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Interaction between β -lactoglobulin and structurally different heteroexopolysaccharides investigated by solution scattering and analytical ultracentrifugation study

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Knowledge on molecular structure of exopolysaccharides (EPSs) and their roles in the associative interactions with proteins is essential to understand the relationship between their structure, physical and rheological properties. Despite their importance, no detailed molecular characterization of bacterial EPSs and their associative interactions with proteins have been reported up to now. By combining X-ray solution scattering (SAXS), dynamic light scattering (DLS) and analytical ultracentrifugation (AUC) in conjunction with scattering modeling, we have characterized four different heteroexopolysaccharides (HePS-1–HePS-4) from lactic acid bacteria (LAB) and their interactions with β -lactoglobulin. We have previously shown that these HePSs exhibited a compact conformation in solution [1]. Here, SAXS data for HePSs (HePS-1–HePS-4) complexes with β -lactoglobulin showed that β -lactoglobulin aggregated strongly with these HePSs. β -lactoglobulin exists as a dimer at pH 4 in the absence of HePSs. When mixed with HePSs, SAXS analysis showed that β -lactoglobulin formed large aggregates. DLS also showed formation of large aggregates of β -lactoglobulin with HePSs, thus validating SAXS data. Turbidity and AUC data indicated that both soluble and insoluble BLG–HePSs complexes were formed. This study provides new insights into the role of molecular structures in associative interactions between HePSs and BLG which has relevance for various industrial applications.

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References

[1] Khan, S.; Birch, J.; Harris, P.; Van Calsteren, M-R.; Ipsen, R.; Peters, G. H. J.; Svensson, B.; Almdal, K. Revealing the compact structure of lactic acid bacterial heteroexopolysaccharides by SAXS and DLS. *Biomacromolecules* **2017**, *18*, 747–756.