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Title:

Unravelling process-structure-function relationships in commercial oat protein ingredients

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1. The title should be as brief as possible but long enough to indicate clearly the nature of the study. Capitalise the first letter of the first word ONLY (place names excluded). No full stop at the end.
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An increasing number of new plant protein ingredients are entering the market, with their industrial-scale extraction processes often prioritising yield and cost over functionality and nutritional value. Despite potentially limited performance, manufacturers frequently make vague claims regarding their suitability for food applications. Understanding process–function linkages is essential for selecting suitable proteins for specific applications and for designing processing methods aimed at maximising functionality. This study investigated the process–structure–function relationships in four commercial oat protein ingredients (COPIs). Key techno-functional properties (solubility across pH 3–8 and water hydration capacity) were evaluated in relation to chemical composition (proximate analysis and SDS-PAGE), structure (confocal microscopy), and physical properties (DSC and average particle diameter $D_{4,3}$), which were further linked to processing history. With protein contents ranging from 31 to 55%, the COPIs are classified as protein-rich flours or concentrates. Oat milk flour and organic oat protein exhibited DSC endotherms around 110 °C, corresponding to the denaturation of native 12S globulins (~54 kDa). Despite retaining native protein structures, both had low solubility (<10%), likely due to large, protein-entrapped cellular and tissue structures ($D_{4,3}$ ~ 276–295 µm) resulting from inefficient breakdown of oat particles during wet milling. In contrast, PrOatein® oat protein and oat protein 60% did not exhibit denaturation endotherms, indicating prior thermal or enzymatic treatment that resulted in denatured or hydrolysed proteins. The latter showed the highest solubility (68–72%) and smallest particle size ($D_{4,3}$ ~ 73.5 µm) due to enzymatic hydrolysis into polypeptides and amino acids. In conclusion, the functionalities of COPIs are strongly influenced by microstructure at the tissue and cellular levels, and by the molecular state of the proteins (denatured or hydrolysed), both imparted by processing. The degree of protein denaturation alone is not a reliable predictor of COPI functionality, contrary to trends commonly observed in commercial protein isolates.