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INFLUENCE OF HOST-ASSOCIATED FACTORS ON THE GUT MICROBIOTA OF ADOLESCENTS FROM GEOGRAPHICALLY DISTANT POPULATIONS

Shreyas Kumbhare, National Centre for Cell Science, Pune, India, R.C. Patel Arts, Science, and Commerce College, Shirpur, India, Children's Hospital Research Institute of Manitoba, Winnipeg, Canada; **Himanshu Kumar**, Functional Foods Forum, University of Turku, Turku, Finland; **Somak Chowdhury**, National Centre for Cell Science, Pune, India; **Samuli Rautava**, Functional Foods Forum, University of Turku, Turku, Finland, University of Turku, Turku, Finland; **Nitinkumar Patil**, Smt. Chandibai Himathmal Mansukhani College, Thane, India; **Ravindra Patil**, R.C. Patel Arts, Science, and Commerce College, Shirpur, India; **Erika Isolauri**, University of Turku, Turku, Finland; **Ashish Bavdekar**, K.E.M. Hospital Research Centre, Pune, India; **Seppo Salminen**, Functional Foods Forum, University of Turku, Turku, Finland; **Yogesh Shouche**, National Centre for Cell Science, Pune, India

Background:

FUT2 (fucosyl transferase-2) secretor status and birth mode are key determinants of the compositional development of gut microbiota in Western pediatric populations, but these observations may not be representative of other populations globally. The potential interaction and persistence of these effects in later life also remain poorly understood.

Objective:

We compared Finnish and Indian adolescents, to understand geographic variation in the impact of *FUT2* secretor status and birth mode on gut microbial composition.

Methods:

Fecal microbial communities were defined in 52 Finnish and 47 Indian adolescents (aged 13-14) using PCR-DGGE, amplicon sequencing, and qPCR, followed by the analysis of Single Nucleotide Polymorphisms (SNP) to determine *FUT2* secretor status (rs601338). The microbiome analysis toolbox QIIME was used for multivariate analyses comparing gut microbial composition and the differential abundance of bacterial taxa.

Results:

The gut bacterial community structure was significantly different in Indian compared to Finnish children, with a higher abundance of *Blautia* and *Bifidobacterium* in the Finnish group, and predominance of *Prevotella* and *Megasphaera* in the Indian group ($p < 0.001$). We observed a strong influence of *FUT2* secretor status on the abundance of specific bacterial taxa such as *Megamonas*, *Megasphaera* (abundant in non-secretors in Indian group; $p < 0.001$), *Blautia*, *Bifidobacterium* (abundant in Finnish secretors; $p < 0.001$) and *Prevotella* (abundant in Indian secretors; $p < 0.001$). Furthermore, we also observed the influence of birth mode on the abundance of taxa such as *Streptococcus*, *Ruminococcus* (higher in vaginally born; $p < 0.001$) and *Akkermansia* and *Escherichia* (higher in cesarean born children of both the populations; $p < 0.001$). Interestingly, the multi-variate analysis revealed that these host factors influenced different taxa when compared between populations.

Conclusion:

We found substantial differences in the gut microbial composition of the Indian and Finnish adolescents. This study also revealed the differences in the influence of host factors in shaping the microbial community within two distinct populations.