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Abstract Topic:- Genetic, genome and epigenome databases and resources

Abstract Title:- Meta-Analysis of microbiota samples which helps in maintenance of Gut health

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Aims:-The aim of this research was to re-analyze four types of datasets, totaling 141 fecal samples retrieved from the NCBI Sequence Read Archive (SRA), in order to investigate the human microbiome through metagenomic sequencing and identify crucial bacteria associated with carbohydrate metabolism, thereby contributing to gut health and various digestive, fermentation, and metabolic processes.

Methods:- For this study, metagenomic data analysis was conducted on a total of 141 fecal samples obtained from the NCBI SRA. The analysis involved pre-processing, binning, and taxonomic identification of the metagenomic data. This allowed for the re-analysis of four distinct datasets to reveal and characterize key bacteria involved in carbohydrate metabolism essential for gut health.

Results:- Taxonomic classification and analysis of the metagenomic data uncovered ten significant bacterial species crucial for carbohydrate metabolism and beneficial for gut health. These bacteria included *Blautia obeum*, *Bacteroides nordii*, *Bacteroides eggerthii*, *Bacteroides salyersiae*, *Prevotella copri*, *Lactobacillus delbrueckii*, *Alistipes dispar*, *Alistipes shahii*, *Alistipes ihumii*, *Blautia hansenii*, and *Bacteroides caccae*. These bacteria are known to play pivotal roles in the processes of digestion, fermentation, and overall metabolism within the gut.

Conclusions:- The findings of this study highlight ten important bacterial species involved in carbohydrate metabolism, critical for maintaining gut health and contributing to digestive, fermentation, and metabolic processes. The use of metagenomic sequencing facilitated the identification of these key bacteria, offering valuable insights into their roles within the human microbiome. Understanding the significance of these bacteria may contribute to future research focusing on the manipulation and enhancement of the gut microbiota to support overall health and metabolic functions.

Keywords:- Metagenomics; Gut microbiota; Taxonomic identification; Human microbiome; *Lactobacillus*