the long-day-dependent and -independent pathways of floral induction (1, 7, 8, 11). Indeed, in contrast to plants that overexpressed only FT or LFY(12), the vegetative phase was bypassed in 35S::FT 35S::LFY plants, which produced a terminal flower immediately upon germination. The only leaves produced by these plants were the first two leaves, which are already initiated in the embryo (Fig. 2, C, E, and I, and Table 1). A less marked effect was seen in 35S::FT 35S:: AP1 plants (Fig. 2C and Table 1), even though 35S:: AP1 plants on their own flowered considerably earlier than did 35S::LFY plants (7, 12-14) (Table 1). The 35S::FT 35S::LFY phenotype was also more severe than that of 35S::AP1 35S::LFY plants (14), indicating that FT does not only induce AP1, which is confirmed by a failure of an apl mutation to suppress early flowering of 35S::FT plants (Table 1).

The deduced FT protein belongs to a small family of Arabidopsis proteins, which includes the TFL1 protein, whose amino acid sequence is more than 50% identical to that of FT (3, 15). FT and TFL1 have opposite effects on flowering. Loss of FT function causes late flowering (4), whereas loss of TFL1 causes early flowering along with the formation of terminal flowers (16). However, FT and TFL1 effects are not entirely mirror images of each other, because 35S::FT plants flower much earlier than tfl1 loss-of-function mutants, particularly under short days, and 35S::TFL1 plants not only flower late, as do ft loss-of-function mutants, but they also show transformation of individual flowers into shootlike structures (17).

To clarify the relation between FT and TFL1, we tested whether FT promotes flowering by eliminating TFL1 activity. 35S::FT tfl1-1 plants flowered even earlier than 35S::FT plants and often formed only a single, terminal flower on the main shoot, indicating that TFL1 is still active in 35S::FT (Table 1 and Fig. 2, A and H). Consistent with this finding, TFL1 was expressed in 35S: FT plants (Fig. 3, C and F). Independent action of FT and TFL1 was likewise evident from the fact that 35S::TFL1 attenuated the early flowering of 35S:: FT, even though the attenuation was modest (Table 1 and Fig. 2A). Together, these observations suggest that FT and TFL1 act at least partially in parallel.

TFL1 mRNA is highly expressed in a small group of shoot meristem cells (15) (Fig. 3F). Using reverse transcriptase polymerase chain reaction (RT-PCR), we detected FT mRNA throughout the aerial part of the plant (Fig. 1B). In situ hybridization revealed no specific concentration of FT transcripts at the shoot apex, suggesting that FT and TFL1 do not have to be expressed in the same pattern to antagonize each other's effects.

FT and TFL1 are related to a membraneassociated mammalian protein that can bind

hydrophobic ligands (18). This protein also gives rise to hippocampal cholinergic neurostimulating peptide (HNCP), which is generated from its precursor by cleavage after amino acid 12 (19). Comparison of the FT and TFL1 sequences (3) with the crystal structure (20, 21)of HCNP precursor, also called phosphatidylethanolamine binding protein (PEBP), revealed several interesting features. The conserved residue Arg¹¹⁹ has been proposed to activate the bond between Leu¹² and Ser¹³ for cleavage of HCNP (20). Arg¹¹⁹ is important for FT function as well, because this residue was changed to histidine in the strong ft-3 allele (Fig. 1A). It has also been proposed that access to the PEBP ligand-binding site is regulated by a COOH-terminal α helix (20, 21). A missense mutation in ft-1 close to the COOH-terminus indicates that this region is critical for FT as well (Fig. 1A).

In summary, FT and TFL1 encode related proteins with opposite effects on flowering. Similarly to FT, its antagonist TFL1 is positively regulated by CO(6), suggesting that the balance between FT and TFL1 activity serves to fine tune the response to floral inductive signals (3). It remains to be determined how far the sequence similarity between FT, TFL1, and mammalian PEBP reflects similar biochemical modes of action.

Note added in proof: Human PEBP was recently shown to be identical to RKIP (Raf kinase inhibitor protein), which regulates the activity of the RAF/MEK/ERK signal transduction pathway (22).

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Organogenic Role of B Lymphocytes in Mucosal Immunity

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Follicle-associated epithelium (FAE) in the intestinal Peyer's patches contains M cells that deliver pathogens to organized lymphoid tissue. Development of Peyer's patches, FAE, and M cells was found to be impaired in mice that had no B cells. Transgenic expression of membrane-bound immunoglobulin M restored B cells and FAE development. The lack of M cells abrogated infection with a milk-borne retrovirus. Thus, in addition to secretion of antibodies and presentation of antigens, B cells are important for organogenesis of the mucosal immune barriers.

The gut-associated lymphoid tissue (GALT) consists of highly organized Peyer's patches (PPs) in the small intestine and intraepithelial lymphocytes (IELs) found throughout the length of the gastrointestinal tract. The intes-

tinal surface of PPs is characterized by the presence of FAE-covering "domes," regions free of intestinal villi (1). M cells are found in these domes, scattered among enterocytes (2). M cells lack microvilli on their apical

surface (hence the term M, denoting microfold or membranous cells) and are able to tunnel pathogens through the cytoplasm to the basal surface, where deep invaginations of their membrane allow close contact with lymphocytes and macrophages (3). In respiratory epithelium, where M cells are also found, they serve as the entrance gates for pathogens such as mycobacteria (4). In vitro, M cells were shown to develop from a human intestinal epithelial cell line under the influence of lymphocytes, and a B cell lymphoma was a stronger converter of epithelial cells into M cells than was a T cell lymphoma (5). Thus, we investigated whether B cells are responsible for the generation of FAE and M cells in vivo and whether B cell deficiency could affect transepithelial transport of an

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Fig. 1. Full development of PPs and FAE is affected in B cell-negative mice and can be restored by transgenic expression of mlgM. Relative to normal B6 mice (A and B), two B cell-deficient mouse stocks analyzed— Igh-6 (C and D) and J_HD (G)—showed reductions in PP size, dome numbers, and dome size. Transgenic expression of mlgM led to development of B cells (H), PPs, and domes (E and F). The inner surface of PPs was photographed in transmitted light using a Wild M10 Stereoscope (Leica) and SPOT charge-coupled device camera (Diagnostic Instruments, Sterling Heights. Michigan). Black rectangle, PP in Igh-6 mouse; black and white arrows, FAE; white rectangle, FAE in Igh-6 mouse. Scale bar for (A), (C), and (E) is shown in (A); bar for (B), (D), and (F) is shown in (B). Cryostat sections of PPs from J_HD (G) and transgenic migM (H) mice were stained with fluorescein isothiocvanate-



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enterally transmitted retroviral pathogen.

We examined knockout (KO) mice with targeted mutations that lack specific lymphocyte subsets (6) for abnormalities in PP and FAE generation. The absence of B cells, due to KO of either the µ membrane segment (Igh-6) or J_H segments of immunoglobulin (Ig) genes (J_HD) , caused a diminution of numbers of detectable PPs (Table 1). In contrast, mice deficient in either $\alpha\beta$ T cells [T cell receptor (TCR) β KO] or $\gamma\delta$ T cells (TCR^{\delta} KO) had normal numbers of PPs, as did mice deficient in both $\alpha\beta$ and $\gamma\delta$ T cells (TCRβ, TCRδ KO). The strongest PP deficiency has been observed in mice lacking both B and T cells as a result of the absence of RAG1 recombinase (RAG1 KO). In B cell-negative mice, the size of PPs was much smaller and FAE was abnormal, as revealed in unfixed preparations of PPs seen in transmitted light (Fig. 1, C and D) or in a cryostat section (Fig. 1G). The transgenic expression of a membrane-bound immunoglobulin M (mIgM) on the J_HD background, allowing generation of B cells with surface but not

secreted IgM, completely restored the development of PPs (Table 1) and FAE (Fig. 1, E, F, and H).

Scanning electron microscopy (SEM) was used for further analysis of FAE in mutant mice (Fig. 2). SEM is the most adequate approach for M cell detection, as the luminal surface of M cells has very distinct microfold morphology (Fig. 2C) (7). SEM allows analysis of the large FAE surfaces, an advantage over transmission electron microscopy or histochemical detection of M cells (8). M cells could be found in abundance in the large domes in the PPs of normal mice (Fig. 2B) (9). In contrast, only a few cells with a characteristic microfold surface could be detected in the smaller domes of B cell-deficient animals (Fig. 2, E to G) (9). Cells with an unusual brush border (Fig. 2, F and G) were also found in mice without B cells. These cells are most likely M cell maturation intermediates (9).

Reconstitution of B cells by mIgM transgene expression resulted in the complete development of FAE and M cells (Fig. 2, H and I). Nonactivated B lymphocytes are likely sufficient for organogenesis, as FAE-containing M cells were normally developed in CD40 ligand-negative (CD40L KO) mice (Fig. 2J), even though B cells in these mice cannot be properly activated (10, 11). The lack of T cells did not have any significant influence on FAE development because TCRβ, TCRδ KO mice had normally developed M cells (Fig. 2K). However, in RAG1 KO mice, domes were even more difficult to find than in mice with no B cells, and there was no evidence of M cells (12); this suggests that the development of residual M cells found in the absence of B cells (Fig. 2, F and G) (9) may be promoted by T lymphocytes, although the input of T cells in M cell devel-

Table 1. Development of Peyer's patches is affected in mice lacking B lymphocytes.

Mouse strain	PP numbers	
	Average	Individual mice
B6	6.8	7, 5, 7, 6, 5, 9, 8, 7, 6, 8, 7
B6-Igh-6	2.1*	3, 2, 2, 2, 3, 2, 2, 3, 2, 1, 2, 2, 2, 2, 2
B6-TCRβ KO	7.0	7, 7, 6, 8, 7, 7
B6-TCRδ KO	6.3	5, 7, 6, 7
B6-TCR β, TCRδ KO	6.8	6, 8, 7, 6, 7, 7
B6-Rag1 KO	0.6*	1, 0, 1, 0
BALB/cj	10.3	11, 9, 10, 11
BALB/c-J _H D	1.6*	2, 0, 2, 0, 1, 2, 4, 2, 2, 1, 2
mlgM Tg	9.0	10, 11, 11, 8, 9, 10, 10, 7, 9, 10, 8, 8, 7

*The size of PPs was significantly diminished. PPs on isolated intestines were counted using a Leica MZ6 zoom stereo microscope (28).

coupled polyclonal antibodies to Ig (Sigma).

0.1mm

0.1mm

opment is very limited. A conservative estimate suggests that the overall number of M cells in B cell–deficient mice is smaller by a factor of at least 150 to 840 (one-sixth to one-third the number of PPs \times one-quarter to one-half the number of domes \times one-fifth the dome surface area \times one-seventh to one-fifth the number of M cells in the field). Thus, only 1.2 to 6.6 M cells are present in B cell–deficient mice per every 1000 M cells in normal intestine.

Substantial diminution of M cell numbers should lead to a strong functional impairment. We used mouse mammary tumor virus (MMTV), a classical retrovirus suspected to use M cells to enter GALT (13), to show functional involvement of M cells in retroviral transport from the intestinal lumen. MMTV infects only dividing cells, and it relies on its superantigen (SAg) to induce proliferation of T cells expressing certain VB chains (14). T cell activation by SAg depends on direct interaction with B lymphocytes (15). Elimination of either T cells with appropriate V β chains (16) or B cells (17) abrogates MMTV infection. Thus, B cells may be needed both for T cell activation and for M cell-dependent translocation of MMTV.

To unmask the possible role of M cells in channeling MMTV through the intestinal wall, we used a bone marrow (BM) chimera approach (18). Newborn Igh-6 or TCR β KO mice

Fig. 2. SEM (29) showed normal FAE and the presence of M cells (marked "M") in BALB/cJ (A to D) and transgenic mIgM (H and I) mice. Goblet cells are indicated by "G"; enlarged images of a typical M cell (C) and goblet cell (D) are shown. In J_HD mice, FAE was small (E and G) and M cell generation (F and G) (9) was affected by the lack of B cells. Cells with an unusual brush border are marked with an asterisk in (F) and (G). (J) B cells in mice lacking CD40L stimulate normal development of FAE and M cells. (K) The absence of both $\alpha\beta$ and $\gamma\delta$ T cells did not affect M cell development.

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were used as recipients of normal adult B6 BM and were simultaneously briefly exposed to MMTV (19). In all TCR β KO (having intact B and M cells) recipients of B6 BM, MMTV infection was readily detectable (Fig. 3). In contrast, chimeras with a reconstituted immune system but with underdeveloped FAE were significantly resistant to MMTV infection: Most Igh-6 recipients had severely diminished viral load or had no detectable MMTV proviruses at

Fig. 3. Infection with milkborne retrovirus (MMTV) is controlled by B cell-dependent FAE. (A) Control B6 mice, but not TCRβ KO or Igh-6 mice, fed with MMTV-laden milk became infected. Integrated MMTV proviruses were detected in the spleens at 8 weeks by semiquantitative PCR. Each lane represents a different mouse. (B) When the two immunodeficient strains were reconstituted at birth with B6 BM (18), only B6 \rightarrow TCR β KO chimeras demonstrated fullscale infection. Mice in the experiments shown two were fostered by MMTV+ foster mothers for 7 and 3 days, respectively. Densitometric analysis of the PCR bands is shown below

all (Fig. 3). Only a small fraction of total T cells (T cells expressing cognate V β regions) can be used by MMTV (20). Nevertheless, T cell numbers originating from donor BM were sufficient to allow MMTV infection in B6 \rightarrow TCR β KO chimeras. Because mouse BM contains 15 to 20% cells of the B cell lineage versus 1 to 2% of the T cell lineage, the number of B cells introduced should be sufficient to support SAg-dependent T cell activation.





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The B cell-controlled development of FAE (as opposed to mere reduction of PP numbers) is crucial for retroviral infection, as tumor necrosis factor receptor 1 (TNFR1) KO mice with the same reduction in number and size of PPs (21, 22) as B cell-negative mice but with significant numbers of M cells were found to harbor MMTV efficiently (9).

The precise mechanisms of the organogenic function of B cells are unknown. B cells in transgenic mIgM mice do not produce any secreted Ig, excluding involvement of soluble Ig or signaling through Fc receptors in FAE development. The members of the TNFR family have been implicated in organogenesis of lymphoid tissue, including GALT (23), and are likely to be involved in the B cell-dependent development of FAE, similar to B cell-dependent generation of follicular dendritic cells (FDCs) (24).

The organogenic function of B cells in GALT (and possibly in other mucosal barriers, such as respiratory epithelium) is distinct from their immune functions of Ig secretion or antigen presentation. It affects M cell-dependent translocation of pathogens through mucosal barriers, influences an organism's interactions with environmental flora (25), and must be taken into account when interpreting studies that implicate B cells as antigen-presenting cells in immunity and autoimmunity (26, 27).

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Use of Chemokine Receptors by Poxviruses

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Chemokine receptors serve as portals of entry for certain intracellular pathogens, most notably human immunodeficiency virus (HIV). Myxoma virus is a member of the poxvirus family that induces a lethal systemic disease in rabbits, but no poxvirus receptor has ever been defined. Rodent fibroblasts (3T3) that cannot be infected with myxoma virus could be made fully permissive for myxoma virus infection by expression of any one of several human chemokine receptors, including CCR1, CCR5, and CXCR4. Conversely, infection of 3T3-CCR5 cells can be inhibited by RANTES, anti-CCR5 polyclonal antibody, or herbimycin A but not by monoclonal antibodies that block HIV-1 infection or by pertussis toxin. These findings suggest that poxviruses, like HIV, are able to use chemokine receptors to infect specific cell subtypes, notably migratory leukocytes, but that their mechanisms of receptor interactions are distinct.

Viruses can use a wide spectrum of cellular receptors for binding and entry to initiate an infectious process (1, 2). For example, HIV and simian immunodeficiency virus (SIV) are known to exploit a variety of members be-

longing to the chemokine receptor superfamily, most notably CXCR4 and CCR5, which, along with CD4, act as coreceptors to govern viral tropism [reviewed in (3)]. The identification of cell-surface receptors for poxvirus http://www.jstor.org

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¹⁰A 39-kDa Protein on Activated Helper T Cells Binds CD40 and Transduces the Signal for Cognate Activation of B Cells

Randolph J. Noelle; Meenakshi Roy; David M. Shepherd; Ivan Stamenkovic; Jeffrey A. Ledbetter; Alejandro Aruffo

Proceedings of the National Academy of Sciences of the United States of America, Vol. 89, No. 14. (Jul. 15, 1992), pp. 6550-6554.

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²² Peyer's Patch Organogenesis is Intact yet Formation of B Lymphocyte Follicles is Defective in Peripheral Lymphoid Organs of Mice Deficient for Tumor Necrosis Factor and its 55-kDa Receptor

Manolis Pasparakis; Lena Alexopoulou; Matthias Grell; Klaus Pfizenmaier; Horst Bluethmann; George Kollias

Proceedings of the National Academy of Sciences of the United States of America, Vol. 94, No. 12. (Jun. 10, 1997), pp. 6319-6323.

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