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Investigating the degradation pathways of fungal mannoproteins as carried out by different bacteria found in the human gut

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PURPOSE OF THE ABSTRACT

As we transition to more sustainable food sources in order to reduce resource consumption and our ecological footprint, it is critical we investigate the effects new food sources have on the health of consumers. Changes in diet can particularly influence the structure and diversity of the human gut microbiome (HGM) which previous research has indicated contributes to overall host health, particularly of the gut and brain via the gut-brain axis [1]. Quorn is currently one of the leading brands in Europe promoting sustainably produced meat alternatives manufactured from the fermentation of the fungal species Fusarium venenatum (F. venenatum) [2]. Humans lack the capacity to fully digest F. venenatum due to not having the necessary enzymes to degrade the complex sugars (dietary fibres) that constitute its cell wall, instead, we rely solely on bacteria that make up the HGM. Different bacterial species endogenous to the gut utilise diverse dietary fibre through the process of fermentation by primary and secondary degraders. Cross-feeding interactions between different degraders are essential to ensuring the health of the HGM during dietary changes. To degrade a polysaccharide, bacteria rely on glycoside hydrolases (GHs) which cleave specific bonds in the structure of a polysaccharide through hydrolysis reactions. Bacteria native to the HGM group enzymes (GHs) specific to a single substrate in co-localised, co-regulated gene clusters known as polysaccharide utilisation loci (PUL) the transcription of which is initiated in the presence of their target polysaccharide [3]. This project aims to find out which known gut bacteria are capable of growth on mannoproteins (fibre) obtained from F. venenatum as the sole carbon source and the methods in which they do so. It is beneficial to determine which PULs and GHs the primary degrader species use in order to ascertain some of the structural elements of this novel fibre and the products of fermentation that may be made available to secondary degrader species. Mannoproteins are the fibre of interest as they form the outermost layer of the cell wall, so are responsible for coordinating many of F. venenatum's extracellular interactions, especially during fermentation and processing to form Quorn's products. Based on current research we expect PULs that degrade mannoproteins to include alpha-mannanases (e.g. GH76) as the mannoproteins structure is majoritively alpha-mannan bonds [4], once PULs containing alpha-mannanases are identified from known primary degrader species, other enzymes in the PULs may be investigated to determine what activity they may have on mannoproteins in order to build a comprehensive picture of its total degradation. The implications of this research will pave the way to an increased understanding of how the different enzymatic mechanisms deployed by bacteria native to the HGM maintain gut health in the presence of new food sources.

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FIGURES

FIGURE 1

FIGURE 2

KEYWORDS

gut microbiota bioprospecting | glycoside hydrolase | mannan | enzymology

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BIBLIOGRAPHY