

**P1402**

**Paper Poster Session**

**Influenza - clinical epidemiology**

**Cellular microRNAs profiling in response to influenza A viruses infection based on high-throughput sequencing**

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**Background:** MicroRNAs (miRNAs) play many essential roles in mechanisms of gene regulation of gene in terms of post transcription gene silencing, resulting in many cellular mechanisms including infected viral replication inhibition or supports. This study aimed to profile the human cellular miRNAs involved in early stage of influenza virus infection to understand more of viral mechanisms and control.

**Material/methods:** Infection of different subtypes of influenza virus (pH1N1, H3N2 and H5N1) was performed in A549 cells. Total miRNAs were extracted at 24 h.p.i. for DNA library preparation for Next-generation Sequencing (NGS). All DNA libraries were pooled together in similar concentration with various indices, followed by NGS operation based on MiSeq (Illumina) platform before MiSeq reporter software was used for profiling and quantifying the sequencing data of the total miRNAs. The miRNAs expression levels were categorized into 2 groups; up and down-regulated miRNAs, compared to miRNAs expression level in non-infected cells. The NGS data were used for target gene prediction after analysis.

**Results:** The infection of each subtype of influenza A virus mostly could trigger the miRNAs expression level to be up-regulated in miRNA expression profiles. Some considerable miRNAs such as hsa-miR-101, hsa-miR-193b, hsa-miR-23b and hsa-miR-30e\*, which were up-regulated when infected with all 3 subtypes of influenza A virus, were further analysis in target prediction. The prediction results showed that many genes in cellular process, metabolic process, developmental process and biological regulation could be triggered by influenza virus infection.

**Conclusions:** The infection of influenza virus infection can regulate the cellular processes via miRNAs mechanisms, which can be the viral processes or host cellular defense responded to influenza virus infection. This study provided some understanding into the cellular miRNA profiling in response to various subtypes of influenza A viruses in circulation and which have caused outbreaks in human population.