Dietary fiber has been shown to influence the gut microbiota community which is associated with chronic metabolic diseases such as inflammatory bowel disease, obesity and diabetes. It remains unclear, though, whether and how bacteria can be modulated via specific fiber substrates in a controlled manner. Here, we have addressed this question by using Bacteroides isolates to study subtle variations in structure of a common cereal bran fiber, corn arabinoxylan. Bacteroides xylanisolvens XB1A, Bacteroides ovatus 3-1-23 and Bacteroides cellulosolyticus DSM 14838, were used to investigate partially debranched hydrolyzates of corn arabinoxylan by an enzymatic method to understand the degree of specificity of dietary fiber molecular fine structure on the utilization of target strains. Using a pure culture of Bacteroides xylanisolvens XB1A, a large lag phase shift was linked to change arabinosyl moieties on the xylan backbone. In a multi-strain environment, B. xylanisolvens XB1A showed the support on the growth of B. ovatus on complex fiber structures. In addition, B. xylanisolvens XB1A was apparently suppressed by other strains when it was fed on a structure that induced the longer lag phase, i.e. response time to a new nutrient) is important to a strain’s ability to compete for specific fiber substrates. This study shows a clear connection between subtle fiber structural features and utilization of target colonic bacteria. A high dependence of strains on specific fiber structural features for growth was observed, and implies the potential to deliberately change target strains within the competitive environment of the human colonic microbiota using proper dietary fibers.

**Materials and Methods**

- Dry-milled corn bran, particle size < 50 μm from Bunge Ltd., Darien, IL; α-amylase from Bacillus licheniformis, protease from Bacillus amyloliquefaciens and other analytical chemicals were purchased from Sigma; Multi Tech 40% AXH-43, AXH-m, endo-β-xylosidase gifts of Genencor International, Inc., Rochester NY.

- AXH-m: release arabinosyl group linked to the C-2 and C-3 position of monosubstituted xylose residues
- AXH-43: release only arabinosyl group linked to the C-3 position of diethanolated xylose residues

- Structural comparison of designed substrates was performed including sugar composition by the GC analytical chemicals were purchased from Sigma; Multi Tech 40% AXH-43, AXH-m, endo-β-xylosidase gifts of Genencor International, Inc., Rochester NY.
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- AXH-m: release arabinosyl group linked to the C-2 and C-3 position of monosubstituted xylose residues

**Results**

- Growth of B. xylanisolvens XB1A was induced by Subtle Structural Difference of Two Fiber Substrates in Pure Culture
- Structural patterns from corn arabinoxylan fragments
- Bacterial composition on different fiber substrates

**Discussion:** In complex corn fiber molecules (Fig. 1), specific structural features, as shown in Fig. 1, are responsible for a notable lag phase change of B. xylanisolvens (Fig. 2), suggesting the high dependence of bacteria growth on dietary fiber structures and implying the possibility of gut microbiota alteration via diet.

**Discussion:** In complex corn fiber molecules (Fig. 1), specific structural features, as shown in Fig. 1, are responsible for a notable lag phase change of B. xylanisolvens (Fig. 2), suggesting the high dependence of bacteria growth on dietary fiber structures and implying the possibility of gut microbiota alteration via diet.

**Figure 1:** Proposed structures of dietary fiber substrates CAXH1, and CAXH2

**Figure 2:** Growth curves of xylanisolvens XB1A on CAXH1, (blue) and CAXH2, (red) showing the lag phase change on two fiber structures with specific structural patterns.

**Figure 3:** Growth curves of B. xylanisolvens XB1A in the presence of B. ovatus 3-1-23 on CAXH1 and CAXH2

**Figure 4:** Compositions of bacteria in multi-culture environments on CAXH1 and CAXH2

**Figure 5:** Growth curves of B. ovatus 3-1-23 on CAXH1 and CAXH2

**Results from this study clearly demonstrated that it is possible to manipulate target bacteria’s growth behaviors through the change of specific structural features in fiber molecules.

The growth of B. xylanisolvens XB1A in pure culture is affected by specific structural patterns in fiber molecules, leading to a big lag phase in this study. In multi-culture study, B. ovatus can grow better on complex dietary fiber structures with the presence of B. xylan.

**Future Work**

To investigate the performance of target bacteria using animal study.

To figure out how to understand the nutritional interactions between bacteria when strain number becomes large.

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