Advances in Dairy Research
ISSN: 2329-888X
OPEN ACCESS Freely available online
Commentary

Microorganisms and Structure of Milk Protein-Gel-Based Milk Yoghurt

Vijaya Sharma*

Department of Nutrition, Cornell University, Ithaca, New York, USA

DESCRIPTION

Lactic acid bacteria (LAB) turn milk into yoghurt by causing an acidity reaction. By fermenting milk carbohydrates, Lactic acid bacteria make lactic acid, which lowers pH. Casein micelles, which make up 80% of the total milk proteins and are made up of αS1, αS2, β, and κ-caseins in an approximately 4:1:4:1 molar ratio, are disrupted and gel at the end of this process. Whey proteins, which make up the remaining 20% of milk proteins, are denatured by heat and contribute in network development, changing the gels' mechanical and physical characteristics.

The organization and interactions of these milk proteins with LAB metabolites, like exopolysaccharides, are what give yoghurt its unique sensory and physical characteristics. Milk protein gels are made up of clusters and strands at length scales exceeding tens of micrometres, according to visualizations of yoghurt network development and microstructure produced by electron and fluorescence microscopy. In addition, a number of group studies utilizing nuclear magnetic resonance spectroscopy, spin-echo small angle neutron scattering, and rheology measurements of transglutaminase-crosslinked caseins have shown that significant molecular rearrangements occur during milk acidification.

The final gel's mechanical properties are impacted by these molecular rearrangements as well as modifications to protein conformation and interactions. As of right now, it is understood that acidification causes the calcium phosphate in casein micelles to dissolve as well as the collapse of -casein brushes on the micelle surface and the release of some caseins from the micelles. Due to the low resolution of traditional light microscopy methods and the difficulties in labelling the specificity of the individual components, the precise arrangement of the caseins in the milk gels is still difficult to determine.

These drawbacks would be resolved by the use of new tools that can map the spatial distribution of different proteins in dairy gels at submicron resolution. This would aid in understanding the mechanisms underlying milk gelation as well as the factors affecting network microstructure and mechanics. Super resolution microscopy techniques have become effective tools in the biological sciences that allow complex structures to be visualised with resolution that exceeds the traditional diffraction limit. Super resolution microscopy has recently received a lot of attention for its use in characterising the microstructure of food because it makes it possible to see how fluorescently marked biomacromolecules are arranged in space at the nano- and mesoscales. One of these technologies is stimulated emission depletion microscopy, which use a single excitation laser and a second, doughnut-shaped depletion laser to constrict the area from which light is emitted around the focus point, increasing the optical resolution to 50 nm and higher.

Used a variety of super-resolution microscopy techniques, such as Stimulated Emission Depletion (STED) microscopy, and specific labelling of αs1- and β-caseins to locate the domains within acid milk gels and determine whether the β-caseins are distributed similarly throughout the protein network. We noticed variations in the distribution αs 1-caseins and β-caseins in glucono-δ-lactone(GDL)-acidified milk gels regardless of the microscopy technique applied. STED made it possible to image the murky model yoghurts at a resolution double that of confocal microscopy, which was useful for conducting additional quantitative investigation of the network structure. It's interesting to note that whereas β-caseins spread more heterogeneously in acid milk gels than αs1-caseins do throughout the gel. By evaluating the connection of the two caseins using a skeleton analysis, the differential distribution's magnitude was determined. We explain the variations in αs1-and β-casein distribution and domain connectivity by a reorganisation of s1- and s-caseins in the pH range of 6.8 to 4.6 during GDL-induced gelation, as suggested before. In comparison to β-casein domains, αs1-casein domains were less linked, regardless of the amount of protein or the presence of whey proteins and fat. A lower link density and a higher proportion of short skeleton lengths in the skeleton length distributions in a skeleton analysis verified all of this. Future studies on the connectivity of caseins in real yoghurt fermented with various bacterial strains under physiological conditions would be very interesting. It would also be interesting to look at how the found microstructures relate to the rheological characteristics and quality traits of the yoghurt.

Correspondence to: Vijaya Sharma, Department of Nutrition, Cornell University, Ithaca, New York, USA, E-mail: vijay00@gmail.com

Received: 15-May-2023, Manuscript No. ADR-23-25598; **Editor assigned:** 17-May-2023, PreQC No ADR-23-25598 (PQ); **Reviewed:** 29-May-2023, QC No. ADR-23-25598; **Revised:** 05-Jun-2023, Manuscript No ADR-23-25598; **Published:** 15-Jun-2023, DOI: 10.35248/2329-888X.23.11.626

Citation: Sharma V (2023) Microorganisms and Structure of Milk Protein-Gel-Based Milk Yoghurt . J Adv Dairy Res. 11:626.