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Divide and characterize: partial hydrolysis of a wheat protein

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New exploration of the γ-gliadin structure through its partial hydrolysis.

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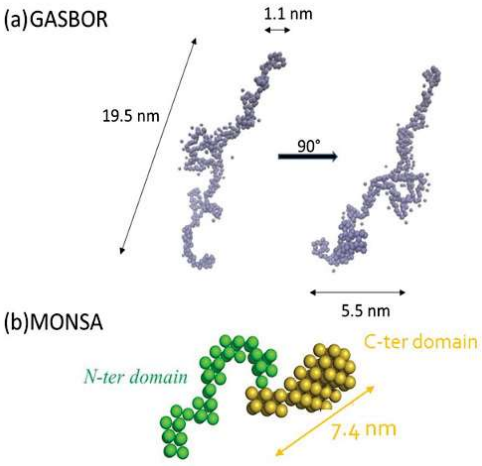

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Low-resolution models of the γ-gliadin obtained from small-angle X-ray scattering curves and displayed by (a) GASBOR (2) and (b) MONSA (3) software.

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Context

In the grain, wheat storage proteins form assemblies in the grain called protein bodies. These assemblies are formed by interactions that depend on biological microenvironment but also on intrinsic structural characteristics of the proteins, whose structures have not been resolved yet. In an effort to probe these characteristics, we set out to study a wheat protein, γ-gliadin, and each of its N-terminal (N-ter) and C-terminal (C-ter) domains obtained after partial hydrolysis. These proteins are known to show broad structural and conformational flexibility, yet the roles played by N-ter and C-ter are unclear. The goal of this research was to mobilize advances in the field of intrinsically-disordered proteins to revisit the wheat gliadin structure.

Results

Biochemical and structural methods (dichroism spectra, small-angle X-ray scattering, ab initio computational modelling) were developed to determine whether or not γ-gliadin is intrinsically disordered. Based on our evidence, we learned that the wheat γ-gliadin is partially disordered–with a disordered N-ter domain and an ordered C-ter domain. We went on to propose a new three-dimensional model of γ-gliadin on the basis of *ab initio* computations and small-angle X-ray scattering curves (Figure 1). We also found that the disordered N-ter domain is resistant to enzymatic hydrolysis, for reasons that remain unknown. Chemically-engineered short peptides mimicking the repeated motifs of amino acids in the N-ter domain showed high structural similarity with the whole N-ter domain. These synthetic peptides could serve as models to make headway in understanding N-ter resistance to hydrolysis and its wider contribution to the wheat storage proteins assembly systems.

Future outlook

A better comprehension of gliadin structure may lead to greater insight into the way gliadins self-assemble during synthsis in wheat grain. This in turn could provide us with a deeper understanding of how the grains respond to cereal commodity processing.