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Comparative transcriptomics reveals small RNA composition and differential MicroRNA responses underlying interferon-mediated antiviral regulation in porcine alveolar macrophages

Previous studies have shown that interferon-mediated antiviral activity is subtype-dependent. Using a whole transcriptome procedure, we aimed to characterize the small RNA transcriptome (sRNA-Seq) and specifically the differential microRNA (miRNA) responses in porcine alveolar macrophages (PAMs) upon antiviral activation during viral infection and interferon (IFN) stimulation. Data showed that near 90% of the qualified reads of sRNA were miRNAs, and about 10% of the other sRNAs included rRNA, snoRNA, snRNA, and tRNA in order of enrichment. As the majority of sRNA (>98%) were commonly detected in all PAM samples under different treatments, about 2% sRNA were differentially expressed between the different antiviral treatments. Focusing on miRNA, 386 miRNA were profiled, including 331 known and 55 novel miRNA sequences, of which most were ascribed to miRNA families conserved among vertebrates, particularly mammalian species. Of the miRNA profiles comparably generated across the different treatments, in general, significantly differentially expressed miRNA (SEM) demonstrated that: (1) the wild-type and vaccine strains of a porcine arterivirus (a.k.a., PRRSV) induced nearly reversed patterns of up- or down-regulated SEMs; (2) similar SEM patterns were found among the treatments by the vaccine strain and antiviral IFN-α1/-ω5 subtypes; and (3) the weak antiviral IFN-ω1, however, remarked a suppressive SEM pattern as to SEMs upregulated in the antiviral treatments by the vaccine and IFN-α1/-ω5 subtypes. Further articulation identified SEMs commonly or uniquely expressed in different treatments, and experimentally validated that some SEMs including miR-10b and particularly miR-9-1 acted significantly in regulation of differential antiviral reactions stimulated by different IFN subtypes. Therefore, this study provides a general picture of porcine sRNA composition and pinpoints key SEMs underlying antiviral regulation in PAMs correlated to a typical respiratory RNA virus in pigs.

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