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ABSTRACT SUBMISSION FORM

CHR D 2022: Abstract & Poster Submission Form

Submitter Name

Jashvi Desai

Submitter Email

jashvidesai@princeton.edu

Presenter Status

- Undergraduate Students
- Masters Student
- PhD Student
- Post-Doctoral Fellows
- Residents
- Non-Trainee

Research Category

- Basic Science
- Clinical
- Community Health / Policy

Role in the project

- Design
- Perform Experiments
- Analyze Data
- Write Abstract

Title

Role of CircRNA in Congenital Diaphragmatic Hernia

Background

Congenital diaphragmatic hernia (CDH) is a devastating congenital anomaly. CDH babies are born with a hole in their diaphragm and abnormal lung development. There is a lack of biomarkers in detecting CDH.

Objective

In the present study, we have analyzed the expression profile of circRNAs from the lung samples collected from control and CDH rats and amniotic fluid samples from survivors and non-survivors to explore the role of CircRNAs in CDH.

Methods

CircRNA arrays were carried out on lung tissue collected from E15 rats (3 control and 3 nitrofen-treated), E21 rats (3 control and 3 nitrofen-treated) rats, and amniotic fluid samples (3 survivors and 3 non-survivors). The data collected was quantile-standardized and processed using R's Limma function. A total of 20 circRNAs were collected ($p < 0.05$). Using CircAtlas and circRNA interactome databases, 12 miRNAs were found to be interacting with these circRNAs. Relevant genes associated with CDH were first sorted into functional gene groups. The interactions between the miRNAs and these relevant genes were then analyzed through the MirWalk and TargetScan databases.

Results

This study suggested that both the CDH lungs and amniotic fluid have a unique circRNA profile compared to control. Interestingly, we have found that similar differentially expressed CircRNAs are present in both amniotic fluid and rat samples. The differentially expressed circRNAs acted as a sponge for a range of miRNAs (hsa-miR-22-5p, hsa-miR-211-3p, hsa-miR-198, hsa-miR-134-3p, hsa-miR-183-3p, hsa-miR-7, hsa-miR-149-5p, hsa-miR-150-3p, hsa-miR-182-5p, hsa-miR-103a-2-5p, hsa-miR-92a-1-5p, hsa-miR-139).

All the miRNAs interacting with genes (EYA1, GAB1, SLIT3, ROBO2, ROBO1) were related to cell migration, axon formation, and angiogenesis.

Conclusion

We have identified that circRNAs can serve as a biomarker to predict outcomes in CDH.

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Authors

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Name	Email	Role	Profession
Jashvi Desai	jashvidesai@princeton.edu	Presenting Author	Undergraduate Student
Muntahi Mourin	Muntahi.Mourin@umani-toba.ca	Co Author	Post-Doc

Richard Keijzer

Richard.Keijzer@umani
toba.ca

Co Author

Surgeon-Research
Scientist