

# The involvement of miR-21 in the molecular pathogenesis of Richter transformation

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### Introduction

- RNA non-coding miRNAs are that play roles molecules in posttranscriptional gene regulation and in translation.
- Our preliminary data indicates that miR-21 is overexpressed in patients with Richter transformation (RT).
- Therefore, the investigating the role of miR-21 could be associated with the development of RT in patients with chronic lymphocytic leukemia (CLL).
- unknown.

# **Methods**

- miR-21 KO cells were generated using CRISPR-Cas9 technology
- Genomic DNA extraction, PCR, and gel electrophoresis were conducted to genotype knockout cells.
- Sanger sequencing was conducted to sequence specific areas of knockout cells.
- RNA extraction, cDNA synthesis, and RT-qPCR were conducted to compare miRNA levels
- Cell viability was measured MTS assay.
- Flow cytometry was performed to determine the effects the miRNAs had on the cell cycle and apoptosis



### **Results**

SSC



Figure 7. miR-21 KO cells induce apoptosis. (A) Flow graphs for MEC1 cell line (parental on left) (B) Flow graphs for RT5 cell line (parental on left) **MEC1 Cells** 



# Conclusions

- We confirmed the oncogenic role of miR-21 in CLL and Richter transformation.
- Potential targets for miR-21 should be identified for future research
- The pre-Richter mouse model can be used with miR-21 knockout cells for future investigations.
- Exploring the function and possible implications of miR-21 during the transition from CLL to RT is a crucial area of investigation since miR-21 could potentially serve as

#### **Richter transformation/** diffuse large B cell lymphoma

**Figure 1.** *miR-21 is significantly upregulated at* the time of RT when compared to at CLL diagnosis.

### **Hypothesis**

In this study, we hypothesized that miR-21 overexpression is related to the molecular pathogenesis of RT

# **Research Aims**

- Generate knock-out (KO) miR-21 stable CLL and RT cells using CRISPR/Cas9 technology.
- Determine effects of miR-21 on the cell cycle, apoptosis, and cell viability



**Figure 4.** Sanger sequencing for miR-21 KO cells.



Figure 6. miR-21 KO cells induce proliferation **Figure 5.** *miR-21 expression levels for KO* of cells. cells.

therapeutic target.

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#### References

1) Roosbroeck, Bayraktar, et al. (2019). The involvement of microRNA in the pathogenesis of Richter syndrome. Haematologica v. 104 (5). 2) Rossi, Davide, and Gianluca Gaidano. "Richter syndrome: pathogenesis and management." Seminars in oncology vol. 43,2 (2016): 311-9. doi:10.1053/j.seminoncol.2016.02.012 3) UCSC Gene Browser on Human. https://genome.ucsc.edu/cgibin/hgTracks?db=hg38&lastVirtModeType=default&lastVirtModeExtraState=&virtModeType =default&virtMode=0&nonVirtPosition=&position=chr17%3A59841266%2D59841337&hgsi d=1668084494\_Xnax7F8r5pscRAsSzNgiG5SaQSvu