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Vaginal microbiota and its role in preterm births among Indian women

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Dr. Bhabatosh Das and his team at Faridabad based Translational Health Science and Technology Institute (THSTI) is inquiring the nature of Indian vaginal microbiota as an essential exercise to find its role in virginal health, and pre term births among Indian women. Under the flagship GARBH-Ini project, samples from 40 pregnant women were investigated to identify the microbial species populating the vaginal environment in Indian women.

In a first of its kind, the understanding of Indian women was developed further by adopting a metagenomic approach of culture-independent high-throughput sequencing of the 16S rRNA gene. The adopted methodology rendered the present study advantage over the previous investigations, which adopted a culture-based method for studying the vaginal microbiota. Such selected amplification of genomic signatures (rRNA sequence) for the microbes identified in the culture-based method remains inadequate in painting a holistic picture of the vaginal microbiota.

Thus, findings from several studies revealed that the Indian women of reproductive age have an acidic vaginal environment. The vaginal bacteria belong to four different phyla, highly dominated Firmicutes (85%). Other phyla include Proteobacteria (9%), Bacteroidetes (3%), and Actinobacteria (2%). A total of 12 bacterial genera were also identified. *Lactobacillus*, the lactic acid-producing bacteria, dominates the bacterial population.

The presence of *Lactobacillus* species marks a healthy vaginal environment by preventing the growth of all ochthonous bacterial taxa and reducing the risk for urogenital diseases. Amongst the different *Lactobacillus* species, *L. iners, L. crispatus,* and *L. gasseri* were found prevalent. Moreover, an insight into the genome of different lactic acid bacteria showed their ability to modulate the vaginal microbiota composition favourably and improve the health of the host. Besides *Lactobacillus*, *Halomonas* species were also prevalent, while the *Gardnerella* species associated with pre term birth (PTB) were deficient. Hence, it presents a novel challenge for researchers to find the link between the microbiome and the PTB occurrence in Indian women. Additionally, by understanding the dysbiotic changes in the microbiota during

conditions such as bacterial vaginosis can help establish innovative diagnostic techniques as well.

A complex microbiota inhabits the female vagina, and it earmarks the gut microbial composition of the babies delivered vaginally. The nature of microbes residing in vagina can also serve as a risk factor for preterm birth (PTB). With the issue of PTB at the surge in India, impacting approximately 3.6 million infants annually, such a premise demands investigation.

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