



# Serum miRNAs are crucial for prediction of Asthma Exacerbations in Costa Rica

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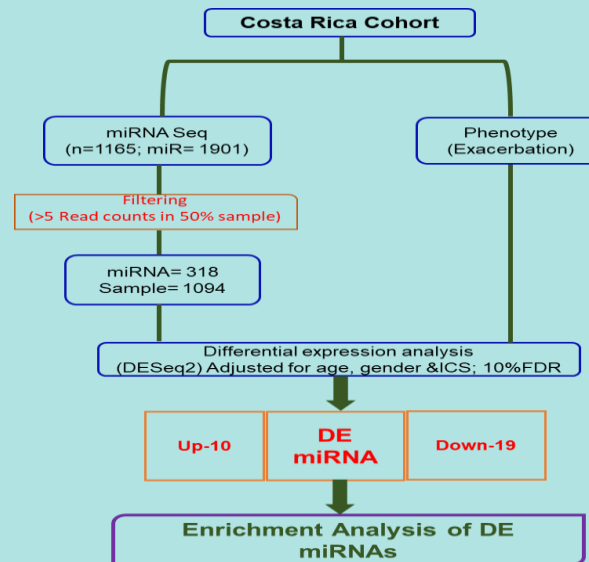
## Rationale

- Asthma is chronic inflammation of the airways characterized by airway obstruction due to both smooth muscle hyperresponsiveness and inflammation.
- Asthma affects >350 million people worldwide.
- It is the leading chronic condition that occurs results in hospitalization and school absences in children.
- MicroRNAs (miRNAs) are small non-coding RNAs that regulate their target mRNAs post-transcriptionally through degradation or translational repression.
- miRNAs have emerged as vital molecules in asthma.
- However, the investigation of circulating miRNAs association with significant clinical events including exacerbations has not been carried out previously.

## Objective

- The purpose of this study was to determine the association between circulating miRNAs & asthma exacerbation.
- miRNAs regulate gene expression, particularly inflammatory pathways
- Airway inflammation is a primary driver of the asthma exacerbation.
- Our primary outcome was severe asthma exacerbations, defined as >2 emergency room or urgent care visits in GACRS .

## Methods

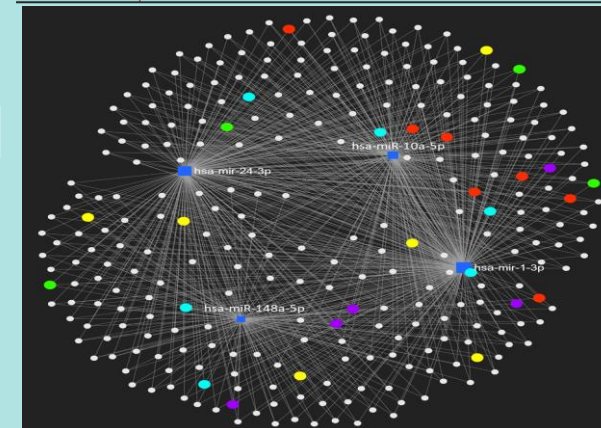


## Results

- We identified 10 upregulated & 19 downregulated miRNAs among 29 differentially expressed miRNAs between frequent exacerbation (n=778) & infrequent exacerbation subjects (n=316).
- To check the ability of 4 DE replicated miRs to predict Asthma exacerbations, we used a linear regression model and obtained an AUC of 63%, indicating a predictive performance statistically better than random guessing.
- Enrichment analysis showed the most enriched pathway cluster was PI3AKT, Ras, RAP and MAPK signaling pathway.

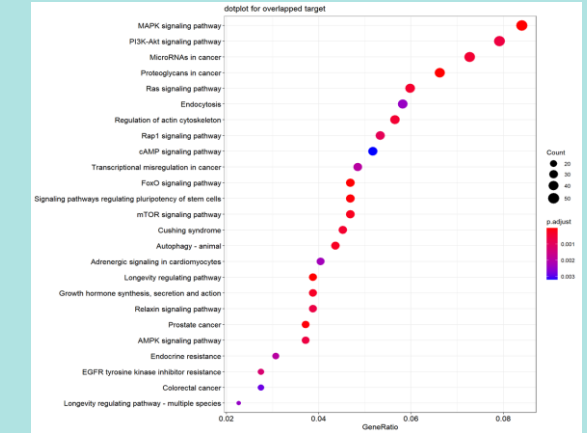
**Table 1.** Significant up- and down-regulated miRNAs between infrequent exacerbators and frequent exacerbators

	baseMean	log2FC	pvalue	padj
hsa-miR-30a-3p	1.43E+02	-1.25286	1.08E-10	1.44E-08
hsa-miR-500b-3p	1.81E+02	-1.00606	6.83E-13	1.82E-10
hsa-miR-411-5p	1.40E+02	-0.7959	1.57E-05	8.40E-04
hsa-miR-766-3p	7.96E+01	-0.7334	1.06E-04	3.15E-03
hsa-miR-3131	7.87E+01	-0.68029	3.00E-03	4.22E-02
hsa-miR-483-5p	6.35E+02	-0.64017	5.89E-05	2.24E-03
hsa-miR-98-5p	5.95E+02	-0.63722	2.71E-06	2.39E-04
hsa-miR-326	1.58E+02	-0.63403	1.74E-03	2.73E-02
hsa-miR-1-3p	2.58E+03	-0.58073	1.93E-04	4.68E-03
hsa-miR-1290	1.10E+02	-0.46007	4.96E-04	9.93E-03
hsa-miR-148a-5p	1.66E+02	-0.4453	1.03E-02	9.79E-02
hsa-miR-7706	1.51E+02	-0.44387	5.35E-03	6.49E-02
hsa-miR-409-5p	5.86E+02	-0.3449	4.24E-03	5.67E-02
hsa-miR-1271-5p	6.03E+02	-0.31445	2.71E-03	4.02E-02
hsa-miR-99a-5p	8.87E+04	-0.21566	7.49E-04	1.33E-02
hsa-miR-500a-3p	3.99E+03	-0.19627	7.67E-03	8.53E-02
hsa-miR-10a-5p	1.56E+05	-0.18285	8.80E-03	9.04E-02
hsa-miR-10b-5p	2.28E+05	-0.18031	1.07E-02	9.81E-02
hsa-miR-24-3p	2.04E+04	-0.13488	9.25E-03	9.15E-02
hsa-miR-21-5p	2.71E+04	0.16217	6.35E-03	7.37E-02
hsa-miR-25-3p	1.06E+04	0.209544	8.54E-03	9.04E-02
hsa-miR-28-3p	4.20E+03	0.260048	2.93E-04	6.52E-03
hsa-miR-101-3p	2.81E+04	0.312038	7.60E-05	2.54E-03
hsa-miR-103a-3p	2.42E+03	0.366806	0.366806	1.58E-04
hsa-miR-443b-5p	3.82E+02	0.397657	4.51E-03	5.73E-02
hsa-miR-342-5p	8.36E+02	0.522224	1.92E-05	8.53E-04
hsa-miR-3158-3p	8.08E+01	0.658961	1.41E-03	2.35E-02
hsa-miR-125b-5p	6.01E+01	0.781527	5.21E-04	9.93E-03
hsa-miR-1307-5p	2.95E+02	0.851277	3.58E-06	2.39E-04



**Figure 1.** Network between DE miRNA and putative target genes from miRNet. Sky-blue color squares represent the miRNAs and different color circles represents the target genes involved in different essential pathways implicated in Asthma.

**Figure 2.** Functional enrichment of putative target genes of DE miRNAs from KEGG



## Conclusion

Results show that 29 DE miRNAs were linked with asthma exacerbation in our discovery cohort and involved in 4 main asthma-related pathways: PI3AKT, Ras, RAP and MAPK signaling pathway.

## Acknowledgement

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## References

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