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Christian Beauvallet, Claudia Bevilacqua, Bouabid Badaoui, Christelle Cebo, Samira Makhzami, Sophie Pollet, Eric Chanat, Patrice Martin

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Accumulation of caseins in the endoplasmic reticulum of mammary epithelial cells due to α_{s1} -casein deficiency, induces a chronic er stress and a milk protein composition signing a singular secretion mode

Beauvallet C., Bevilacqua C., Badaoui B., Cebo C., Makhzami S., Pollet S., Chanat E. and Martin P.

Génomique & Physiologie de la Lactation, INRA Jouy en Josas, France

The extensive polymorphism recorded at the *CSN1S1* locus influences the composition of goat milk and its technological properties. A deficit of α s1-casein is responsible for the accumulation of immature caseins in distended rough endoplasmic reticulum (ER) cisternae and consequently for a perturbation of the secretory process of proteins and lipids. In contrast, no accumulation was found in mammary epithelial cells (MEC) lacking β-casein expression (*CSN2* O/O). This suggests that α s1-casein interacts with the other caseins and that this complex is required for their transport to the Golgi. To understand the underlying mechanisms and go further in the characterization of cell functioning (and dysfunction) we first performed comparative gene expression profiling experiments, starting from mammary tissues and epithelial cells isolated from goats of extreme genotypes (O/O vs. A/A) at the CSN1S1 locus. Since milk fat originates in the MEC, it was expected that ER disorders observed in defective animals affect the protein composition of the milk fat globule membrane (MFGM). Non conventional 2D proteomic analyses were developed to test such an hypothesis in order to identify proteins differentially expressed in the MFGM of goats of extreme CSN1S1 genotypes. Acini from both genotypes were drawn using Laser Capture Microdissection and directly analyzed in Maldi-Tof Mass spectrometry. Several spectra were acquired in different mass ranges, recorded and compared. Some peaks were found to give different intensity levels, specifically in the casein region. Concomitantly, a differential proteomic analysis (2D-DIGE) of milks from goats of extreme genotypes (A/A vs. O/O) has been carried out. Micellar caseins were removed by centrifugation and the supernatants labelled with the three CyDyes, of which one (Cy2) was used as internal standard (equimolar mix of each sample). Statistically, a hundred of spots were significantly discriminated and the most powered spots were identified by Maldi-Tof-MS. The occurrence of ER-resident proteins in O/O milks strongly suggests a singular secretory mechanism for this genotype.

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