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HIGH FIELD NMR SPECTROSCOPY ANALYSIS OF BETA-LIMIT DEXTRINS FROM STARCH LIKE POLYSACCHARIDE.

AN APPROACH TO THE UNDERSTANDING OF AMYLOPECTIN CRYSTALLINITY

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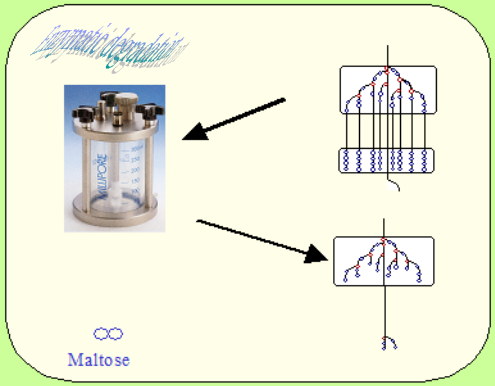
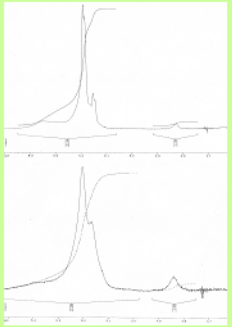
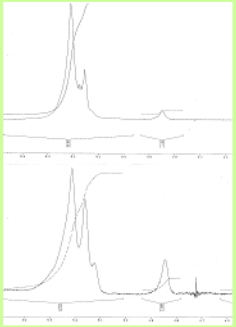
Introduction : Amongst all branched alpha-1,4 glucans, amylopectine is outstanding. Its specific, well-ordered alpha-1,6 branching pattern, originating from a complex enzymatic control, permits a very efficient packing of short linear chains within the currently accepted cluster model and allows amylopectine to grow into exceptionally large macromolecules. These characteristics lead to unique physicochemical properties such as gelling properties, reversible swelling, crystallinity of high water content, complexes with linear and apolar molecules as well as several others. It is essential to uncover this intimate branching organisation in order to understand the unique architecture of amylopectine and its relations to some of starch's macroscopic properties.



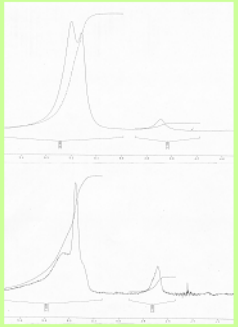
Wheat



Waxy maize



Glycogen



Experimental : The polysaccharides (100 - 1500 mg) were digested with 20- 50 unit of beta amylase in pH 4.8, acetate buffer, in a 47 mm diameter frontal stirred ultrafiltration millipore cell equipped with a 1000 MWCO cellulose membrane. The cell was run under 0.6 mbar of Argon and the cell was regularly refilled with buffer. The production of dialysed maltose was monitored by HPLC. The medium was washed several times with water, concentrated and the remaining dextrins were lyophilised then -OH protons were replaced with deuterium by exchanging twice in D2O. Nmr spectra were recorded in a 4/1 deuterated methyl sulfoxyde / D2O mixture at 500 Mhz at 353 K. The the 4-5 ppm region is displayed.

Aim of the studdy : The aim of the study was to analyse the differences between native and enzymatically degraded dextrins as seen on high field proton nmr spectra. In order to study the branching sequences, we have used a beta-amylase degradation on structurally related glucans : glycogen, waxy maize amylopectine as well as native wheat. The beta amylase degradation trims off all branches by removing maltose residues from the non-reducing ends until it reaches a branching-off point, where it leaves a short stem of only a few glucose residues. The digestion removes half the mass of the starting glucan. The betalimit dextrins so obtained are depleted in short chains and proportionally « enriched » with branched points as seen on the integration of the H1 of the branched glucose at 4.84 ppm the 4-5 ppm region.

Abstract: Wheat, waxy maize starch and glycogen were treated with beta-amylase degradation. Proton nmr spectra of the resulting limit dextrin show differences characteristic of a branching pattern.

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