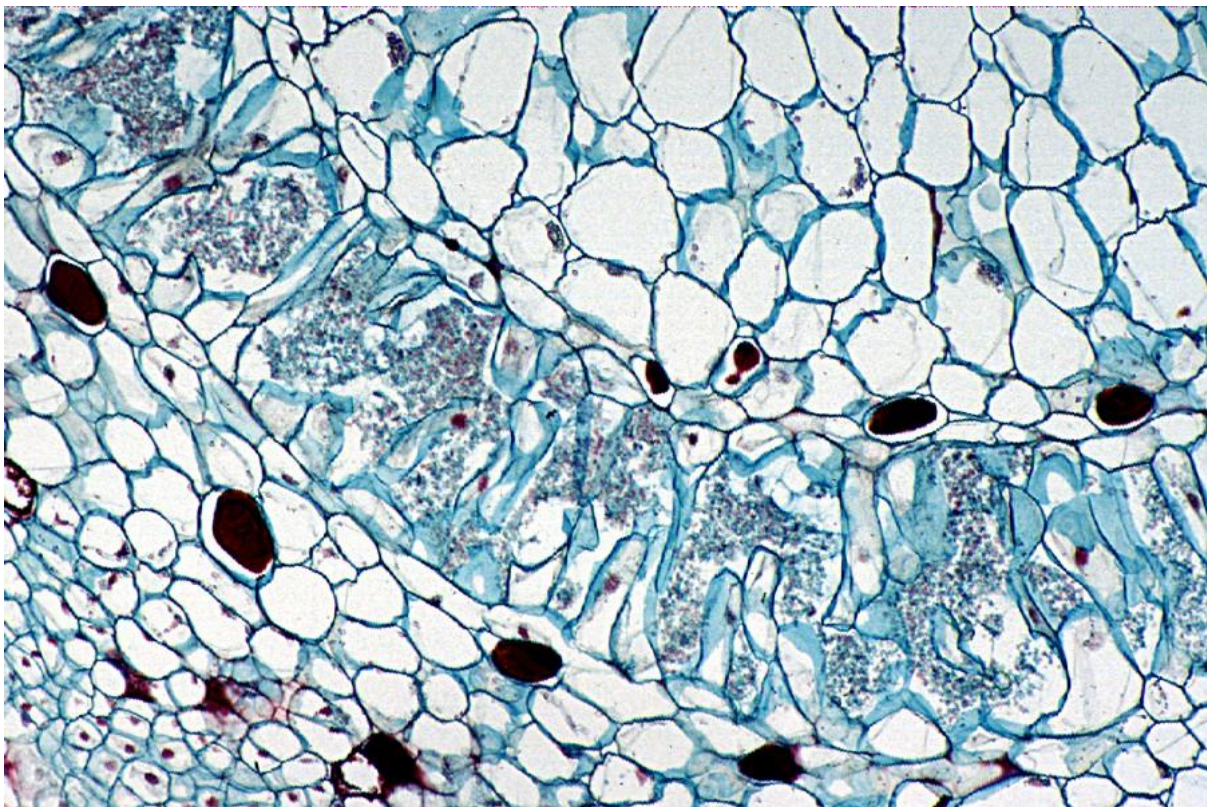


DBT-NCCS studies on joint families show association of microbiome with age

New Delhi, July 15: The human microbiome refers to the community of microorganisms associated with the human body, including those present inside and on external surfaces. The importance of the role played by this microbial ecosystem in maintaining human health, and its association with various diseases, has been gaining increasing recognition and attention.



The microbiome comprises many different types of microbes that contribute in various ways to human health, such as by aiding digestion, protecting the body against pathogens, and regulating the central nervous system. Several factors like age, diet, ethnicity, geographic location, etc., can influence the human microbiome. To understand the individual influence of a single determinant, the microbiomes of people who share similarities with respect to the other influencing factors, would need to be examined.

Ageing is a complex, progressive process involving several factors, which gradually results in decreased efficiency of functioning of the systems of the body. Studies in humans and laboratory animals have revealed that the microbiome also changes with age. Most of these changes may not have any significant influence on health, but some types of microbes found to be especially associated with the elderly, appear to be important.

Artificially changing the gut microbiome of test animals like fruit flies and mice in the laboratory, has been shown to cause changes in the physiology, with a concomitant influence on health, and to even increase lifespan. It is no surprise, therefore, that the correlation of the microbiome and age has been an important subject of research.

The majority of earlier studies to understand age-related changes in the human microbiome had mainly focused on the gut microbiome, or were conducted on populations from different geographical locations or with different dietary habits. Therefore, to more comprehensively understand this association, Dr. Yogesh Shouche and his group at the National Centre for Cell Science (NCCS), Pune, leveraged the unique joint family arrangement to track age-associated changes in the human microbiome.

Extended Indian families, with multiple generations living together, are well suited for such studies, since they share similar dietary and social habits, sanitation conditions, economic status and geographic location. The researchers conducted an analysis of the microbial community from the gut, mouth and skin of healthy individuals, in collaboration with the KEM Hospital Research Centre, Pune, Government Institute of Science, Aurangabad, and Chest Research Foundation, Pune. The individuals selected for this study belonged to six different patrilineal families with three generations living together, from the same location in rural India.

The studies have helped understand the precise and perceptible associations between age and the human microbiome. A larger variation with age was observed in the composition of the skin microbiome, than that of the gut and oral cavity. Bacteria belonging to the phylum Proteobacteria in the gut microbiome and phylum Fusobacteria in the oral microbiome showed higher abundance with increasing age. Such correlations were not observed with the skin microbiome.

From amongst over a hundred and seventy bacterial genera in the gut microbiome, only those bacterial species that belong to the genus *Bacteroides* showed age-associated changes, and the abundance of *Bacteroides* species was found to decrease with increasing age. These studies suggest that the microbiomes undergo very specific age-related changes, which warrant further exploration.

For example, it would be worthwhile to investigate the specific physiological role played by Proteobacteria in the gut. Similarly, understanding the influence of bacteria belonging to *Treponema*, *Fusobacterium*, *Granulicatella* and *Streptococcus* found in the human oral microbiome could reveal pertinent information. Moreover, data obtained from a section of the healthy Indian population, such as these, could serve as baseline reference for further microbiome studies focused on individuals with disease like diabetes and obesity.

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