



Comparative proteomic analysis of the lactating and nonlactating bovine mammary gland

W. T. Dai,* Q. J. Wang,* Y. X. Zou,* R. R. White,† J. X. Liu,* and H. Y. Liu*¹

*College of Animal Sciences, Zhejiang University, Hangzhou 310058, P.R. China

†Department of Dairy Science, Virginia Tech, Blacksburg 24060

ABSTRACT

Proteomic analysis of the lactating and nonlactating bovine mammary gland (MG) was performed using 2D-PAGE and MS/MS. A total of 1,236 protein spots were identified, of which 320 were unique to the lactating MG, 1,016 were unique to the nonlactating MG, and 90 were shared between the two. The 320 unique proteins in the lactating MG were further categorized into 15 functional groups, including 100 related to milk production, 100 related to cell growth and differentiation, 100 related to energy metabolism, and 120 related to other functions. The 1,016 unique proteins in the nonlactating MG were further categorized into 15 functional groups, including 100 related to cell growth and differentiation, 100 related to energy metabolism, 100 related to protein synthesis, and 760 related to other functions. The 90 shared proteins were further categorized into 15 functional groups, including 100 related to cell growth and differentiation, 100 related to energy metabolism, 100 related to protein synthesis, and 100 related to other functions. The results of this study provide a comprehensive overview of the proteomic changes in the bovine MG during lactation and nonlactation, and may be useful for understanding the underlying mechanisms of mammary gland development and function.

Key words: proteomics, lactation, mammary gland

Short Communication

(MG)
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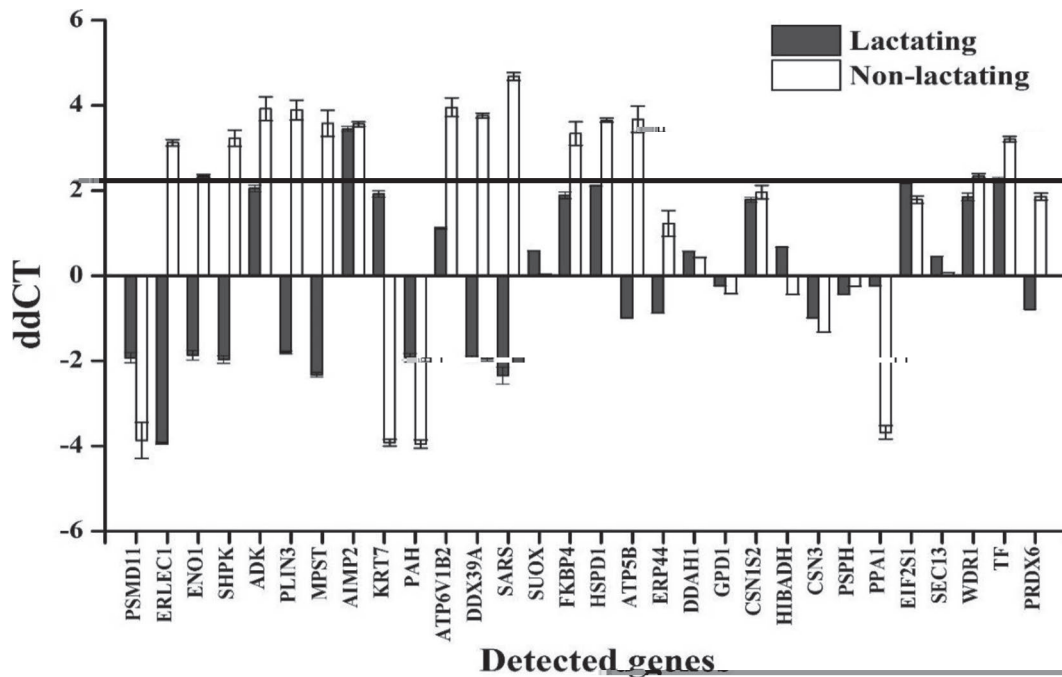


Figure 3.

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ACKNOWLEDGMENTS

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