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Deciphering the dietary fibre-degrading enzyme system of the human gut bacterium *Bacteroides xylanisolvens* using transcriptomic, proteomic and mutagenesis approaches

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In humans, the degradation of dietary fibers is a metabolic function undertaken by the intestinal microbiota. This metabolic function favors the homeostasis of the digestive ecosystem and participates in the prevention of several chronic disorders like metabolic diseases. The bacteria able to initiate this process possess complex enzymatic systems that deconstruct polysaccharides into compounds (oligosaccharides, sugars) that serve as energetic substrates to the whole microbial community. *Bacteroides xylanisolvens* is a prevalent bacterial species in the human gut that has the particularity to degrade both pectins (soluble fibers found in fruits) and xylans (insoluble fibers found in cereals). The type strain XB1A was isolated in our laboratory and was shown to harbor more than 300 genes encoding carbohydrate active enzymes (CAZymes) that are distributed in 74 genomic loci called Polysaccharide Utilization Loci (PUL). Considering the complexity of *B. xylanisolvens* enzyme system, the pectinolytic and xylanolytic function was studied using transcriptomics (RNAseq), proteomics and directed mutagenesis. The results highlighted the existence of 6 and 2 PULs involved in pectin and xylan degradation, respectively. Our findings highlight the metabolic plasticity of *B. xylanisolvens* towards non-starch dietary polysaccharides which contributes to its competitive fitness within the human gut ecosystem.