

Title: Genomic diversity and carbohydrate utilisation in human-associated bifidobacterial isolates

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Bifidobacteria are beneficial commensals of the human gastrointestinal tract and their presence in the gut has been associated with positive health effects on the host. They account for a vast proportion of the infant gut microbiota, when the infant is fed on a milk-based diet, with their number progressively decreasing in adult and elderly. The gut microbiota and associated metabolic activities significantly impact on human health by promoting appropriate development of the infant immune system and contributing to the maintenance of the intestinal homeostasis. In recent years it has become clear that microbial colonization of the gut immediately following birth represents a crucial phase in the development of host metabolism and physiology, in some case promoted by prebiotic substrates such as Human Milk Oligosaccharides (HMOs). For this reason, gut microbiota research has shown particular interest on early colonisers of the infant gut capable of metabolising those prebiotic substrates. In the current study an extensive comparative and functional genomic analysis of 10 novel bifidobacterial isolates have highlighted the presence of genetic loci responsible for HMOs utilisation, production of extracellular structures involved in bacteria-host interaction and production of antimicrobials in the strains, thus showing how comparative genomic approaches can support the phenotypic characterisation of novel bifidobacterial isolates.