

Separation and quantification of milk protein from different buffalo breeds

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Summary

Understanding the milk protein expression profile in different buffalo breeds plays an important role in improving hybrid selection and determining the effects on milk protein synthesis. The aim of this research is to compare the differences in milk protein content, composition and distribution between River buffalo and their crossbreeds for hybrid screening. Four groups of milk samples that included Nili-Ravi (N), Murrah (M), a Nili-Ravi-Murrah crossbreed (M-N), and a crossbreed of river buffalo with local swamp buffalo (C) were collected. The protein composition of the buffalo milk was determined by RP-HPLC. A gel-based proteomic approach consisting of two-dimensional gel electrophoresis coupled with mass spectrometry was utilized for the detailed protein characterization of milk from different breeds. The results of this analysis showed that the river/swamp buffalo crossbreed (C) displayed the highest content of total protein (4.46%) and κ -casein (11.14%) but the lowest content of α -lactalbumin (6.79%). By selecting 23 different protein spots among the four types of milk that contained the most spots corresponding to κ -casein, β -casein and α_{s1} -casein, correlations between the crossbreeds, protein polymorphism and phosphorylation could be made. The results of this study indicate that crossbreeding a swamp buffalo with a river buffalo has a notable effect on the protein content and composition that may be exploited for producing high-quality raw milk in food technology applications and dairy food production.

Keywords: swamp buffalo, river buffalo, crossbreed, milk protein, comparative proteomics