Circulating MicroRNA: A potential biomarker for ICS treatment response

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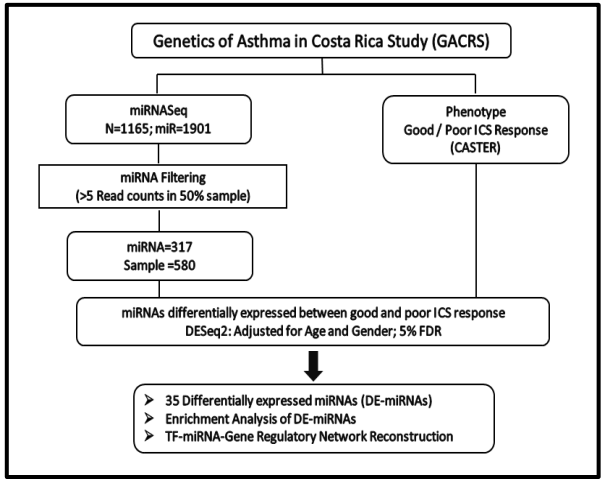
Background & Objective

- Inhaled corticosteroids (ICS) are the most effective and most prescribed asthma controller medications.
- However, the response of asthma patients to ICS is inconsistent and difficult to measure.
- We have previously defined a Cross-sectional Asthma STEroid Response (CASTER) measure of ICS response, based on a combination of asthma control indicators and spirometry measures.
- MicroRNAs (miRNAs) can be effective tools as a biomarker that predict the response to ICS treatment.
- The purpose of this study was to identify key associations between circulating miRNAs and ICS response in childhood asthma.

Methods

Figure 1. Workflow for miRNASeq data analysis



Results

- We identified 34 upregulated & 1 downregulated miRNAs among 35 differentially expressed miRNAs between good (n=379) & poor CASTER/ICS response subjects (n=201) at 5% FDR.
- Enrichment analysis showed the most enriched pathway cluster was Rap1, Toll-like receptor, ErbB, T cell receptor, TGF-beta, p53, Ras, Jak-STAT, Wnt, Chemokine and B cell receptor signaling pathways at FDR <0.01

Figure 2. Significant up- and down-regulated miRNAs between good and poor CASTER/ICS response

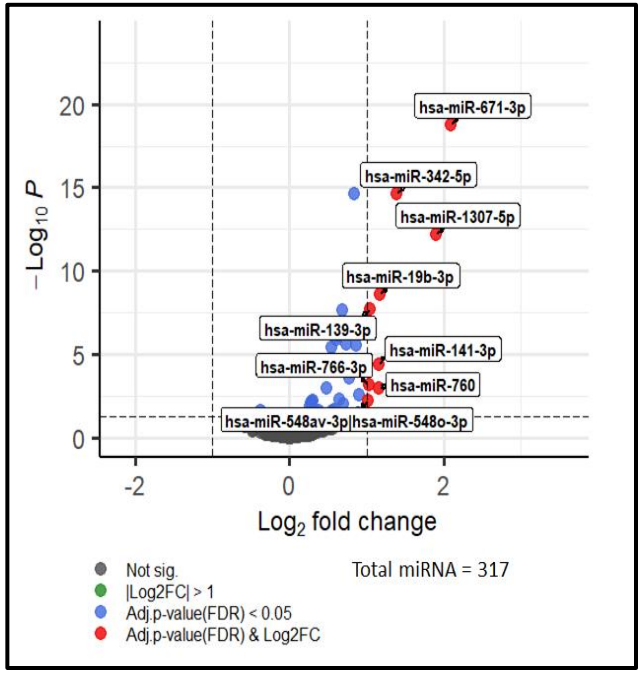


Figure 3. miRNA-TF-gene Regulatory Network (showing 1st neighboring nodes of steroid hormone signaling pathway enriched target genes)

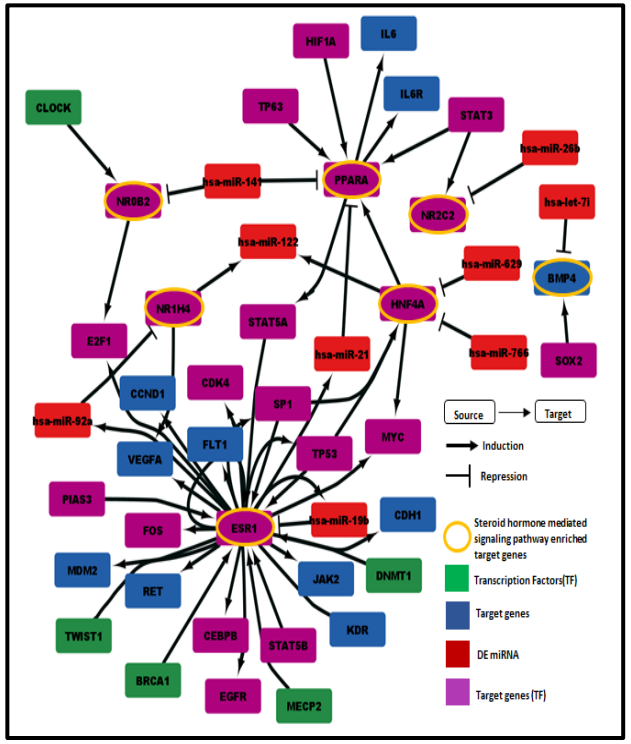
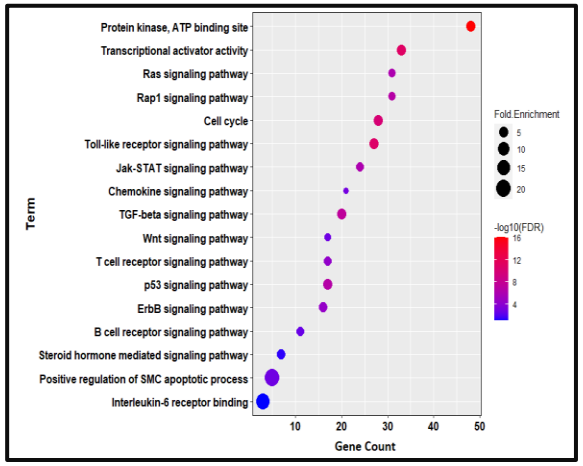


Figure 4. Functional enrichment of putative (validated) target genes of DE miRNAs from KEGG and gene ontology



Conclusion

Identified 35 dysregulated miRNAs between good and poor ICS response groups at 5% FDR. Biological pathway enrichment analysis of target genes highlighted Rap1, Toll-like receptor, ErbB, T cell receptor, TGF-beta, p53, Ras, Jak-STAT, Wnt, Chemokine and B cell receptor signaling pathways at FDR <0.01.

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