

MicroRNA transcriptome of duodenum tissues in Chinese Meishan weaned piglets challenged with *E. coli* F18

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Escherichia coli F18 is mainly responsible for post-weaning diarrhea (PWD) in piglets. The molecular regulation of *E. coli* F18 resistance in Chinese domestic weaned piglets is still obscure. We used Meishan piglets as model animals to test their susceptibility to *E. coli* F18. Small RNA duodenal libraries were constructed for *E. coli* F18-sensitive and resistant weaned piglets challenged with *E. coli* F18 and sequenced using Illumina Solexa high-throughput sequencing technology. Sequencing results showed that 3,475,231 and 37,198,259 clean reads were obtained with 305 known and 681 novel microRNAs (miRNAs) differently expressed in resistant and sensitive groups, respectively. Twenty-four miRNAs including 15 up-regulated and 9 down-regulated demonstrated more than a 2-fold differential expression between the F18-resistant and sensitive pigs. Stem-loop RT-qPCR validation indicated that most of the differently expressed miRNAs were consistent with the high-throughput sequencing data, including significantly expressed miRNAs, such as miR-136, miR-196b, miR-499-5p and miR-218-3p ($p < 0.05$). KEGG pathway analysis for target genes revealed that differently expressed miRNAs were involved in infectious diseases, signal transduction and immune system pathways. According to the function of the target genes and previous sequencing results, miR-196b, miR-499-5p and miR-218-3p appear to be very promising candidates for miRNAs involved in response to *E. coli* F18 infection. The present study provides improved database information on pig miRNAs, better understanding of the genetic basis of *E. coli* F18 resistance in local Chinese pig breeds and lays a new foundation for identifying novel markers of *E. coli* F18 resistance.

Biography

Ying Liu is a Doctor of Yangzhou University, China. She is mainly engaged in pig disease-resistant breeding and reproduction.

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