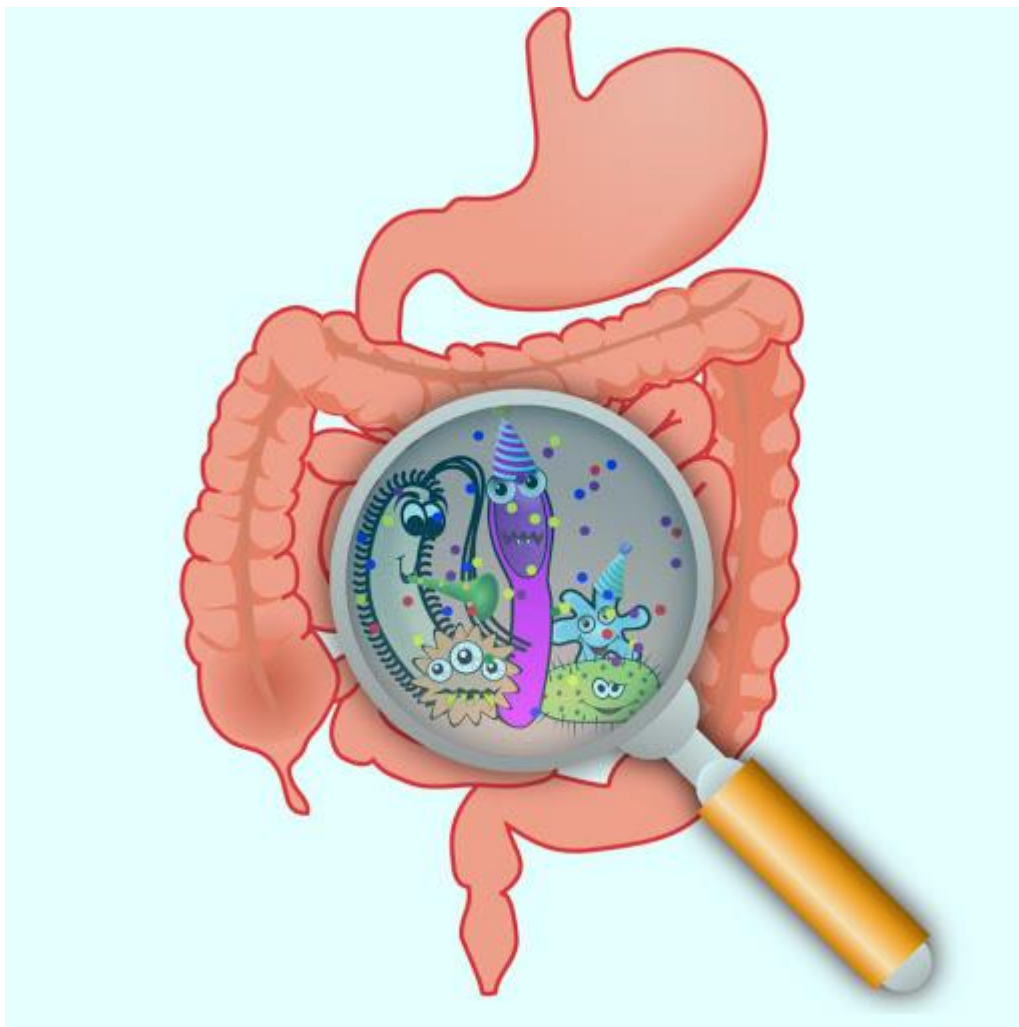


DBT-THSTI team studies gut microbiota of diabetic patients

New Delhi, April 05: Type 2 diabetes (T2D), a multifactorial disease influenced by host genetics and environmental factors, is the most common endocrine disease in India and across the world. Researchers from Translational Health Science and Technology Institute (DBT-THSTI), Madras Diabetes Research Foundation (MDRF), Tata Consultancy Services (TCS) Ltd. and University of Copenhagen, Denmark examined the compositional and functional potential of the gut microbiota of 1,110 individuals from Denmark and India with a focus on T2D.



The research scientists decoded and investigated the metagenomics DNA sequences of the samples. They observed that the T2D patients have an increased relative abundance of some of the bacteria comprising of three operational taxonomic units (OTUs) from the *Lachnospiraceae* family, and a decreased abundance of *Subdoligranulum*, *Butyricicoccus* and

Anaerosporbacter. The study reports a possible association of *Megasphaera* OTU(s) with impaired glucose tolerance, which is significantly pronounced in Indian subjects.

Metformin is the most commonly used drug for diabetes across the world. There are several reports indicating non-antibiotic drugs can also change the composition of gut microbiome. To address this question, the researchers included metformin treated and metformin naive diabetic patients. It was observed that metformin can also change the composition of gut microbiome. However, specific changes are also observed in the metformin naive patients. Supporting the hypothesis, dysbiosis in the gut microbiome may also be a potential risk for diabetes. The results present trans-ethnic gut microbiome and inflammation signatures associated with prediabetes, in Indian and Danish populations. The identified microbial signatures and their associations with T2D may serve as potential early indicators for individuals at risk of dysglycemia.

Complete paper: <https://pubmed.ncbi.nlm.nih.gov/33658065/>

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