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Epigenetic alterations induced by chronic inflammation and influence of colonic microbiome on them

Toshikazu Ushijima
Chief of Division of Epigenomics, National Cancer Center Research Institute

Epigenetic modifications, namely histone modifications and DNA methylation, are inherited upon somatic cell divisions, and function as an interface between the genome and environment. Their alterations are causally involved in cancer and potentially in other chronic disorders, and induced by chronic inflammation, such as ulcerative colitis and *Helicobacter pylori*-induced gastritis [Ushijima, Clin Cancer Res, 18: 923, 2012]. Using dextran sodium sulfate (DSS)-induced mouse colitis, we demonstrated that alteration of trimethylation of histone H3 lysine 27 (H3K27me3) in colonic epithelial cells is induced relatively early after exposure to inflammation, and that some of the induced H3K27me3 can lead to aberrant DNA methylation [Takeshima, Carcinogenesis, 33: 2384, 2012]. The accumulation of aberrant DNA methylation is associated with development of colonic tumors, producing "epigenetic field defect" [Katsurano, Oncogene, 31: 342, 2012]. Modulation of colonic microbiome has strong effects on the degree of the defect and eventually on tumor incidence, showing the usefulness of the degree of epigenetic field defect as an early-stage marker to assess the effect of intervention into colitis. Epigenetic alterations are an important player in disorders associated with altered microbiome.