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Milk Protein Polymorphism of Buffaloes in Southern Area of Sri Lanka

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Water buffaloes contribute around 17% of the total milk production of the country. The buffalo population shows an increment during last decade and it was 318,530 in the year 2008. The buffalo is spread all over the country and southern province of Sri Lanka is becoming an important area for buffalo farming. However, due to the present breed structure of the population; a detailed study has to be conducted to improve buffalo production through breeding. The selection of suitable animals plays an important role and genetic markers have a great potential in the process of selection. But new sophisticated techniques based on DNA technology are expensive to practice and more sophisticated facilities are essential. Therefore, conventional protein evaluating techniques based on polymorphism can be used as low cost methods.

The study was conducted for identify the milk protein polymorphism of the buffalo milk and identify the relationships of the animals according to the milk protein polymorphism. Milk samples of four distinct groups of buffaloes (Surti cross bred, Local wild type, Upgraded Murah and Local crossed) were collected and used for protein separation by $(\text{NH}_4)_2\text{SO}_4$. The separated proteins were run in Polyacrylamide gel using Sodium Dodecyl Sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) method and the polymorphism in the milk proteins was studied. The Coomassie blue and silver staining methods were used for staining the gels.

Milk proteins of the local wild type animals show a clear difference from other three groups of animals due to the absence of a protein band of 87 kDa in 10 % SDS gel. There were differences in proteins between animal groups as well as within the same group. The most possible reason for that is the genetic diversity between the groups and within the group. For