

Functional analysis of the dairy cow mammary transcriptome during the lactation cycle

Ye Lin^{1,3}, He Lv³, Minghui Jiang³, Jinyu Zhou³, Shuyuan Song³, Xiaoyu Duan³, and Xiaoming Hou^{2,3*}

¹Key Laboratory of Dairy Science of Education Ministry, Northeast Agricultural University, Harbin 150030, China

²Key Laboratory of Animal Cellular and Genetics Engineering of Heilongjiang Province, Northeast Agricultural University, Harbin 150030, China

³College of Life Science, Northeast Agricultural University, Harbin 150030, China

Short title: **Mammary transcriptome during lactation cycle**

*Correspondence: Xiaoming Hou

College of Life Science

Northeast Agricultural University

Harbin 150030

China

Phone +86-451-55191416

FAX +86-451-55190244

E-Mail: xiaominghou@126.com

Summary

The mammary gland is a dynamic organ that experiences regular proliferation, differentiation, and involution cycles after maturity. Investigation of the molecular events underlying these changes will provide fundamental insights into milk production, as well as a better standing of tissue remodeling in dry period. The objective of this study was to screen the target genes and pathways involved in normal dairy cow mammary lactation cycle. We used digital gene expression (DGE) analysis to identify differences in gene expression in the mammary gland of dairy cow between lactation and dry period. A total of 741 genes were identified as differentially expressed by DGE analysis. Compared to dry cows, 214 genes were up-regulated and 527 genes were down-regulated in lactating cow mammary gland. Gene ontology analysis showed that lactation was supported by increased gene expression in metabolic process, nutrient transport, and was couple with decreased gene expression in cell proliferation. Pathway mapping using the Kyoto Encyclopedia of Genes and Genomes (KEGG) showed that 579 differentially expressed genes were given pathway annotations that were related to 204 pathways. The metabolic pathway-related genes were the most significantly enriched. Our DGE data provide insight into the molecular events in the mammary gland in the lactation cycle, which provide a platform for future research into the management of mammary development and function.