

IL-1 β maintains the DNA hypermethylation of anti-inflammatory IL-10 gene in a human intestinal epithelial cell line

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Intestinal inflammation is a natural process crucial to maintain gut integrity, but its deregulation is involved in the pathogenesis of severe intestinal disorders^[1]. Intestinal epithelial cells play a crucial role in the inflammatory response, modulating the immune cell exposure to antigens and by their ability to secrete many inflammatory mediators. IL-1 β represents a pivotal player: secreted by infiltrated leucocytes, it induces the expression of several pro-inflammatory genes. Also the anti-inflammatory IL-10, whose function is to terminate the inflammatory process, modulates the intestinal physiology^[2]. Recent clinical reports showed that patients with ulcerative colitis in remission phase have significantly higher *IL10* gene expression in mucosa compared with active patients and controls^[3]. Moreover, in the latest years aberrant epigenetic mechanisms were put in binomial relationship with chronic inflammatory diseases^[4].

Previously, we described a demethylation of pro-inflammatory *IL6* and *IL8* genes in human colonic Caco-2 cells differentiated into an enterocyte-like phenotype and exposed to the inflammatory action of IL-1 β ^[5].

In the present study we evaluate whether the IL-1 β treatment affected the methylation status of the anti-inflammatory *IL10* gene, in the same *in vitro* model. Our results showed that IL-1 β treatment did not change the hypermethylation status of the *IL10* promoter. Moreover, in cell lysates from IL-1 β -treated Caco-2 cells, we observed a dose-dependent increase of DNMTs activity and, surprisingly, a decrease of DNMT3b expression. These findings put in evidence the complexity of relationship between IL-1 β and DNMTs, and may suggest a potential role of IL-1 β as pleiotropic modulator of DNA methylation in Caco-2 cell line.

References

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