Structural Heterogeneities & Physiological Responsivity of Starch Hydrogels

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Introduction

Hydrogels are highly promising candidates for the development of "smart" drug delivery materials for targeted release of physiologically active compounds.[1] Starch can associate into a range of semi-crystalline arrangements and form a variety of aggregates and hydrogels, as a result of a range of processing conditions. Hydrothermally treated and subsequently retrograded starch has been shown to escape small intestinal digestion, and instead is fermented by commensal bacteria in the large intestine, which has been associated with positive impact on the host's overall health and wellbeing.[2-4]

Aims & Objectives

In this initiative, we have probed the structural changes starch hydrogels undergo as they traverse the entire length of the gastrointestinal tract (GIT). Our work aims at providing important insights into the role and function of hydrogel structure on its impact and interaction with the GIT, shedding light on the role of individual components of the digestive system. Furthermore, we show how structure governs interactions of starch gel systems with host's gut microbiota on a species-level, and the impact of this interplay on the production of important physiologically relevant microbial metabolites, such as short-chain fatty acids (SCFA).

Results & Future Work

We have probed the structural changes starch hydrogels experience across the entire length of the human GIT. We report the existence of undocumented level of structural organisation, its origin, impact on bulk hydrogel properties[5], and how these change across a wide range of physiological conditions.
Our work demonstrates the viability of starch hydrogels as orally administrable drug delivery systems for targeted delivery of physiologically active compounds to the large intestine. Furthermore, the composition of our matrices has been shown to lead to the production of secondary bacterial metabolites, such as SCFA, associated with beneficial effects on the host.

Current and future work involves probing the drug release kinetic profiles of three guest molecules and quantifying the guest-host interactions between the small molecules and the hydrogel excipients. This will be followed by putting these drug delivery matrices through *in vivo* experimental conditions.

References

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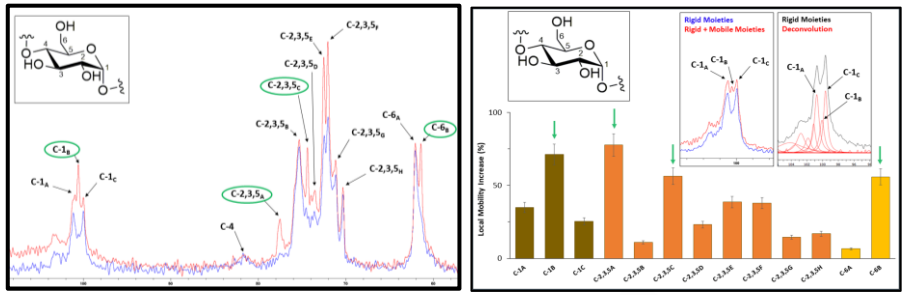
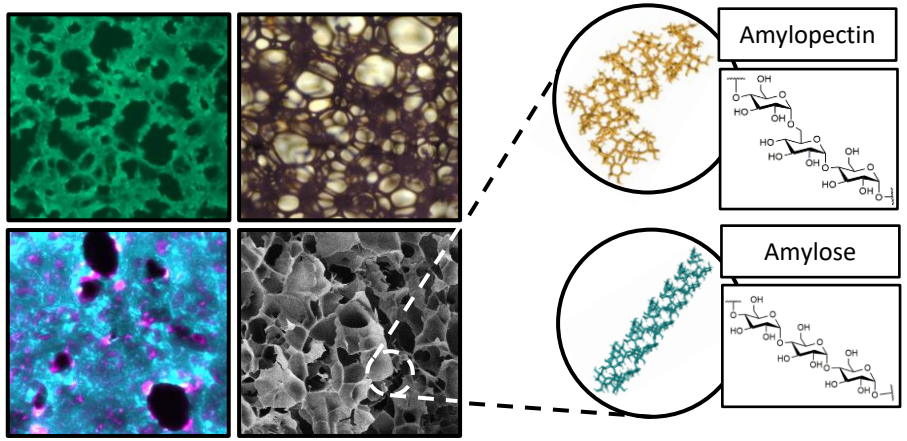
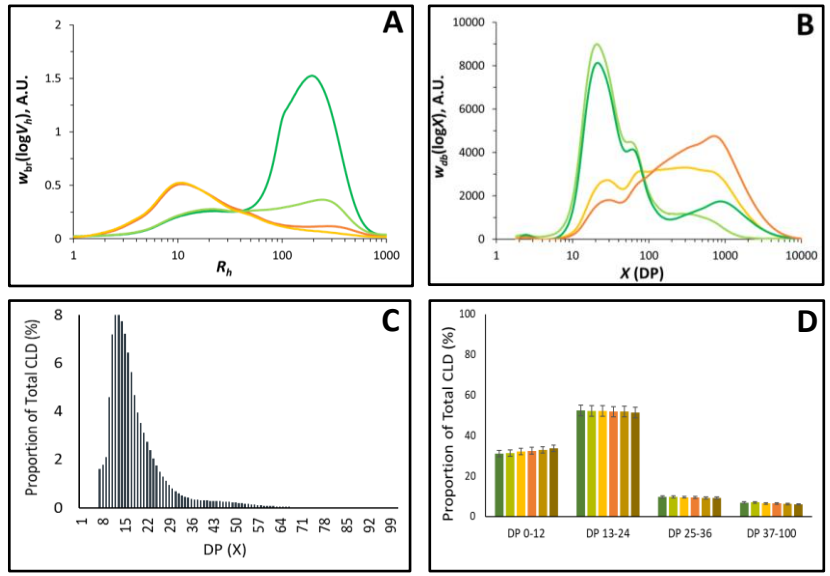
Detection & Quantification of Local Mobility



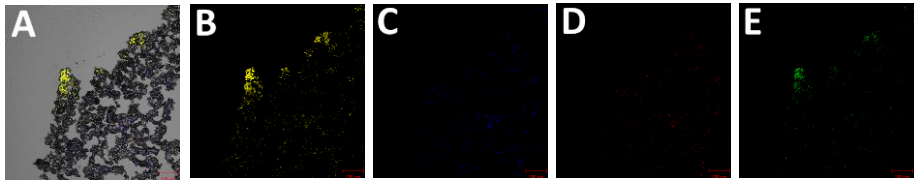


Molecular Structural Parameter Changes



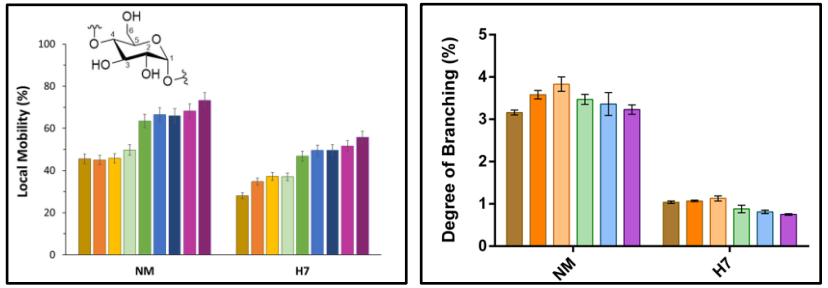
Structural parameter changes before and after of *in vitro* digestion of two distinct branched (A) and debranched (B) starch hydrogels via HPLC-SEC. Chain length distribution (CLD) and degree of polymerisation (DP) changes at successive stages of *in vitro* digestion (C & D).

Matrix Interaction with Colonic Microbiota



Confocal microscopy images of NM starch hydrogels fermented for 48 h, with bacterial species-specific fluorescent probes (A) indicating the presence of all bacteria (B); *Ruminococcus bromii* (C); *Bacteroides* (D); and *Bifidobacterium* (E);

Local Structural Changes



Local structural mobility changes at various stages of *in vitro* digestion and fermentation of starch hydrogels (left). Degree of branching of starch hydrogels at successive stages of *in vitro* digestion and fermentation (right).

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