

Immune response regulation through non-coding RNA-target interactomes

Lanre Morenikeji, PhD
University of Pittsburgh @ Bradford

Motivation

- To understand how immune systems are regulated through non-coding ribonucleic acids (ncRNA) in the presence of exogenous stimuli
- Variation in host-pathogen interactomes
- Would benefit disease surveillance and therapeutic intervention
 - Infectious diseases
 - Coronavirus infection

Project Description

- Targeting specific immune response genes with ncRNAs in cells
- Gene expression profiling at transcriptomic and proteomic levels
- **Manipulating ncRNA-targets to circumvent negative regulators of immune responses.**

Context

- There is paucity of information on the involvement of ncRNAs in infectious diseases
- They are important as diagnostic markers and drug targets, because they can bind multiple targets to regulate their expression through complimentary base pairing.
- Elucidating these small molecules in the context of immune system regulation and response (cytokine storms) to infectious diseases such as coronaviruses is highly pertinent.
- We have shown that some miRNAs target two or more genes in the same pathway, indicating their importance as molecular regulators (Figure 1)



This project brings hands-on experiential research opportunity for undergraduate students in STEM at Pitt-Bradford and contributes to understanding mammalian RNA biology in infectious disease.

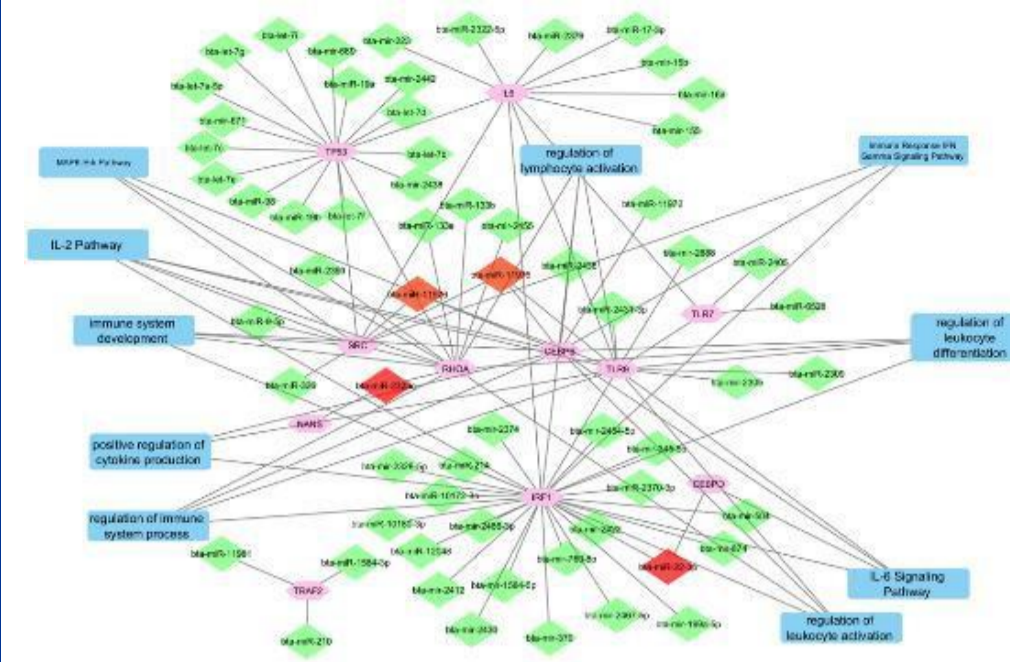


Fig 1: Multiple miRNA-targets has potential impact on several disease pathways (with bovine coronavirus infection) (Morenikeji et al., 2022)

Project Deliverables

1. Markers for molecular disease detection, vaccine production or therapeutic targets against coronavirus infection (B-CoV).
2. Conference abstract presentations and peer reviewed publications
3. Significant capacity development of undergraduate students.
4. Generate preliminary data to source for external funding after the funding period ends
5. To measure our progress and success, my research team should have generated and analyze data on ncRNA-target interactions within the first six to seven months of this project.

Potential Impact

- This project will lay a strong foundation to better understand the regulatory role of ncRNA in infectious diseases.
- It will fill many gaps in our knowledge of mammalian RNA and contribute to systems immunology.

References and/or Acknowledgements

- Morenikeji OB, *Wallace M, *Strutton E, *Bernard K, *Yip E and Thomas BN. Integrative network analysis of predicted miRNA-targets regulating expression of immune response genes in bovine coronavirus infection. *Frontiers in Genetics* 2020; 11, 584392
- * Student coauthors