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In Silico Study of Cell Surface Structures of Parabacteroides distasonis Involved in Its Maintain Within the Gut Microbiota and Its Potential Pathogenicity

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Abstract : Gut microbiota (GM) is now considered a new organ mainly due to the microorganism's specific biochemical interaction with its host. Although mechanisms underlying host-microbiota interactions are not fully described, it is now well-defined that cell surface molecules and structures of the GM play a key role in such relation. The study of surface structures of GM members is also fundamental for their role in the establishment of species in the versatile and competitive environment of the digestive tract and as a potential virulence factor. Among these structures are capsular polysaccharides (CPS), fimbriae, pili and lipopolysaccharides (LPS), all well-described for their central role in microorganism colonization and communication with host epithelium. The health-promoting Parabacteroides distasonis, which is part of the core microbiome, has recently received a lot of attention, showing beneficial properties for its host and as a new potential biotherapeutic product. However, to the best of the authors' knowledge, the cell surface molecules and structures of P. distasonis that allow its maintain within the GM are not identified. Moreover, although P. distasonis is strongly recognized as intestinal commensal species with benefits for its host, it has also been recognized as an opportunistic pathogen. In this study, we reported gene clusters potentially involved in the synthesis of the capsule, fimbriae-like and pili-like cell surface structures in 26 P. distasonis genomes and applied the new RfbA-Typing classification in order to better understand and characterize the beneficial/pathogenic behaviour related to P. distasonis strains. In context, 2 different types of fimbriae, 3 of pilus and up to 14 capsular polysaccharide loci, have been identified over the 26 genomes studied. Moreover, the addition of data to the rfbA-Type classification modified the outcome by rearranging rfbA genes and adding a fifth group to the classification. In conclusion, the strain variability in terms of external proteinaceous structure could explain the inter-strain differences previously observed in P. distasonis adhesion capacities and its potential pathogenicity.

Keywords : gut microbiota, Parabacteroides distasonis, capsular polysaccharide, fimbriae, pilus, O-antigen, pathogenicity, probiotic, comparative genomics
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