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Commensal bacteria-derived metabolites shape the intestinal immune system through epigenetic modifications

○ Koji Hase¹, Yukihiro Furusawa¹, Yuuki Obata¹, Shinji Fukuda², Hiroshi Ohno³¹International R&D Center for Mucosal Vaccines, The Institute of Medical Science, The University of Tokyo,²Institute for Advanced Biosciences, Keio University,³RIKEN Center for Integrative Medical Sciences (IMS-RCAI)

Gut commensal microbes shape the mucosal immune system by regulating differentiation and expansion of several types of T cells (1). *Clostridia*, a dominant class of commensal microbe, can induce colonic regulatory T (Treg) cells, which play a central role in the suppression of inflammatory and allergic responses (2). However, the molecular mechanisms by which commensal microbes induce colonic Treg cells have been unclear. Here we show that a large bowel microbial fermentation product, butyrate, induces the differentiation of colonic Treg cells. A comparative NMR-based metabolome analysis suggested that the luminal concentrations of short-chain fatty acids (SCFAs) positively correlated with the number of Treg cells in the colon. Among SCFAs, butyrate induced the differentiation of Treg cells *in vitro* and *in vivo* and ameliorated the development of colitis induced by adoptive transfer of CD4⁺CD45RB^{hi}T cells in Rag1^{-/-} mice. Treatment of naïve T cells under the Treg-polarizing conditions with butyrate enhanced histone H3 acetylation in the promoter and conserved non-coding sequence (CNS) regions of the *Foxp3* locus. These data indicate that the microbial-derived butyrate can regulate differentiation of Treg cells by epigenetic changes. Our findings provide new insight into the mechanisms by which host-microbe interactions establish immunological homeostasis in the gut (3).

[References]

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