

P656 - 217: EPIGENETIC MODIFICATION OF ALLERGIC ASTHMA BY GUT MICROBIOTA

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**Background and Aim:** Asthma is a highly prevalent chronic disease extremely affects quality of life. Allergic asthma initiates from immune deregulation in early infantile. Role of gut microbiota on asthma initiation and development has been discovered. Also impact of epigenetic mechanisms in regulation of asthma has been reported. In this article, intestinal microbiome impact on epigenetic modulation of allergic asthma has been reviewed.

**Methods:** Articles between years 1965 and 2016 were searched and studied precisely in medline. The key words "asthma, epigenetic and gut microbiome" were used. The associated articles were studied and summarized.

**Results:** Intestinal microbiota is a reservoir of epigenetic constituents. Gut microbiota containing high fibre suppresses expression of certain genes in fetal lung lead to inhibition of airway responses in asthmatic patients. Moreover commensal gut microbes produce epigenetically modifiers including short chain fatty acids affect asthma development. Also probiotic bacteria, could induce production of some metabolites including short-chain fatty acids acetate regulate the methylation of gene promoters and histone acetylations in macrophages/ regulatory T cells suppress intestinal inflammation. Besides numerous epigenetic factors present in gut like early infancy enteroviruses, nutrients and contact to air contaminants have adverse epigenetic effects on immune system could exacerbate asthma.

**Conclusion:** The gut microbiota, as part of epigenetic location, has an intensive effect on intestinal immune system and plays an important role in immunopathogenesis of asthma. Therefore adaptation of gut microbiome profile and products including lipopolysaccharide, alimentary interventions and probiotic bacteria might be efficient epigenetic-mediated modulation of immune cells and could be a potential therapeutic strategy in asthma.

**Keywords:** Asthma, epigenetic, gut, microbiome



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