# Identification of conserved microRNAs in peripheral blood from giant panda: expression of mammary gland-related microRNAs during late pregnancy and early lactation

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**ABSTRACT.** The giant panda (*Ailuropoda melanoleuca*) is one of the world's most endangered mammals, and it has evolved several unusual biological and behavioral traits. During puberty, pregnancy, lactation, and involution, the mammary gland undergoes profound morphological and functional changes. A large number of microRNAs (miRNAs) have been identified to be involved in mammary gland development and lactation. In this study, we identified 202 conserved mature miRNAs, corresponding to 147 pre-miRNAs, in giant panda peripheral blood using a small RNA-sequencing approach. In addition, 27 miRNA families and 29 miRNA clusters

were identified. We analyzed the arm selection preference of pre-miRNAs and found that: 1) most giant panda pre-miRNAs generated one-strand miRNAs, and the 5p-arm only miRNAs have a higher expression level than 3p-arm only miRNAs; 2) there were more 5p-arm dominant miRNAs than 3p-arm dominant miRNAs; and 3) 5p-arm dominant miRNAs have a larger fold change within miRNA pairs than 3p-arm dominant miRNAs. Expression of 12 lactation-related miRNAs was detected across late pregnancy and early lactation stages by qPCR, and seven miRNAs were identified as clustered in one significant model. Most of these clustered miRNAs exhibited inhibitory roles in proliferation and differentiation of mammary epithelial cells. Functional analysis highlighted important roles of the seven as signed miRNAs in mammary development and metabolic changes, including blood vessel morphogenesis, macromolecule biosynthesis, cell cycle regulation, and protein transport.

**Key words:** Giant panda; miRNA; Mammary gland; Lactation