



## Commentary

## Allergy Associations with the Adult Fecal Microbiota: Cause, Effect or Biomarker?



Seppo Salminen

Functional Foods Forum, Faculty of Medicine, University of Turku, 20014 Turku, Finland

## ARTICLE INFO

## Article history:

Received 27 November 2015

Accepted 27 November 2015

Available online 28 November 2015

Several studies have suggested that the intestinal microbiota has an important role in host physiology and pathophysiology and in health and disease (Palm et al., 2015). The so called hygiene hypothesis describes the potentially protective influence of microbial exposures in early life and their impact on the development of allergic diseases (Liu, 2015). A recent report described the impact of normal American diet or vegan diet versus USDA recommended diet on the daily intake of microbes. Surprisingly, the diet according to nutrition recommendations provided a significantly higher microbial load to the gut when compared with the diet based on convenience foods (Lang et al., 2014). This certainly demonstrates the altered exposure to microbes due to changes in our eating habits.

Recent investigations have suggested an overall “microbiome hypothesis” associated with factors in the home environment, medical practices such as antibiotics and c-section deliveries, and hygienic behavior as well as industrialized food supply (Liu, 2015). Earlier reports based on conventional and molecular microbiology methods describe deviations in microbiota development during the early childhood preceding the development of atopic eczema (Kalliomäki et al., 2001; Nylund et al., 2015). Little is known on the microbiota in adults associated with allergic disease and therefore new information is urgently required. Relatively crude markers of a potentially protective microbial environment have been reported and most do not distinguish features that differ from pathologic features.

Several studies have focused on succession of microbes developing to a relatively stable intestinal microbiota composition, which appears to be specific to each individual (Rautava et al., 2012). Modification of microbiota by specific probiotics has already led to recommendations of probiotic use in at risk populations (Fiocchi et al., 2015).

In this issue of *EBioMedicine*, Hua et al. report a study which used the publicly available data from the American Gut Project including questionnaires and fecal 16S rRNA sequence data. The report focuses on associations between self-reported allergies and the adult fecal microbiota composition. Self-reported allergy prevalence among the 1879 subjects was more than 80% which is likely to have overestimated the problem. Subjects with self-reported allergies had significantly less diverse microbiota with differences also in specific components of the microbiota as compared to individuals with no reported allergies.

The data presented in the current article provide interesting cross-sectional associations between the gut microbiota and allergic symptoms. However, the presence of an altered microbiota in the gut associated with allergy or intolerance symptoms cannot be considered as a cause or even an effect as the questions related to the association with microbiota composition are likely to be overestimated and in some cases even untrue. However, the study provides new clues to define microbiota deviations, which could serve as markers of increased risk or treatment success in adult subjects who suffer from allergic diseases of intestinal origin.

Allergic participants also had markedly altered microbiota composition and the results were especially significant in the case of subjects with nut and seasonal allergies. Thus, the results are in concordance with allergy-associated gut microbiota deviations and they are consistent with the hygiene hypothesis. These results may provide clues to devising treatment or prevention strategies for allergic disease in adults. However, more work is needed on potential markers which could support prevention strategies also in infants and children.

## Disclosure

The author declared no conflicts of interest.

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DOI of original article: <http://dx.doi.org/10.1016/j.ebiom.2015.11.038>.

E-mail address: [sepsal@utu.fi](mailto:sepsal@utu.fi).

<http://dx.doi.org/10.1016/j.ebiom.2015.11.051>

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