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MICROBIOME

Cell surface polysaccharides of *Bifidobacterium bifidum* induce the generation of Foxp3$^+$ regulatory T cells

Ravi Verma[1], Changhon Lee[2], Eun-Ji Jeun[2], Jaeu Yi[2], Kwang Soon Kim[1], Ambarnil Ghosh[1], Seohyun Byun[2], Choong-Gu Lee[1], Hye-Ji Kang[1], Gi-Cheon Kim[1], Chang-Duk Jun[3], Gwenaël Jan[4], Chang-Hee Suh[5], Ju-Yang Jung[5], Jonathan Sprent[2,6], Dipayan Rudra[1,2], Cristina De Castro[7,8], Antonio Molinaro[8,9], Charles D. Surh[1,2], Sin-Hyeog Im[1,2]*

Dysregulation of intestinal microflora is linked to inflammatory disorders associated with compromised immunosuppressive functions of Foxp3$^+$ T regulatory (T_{reg}) cells. Although mucosa-associated commensal microbiota has been implicated in T_{reg} generation, molecular identities of the "effector" components controlling this process remain largely unknown. Here, we have defined *Bifidobacterium bifidum* as a potent inducer of Foxp3$^+$ T_{reg} cells with diverse T cell receptor specificity to dietary antigens, commensal bacteria, and *B. bifidum* itself. Cell surface β-glucan/galactan (CSGG) polysaccharides of *B. bifidum* were identified as key components responsible for T_{reg} induction. CSGG efficiently recapitulated the activity of whole bacteria and acted via regulatory dendritic cells through a partially Toll-like receptor 2–mediated mechanism. T_{reg} cells induced by *B. bifidum* or purified CSGG display stable and robust suppressive capacity toward experimental colitis. By identifying CSGG as a functional component of T_{reg}-inducing bacteria, our studies highlight the immunomodulatory potential of CSGG and CSGG-producing microbes.

INTRODUCTION

The mammalian gastrointestinal tract harbors numerous species of commensal organisms that constitute the intestinal microbiota. Dysregulation in the composition and diversity of microbiota (dysbiosis) is closely associated with diverse immune disorders, such as allergy, autoimmunity, and gastrointestinal inflammatory disorders. Compared with specific pathogen–free (SPF) conditions, mice raised in complete germ-free (GF) settings display disorganized lymphoid tissues and abnormal immune responses; these deficits are corrected by the provision of commensal microbial species (*1*–*3*). The intestinal microbiota have also been implicated in diversified functions of host immunity by potentiating generation of particular immune cell types with reciprocal functions, notably proinflammatory T helper 17 (T_H17) or anti-inflammatory regulatory T (T_{reg}) cell populations (*1, 4*–*7*). T_{reg} cells are a subset of CD4$^+$ T cells with suppressive function and are characterized by expression of the transcription factor Foxp3 (*8, 9*). T_{reg} cells are generally formed in the thymus (nT_{reg}) but can also arise in the periphery from normal CD4$^+$ cells (pT_{reg}).

In recent years, individual species of the microbial community have been shown to shape the immune composition of the host. For example, colonization with segmented filamentous bacteria (SFB) results in strong induction of T_H17 cells in the small intestine, which is associated with host resistance against intestinal pathogens while exacerbating autoimmune syndromes (*10*–*12*). Several studies have implicated specific strains or a mixture of the commensal microbiota in homeostasis and function of mucosa-associated T_{reg} cells (*13*). In particular, a mixture of 17 strains residing within clusters IV, XIVa, and XVIII of *Clostridia* was shown to enhance colonic T_{reg} cell differentiation and function in mice (*14*). Also, colonization of mice with human commensal *Bacteroides fragilis* (*Bf*) potentiates interleukin-10 (IL-10)–producing T_{reg} cells (*2, 15*–*17*). We have previously reported that a mixture of five probiotic strains, IRT5, has the capacity to induce Foxp3$^+$ T_{reg} cells and to suppress diverse immune responses in several experimental disease models, such as atopic dermatitis, rheumatoid arthritis, myasthenia gravis, and multiple sclerosis (*18*–*20*).

Although these studies demonstrate immunomodulatory properties of specific bacterial species, the underlying molecular events driving these processes remain elusive. Several bacteria-derived metabolites and cell wall components have previously been implicated. For example, butyrate was reported as a key effector molecule produced by *Clostridia*, which can potentiate colonic T_{reg} cell induction (*21*). The polysaccharide A (PSA) of *Bf* was identified as a key effector molecule for IL-10–producing T_{reg} induction (*2, 22*).

Supplementing patients with missing microorganisms might be effective in restoring dysregulated microbiota. Fecal microbiota transplants (FMTs) from healthy donors to patients have been shown to have beneficial effects in treating gastrointestinal disorders (*23*). However, given that FMT has not yet been approved as a therapeutic modality due to safety issues, administration of probiotics could provide an alternative approach to achieve the same goal. Several studies have reported that consumption of safety-assured bacteria-like probiotics could ameliorate diverse immune disorders, such as allergies and inflammatory bowel disorders (*24, 25*). However, the functionality of probiotics might depend on the particular health disorder of the patients. For this approach to be successful, it is vital to identify beneficial microorganisms and to elucidate effector mechanisms that regulate their immunomodulatory activity.

Here, we have screened a large collection of probiotic strains for their T_{reg}-inducing capacity and report a *Bifidobacterium bifidum* strain *PRI1* (*Bb*) to be the best candidate. Using GF mice, we have established that this strain facilitates efficient de novo generation of T_{reg} cells with specificity for dietary antigens (Ags), commensal microbiota, and *Bb* itself. Further, we have identified a class of bacterial cell surface β-glucan/galactan

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(CSGG) polysaccharides as the key effector component able to induce T_{reg} cells with the capacity to ameliorate intestinal inflammation.

RESULTS

Bb monocolonization induces de novo generation of pT_{reg} cells

To identify T_{reg}-inducing bacteria among the commensal microorganisms, we screened probiotic strains using our ex vivo screening protocol (*20, 26*). Briefly, individual bacterial strains were cultured in the presence of antibiotics with a suspension of total mesenteric lymph node (mLN) cells from Foxp3-GFP (green fluorescent protein) ($Foxp3^{GFP}$) reporter mice, thereby enabling detection of T_{reg} cells (*9*). Bacterial strains that induced at least 10-fold greater production of IL-10 than IL-12 and also a > 50% higher frequency of $CD4^+GFP^+$ T_{reg} cells than mock-treated cultures were selected. Among these, *Bb* was chosen as the best candidate (fig. S1, A and B). *Lactobacillus paracasei sub. Tolerans* 467 (*Lpa*), which displayed no noticeable immune response, was selected as a control inert strain (fig. S1A). *Bf* [American Type Culture Collection (ATCC) 25285] (*2, 15–17*) was also used to compare the T_{reg}-inducing capability among the bacterial species.

Single administration of *Bb* to GF mice led to its stable colonization primarily in the colon (Fig. 1A) and normalized the enlarged

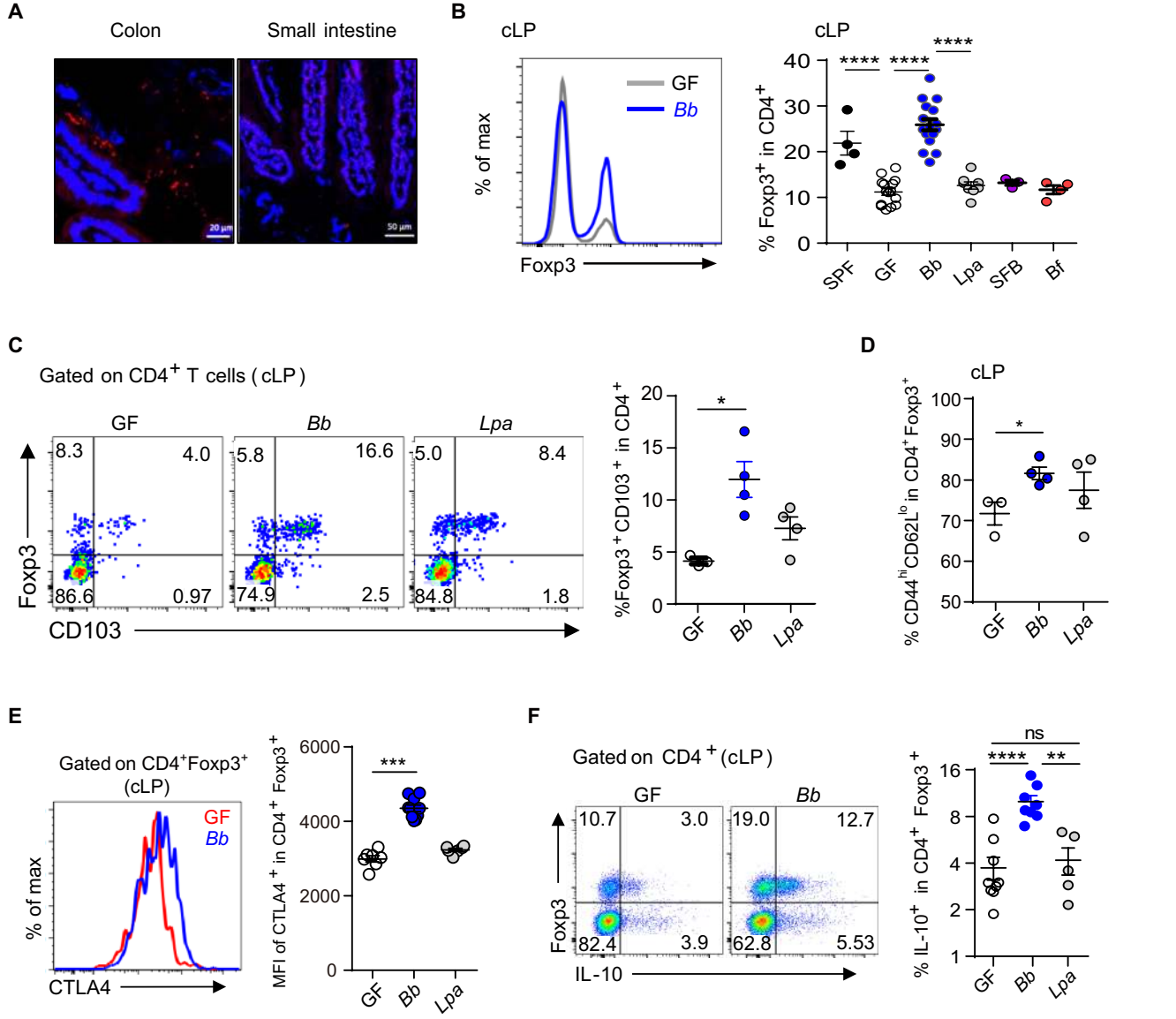


Fig. 1. *Bb* monocolonization enhances T_{reg} population in the cLP. (**A**) Localization analysis of *Bb* in the intestinal niches of GF mice by HISTO-FISH staining with DNA-Cy5 probes (EUB338, red) 3 weeks after colonization. (**B**) Representative flow cytometry plots and percentage analyses of $CD4^+Foxp3^+$ cells in cLP of GF mice colonized with indicated bacterial strains. (**C** to **F**) Representative flow cytometry plots and frequencies of $CD103^+$ and $CD62L^{lo}CD44^{hi}$, $CTLA4^+$, and $IL10^+$ in T_{reg} cells in GF mice or those monocolonized with *Lpa* or *Bb*. Numbers in the quadrants represent cell percentage, and circles in the graph plots represent individual mouse corresponding to each parameter. Data are representative of three to five independent experiments with similar results ($n \geq 3$ mice). All graph plots show means ± SEM. $^*P < 0.05$, $^{**}P < 0.01$, $^{***}P < 0.001$, $^{****}P < 0.0001$ (Student's *t* test). MFI, mean fluorescence intensity; ns, not significant.

cecum size of GF mice (fig. S1C). Three-week colonization with *Bb*, but not with *Lpa*, *SFB*, or *Bf*, led to a marked increase in the frequency of Foxp3$^+$ T_{reg} cells in the colonic lamina propria (cLP; Fig. 1B and fig. S1, D and E) as well as in other organs, including mLN, spleen, and, to a lesser degree, small intestinal lamina propria (siLP) and peripheral LN (pLN) (fig. S1F). Compared with GF mice, mice monocolonized with the *Bf* that was previously reported to induce T_{reg} cells (*2, 16, 22*) did not show any substantial increase in Foxp3$^+$ T_{reg} cells (Fig. 1B and fig. S1D). T_{reg} cells in the cLP of *Bb*-monocolonized mice displayed a significantly higher proportion of CD103$^+$ and memory-phenotype (CD62L^{lo}CD44^{hi}) cells compared with T_{reg} cells in unmanipulated GF mice, suggesting a higher state of T_{reg} cell activation (Fig. 1, C and D, and fig. S1, G and H). Consistent with this idea, cLP T_{reg} cells induced by *Bb* colonization also expressed higher levels of CTLA4 and IL-10, two key molecules indicative of enhanced suppressive properties (Fig. 1, E and F). Although levels of interferon-γ (IFNγ) and IL-13 were not altered, IL-17 levels were increased in T_{reg} cells (fig. S2, A and B). A slight increase in IFNγ levels was observed in CD4$^+$Foxp3$^-$ non-T_{reg} cells in the *Bb* monoassociated mice (fig. S2, A and B).

Expression of the IKAROS family transcription factor Helios and neuropilin 1 (Nrp1) is widely used to distinguish Helios$^+$Nrp1$^+$ thymically generated T_{reg} (tT_{reg}) cells from Helios$^-$Nrp1$^-$ peripherally generated T_{reg} (pT_{reg}) cells (called induced "iT_{reg}" when generated in in vitro culture conditions) (*27–29*). Whereas a small increase in Nrp1$^+$ tT_{reg} cells was observed in *Bb*-colonized cLP, a much greater increase was observed for Nrp1$^-$ and Helios^{lo} pT_{reg} cells in all organs tested, indicating that *Bb* primarily promotes generation of pT_{reg} cells (Fig. 2, A to D, and fig. S3, A and B). Furthermore, a large proportion of the newly generated pT_{reg} cells expressed the transcription factor RORγt (RORγt$^+$Helios$^-$ Foxp3$^+$ and RORγt$^+$ Foxp3$^+$), which is up-regulated upon interactions with microbes in cLP and siLP (Fig. 2, E and F, and fig. S3, C and D) (*30–32*).

To further confirm the peripheral origin of the *Bb*-induced T_{reg} cells, we adoptively transferred allelically marked naïve phenotype CD4$^+$CD45.1$^+$Foxp3$^-$CD62L^{hi}CD44^{lo} T cells sorted from Foxp3^{GFP} mice into mice monocolonized with *Bb* (fig. S3E). Analysis of the donor cells 3 weeks later revealed emergence of a significant proportion of Foxp3$^+$ T_{reg} cells among donor cells in the intestine (cLP and siLP) of *Bb*-monocolonized mice, whereas such cells were sparse among the donor cells in mock-colonized control GF hosts (Fig. 2G and fig. S3, F and G).

Together, these data establish *Bb* as a potent inducer of pT_{reg} cells by eliciting de novo up-regulation of Foxp3 in naïve CD4$^+$ T cells, primarily at the sites of colonization. Similarly enhanced induction of pT_{reg} cells was observed in SPF mice. Here, SPF mice were adoptively transferred with allelically marked purified naïve T cells and then gavaged repeatedly with *Bb* for 3 weeks. These mice developed a high proportion of donor-derived CD4$^+$Foxp3$^+$ cells, strongly suggesting that the T_{reg} cell–inducing property of *Bb* is physiologically relevant (Fig. 2H).

Bb colonization induces pT_{reg} cells with a broad range of TCR specificity to diverse Ags

Next, we analyzed the T cell receptor (TCR) specificity of pT_{reg} cells generated in the presence of *Bb*. pT_{reg} cells generated in the presence of *Bb* could be reactive to dietary Ags and/or reactive to a variety of species of commensal bacteria, including *Bb* itself. To test whether colonization of *Bb* promotes pT_{reg} cells to dietary Ags, we adoptively transferred Cell Trace Violet (CTV)–labeled ovalbumin (OVA)–specific naïve OT-II TCR transgenic CD4$^+$ cells from OT-II. Thy1.1$^+$Foxp3^{GFP} mice into normal GF or *Bb*-monocolonized mice that were then gavaged with OVA protein (fig. S4A). As previously observed (*33*), a small fraction of OT-II cells that underwent expansion in normal GF hosts up-regulated Foxp3 in the siLP and cLP. Notably, in *Bb*-monocolonized mice, but not in the *Lpa*-monocolonized mice, the efficiency of Foxp3 up-regulation by donor OT-II cells increased about two- to threefold in cLP (Fig. 3, A and B).

To determine whether the administration of *Bb* promotes generation of pT_{reg} cells specific to microbiota, we used CBir TCR transgenic mice that recognize bacterial flagellin (*34*). Naïve CD4$^+$Foxp3$^-$ T cells sorted from CBir transgenic mice on a CD45.1$^+$Foxp3^{GFP} background were adoptively transferred into SPF *Rag1*$^{-/-}$ recipients, and then mock [phosphate-buffered saline (PBS)] or *Bb* was gavaged every other day until the end of the experiment (fig. S4B). Control SPF *Rag1*$^{-/-}$ recipients of CBir T cells alone showed prominent signs of colitis as indicated by progressive weight loss (Fig. 3C), a shortened colon with thickened mucosa (Fig. 3D), a change in colonic thickness, and increased infiltration of lymphocytes along with a high histological score that contained few T_{reg} cells (Fig. 3, E and F) but a high proportion of CD4$^+$IFNγ$^+$ and RORγ$^+$Foxp3$^-$ T cells (Fig. 3G and fig. S4C). These various signs of pathology were absent or much less marked in hosts injected with CBir T cells plus *Bb* administration. In this situation, weight loss was minimal, the colon was normal with low histology score, and the cLP contained elevated numbers of T_{reg} cells along with RORγ$^+$Foxp3$^+$ T_{reg} cells but few CD4$^+$IFNγ$^+$ cells (Fig. 3, C to G, and fig. S4C).

To test whether the pT_{reg} cells induced by *Bb* monocolonization have specificity for *Bb* itself, we performed the following experiments. Total colonic CD4$^+$ T cells containing Foxp3$^+$ T_{reg} cells from the GF mice and *Bb*-monocolonized mice were sorted and labeled with CTV and then cocultured with T cell–depleted splenic antigen-presenting cells (APCs) pretreated with fecal Ags from normal GF mice and mice monocolonized with *Bb* or irrelevant control bacteria *Lpa*; these cells were then analyzed for T cell proliferation (CTV dilution) 3 days later (fig. S5A). The results showed that Foxp3$^+$ T_{reg} cells from *Bb*-monocolonized mice displayed sustained Foxp3 expression and proliferation when stimulated with *Bb* fecal Ag-treated APC (Fig. 4A). By contrast, coculturing of total colonic CD4$^+$ with APCs treated with fecal Ags from GF- or *Lpa*-monocolonized mice failed to sustain T_{reg} cell proliferation and stability under identical conditions (Fig. 4A).

We also compared the TCR specificity of GF and *Bb*-monocolonized mice by sequencing the CDR3 region of TCR α and β chains of Foxp3$^+$ T_{reg} cells sorted from colon, mLN, and spleen. Although both T_{reg} cells showed a similar pattern of diversity in TCR α and β chains in spleen and mLN, colonic T_{reg} cells from *Bb*-monocolonized mice showed enhanced diversity with distinct TCR patterns that were not present in GF control (Fig. 4, B to E, and fig. S5B). Moreover, we observed that some of the colonic T_{reg} cells with specific TCR sequences were predominantly enriched (>0.1% frequency) compared with those of mLN and spleen (marked with asterisks in Fig. 4E; tables S1 and S2). Collectively, these results suggest that *Bb* colonization induces the generation of CD4$^+$Foxp3$^+$ T_{reg} cells with a broad range of TCR specificity to dietary Ags and/or commensal microbiota and *Bb* itself.

Bb facilitates T_{reg} cell induction through a dendritic cell–dependent mechanism

Because intestinal induction of pT_{reg} cells from naïve T cells requires an immunoregulatory cytokine milieu, we tested whether colonization

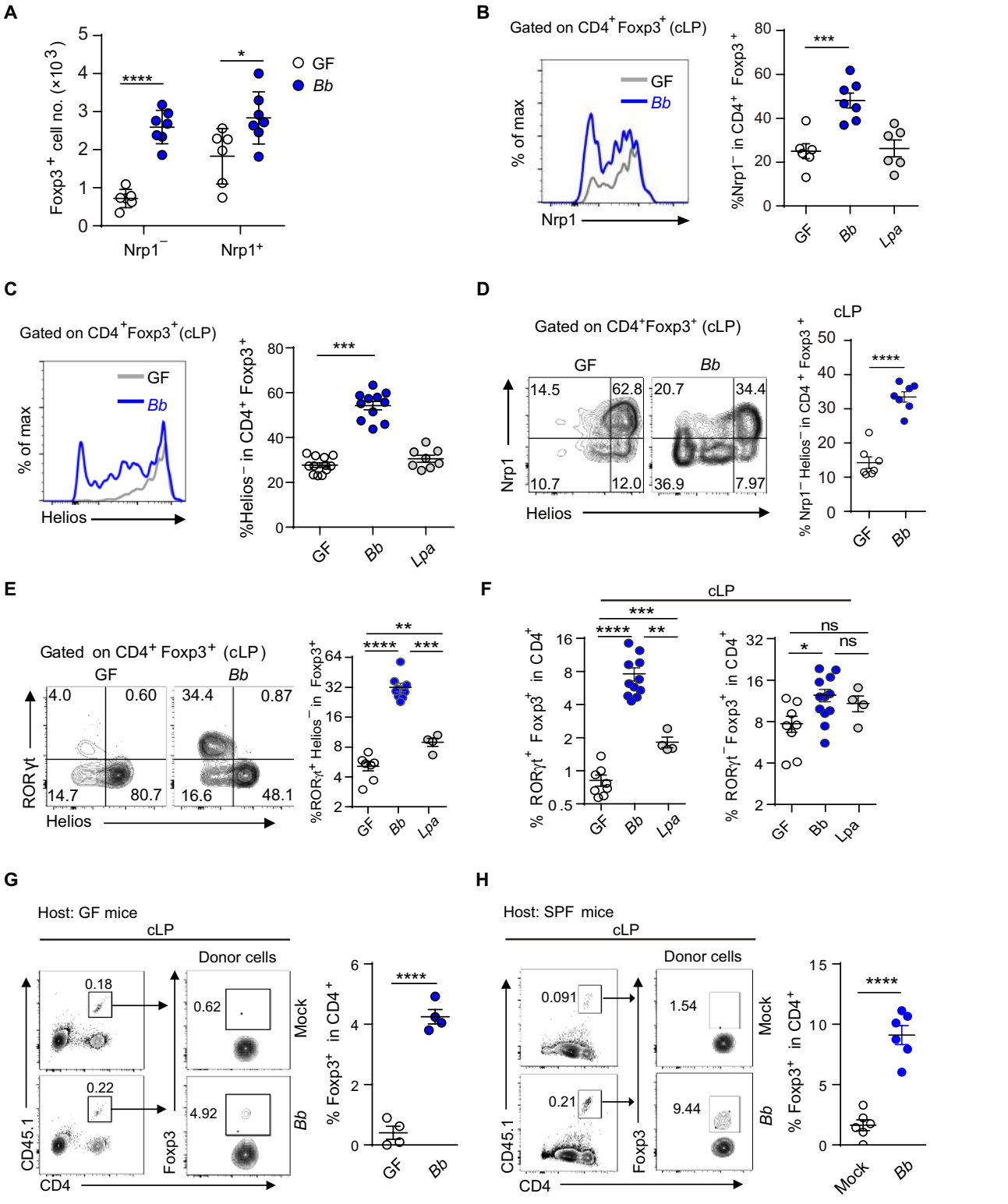
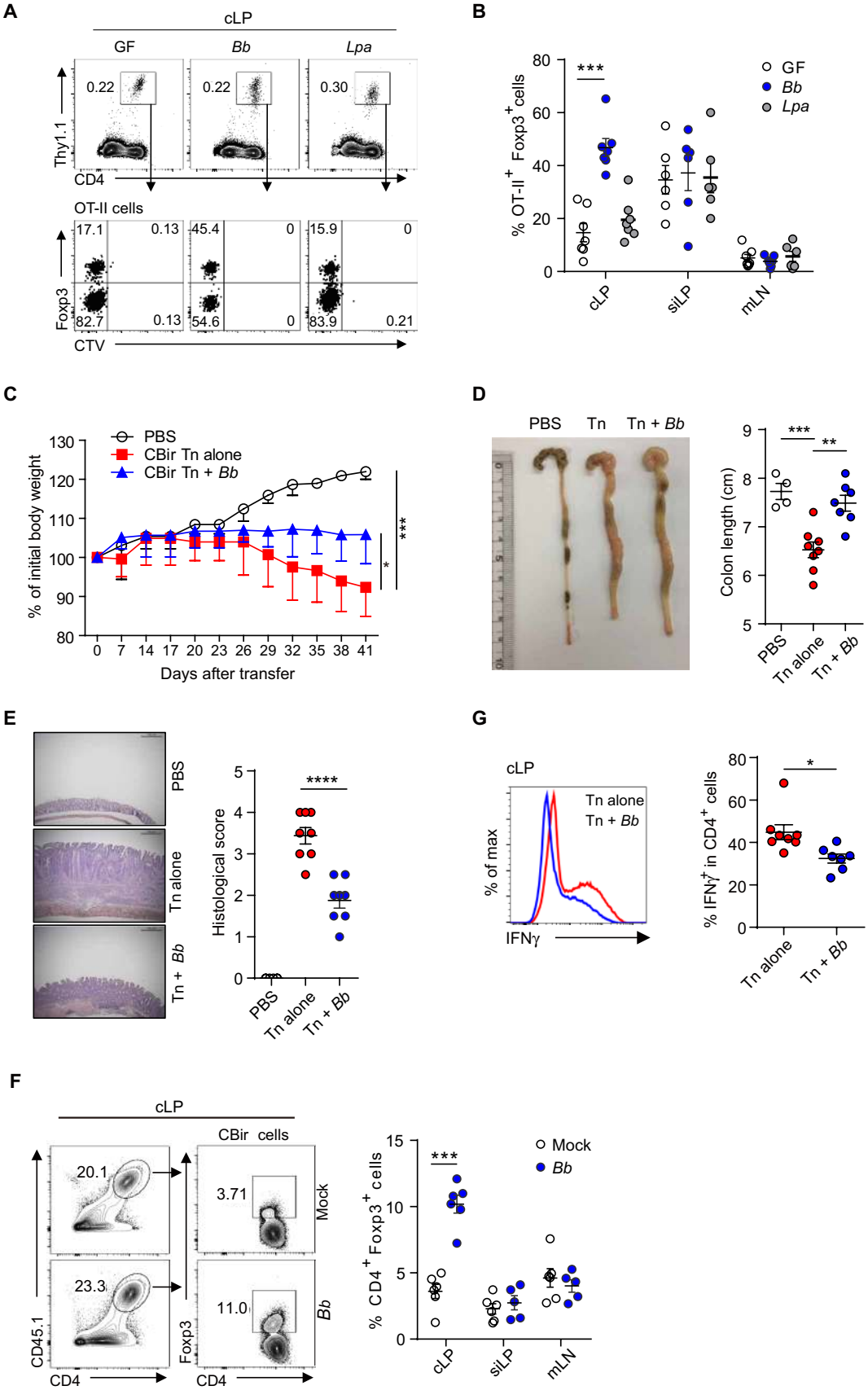


Fig. 2. *Bb* monocolonization facilitates de novo generation of pT_{reg} cells. cLP cells were isolated from the GF mice or mice monocolonized with *Lpa* or *Bb* 3 weeks after colonization. (**A**) Absolute numbers of $Nrp1^+$ and $Nrp1^-$ T_{reg} cells. (**B** to **F**) Representative flow cytometry plots and frequencies for $Nrp1^-Foxp3^+$ (B), $Helios^-Foxp3^+$ (C), $Helios^-Nrp1^-Foxp3^+$ (D), $ROR\gamma t^+Helios^-$ $Foxp3^+$ (E), and $ROR\gamma t^+Foxp3^+$, $ROR\gamma t^-Foxp3^+$ (F) T_{reg} cells in the cLP of GF or *Bb*- or *Lpa*-monocolonized mice. (**G**) Naïve $CD4^+Foxp3^-$ T cells sorted from $CD45.1^+Foxp3^{GFP}$ reporter mice were transferred into GF mice. Animals were either left GF or monocolonized with *Bb* for 3weeks. $Foxp3^+$ T_{reg} population was analyzed by GFP expression in the cLP. (**H**) Naïve $CD4^+Foxp3^-$ T cells sorted from $CD45.1^+Foxp3^{GFP}$ reporter mice were transferred into SPF mice, and then mice were fed with mock (PBS) or *Bb* (5×10^8 CFU) every other day for 3 weeks and analyzed for $Foxp3^+$ T_{reg} cells. Data are representative of at least five independent experiments with similar results ($n \geq 3$ mice). All graph plots show means ± SEM. $^*P < 0.05$, $^{**}P < 0.01$, $^{***}P < 0.001$, $^{****}P < 0.0001$ (Student's *t* test).

Fig. 3. *Bb* colonization induces dietary Ag– and microbiota-reactive T_{reg} cells. (**A** and **B**) CTV-labeled naïve allelically marked $CD4^+Thy1.1^+Foxp3^-$ T cells from OT-II.$Thy1.1^+Foxp3^{GFP}$ mice were adoptively transferred into GF mice or mice premonocolonized with *Bb* or *Lpa* for 14 days. The mice were fed with OVA (20 mg) every other day for 7 days. The cLP $CD4^+Foxp3^+$ population of the donor ($Thy1^+$OT-II) cells was analyzed. Representative fluorescence-activated cell sorting (FACS) plots (A) and frequencies of T_{reg} cells generated in vivo (B) are shown. (**C** to **E**) Naïve $CD4^+CBir^+CD45.1^+Foxp3^-$ T cells sorted from $CBir^{Tg}CD45.1^+Foxp3^{GFP}$ mice were adoptively transferred into the SPF *Rag1*$^{-/-}$ recipients. The recipient mice were fed with either *Bb* or PBS every other day until the end of the experiment. Changes in the body weight (C), colon length (D), and histopathology and histological score (E) in colonic tissue were measured and analyzed. (**F** and **G**) Representative FACS plots and frequencies of $CBir^+CD45.1^+Foxp3^+$ T_{reg} cells (F) and $CD4^+IFN\gamma^+$ cells (G) within cLP of mock- or *Bb*-administered mice analyzed at the end of experiment. Numbers indicate cell percentages in the quadrants, and circles in the graph plots represent individual mouse corresponding to each parameter, respectively. Data are representative of at least three independent experiments with similar results ($n \geq 3$ mice). Graphs with error bars show means ± SEM. *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$, ****$P < 0.0001$ (Student's *t* test).



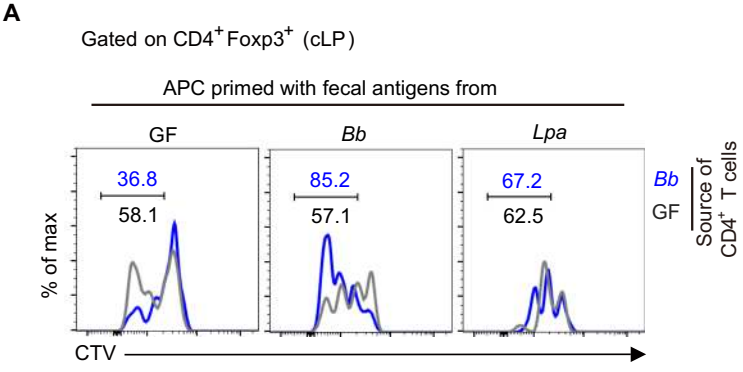
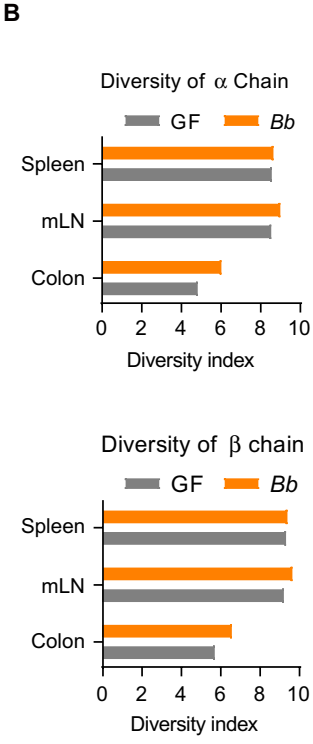
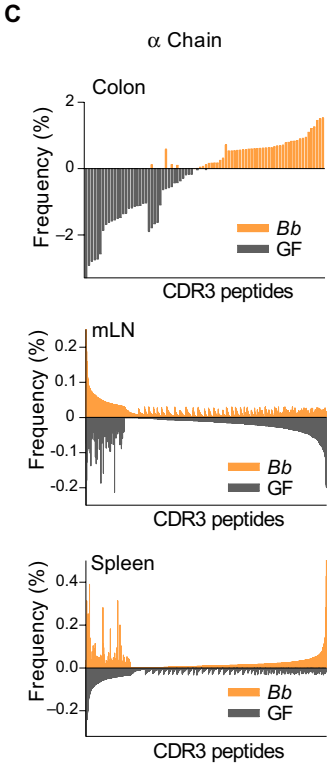
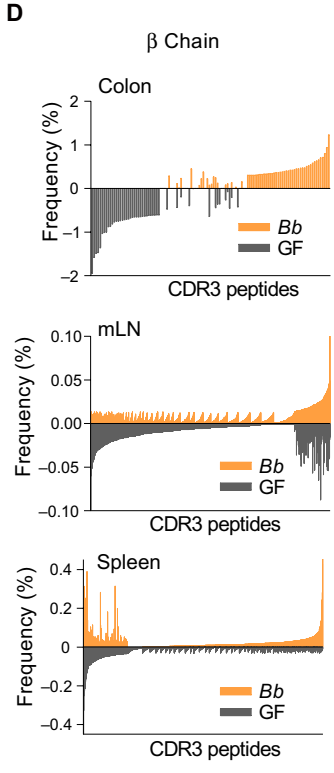
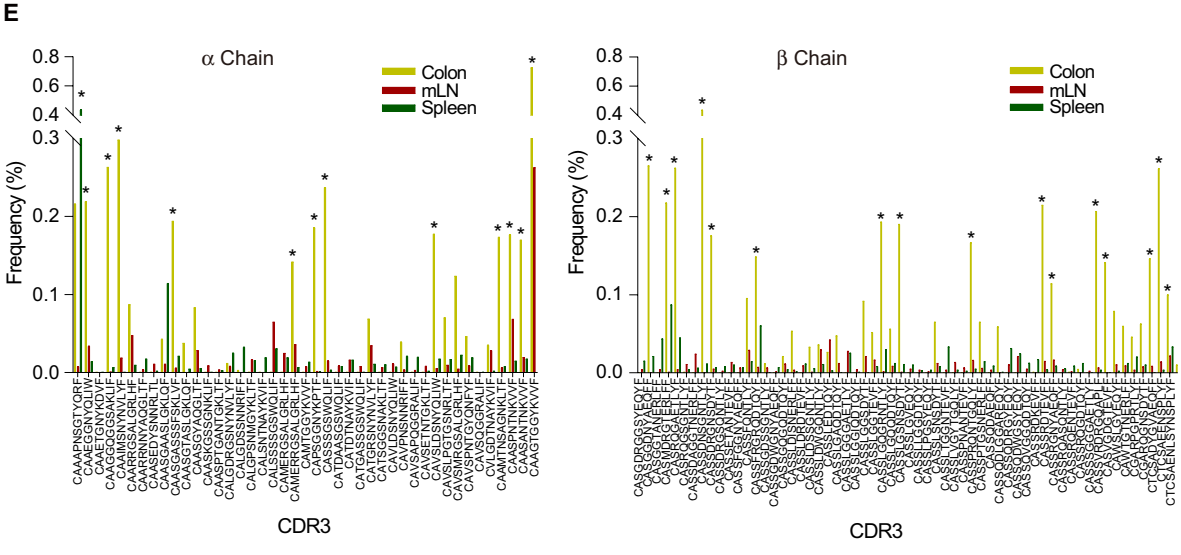


Fig. 4. *Bb* monocolonization induces *Bb*-reactive colonic T_{reg} cells with distinctive TCR repertoires. (**A**) Total colonic $CD4^+$ T cells containing $Foxp3^+$ T_{reg} cells from the GF mice or *Bb*-monocolonized mice were sorted and labeled with CTV and then cocultured with T cell–depleted splenic APC in the presence of indicated fecal Ags from GF or *Bb*- or *Lpa*-monocolonized mice. Three days later, relative proliferation of T_{reg} cells was analyzed by FACS. (**B**) Comparison of Shannon diversity from TCR α and β chains of T_{reg} cell repertoires obtained from different lymphoid organs of GF or *Bb*-monocolonized mice. (**C** and **D**) Frequency distribution two-way bar plot representation of common TCR-CDR3 α regions (85 from colon, 1469 from mLN, and 1381 from spleen) (C) and β regions (118 from colon, 1724 from mLN, and 1381 from spleen) (D). (**E**) Comparative enrichment frequency distribution of unique α and β chains of TCR-CDR3 regions of T_{reg} cells isolated from colon, mLN, and spleen of *Bb*-monocolonized mice compared with GF mice.









with *Bb* induces a tolerogenic microenvironment in the colon. Compared with normal GF mice, total colonic cells (fig. S6A) as well as cLP-DCs ($MHCII^+CD11c^+CD11b^+CD103^+F4/80^-$) isolated from the *Bb*-monocolonized mice displayed a significant increase in the expression of mRNA for a number of inhibitory molecules, namely, *il10*, *Csf2*,*Tgfβ1*, *ido*, *Ptgs2*, and *Pdcd1*, as well as costimulatory molecules *Cd86* and *Cd40* (Fig. 5, A to C, and fig. S6A). These findings suggest that colonization with *Bb* induces a population of regulatory dendritic cells (rDCs), which, in turn, may enhance de novo pT_{reg} differentiation. We further analyzed the different subtypes of DCs affected by *Bb* monocolonization in the cLP, siLP, and mLN. In the cLP, we could observe a slight increase in $CD103^+CD11b^+$ and plasmacytoid DC (pDC) ($Bst2^+CD11c^{lo}$) population but not in $CX3CR1^+CD11b^+$ population (Fig. 5D and fig. S6, B to D). In the mLN, but not in siLP, a significant increase in $CD103^+CD11b^+$ DCs and $CX3CR1^+CD11b^+$ population was observed (fig. S7, A and B). These results indicate that $CD103^+$ cLP-DCs may play a key role in *Bb*-mediated T_{reg} induction in the colon. To examine this possibility, we performed an in vivo mimicking experiment by culturing sorted cLP-DCs ($MHCII^+CD11c^+CD11b^+CD103^+F4/80^-$) with *Bb* for 10 to 12 hours followed by washing and then coculture with naïve $CD4^+Foxp3^-$ T cells for 3 days in suboptimal T_{reg}-inducing conditions. Notably, pretreatment of cLP-DCs with *Bb* resulted in the significant induction and proliferation of iT_{reg} cells relative to mock treatment or exposure to control *Lpa* (Fig. 5E). IL-10 secretion in the *Bb*-treated culture was also increased compared with mock-treated group (Fig. 5E, bottom panel). By contrast, cLP-DC–treated *Lpa* did not induce iT_{reg} or IL-10 production in these culture conditions (Fig. 5E).

CSGG are the active components of *Bb* facilitating T_{reg} cell induction

Using the above in vitro system, we performed experiments to identify *Bb*-derived effector molecules that facilitate iT_{reg} differentiation. Because of limited availability of cLP-DCs, we used splenic DCs for these experiments in suboptimal T_{reg}-inducing conditions. Because *Bb* is strictly anaerobic and mostly nonviable during coculture with DCs, we tested whether some of its cellular components might act as effector molecules with iT_{reg}-inducing activity. Among the subcellular fractionates comprising cell surface, cell membrane, and cytosol components, only the cell surface extract effectively promoted iT_{reg} generation (fig. S8A). Treatment of cell surface extract with ribonuclease (RNase), deoxyribonuclease (DNase), Pronase, or boiling at high temperature did not reduce the T_{reg}-inducing activity, suggesting that polysaccharides might be the effector molecules. Incubating DCs with total cell surface polysaccharide (tCSPS) extract effectively induced iT_{reg} cells in a dose-dependent manner under similar culture conditions (fig. S8B).

We further purified polysaccharides by two successive chromatography steps. On the basis of its molecular weight features, tCSPS was further separated by ion exclusion chromatography, followed by in-depth nuclear magnetic resonance (NMR) analysis of the fractions eluted at low ionic strength. Cell surface polysaccharides of *Bb* consisted of at least five different polysaccharides. Among these, the 8000-Da (average molecular weight), negatively charged polysaccharide phosphoglycero-β-galactofuran (PGβG), with 64% abundance, was the most prevalent (Fig. 5F). The remaining four polysaccharides (β-1-6-glucan, β-1-4-glalactan, β-1-6-glalactan, and β-galactofuranan) had similar molecular weights (average ~4000 Da) without charge differences (neutral), precluding their further separation. We tested which of the polysaccharides, the neutral mixture or PGβG, have the activity to induce T_{reg} cells in vitro. Significantly, only the neutral polysaccharides, and not the negatively charged PGβG, facilitated induction of T_{reg} cells (Fig. 5G). We named this mixture of neutral polysaccharides derived from the *Bb* as CSGG. Among the CSGG, cell surface β-1-6-glucan (CSβG) might be the key effector molecule. Treatment of CSGG with β-1,6-glucanase reduced CSGG-induced iT_{reg} cell levels in a dose-dependent manner, whereas other enzyme treatments such as β-1,4-galactanase or β-1,6-galactanase displayed no significant reduction (Fig. 5H and fig. S8C).

Next, we tested whether CSGG could recapitulate the capacity of whole bacteria to induce T_{reg} cells in vitro and in vivo. Naïve $CD4^+Foxp3^-$ T cells were cocultured with DCs pretreated with *Bb*, CSGG, *Bf*, or *Lpa* in suboptimal T_{reg}-inducing conditions. Significantly, the CSGG-treated DCs induced $Foxp3^+$ iT_{reg} cells as effectively as *Bb*-treated DCs, whereas *Bf- or Lpa*-treated DCs failed to induce iT_{reg} cells (fig. S8D). Coculturing of naïve $CD4^+Foxp3^-$ T cells with DCs pretreated with *Bf* induced high levels of $IFNγ^+IL\text{-}10^+$ mostly in $Foxp3^-$ T cells (fig. S8E). Next, we tested whether CSGG could induce pT_{reg} cells in vivo. Intraperitoneal injections of CSGG (100 μg per dose) into GF mice for 3 weeks induced $CD4^+Foxp3^+$ and $Nrp1^-Rorγt^+$ T_{reg} cells similar to the levels of *Bb*-monocolonized mice in the cLP and mLN (Fig. 5I and fig. S8F). These T_{reg} cells displayed a higher proportion of $CD103^+$ and activated $CD44^{hi}CD62L^{lo}$ cells than T_{reg} cells from control GF mice (fig. S8G). Next, we tested whether CSGG treatment could induce T_{reg} cells in the human $CD4^+$ T cells. Coculturing of CSGG-treated human DCs and naïve $CD4^+$ T cells isolated from peripheral blood mononuclear cells (PBMCs) of healthy donors significantly induced $CD25^+Foxp3^+$ T_{reg} cells in a dose-dependent manner (Fig. 5J).

CSGG induces T_{reg} cells through generation of regulatory DCs

Treatment of naïve $CD4^+$ T cells with CSGG in the absence of DCs failed to induce $Foxp3^+$ T_{reg} cells, implying a DC-dependent mechanism for iT_{reg} induction (fig. S9A). We therefore tested the role of different DC subtypes for generation of CSGG-induced iT_{reg} cells (fig. S9B). pDCs, cDCs, and $CX3CR1^+$ and $CX3CR1^-$ DCs were sorted from the spleen; treated with mock, *Bb*, or CSGG; and then cocultured with naïve $CD4^+Foxp3^-$ T cells in suboptimal T_{reg}-inducing conditions. Although all the tested DC subtypes were able to induce iT_{reg} cells upon *Bb* or CSGG treatment, cDCs, pDCs, and $CX3CR1^-$ cells induced high levels of iT_{reg} (fig. S9, C and D). We also tested whether pretreatment of DCs with CSGG could induce Ag-specific iT_{reg} generation because *Bb* administration induced pT_{reg} cells with a broad range of TCR specificity to diverse Ags in vivo (Figs. 3 and 4). Sorted total splenic DCs ($MHCII^+CD11c^+$), as well as either of the two main types of DCs ($CD8α^+$; $MHCII^+CD11c^+CD11b^-$ and $CD8α^-$; $MHCII^+CD11c^+CD11b^+$), were pretreated with CSGG, and then naïve OT-II TCR transgenic $CD4^+$ cells from $OT\text{-}II.Thy1.1^+Foxp3^{GFP}$ mice were cultured in the presence of OVA Ag (fig. S9E). CSGG treatment potentiated Ag-specific iT_{reg} generation (fig. S9E). These results suggest that the CSGG treatment acts by converting conventional DCs into rDCs, similar to the above findings for the cLP-DC populations of *Bb*-colonized mice (Fig. 5, A to D). To test this possibility, we performed RNA sequencing (RNA-seq) analysis of the $CD11c^+$ splenic DCs treated for 4 hours with CSGG. Compared with mock control treatment, CSGG treatment significantly enhanced levels of rDC-associated markers such as *Ifna2*, *Pdcd1*, *Tgfβ1*, *Csf2*, *Ptgs2*, *il10*, and

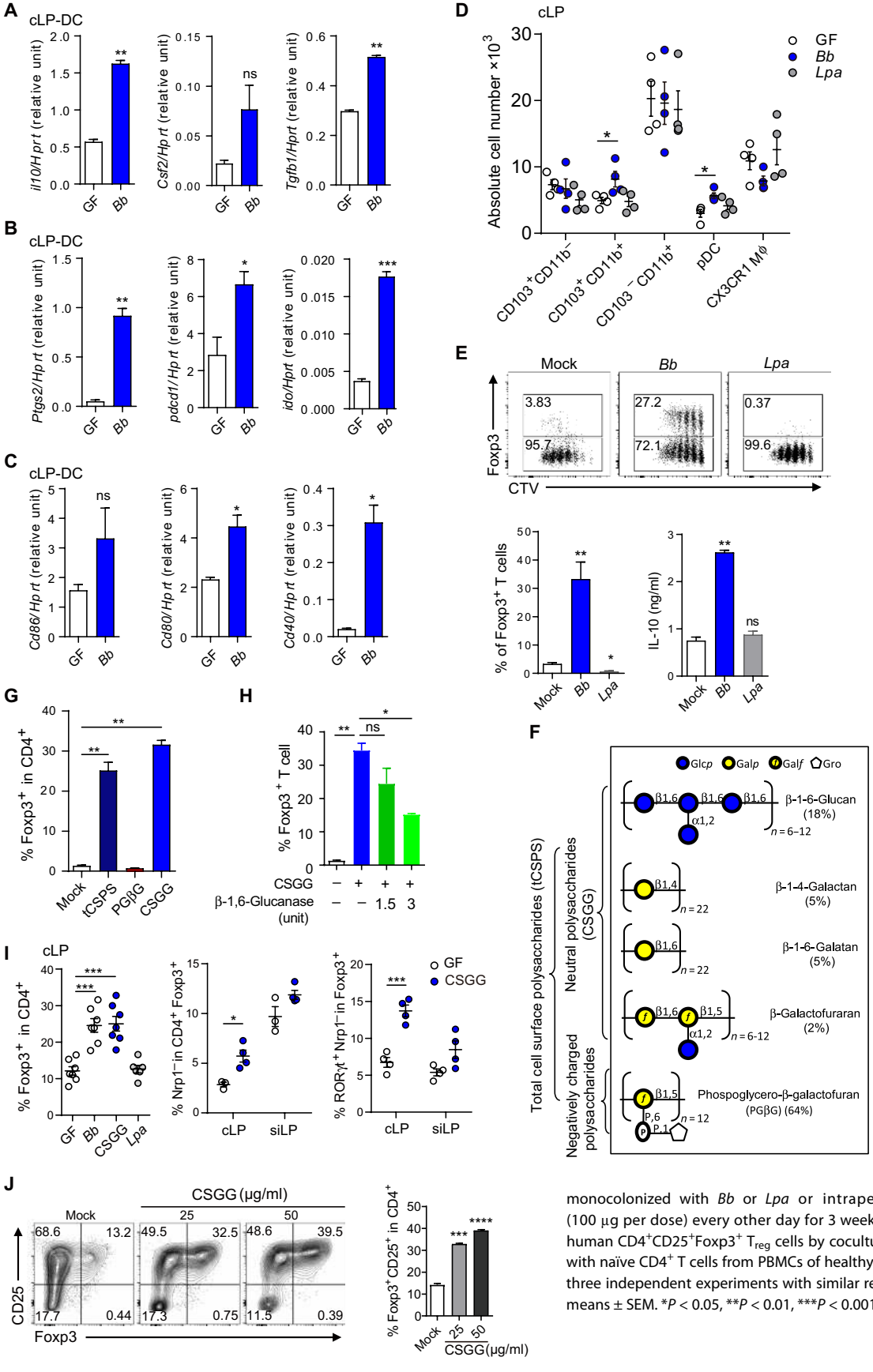


Fig. 5. Cell surface CSGG of *Bb* mediates T_{reg} cell induction. (**A** to **C**) Quantitative polymerase chain reaction analysis of mRNA for cytokines and inhibitory and costimulatory molecules plotted as fold change in the cLP-DCs ($MHCII^+CD11c^+CD11b^+CD103^+F4/80^-$) of GF or *Bb*-monocolonized mice. Data are representative of three independent experiments with similar results. (**D**) Graph shows absolute number of cLP-DCs from GF mice or monocolonized mice with *Lpa* or *Bb* for CD103, CD11b, CX3CR1, and pDCs ($Bst2^+CD11c^{lo}$). Numbers represent the frequency of each population from the total $CD11c^+MHCII^+$ cells. Data are representative of two independent experiments with similar results ($n = 4$ mice). (**E**) $CD11c^+$DCs pretreated with *Bb* or *Lpa* were cocultured with naïve $CD4^+$ T cells in suboptimal T_{reg}-inducing conditions for 3 days, after which $Foxp3^+$ T_{reg} cells were analyzed within live cells. Representative flow cytometric analysis and mean frequencies of $CD4^+Foxp3^+$ T_{reg} cells are shown. From culture supernatant, IL-10 secretion was determined by enzyme-linked immunosorbent assay. Data are representative of five independent experiments with similar results. (**F**) Structures of neutral (CSGG) or negatively charged polysaccharides (PGβG) isolated from the tCSPS of *Bb*. Glc*p*, glucopyranos; Gal*p*, galactopyranose; Gal*f*, glucofuranose; Gro, glycerol. *n* = repeating unit. Relative abundances of each polysaccharide are shown as % (mol/mol). (**G**) Comparison of $CD4^+Foxp3^+$ T_{reg}-inducing activity between the neutral (CSGG, 50 μg/ml) and negatively charged polysaccharides (PGβG, 100 μg/ml) compared with tCSPS (100 μg/ml). (**H**) Effect of β-1,6-glucanase treatment on CSGG-induced iT_{reg} cells. (**I**) Populations and phenotypes of T_{reg} cells in GF mice or mice monocolonized with *Bb* or *Lpa* or intraperitoneally injected with CSGG (100 μg per dose) every other day for 3 weeks. (**J**) Dose-dependent induction of human $CD4^+CD25^+Foxp3^+$ T_{reg} cells by coculturing of DCs pretreated with CSGG with naïve $CD4^+$ T cells from PBMCs of healthy donors. Data are representative of three independent experiments with similar results. Graphs with error bars show means ± SEM. **P* < 0.05, ***P* < 0.01, ****P* < 0.001, *****P* < 0.0001 (Student's *t* test).

il27 (Fig. 6A). CSGG treatment also significantly increased the protein levels of IL-10 and TGF-β1 and decreased IFNγ levels measured from culture supernatants (Fig. 6B). Moreover, compared with IL-10, TGF-β played a pivotal role in iT_{reg} generation because addition of anti–TGF-β–neutralizing antibody (Ab) almost completely abolished CSGG-mediated iT_{reg} induction (Fig. 6C). IL-10–deficient DCs also displayed a tendency toward reduced iT_{reg} generation compared with wild-type (WT) DCs, although statistical significance was not achieved (Fig. 6D).

To determine the role of pattern recognition receptors (PRRs) on DCs, we reanalyzed the RNA-seq data for the expression of genes encoding all the Toll-like receptor (TLR) subtypes upon CSGG treatment. We observed a prominent selective increase in *TLR2* expression, suggesting CSGG recognition via TLR2 (Fig. 6E). When cocultured with CSGG and assessed in vitro, $CD11c^+$ DCs isolated from mouse strain lacking TLR2 ($TLR2^{-/-}$) displayed a significant reduction in iT_{reg}-inducing activity compared with WT DCs (Fig. 6F and fig. S10A). TLR2-deficient DCs elicited reduced levels of IL-10 and TGF-β1 in the cultures (Fig. 6, G and H) but no change in IFNγ levels (fig. S10D). The defect seen with TLR2-deficient DCs was not further enhanced by additional blocking of TLR6 signaling (fig. 10B). A similar defect was also observed when DCs were isolated from mice lacking the downstream adaptor protein MyD88 (Fig. 6F and fig. S10A). TLR4- or TLR6-deficient DCs displayed no significant defect (Fig. 6F and fig. S10A). Also, T_{reg} induction was unaffected when $TLR3^{-/-}TLR7^{-/-}TLR9^{-/-}$ triple knockout DCs were used (fig. 10C). To test potential involvement of C-type lectin receptors, we cultured $Dectin1^{-/-}$ and $Dectin2^{-/-}$ DCs or $CD11c^+$ DCs pretreated with blocking Ab for DC-SIGN and mannose receptor with naïve $CD4^+$ T cell in the presence of CSGG. However, no significant reduction was observed in the level of CSGG-induced iT_{reg} cell generation among the tested experimental groups (fig. S10, E and F). Together, these data strongly suggested that the TLR2/MyD88 signaling pathway is required for CSGG-mediated induction of iT_{reg} cells. However, provided that the $TLR2^{-/-}$ DCs still retained low degree of T_{reg} induction activity upon CSGG treatment (Fig. 6F), it seems possible that additional signaling pathways may also be involved.

CSGG-induced iT_{reg} cells are capable of suppressing intestinal inflammation

The identification of CSGG as the major T_{reg}-inducing component of *Bb* suggested that administration of CSGG might be effective in generating and boosting T_{reg} cell function and thereby suppressing inflammatory conditions. Under in vitro conditions, sorted iT_{reg} cells generated in the presence of CSGG-treated DCs displayed significantly enhanced suppressive capacity relative to iT_{reg} cells induced with mock-treated DCs (fig. S11A). For in vivo studies, we used the T cell transfer model of colitis induction. Naïve $CD4^+$ T cells were transferred into $Rag1^{-/-}$ lymphopenic hosts, either alone or together with various types of sorted allelically marked ($CD45.1^+$) iT_{reg} cells. nT_{reg} cells sorted from the $Foxp3^{GFP}$ mice were used as a positive control. As expected, mice injected with naïve T cells alone developed severe signs of colitis, as indicated by weight loss (Fig. 7A), shortening of the colon (Fig. 7B and fig. S11B), observed by histological staining, changes in colonic thickness, and tissue histology with high histology score (Fig. 7, C and D). For iT_{reg} cells, co-injection of control mock-induced iT_{reg} cells was ineffective and failed to inhibit signs of colitis (Fig. 7A). In marked contrast, *Bb*-induced iT_{reg} cells were highly efficient in suppressing colitis, as too were nT_{reg} cells (Fig. 7A). Equivalent suppression of colitis was mediated by CSGG-induced iT_{reg} cells (Fig. 7A). Like *Bb*-induced iT_{reg} cells, CSGG-induced iT_{reg} analysis from cLP at the end of the experiment present at a much higher proportion than in the mock-treated control group, indicating enhanced stability of the *Foxp3* locus (Fig. 7E). However, as expected, nT_{reg} cells are more stable than the iT_{reg} cells induced in vitro by *Bb* or CSGG treatment (Fig. 7E).

To test whether administration of CSGG itself could suppress colitis development, we adoptively transferred naïve $CD4^+Foxp3^-$ T cells sorted from $CD45.1^+Foxp3^{GFP}$ mice into SPF $Rag1^{-/-}$ hosts, followed by intraperitoneal administration of PBS or CSGG (100 μg per dose) three times a week until the end of the experiment. CSGG administration suppressed colitis development (Fig. 7, F to H, and fig. S11C). Thus, whereas the PBS-treated animals developed colitis and displayed progressive weight loss and enhanced histopathology with high histology score, CSGG treatment largely ameliorated the disease progression (Fig. 7, F to H, and fig. S11C). The protective effect of CSGG treatment was well correlated with an increase in total $Foxp3^+$ T_{reg} cells (fig. S11D) and reduced frequency of IFNγ-producing effector T cells (Fig. 7I). Together, these data suggest that $CD4^+Foxp3^+$ T_{reg} cells induced by CSGG treatment are functionally active to suppress the progression of inflammatory colitis.

DISCUSSION

Here, we have demonstrated that *Bb*, a component of the human gut microbiome, can induce the generation of $Foxp3^+$ pT_{reg} cells that have diverse TCR specificity to dietary Ags, commensal bacteria, and *Bb* itself and that these T cells can potently suppress intestinal inflammation. Furthermore, we have identified *Bb*-derived CSGG as a key effector component that promotes the *Bb*-dependent induction of T_{reg} cells.

Previous work has shown that the T_{reg}-inducing activity of bacterial metabolites involves both T cell intrinsic and extrinsic molecular events that affect generation and function of various immune cells. For example, by virtue of histone deacetylase inhibitory activity, short-chain fatty acids (SCFAs) like butyrate and propionate enhance histone acetylation of the *Foxp3* locus and the acetylated state of the Foxp3 protein itself, a modification that correlates with enhanced T_{reg} function (*21, 35*). In parallel, butyrate negatively affects proinflammatory cytokine production from DCs, thereby facilitating de novo T_{reg} generation (*35*). Although a number of studies have established the ability of distinct microbes to drive intestinal T cells to specific fates, identification of the microbial components responsible has not always been feasible.

Here, we have established that *Bb*-dependent $Foxp3^+$ pT_{reg} induction is mediated by the cell surface polysaccharides CSGG. Although previous reports suggest that PSA or outer membrane vesicles from the *Bf* can induce T_{reg} cells, the types of T_{reg} cells might be quite different compared with CSGG-induced cells. PSA mainly generated a $Foxp3^-$ population of T_{reg} cells with an $IL\text{-}10^{high}IFN\gamma^{high}$ phenotype (*2, 6, 15–17, 36*), whereas CSGG-induced T_{reg} cells are mostly $Foxp3^+IL\text{-}10^{high}IFN\gamma^{low}$ phenotype. *Bf* monocolonization mainly generated $IFN\gamma^+IL\text{-}10^{high}$ cells with a slight increase in $Foxp3^+$ T_{reg} cells (*2*). This discrepancy may be attributed to the differences in the experimental systems such as mouse strain (B6 mice versus Swiss-Webster mice), route of bacterial administration (oral gavage versus spread on food and bedding), and analysis time point after monoassociation of the bacteria (3 weeks versus 60 days).

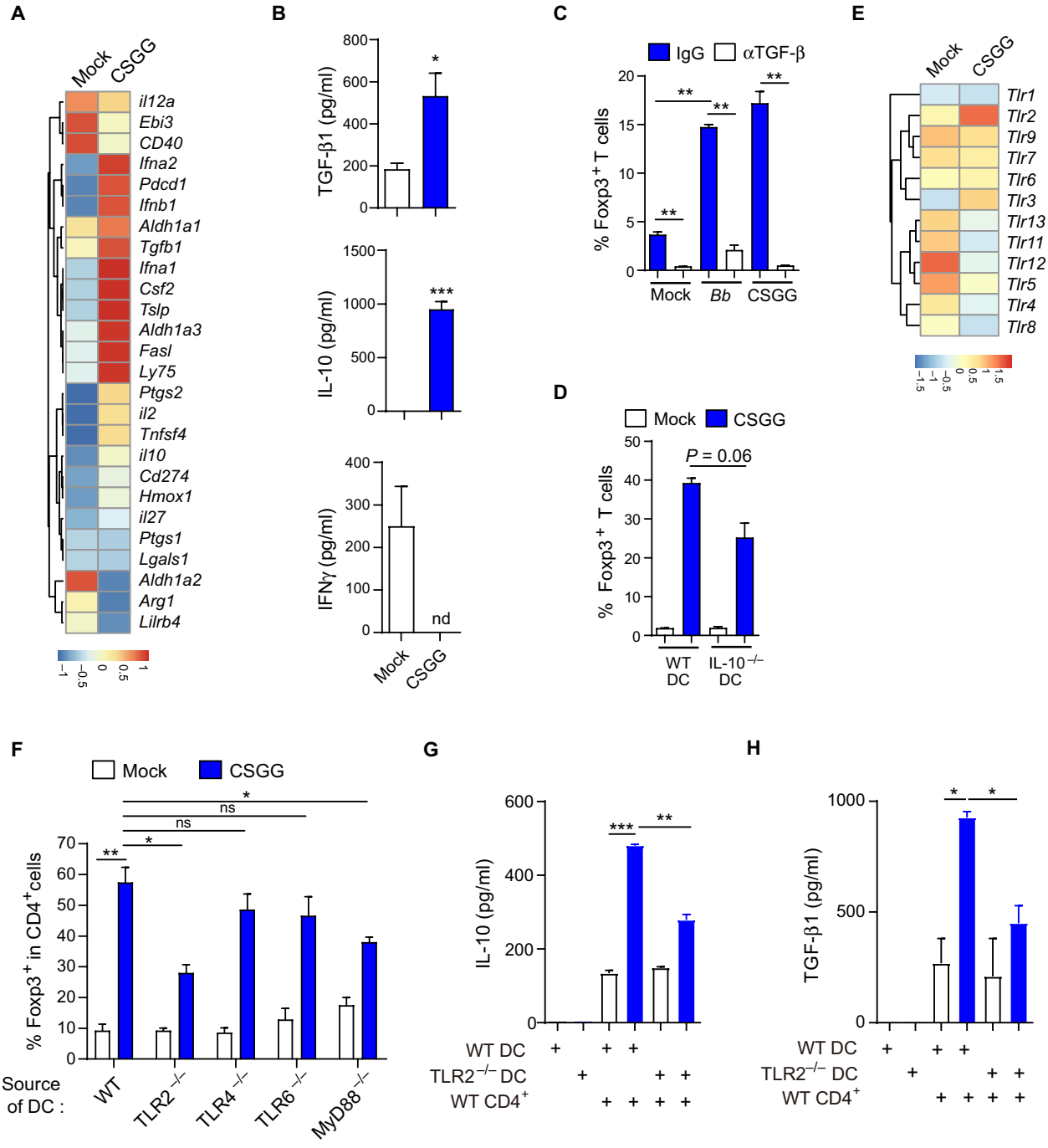


Fig. 6. CSGG facilitates iT$_{reg}$ induction through TLR2-dependent generation of regulatory DCs. (**A**) RNA-seq analysis of CD11c$^+$ splenic DCs treated with mock or CSGG for 4hours. (**B**) Cytokine levels in the culture supernatants after coculturing naïve CD4$^+$ T cells with CD11c$^+$ DCs pretreated with mock or CSGG. Data are representative of four independent experiments with similar results. nd, not detected. (**C**) Effect of anti–TGF-β Ab treatment on in vitro CD4$^+$Foxp3$^+$ T$_{reg}$ induction after *Bb* or CSGG treatment. (**D**) CD11c$^+$ DCs from the WT or IL-10$^{-/-}$ mice pretreated with CSGG were cocultured with WT naïve CD4$^+$ T cells, and iT$_{reg}$ induction was determined after 3 days. Data are representative of three independent experiments with similar results (C and D). (**E**) RNA-seq data were analyzed to determine the expression of genes encoding the TLR subtypes upon CSGG treatment. (**F**) Naïve CD4$^+$ T cells and CD11c$^+$ DCs derived from indicated mice, pretreated with mock or CSGG, were cocultured in suboptimal iT$_{reg}$ generation condition. CD4$^+$Foxp3$^+$ iT$_{reg}$ population was determined by flow cytometry. Data are representative of five independent experiments with similar results. (**G** and **H**) IL-10 and TGF-β1 cytokine levels in the culture supernatants after naïve CD4$^+$ T cells were cocultured with WT or TLR2-deficient CD11c$^+$ DCs pretreated with mock or CSGG. Data are representative of at least three independent experiments with similar results. All bar graphs show means ± SEM. *P < 0.05, **P < 0.01, ***P < 0.001 (Student's t test).

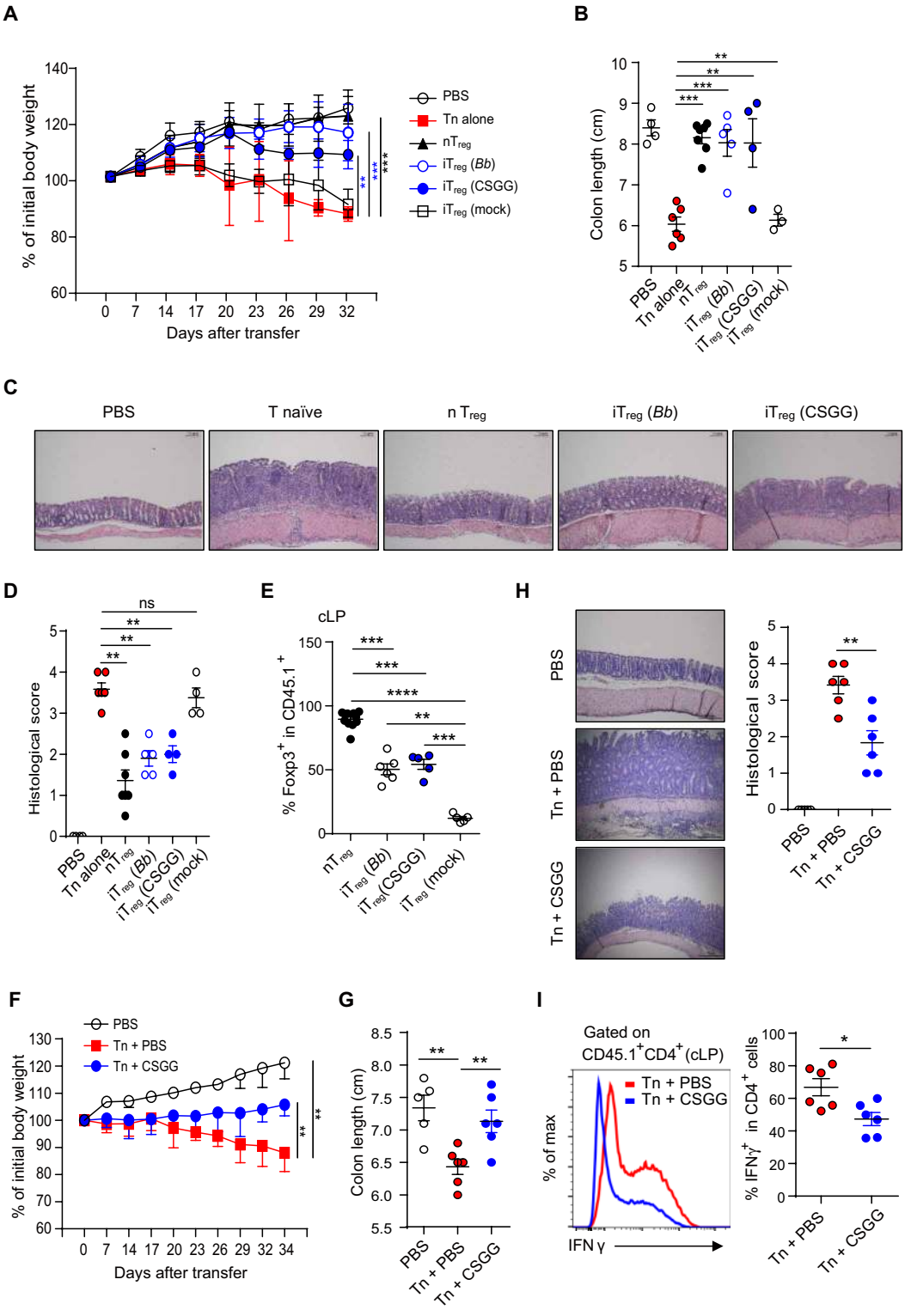


Fig. 7. CSGG-induced iT_{reg} cells are capable of suppressing intestinal inflammation. (**A** to **D**) Naïve $CD4^+Foxp3^-$ T cells sorted from $Thy1.1^+Foxp3^{GFP}$ reporter mice were adoptively cotransferred into *Rag1*$^{-/-}$ recipients in indicated combinations of iT_{reg} cells or nT_{reg} cells. Changes in body weight, colon length, histopathology, and histological score of colonic tissue were measured. (**E**) Analysis of the Foxp3 stability of transferred T_{reg} cells in the cLP at the end of the experiment. At the time of transfer, the purity of the sorted $CD4^+Foxp3^{GFP+}$ cells was more than 98%. (**F** to **H**) Naïve $CD4^+Foxp3^-$ T cells sorted from $CD45.1^+Foxp3^{GFP}$ reporter mice were adoptively transferred into *Rag1*$^{-/-}$ mice, followed by intraperitoneal administration of PBS or CSGG (100 μg/ml). Changes in body weight, colon length, histopathology, and histological score in colonic tissue were measured. (**I**) Analysis of the IFNγ-producing effector T cells in cLP at the end of the experiment. Data are representative of at least three independent experiments with similar results ($n \geq 3$ mice). Graphs with error bars show means ± SEM. *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$, ****$P < 0.0001$ (Student's *t* test).

Our data also suggest that *Bb*/CSGG induces T_{reg} cells via a DC-dependent mechanism, which involves phenotypic conversion of conventional DCs into a population of rDCs that produce abundant levels of inhibitory cytokines, namely, TGF-β1 (*4*) and IL-10 (*37*). *Bb* monocolonization also enriches the number of $CD103^+CD11b^+$ DCs in cLP, which potentiates conversion of naïve CD4 T cells into T_{reg} cells with TCR specificity to diverse Ags. We also provide evidence that TLR2 expression on DCs, and not on $CD4^+$ T cells, is largely responsible for the sensing and delivery of CSGG-induced tolerance signals for secretion of IL-10 and TGF-β1, which induce T_{reg} cell generation. Previous studies have suggested that bacterial components could induce IL-10–producing T_{reg} cells via activation of DCs in a TLR2-dependent manner (*16, 17, 38*). PSA could directly convert naïve $CD4^+$ T cells into T_{reg} cells in a TLR2-dependent manner (*6, 39*). However, it is still unclear how TLR2 signaling is involved in the generation of rDCs or T_{reg} cells. Previous studies reported that treatment of splenic DCs with TLR2 ligand induces IL-10 and a retinoic acid–metabolizing enzyme, Raldh, thereby inducing iT_{reg} cells (*38, 40*). In addition, it is also reported that, depending on the types of TLR agonists, they differentially modulate extracellular signal–regulated kinase signaling, c-Fos activity, and cytokine responses in DCs to induce different T_H responses (*41*). Although TLR2 and MyD88 are important for *Bb*/CSGG-dependent induction of T_{reg} cells, other PRRs might also be involved. In the future, we will direct our studies to identify these molecules and to understand the relative contributions of these pathways to *Bb*/CSGG-dependent induction of T_{reg} cells. In addition, further investigations are required to understand how *Bb*/CSGG could induce T_{reg} cells in the spleen and pLN in addition to the mucosal lymphocytes. These could be exerted by several possibilities: (i) CSGG may circulate systemically, thereby inducing T_{reg} cells elsewhere; (ii) T_{reg} cells generated at the mucosal sites (colon, siLP, and mLN) may emigrate to spleen and pLN; and/or (iii) alteration of intestinal permeability may account for the observed induction of T_{reg} cells at these sites in monocolonized mice.

Bb induced pT_{reg} cells that display potent suppressive capacity against intestinal inflammation. Colonic T_{reg} cells isolated from *Bb*-monocolonized mice have distinct TCR repertoire and could proliferate in response to *Bb*-derived Ags. These findings suggest that, although dominant colonic T_{reg} cell clones may be originated from thymic selection (*42*), *Bb* administration could induce the conversion of naïve $CD4^+Foxp3^-$ cells into the $CD4^+Foxp3^+$ cells in the colon, which could suppress colitis mediated by commensal-induced inflammatory T cells. Patients with inflammatory bowel disease were reported to have specific reduction in *Bifidobacterium* as compared with healthy controls (*43*). *Bifidobacterium* are members of bacterial species known to colonize the gut of breastfed infants early in life (*44*). Administration of *Bifidobacterium* to the allergic infants with aberrant composition of gut microbiota alleviated allergic inflammation (*45*). The identification of CSGG as an active component of T_{reg}-inducing *Bb* able to suppress colitis thus emerges as a potentially important mediator for establishing immune homeostasis in the gut. Moreover, because *Bb* could induce food-reactive T_{reg} cells, administration of CSGG-producing *Bb* could be considered for the treatment of allergic diseases.

MATERIALS AND METHODS

Mice

Mice were maintained in the animal facility of POSTECH Biotech Center, and all the experimental procedures were approved by the POSTECH Institutional Animal Care and Use Committee. A colony of GF C57BL/6 (B6) mice was established at POSTECH from breeders obtained from A. Macpherson (Bern University, Switzerland) and D. Artis (then at University of Pennsylvania, currently at Cornell University, USA) and maintained in sterile flexible film isolators (Class Biological Clean Ltd., USA). GF status was monitored monthly by culture of cecal contents. *Foxp3*-eGFP, $Tlr2^{-/-}$, $Tlr4^{-/-}$, $Tlr6^{-/-}$, and $MyD88^{-/-}$ animals were obtained from the Jackson Laboratory. C57BL/6-CD45a(*Ly5a*)-$Rag1^{-/-}$ TCR OT-II ($Rag1^{-/-}$ OT-II TCR transgenic) and $Rag1^{-/-}$ mice were obtained from Taconic. $Dectin1^{-/-}$ and $Dectin2^{-/-}$ mice were provided by Y. Iwakura (Tokyo University of Science, Japan). The CBir mouse was a gift from C. O. Elson (University of Alabama at Birmingham). Gender- and age-matched mice between 6 and 12 weeks old were used.

Bacterial strain and analysis of bacterial colonization

Bb was anaerobically cultured in MRS media (BD Difco) supplemented with 0.1% L-cysteine. *Lpa* was cultured in MRS media. *Bf* (ATCC 25285; NCTC 9343) was obtained from ATCC and anaerobically cultured in GAM Broth (code: 05422; Nissui, Japan) (*46*). For monocolonization, lyophilized bacteria [5×10^8 colony-forming units (CFU)/200 μl] were administered once orally to GF mice, and their colonization was confirmed by HISTO-FISH or DNA sequencing. *Bf* monocolonization was confirmed by DNA sequencing. National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) analysis confirmed that nucleotide sequences correspond to the *Bf* NCTC 9343 (https://blast.ncbi.nlm.nih.gov/Blast.cgi) (fig. S12).

Data availability for RNA-seq

Total RNA was extracted from the splenic $CD11c^+$ DCs stimulated with mock or CSGG (100 μg/ml) for 4 hours and purified with Ribospin II (GeneAll Biotechnology). RNA quantitation and quality control were performed using NanoDrop 2000 (Thermo Fisher Scientific, Wilmington, DE). Library preparation was performed using the TruSeq Stranded mRNA Sample Preparation Kit (Illumina, San Diego, CA), and RNA-seq was performed using the NextSeq 500 Sequencing System.

Purification of cell surface polysaccharides from *Bb*

Cultured *Bb* was harvested and washed by PBS two times. Purification of cell surface polysaccharide was performed as previously described (*47*) with minor modifications. Briefly, acidic phenol (Sigma-Aldrich) treatment was performed at 68°C to extract capsular polysaccharides, and residual phenol was removed by ether treatment followed by dialysis against distilled water for 3 days. To remove nucleic acids and proteins, we performed DNase I (Roche) and RNase (Sigma-Aldrich) digestion overnight at 37°C, followed by Pronase (protease from *Streptomyces griseus*; Sigma-Aldrich) digestion at 37°C overnight. After acetic acid treatment, centrifugation was performed to remove precipitates. Chilled ethanol was added to precipitate polysaccharides and then dialyzed against distilled water for 3 days and freeze dried. Purified polysaccharides were dissolved in water, and gel filtration was performed by high-performance liquid chromatography (HPLC) column (TSKgel G5000PWXL, Tosho). Anion exchange chromatography was performed (HiPrep Q FF 16/10, GE Healthcare) to further separate neutral and negative charge polysaccharides. The concentration of polysaccharide was determined by acid phenol assay (*48*).

SUPPLEMENTARY MATERIALS

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Materials and Methods
Fig. S1. Identification of *Bb* as T_{reg}-inducing bacteria.
Fig. S2. Effect of *Bb* monocolonization on cytokine levels in T_{reg} and non-T_{reg} cells.
Fig. S3. *Bb* monocolonization facilitates de novo generation of pT_{reg} cells.
Fig. S4. *Bb* colonization induces dietary Ag– and/or microbiota-reactive T_{reg} cells.
Fig. S5. Effect of *Bb* monocolonization on the TCR repertoire of T_{reg} cells.
Fig. S6. Effect of *Bb* monocolonization on phenotypes and population of cLP-DC subtypes.
Fig. S7. Effect of *Bb* monocolonization on phenotypes and population of DC subtypes in mLN and siLP.
Fig. S8. CSGG of the *Bb* enhances T_{reg} cell induction.
Fig. S9. Role of DC subtypes in inducing *Bb*/CSGG-mediated iT_{reg} cells.
Fig. S10. CSGG facilitates iT_{reg} induction through TLR2-mediated generation of regulatory DCs.
Fig. S11. CSGG-induced iT_{reg} cells are capable of suppressing intestinal inflammation.
Fig. S12. Confirmation of *Bf* monocolonization by DNA sequencing.
Table S1. Peptide sequences of α-chain CDR3 region of T_{reg} cells sorted from colon, mLN, and spleen of *Bb*-monocolonized mice compared with GF mice.
Table S2. Peptide sequences of β-chain CDR3 region of T_{reg} cells sorted from colon, mLN, and spleen of *Bb*-monocolonized mice compared with GF mice.
Table S3. Raw data (Excel file).
References (*49*–*55*)

REFERENCES AND NOTES

1. A. J. Macpherson, N. L. Harris, Interactions between commensal intestinal bacteria and the immune system. *Nat. Rev. Immunol.* 4, 478–485 (2004).
2. S. K. Mazmanian, C. H. Liu, A. O. Tzianabos, D. L. Kasper, An immunomodulatory molecule of symbiotic bacteria directs maturation of the host immune system. *Cell* **122**, 107–118 (2005).
3. T. Gensollen, S. S. Iyer, D. L. Kasper, R. S. Blumberg, How colonization by microbiota in early life shapes the immune system. *Science* **352**, 539–544 (2016).
4. K. Atarashi, T. Tanoue, T. Shima, A. Imaoka, T. Kuwahara, Y. Momose, G. Cheng, S. Yamasaki, T. Saito, Y. Ohba, T. Taniguchi, K. Takeda, S. Hori, I. I. Ivanov, Y. Umesaki, K. Itoh, K. Honda, Induction of colonic regulatory T cells by indigenous *Clostridium* species. *Science* **331**, 337–341 (2011).
5. I. I. Ivanov, K. Honda, Intestinal commensal microbes as immune modulators. *Cell Host Microbe* **12**, 496–508 (2012).
6. J. L. Round, S. M. Lee, J. Li, G. Tran, B. Jabri, T. A. Chatila, S. K. Mazmanian, The Toll-like receptor 2 pathway establishes colonization by a commensal of the human microbiota. *Science* **332**, 974–977 (2011).
7. H.-J. Wu, E. Wu, The role of gut microbiota in immune homeostasis and autoimmunity. *Gut Microbes* **3**, 4–14 (2012).
8. S. Hori, T. Nomura, S. Sakaguchi, Control of regulatory T cell development by the transcription factor Foxp3. *Science* **299**, 1057–1061 (2003).
9. J. D. Fontenot, J. P. Rasmussen, L. M. Williams, J. L. Dooley, A. G. Farr, A. Y. Rudensky, Regulatory T cell lineage specification by the forkhead transcription factor foxp3. *Immunity* **22**, 329–341 (2005).
10. V. Gaboriau-Routhiau, S. Rakotobe, E. Lécuyer, I. Mulder, A. Lan, C. Bridonneau, V. Rochet, A. Pisi, M. De Paepe, G. Brandi, The key role of segmented filamentous bacteria in the coordinated maturation of gut helper T cell responses. *Immunity* **31**, 677–689 (2009).
11. I. I. Ivanov, K. Atarashi, N. Manel, E. L. Brodie, T. Shima, U. Karaoz, D. Wei, K. C. Goldfarb, C. A. Santee, S. V. Lynch, T. Tanoue, A. Imaoka, K. Itoh, K. Takeda, Y. Umesaki, K. Honda, D. R. Littman, Induction of intestinal Th17 cells by segmented filamentous bacteria. *Cell* **139**, 485–498 (2009).
12. H.-J. Wu, I. I. Ivanov, J. Darce, K. Hattori, T. Shima, Y. Umesaki, D. R. Littman, C. Benoist, D. Mathis, Gut-residing segmented filamentous bacteria drive autoimmune arthritis via T helper 17 cells. *Immunity* **32**, 815–827 (2010).
13. T. Tanoue, K. Atarashi, K. Honda, Development and maintenance of intestinal regulatory T cells. *Nat. Rev. Immunol.* **16**, 295–309 (2016).
14. K. Atarashi, T. Tanoue, K. Oshima, W. Suda, Y. Nagano, H. Nishikawa, S. Fukuda, T. Saito, S. Narushima, K. Hase, S. Kim, J. V. Fritz, P. Wilmes, S. Ueha, K. Matsushima, H. Ohno, B. Olle, S. Sakaguchi, T. Taniguchi, H. Morita, M. Hattori, K. Honda, T_{reg} induction by a rationally selected mixture of Clostridia strains from the human microbiota. *Nature* **500**, 232–236 (2013).
15. Y. Shen, M. L. G. Torchia, G. W. Lawson, C. L. Karp, J. D. Ashwell, S. K. Mazmanian, Outer membrane vesicles of a human commensal mediate immune regulation and disease protection. *Cell Host Microbe* **12**, 509–520 (2012).
16. J. L. Round, S. K. Mazmanian, Inducible $Foxp3^+$ regulatory T-cell development by a commensal bacterium of the intestinal microbiota. *Proc. Natl. Acad. Sci. U.S.A.* **107**, 12204–12209 (2010).
17. K. M. Telesford, W. Yan, J. Ochoa-Reparaz, A. Pant, C. Kircher, M. A. Christy, S. Begum-Haque, D. L. Kasper, L. H. Kasper, A commensal symbiotic factor derived from *Bacteroides fragilis* promotes human $CD39^+$ $Foxp3^+$ T cells and T_{reg} function. *Gut Microbes* **6**, 234–242 (2015).
18. C.-S. Chae, H.-K. Kwon, J.-S. Hwang, J.-E. Kim, S.-H. Im, Prophylactic effect of probiotics on the development of experimental autoimmune myasthenia gravis. *PLOS ONE* **7**, e52119 (2012).
19. H.-K. Kwon, G.-C. Kim, Y. Kim, W. Hwang, A. Jash, A. Sahoo, J.-E. Kim, J. H. Nam, S.-H. Im, Amelioration of experimental autoimmune encephalomyelitis by probiotic mixture is mediated by a shift in T helper cell immune response. *Clin. Immunol.* **146**, 217–227 (2013).
20. H.-K. Kwon, C.-G. Lee, J.-S. So, C.-S. Chae, J.-S. Hwang, A. Sahoo, J. H. Nam, J. H. Rhee, K.-C. Hwang, S.-H. Im, Generation of regulatory dendritic cells and $CD4^+Foxp3^+$ T cells by probiotics administration suppresses immune disorders. *Proc. Natl. Acad. Sci. U.S.A.* **107**, 2159–2164 (2010).
21. Y. Furusawa, Y. Obata, S. Fukuda, T. A. Endo, G. Nakato, D. Takahashi, Y. Nakanishi, C. Uetake, K. Kato, T. Kato, T. Kato, M. Takahashi, N. N. Fukuda, S. Murakami, E. Miyauchi, S. Hino, K. Atarashi, S. Onawa, Y. Fujimura, T. Lockett, J. M. Clarke, D. L. Topping, M. Tomita, S. Hori, O. Ohara, T. Morita, H. Koseki, J. Kikuchi, K. Honda, K. Hase, H. Ohno, Commensal microbe-derived butyrate induces the differentiation of colonic regulatory T cells. *Nature* **504**, 446–450 (2013).
22. J. Ochoa-Repáraz, D. W. Mielcarz, L. E. Ditrio, A. R. Burroughs, S. Begum-Haque, S. Dasgupta, D. L. Kasper, L. H. Kasper, Central nervous system demyelinating disease protection by the human commensal *Bacteroides fragilis* depends on polysaccharide A expression. *J. Immunol.* **185**, 4101–4108 (2010).
23. T. J. Borody, A. Khoruts, Fecal microbiota transplantation and emerging applications. *Nat. Rev. Gastroenterol. Hepatol.* **9**, 88–96 (2012).
24. F. Yan, D. B. Polk, Probiotics and immune health. *Curr. Opin. Gastroenterol.* **27**, 496–501 (2011).
25. J.-S. Hwang, C.-R. Im, S.-H. Im, Immune disorders and its correlation with gut microbiome. *Immune Netw.* **12**, 129–138 (2012).
26. J.-E. Kim, C. S. Chae, G.-C. Kim, W. Hwang, J.-s. Hwang, S.-M. Hwang, Y. Kim, Y.-T. Ahn, S.-G. Park, C.-D. Jun, D. Rudra, S.-H. Im, *Lactobacillus helveticus* suppresses experimental rheumatoid arthritis by reducing inflammatory T cell responses. *J. Funct. Foods* **13**, 350–362 (2015).
27. J. P. Edwards, A. M. Thornton, E. M. Shevach, Release of active TGF-β1 from the latent TGF-β1/GARP complex on T regulatory cells is mediated by integrin β_8. *J. Immunol.* **193**, 2843–2849 (2014).
28. E. M. Shevach, A. M. Thornton, tTregs, pTregs, and iTregs: Similarities and differences. *Immunol. Rev.* **259**, 88–102 (2014).
29. J. M. Weiss, A. M. Bilate, M. Gobert, Y. Ding, M. A. Curotto de Lafaille, C. N. Parkhurst, H. Xiong, J. Dolpady, A. B. Frey, M. G. Ruocco, Y. Yang, S. Floess, J. Huehn, S. Oh, M. O. Li, R. E. Niec, A. Y. Rudensky, M. L. Dustin, D. R. Littman, J. J. Lafaille, Neuropilin 1 is expressed on thymus-derived natural regulatory T cells, but not mucosa-generated induced $Foxp3^+$ T reg cells. *J. Exp. Med.* **209**, 1723–1742 (2012).
30. B.-H. Yang, S. Hagemann, P. Mamareli, U. Lauer, U. Hoffmann, M. Beckstette, L. Föhse, I. Prinz, J. Pezoldt, S. Suerbaum, T. Sparwasser, A. Hamann, S. Floess, J. Huehn, M. Lochner, $Foxp3^+$ T cells expressing RORγt represent a stable regulatory T-cell effector lineage with enhanced suppressive capacity during intestinal inflammation. *Mucosal Immunol.* **9**, 444–457 (2016).
31. E. Sefik, N. Geva-Zatorsky, S. Oh, L. Konnikova, D. Zemmour, A. M. McGuire, D. Burzyn, A. Ortiz-Lopez, M. Lobera, J. Yang, S. Ghosh, A. Earl, S. B. Snapper, R. Jupp, D. Kasper, D. Mathis, C. Benoist, Individual intestinal symbionts induce a distinct population of $ROR\gamma^+$ regulatory T cells. *Science* **349**, 993–997 (2015).
32. C. Ohnmacht, J.-H. Park, S. Cording, J. B. Wing, K. Atarashi, Y. Obata, V. Gaboriau-Routhiau, R. Marques, S. Dulauroy, M. Fedoseeva, M. Fedoseeva, M. Busslinger, N. Cerf-Bensussan, I. G. Boneca, D. Voehringer, K. Hase, K. Honda, S. Sakaguchi, G. Eberl, The microbiota regulates type 2 immunity through $ROR\gamma t^+$ T cells. *Science* **349**, 989–993 (2015).
33. K. S. Kim, S.-W. Hong, D. Han, J. Yi, J. Jung, B.-G. Yang, J. Y. Lee, M. Lee, C. D. Surh, Dietary antigens limit mucosal immunity by inducing regulatory T cells in the small intestine. *Science* **351**, 858–863 (2016).
34. Y. Cong, C. T. Weaver, A. Lazenby, C. O. Elson, Colitis induced by enteric bacterial antigen-specific CD4+ T cells requires CD40-CD40 ligand interactions for a sustained increase in mucosal IL-12. *J. Immunol.* **165**, 2173–2182 (2000).
35. N. Arpaia, C. Campbell, X. Fan, S. Dikiy, J. van der Veeken, P. deRoos, H. Liu, J. R. Cross, K. Pfeffer, P. J. Coffer, A. Y. Rudensky, Metabolites produced by commensal bacteria promote peripheral regulatory T-cell generation. *Nature* **504**, 451–455 (2013).
36. N. K. Surana, D. L. Kasper, The yin yang of bacterial polysaccharides: Lessons learned from *B. fragilis* PSA. *Immunol. Rev.* **245**, 13–26 (2012).
37. V. K. Raker, M. P. Domogalla, K. Steinbrink, Tolerogenic dendritic cells for regulatory T cell induction in man. *Front. Immunol.* **6**, 569 (2015).

38. S. Dillon, S. Agrawal, K. Banerjee, J. Letterio, T. L. Denning, K. Oswald-Richter, D. J. Kasprowicz, K. Kellar, J. Pare, T. van Dyke, S. Ziegler, D. Unutmaz, B. Pulendran, Yeast zymosan, a stimulus for TLR2 and dectin-1, induces regulatory antigen-presenting cells and immunological tolerance. *J. Clin. Invest.* **116**, 916–928 (2006).
39. S. Dasgupta, D. Erturk-Hasdemir, J. Ochoa-Reparaz, H.-C. Reinecker, D. L. Kasper, Plasmacytoid dendritic cells mediate anti-inflammatory responses to a gut commensal molecule via both innate and adaptive mechanisms. *Cell Host Microbe* **15**, 413–423 (2014).
40. S. Manicassamy, R. Ravindran, J. Deng, H. Oluoch, T. L. Denning, S. P. Kasturi, K. M. Rosenthal, B. D. Evavold, B. Pulendran, Toll-like receptor 2–dependent induction of vitamin A–metabolizing enzymes in dendritic cells promotes T regulatory responses and inhibits autoimmunity. *Nat. Med.* **15**, 401–409 (2009).
41. S. Agrawal, A. Agrawal, B. Doughty, A. Gerwitz, J. Blenis, T. Van Dyke, B. Pulendran, Cutting edge: Different Toll-like receptor agonists instruct dendritic cells to induce distinct Th responses via differential modulation of extracellular signal-regulated kinase-mitogen-activated protein kinase and c-Fos. *J. Immunol.* **171**, 4984–4989 (2003).
42. S. K. Lathrop, S. M. Bloom, S. M. Rao, K. Nutsch, C.-W. Lio, N. Santacruz, D. A. Peterson, T. S. Stappenbeck, C.-S. Hsieh, Peripheral education of the immune system by colonic commensal microbiota. *Nature* **478**, 250–254 (2011).
43. R. Verma, A. K. Verma, V. Ahuja, J. Paul, Real-time analysis of mucosal flora in patients with inflammatory bowel disease in India. *J. Clin. Microbiol.* **48**, 4279–4282 (2010).
44. F. Turroni, E. Foroni, P. Pizzetti, V. Giubellini, A. Ribbera, P. Merusi, P. Cagnasso, B. Bizzarri, G. L. de'Angelis, F. Shanahan, D. van Sinderen, M. Ventura, Exploring the diversity of the bifidobacterial population in the human intestinal tract. *Appl. Environ. Microbiol.* **75**, 1534–1545 (2009).
45. P. V. Kirjavainen, T. Arvola, S. J. Salminen, E. Isolauri, Aberrant composition of gut microbiota of allergic infants: A target of bifidobacterial therapy at weaning? *Gut* **51**, 51–55 (2002).
46. M. Ichimura, H. Nakayama-Imaohji, S. Wakimoto, H. Morita, T. Hayashi, T. Kuwahara, Efficient electrotransformation of *Bacteroides fragilis*. *Appl. Environ. Microbiol.* **76**, 3325–3332 (2010).
47. D. L. Kasper, A. Weintraub, A. A. Lindberg, J. Lönngren, Capsular polysaccharides and lipopolysaccharides from two *Bacteroides fragilis* reference strains: Chemical and immunochemical characterization. *J. Bacteriol.* **153**, 991–997 (1983).
48. M. DuBois, K. A. Gilles, J. K. Hamilton, P. T. Rebers, F. Smith, Colorimetric method for determination of sugars and related substances. *Anal. Chem.* **28**, 350–356 (1956).
49. A. Izcue, J. L. Coombes, F. Powrie, Regulatory lymphocytes and intestinal inflammation. *Annu. Rev. Immunol.* **27**, 313–338 (2009).
50. F. Powrie, T cells in inflammatory bowel disease: Protective and pathogenic roles. *Immunity* **3**, 171–174 (1995).
51. M. Choolani, S. S. Y. Ho, K. Razvi, S. Ponnusamy, S. Baig, N. M. Fisk, A. Biswas; Rapid Molecular Testing in Prenatal Diagnosis Group, FastFISH: Technique for ultrarapid fluorescence in situ hybridization on uncultured amniocytes yielding results within 2 h of amniocentesis. *Mol. Hum. Reprod.* **13**, 355–359 (2007).
52. A. Dinoto, T. M. Marques, K. Sakamoto, S. Fukiya, J. Watanabe, S. Ito, A. Yokota, Population dynamics of *Bifidobacterium* species in human feces during raffinose administration monitored by fluorescence in situ hybridization-flow cytometry. *Appl. Environ. Microbiol.* **72**, 7739–7747 (2006).
53. B. Smith, S. Bodé, B. L. Petersen, T. K. Jensen, C. Pipper, J. Kloppenborg, M. Boyé, K. A. Krogfelt, L. Mølbak, Community analysis of bacteria colonizing intestinal tissue of neonates with necrotizing enterocolitis. *BMC Microbiol.* **11**, 73 (2011).
54. R. Yoshida, T. Yoshioka, S. Yamane, T. Matsutani, T. Toyosaki-Maeda, Y. Tsuruta, R. Suzuki, A new method for quantitative analysis of the mouse T-cell receptor *V* region repertoires: Comparison of repertoires among strains. *Immunogenetics* **52**, 35–45 (2000).
55. K. J. Maloy, L. Salaun, R. Cahill, G. Dougan, N. J. Saunders, F. Powrie, $CD4^+CD25^+T_R$ cells suppress innate immune pathology through cytokine-dependent mechanisms. *J. Exp. Med.* **197**, 111–119 (2003).

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Cell surface polysaccharides of *Bifidobacterium bifidum* induce the generation of Foxp3$^+$ regulatory T cells

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Deconstructing probiotics

Besides supporting host metabolism, our intestinal microbiota also play a vital role in modulating functions of immune cells in the gut. Here, Verma *et al.* have examined how a particular probiotic strain, *Bifidobacterium bifidum*, promotes the generation of T regulatory (T_{reg}) cells in the intestine. They have identified β-glucan/galactan polysaccharides derived from the cell wall of *B. bifidum* to be responsible for promoting T_{reg} cell induction in the intestine. Further, they report this process to be dependent on intestinal dendritic cells that express Toll-like receptor 2. Studies such as this open up the possibility of using microbial components rather than live microbes to treat microbial dysbiosis associated with gastrointestinal disorders including colitis and Crohn's disease.

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