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Opinion Article

Insights of Probiotics: Properties and Analysis

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DESCRIPTION

Probiotics are live bacteria found in fermented foods and cultured milk and are commonly utilized in infant meal preparation. They're known as "healthy bacteria" because they have a variety of health benefits, including preventing bowel ailments, strengthening the immune system, treating lactose intolerance and restoring gut microbial balance, alleviating menopause issues, and lowering traveler's diarrhoea. Recent research has focused on their usage in the treatment of skin and oral ailments. Furthermore, probiotics have been proposed as a unique treatment approach for anxiety and depression *via* modulating the gut-brain axis. The natural and main constituents of gut microbiota are hundreds of different bacteria species. Probiotics are intestinal bacteria that are thought to have potential health benefits to the host *via* modulating the intestinal microbiota. Beneficial probiotic bacterial strains have been reported to belong to the genera *Lactobacillus* and *Bifidobacterium*. *L. acidophilus*, *L. casei*, *L. plantarum*, *B. lactis*, *B. longum*, and *B. bifidum* are all typical species. Improvement of the gastrointestinal microbiota, immune system enhancement, serum cholesterol decreased, cancer prevention, treatment of irritable bowel-associated diarrheas, antihypertensive effects, and lactose metabolism improvement are some of the key health benefits attributed to probiotics.

Proteobacteria (*Acetobacteraceae*) and Firmicutes (*Streptococcaceae, Lactobacillaceae*) were found to be the most prevalent members of the microbial communities in naturally ethnic fermented milk products such as churkam, churpi, mar, and dahi, according to metagenomic studies. The most common lactic acid bacteria found in these fermented goods were *L. helveticus* and *L. lactis*, while the most common acetic acid bacteria found were *Gluconobacter* and *Acetobacter* spp. As a result, these metagenomic and culturomics techniques will reveal a broader range of microbes associated with these indigenous goods, as well as a greater understanding of how their characteristics contribute to human welfare. The comparison of probiotic strains and their associated mutants with fewer or no probiotic benefits is a recent method that is based on genomic technologies. This method aims to find genetic components that are engaged in specific traits. The growing number of bacteria having sequenced genomes, including probiotic strains like *Bifidobacterium longum*, *Lactobacillus plantarum*, and *Lactobacillus acidophilus*, helps to the genomic approach's consolidation. The sequencing of genomes has also paved the door for comparative and functional proteomics, a new approach to studying bacterial characteristics. Whilst also letting for the creation of a global picture of proteins expressed by the genome, including their relative abundance during growth phases, as well as chemical and post-translational modifications, translocation, and synthesis regulation phenomena, a global picture of proteins expressed by the genome can be created. Proteomics sheds new light on Lactic acid bacteria's metabolic characteristics. Lactic acid bacteria are found in the mouth cavity, gastrointestinal system, and female genitourinary tract and constitute an important element of the normal human microbiota. Food supplements containing specific LAB, known as probiotics, have gained appeal as a result of a resurgence of interest in "all-natural" solutions to treat illness. Proteomic investigations also help with the annotation process of genome sequences, which complements the genomic approach.

CONCLUSION

In order to investigate the technical and probiotic qualities of LAB, a mix of both methodologies is required. Comparative proteomics can be used to select probiotic strains based on properties that are currently investigated through *in vitro* screening tests, but it's also likely that proteins and proteomic patterns will be identified that could one day serve as bacterial biomarkers for properties that are currently only revealed through biological tests or extensive clinical trials. Functional proteome studies can aid in elucidating the molecular foundation for a strain's health effects as well as the numerous processes that contribute to the probiotic notion. In modern probiotic studies, for instance, identifying cell components involved in probiotic activity is a difficulty. For the expression of proteomic analysis of differential protein expression using 2-DE, tryptic digestion, chip-LC-QTOF mass analysis, and protein

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identification. The researchers applied a novel approach based on proteomics as an analytical tool to identify distinctive protein profiles related to adherence to mucin as a model probiotic feature. The correlation of proteomic profiles and proteins with specific probiotic capabilities paves the path for their usage as bacterial biomarkers, not only for bacterial traits but also for their potential health impacts.