

Jirapat Ninsuwon 2014: Expression Analysis and Gene Target Prediction of MicroRNA-155 and MicroRNA-181 in Porcine Cells. Master of Science (Veterinary Microbiology), Major Field: Veterinary Microbiology, Department of Veterinary Microbiology and Immunology. Thesis Advisor: Mr. Win Surachetpong, Ph.D. 75 pages.

MicroRNAs (miRNAs) are small non-coding RNA molecules ranging between 18-24 nucleotides. MicroRNAs regulated gene expression through post transcriptional inhibition of target mRNA. The objective of this study is to characterized, predicted target genes and analyzed porcine miR-155 and miR-181 expression. Our results showed that porcine miR-155 and miR-181 had hairpin loop structure resemble to other species including human, mouse, rat, chicken and fish. In addition, the mature sequences of ssc-miR-155 and ssc-miR-181 shared 91.3-95.8% similarity and 100% similarity at the seed region with miR from other species. The miR-155 and miR-181 target genes were predicted by three webserver tool including DIANA-micro T, miRmap and PicTar. The top candidate genes for miR-155 were *BACH1*, *SOCS1*, *MAP3K14* and *MPP5*. The top candidate genes for miR-181 were *DDX3X*, *NFAT5*, *FOXP1* and *MPP5*. Expression analysis revealed that ssc-miR-181 equally expressed in all tissues (spleen, muscle, PBMC and PK15), while ssc-miR-155 highly expressed in PBMC and PK15. Moreover, both miRNAs highly expressed at 12 hours in stimulated peripheral blood mononuclear cells, while lower expression had been observed at 24 and 48 hours. In conclusion, these findings suggested that porcine miR-155 and miR-181 could play an important role in the porcine immune system.

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