

## Fast Determination of the Molar Mass and root-mean-square Radius of Starch from Different Botanical Origins

The molar mass distribution of starches has been conventionally determined by SEC. However, materials with large molecular weights, such as amylopectins, elute in the void volume, may be partially retained in the column as well as suffer degradation due to shearing forces. AFFF coupled with multi-angle light scattering enables the absolute determination of molecular weights of large molecules, which are impossible to analyse by other methods.

In the present study, starches from different botanical sources were characterized. An analysis of the sources of error on the determination of such parameters was also performed. The AFFF instrument was an Eclipse Separation System connected to a DAWN-DSP and an Optilab-RI detector. The starch was dissolved by heat treatment. A programmed cross flow that decreased exponentially was utilised for the Eclipse.

The analysed starches show two size populations. The first and second populations had molar masses below  $10^6$  g/mol. and above  $10^7$  g/mol., respectively. The second population has radii of gyration that varied between 120 and 320 nm with a molecular conformation of a compact sphere in some cases and a flexible chain in others.

The MALS signal helped to reveal starch degradation in a sample solubilised for long time. The use of freshly dissolved samples together with high sample dilution into the channel reduced the risk for amylose aggregation during the analysis.

The present work demonstrates the powerful properties of AFFF+MALS to generate a large number of molar mass and size distribution data in a short time, thus making it suitable for screening of starch characteristics. Large differences were found among varieties of the same starch and among starches from different botanical sources.

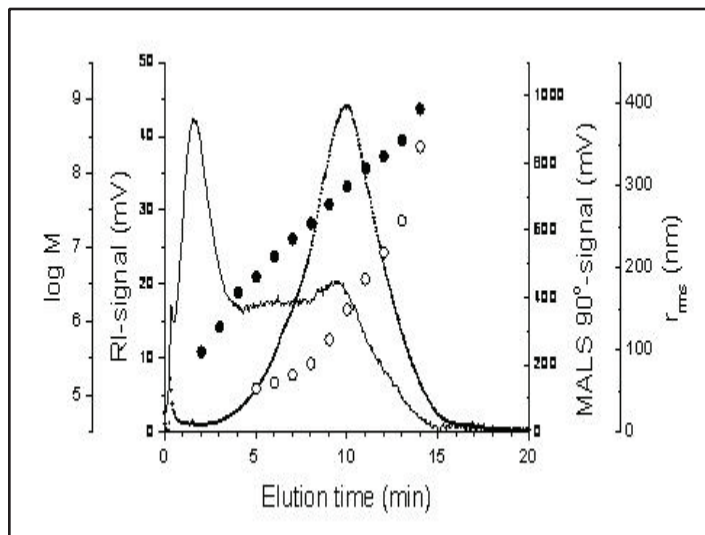
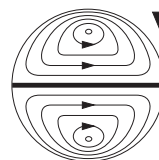


Figure 1. Fractograms of the RI and MALS detectors for a maize starch of normal amylose content.

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