. LT_i cells, a subset of ILC3s, are required for organization and remodeling of lymphoid tissues (276–279). ILC2s also restore epithelium after infection in the lung through amphiregulin, an epidermal growth factor, production (280). In addition, ILC2s have been reported to be involved in metabolic regulation in adipose tissues. IL-5 and IL-13 secreted from ILC2s promote eosinophil accumulation and subsequent macrophage activation in an adipose tissue resulting in protection from obesity (281–283). ILC2s also reduce obesity through production of a peptide which promotes adipose tissue beiging (284). Further, ILC2s can sense nutrient conditions, such as vitamin A deficiency and malnutrition (285, 286). Vitamin A deficiency induces ILC2 increase and ILC3 decrease. Dietary components also affect ILC3 homeostasis through an aryl hydrocarbon receptor (AhR) (287).

§1.6.3 Innate lymphoid cells regulate the host-commensal interaction.

In the intestine, ILCs participate in homeostatic control of the interaction between the host and commensal microbiota. Especially, IL-22 production by ILC3s are largely involved in such regulation. As mentioned above, IL-22 enhance antimicrobial peptides secretion from intestinal epithelial cells (254–256). Such antimicrobial peptides probably suppresses overgrowth of commensal microbes. IL-22 from ILC3s also prevents PP-resident commensal bacteria from spreading systemically and confines the bacteria to the site (288). Further, ILC3-derived IL-22 promotes fucosylation on luminal side of intestinal epithelial cells, which protect the host from infection (257). Fucosylated moiety on intestinal epithelial cells also functions as an environmental niche for commensal bacteria (289). Thus, such ILC3-mediated fucosylation may promote commensal colonization. Conversely, ILC3s are regulated by the intestinal microbiota. The microbiota reduces IL-22 production from ILC3s indirectly through T cell responses (290, 291). Further, aryl hydrocarbon receptor-deficient ILC3s have impaired IL-22 production, which suggests that food components could modulate commensal bacteria through ILC3 function (287, 292).

ILC3s can regulate commensal bacteria also through Ag-presentation to T cells. ILC3s express MHC II and present commensal bacteria-derived Ags to T cells (50, 245, 246). ILC3s in the intestinal LP inhibits T cell responses through the Ag-presentation. Such suppression is due to the absence of co-stimulatory molecules on the ILCs, and may contribute to selection of commensal bacteria (246). The inhibitory state of ILC3s can be reversed in some context through IL-1 β (293).

Some studies have revealed that ILCs regulate IgA production. ILC3s induce IgA production through lymphotoxins activating T cell-dependent and -independent pathways (294). In addition, SPL ILC3s enhance IgA production through BAFF, CD40 ligand, and Notch ligand (295). Further, IL-5, highly produced by ILC2s, promotes B cell differentiation to Ab-secreting cells (28). Thus, ILC2s could enhance IgA secretion (241).

§1.6.4 Short summary

Lin⁻ lymphoid cells, ILCs, are a newly established cell type and have been intensely studied in recent years. These cells express no Ag-specific receptors and secrete various cytokines in response to environmental factors. ILCs are further classified into several subsets, i.e. NK cells, ILC1s, ILC2s, and ILC3s. Each subsets exhibit similarities to T cell subsets in transcription factor dependency and cytokine production. ILCs are involved in a broad spectrum of functions including immunological and non-immunological ones. In the intestine, ILCs regulate homeostasis in the host-commensal interaction through many pathways.

Table 1-2 Lineage markers

Molecules	Lineages
B220	B cell
CD3	T cell
CD4	T cell
CD5	B cell, T cell
CD8	T cell
CD11b	Monocyte
CD11c	Monocyte
CD19	B cell
FcεRIα	Mast cell
GR1	Granulocyte
TER119	Erythrocyte

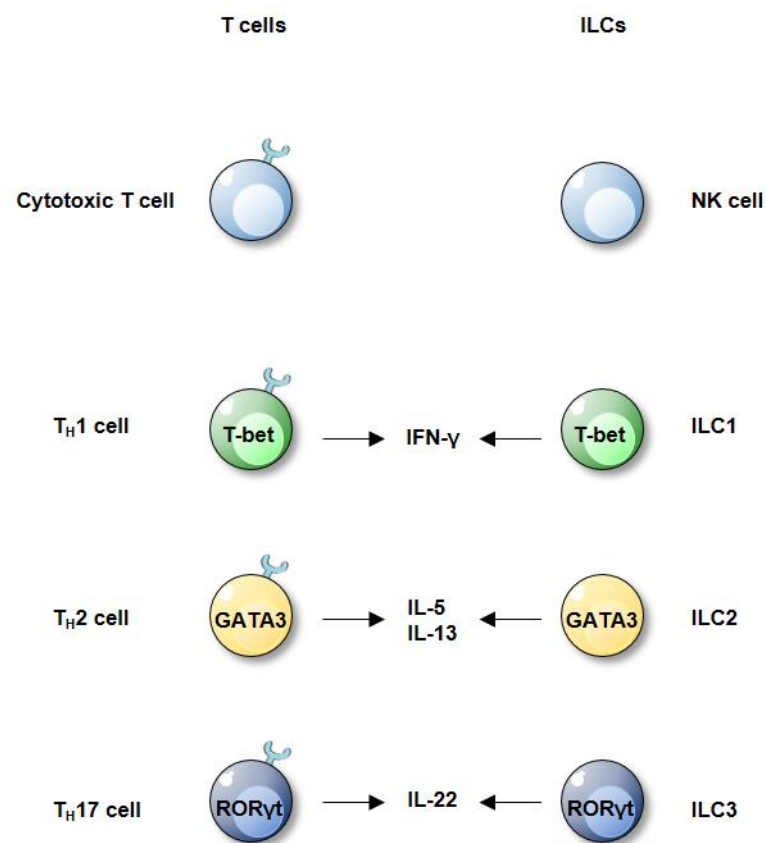


Fig. 1-11 ILC classification

§1.7 Summary

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Chapter 2

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Chapter 3

§3.1 Introduction

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§3.2 Materials and Methods

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§3.3 Results

§3.3.1

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§3.3.3, 3.3.4, 3.3.5

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Chapter 4

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Chapter 5

Overall Discussion

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Acknowledgements

本研究を進めるにあたり、学生の自立・自発的な研究を促して頂いたと同時に、要所での確に温かくご指導くださいました、東京大学大学院農学生命科学研究科食の安全研究センター免疫制御研究室の八村 敏志 准教授に心から感謝致します。

研究や進路のことなど、たくさんのためになるご助言を頂きました、東京大学大学院農学生命科学研究科食の安全研究センター免疫制御研究室 足立 はるよ 特任助教に心から感謝致します。

ILC 研究において、鋭く的確なご意見を頂くなど、とてもお世話になりました、国立感染症研究所 高橋 宜聖 主任研究員に深く感謝致します。

大腸免疫系の研究の基礎をお教え頂きました、日本大学生物資源科学部食品生命学科 細野 朗 教授に深く感謝いたします。

無菌動物をご供与頂き、またそれに関連することなども丁寧にお教えいただきました、東京大学大学院農学生命科学研究科獣医公衆衛生学研究室 平山 和宏 准教授に深く感謝いたします。

合同ゼミなどで鋭いご意見を頂き、大変お世話になりました、東京大学大学院農学生命科学研究科食糧化学研究室 戸塚 護 准教授に深く感謝いたします。

実験にあたり、実験器具をお貸し頂いた東京大学大学院農学生命科学研究科食品生化学研究室 佐藤 隆一郎 教授に深く感謝致します。

研究生活を共にし、とてもお世話になりました、免疫制御研究室の皆様は心より感謝致します。

合同ゼミなどでとても良い刺激を頂きました、食糧化学研究室の皆様は心より感謝致します。
最後に、長い学生生活を様々な面で支えて頂いた家族に深く感謝致します。

2015 年 12 月
上滝 隆太郎