

## A comprehensive Analysis of MicroRNAs Involved in Mammary Gland

Johan Botha\*

Department of Obstetrics and Gynecology, University of Abuja Teaching Hospital Abuja, Abuja, Nigeria

### ABOUT THE STUDY

Long noncoding RNA (lncRNA) can influence the physiological processes of the mammary gland during development and lactation. The underlying genetic processes of lncRNA in mammary gland involution and cell remodelling, however, remain unknown. This study looked at the expression patterns and molecular roles of lncRNA in goat mammary gland tissue during Late Lactation (LL), the Dry Period (DP), and Late Gestation (LG). Sequencing results revealed 3074 lncRNAs in non-lactating goat mammary gland tissue. According to a statistical examination of lncRNA length characteristics and exon number, goat lncRNAs were shorter in length, had fewer exons, and had much lower expression levels than protein-coding genes.

331 differentially expressed lncRNAs were discovered in the three comparison groups (LLvsDP, DPvsLG, and LLvsLG), indicating that lncRNA transcriptional expression was altered during mammary involution. Interestingly, lncRNAs were shown to be more active during the dry phase than during breastfeeding, indicating that lncRNAs in mammary glands are developmentally specialised. Pathway enrichment analyses in the Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) revealed that lncRNAs could regulate immune function, cell proliferation, apoptosis, hormones, substance metabolism, transport, and intercellular communication in the mammary gland *via* various action modes. Among these, cis-acting lncRNAs improved mammary gland health protection throughout the dry phase and late gestation.

The preceding describes the specific strategies used by lncRNA to adjust to the developmental demands of mammary involution and remodelling. Furthermore, expression was greater in late gestation than in the dry period and late lactation in the lncRNA-miRNA-mRNA network related with mammary gland development. Its expression was shown to be favourably connected to PRLR and negatively related to chi-miR-324-3p.

In goat mammary epithelial cells cultivated *in vitro*, overexpression of might activate the prolactin signalling pathway by competitively binding to chi-miR-324-3p, boosting cell proliferation, lowering cell cycle arrest in the G1 / S phase, and

suppressing apoptosis. Overexpression of alone, however, had no effect on mammary cell proliferation or the prolactin signaling pathway.

This suggests that relies on chi-miR-324-3p to prevent mammary cell death. In conclusion, the aforementioned study found that lncRNAs in goat mammary tissue are expressed differently at different phases of involution. As predicted, lncRNAs control many physiological processes during mammary gland involution *via* several mechanisms in preparation for a new round of breastfeeding. These findings serve as a reference and contribute to a better understanding of the regulatory role of lncRNAs in mammary cell involution and modification. Despite growing interest in the role of milk Extracellular Vesicle (EV)-derived microRNAs (miRNAs), little is known about the link between miRNAs in milk EVs and bovine mammary glands. Using short RNA sequencing, we studied the miRNA profile in milk EVs and bovine mammary glands at three lactation phases (60d, 120d and 240d).

In milk EVs and mammary glands, 70 uniformly highly expressed miRNAs were found. When the kinds of miRNAs in milk EVs were compared to those in mammary gland tissue, the consistency rate was more than 90%. There were four kinds of highly expressed miRNAs in milk EVs that were not seen in the mammary gland. MiRNA expression level correlation study indicated significantly substantial connections between milk EVs and mammary gland tissue ( $P < 0.01$ ). Our findings indicated that milk EVs had a very close link with bovine mammary glands in terms of miRNA type and expression. Regenerative involution is necessary for future breastfeeding, although the molecular mechanism is unknown. The importance of miRNAs in tissue development suggests that they may play a role in restorative evolution. The mammary tissues of dairy goats ( $n=3$ ) were taken through biopsy at wk-8 (time to dry off), -6, -4, -1, and +1 relative to lambing for Hematoxylin and Eosin staining and miRNA sequencing in the current work. During regenerative involution, alveolar structures contracted, but the structures remained intact and distended.

Two notable patterns were found among the 50 miRNA expression trajectories classified by the short time-series

**Correspondence to:** Johan Botha, Department of Obstetrics and Gynecology, University of Abuja Teaching Hospital Abuja, Abuja, Nigeria, E-mail: bothajon@213gmail.edu

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expression miner. The differentially expressed miRNAs in the two patterns were mostly associated with tissue self-renewal and were enriched in pathways involving vesical-mediated transport, tissue development, tube formation, vasculature development,

and epithelial development. The discovery of the miRNAs will aid in the understanding of their regulatory roles in mammary gland development.