CHRD 2021: Abstract & Poster Submission Form

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Research Category:

- ◉ Basic Science
- ○ Clinical
- ○ Community Health / Policy

What was your role in the project?

- ☑ Design
- ☑ Perform Experiments
- ☑ Analyze Data
- ☑ Write Abstract
- ☐

Presenter Status:

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

Title

The Bowen-Conradi EMG1 Variant is a Hypomorphic Allele

Background

Bowen-Conradi Syndrome (BCS) is a ribosomopathy (ribosome assembly disorder) present in the prairie Hutterite population. It is characterized by severe development delay leading to death in early childhood. Clinical care for individuals with BCS is primarily supportive. Therefore, further research needs to be conducted to better understand the disease and to propose possible treatment options.

Objective

The aim of this project is to test whether the BCS variant (D86G) of the ribosome assembly protein Emg1 is hypomorphic. In such situations a sequence variant causes structural changes in the protein that result in decreased protein abundance, loss of protein structure, and function. Here we assess the levels of the wild-type and BCS variant EMG1 protein along with probing for structural changes in the protein.

Methods

Using a yeast model of BCS, we assessed the levels of FLAG tagged wild-type and BCS variant EMG1 by western analysis. A cyclohexamide chase assay was used to assess EMG1 protein stability. Structure probing was done by partial trypsin digestion and western blotting.

Results

We observe a decrease in the protein levels of BCS variant EMG1 compared to wild-type for cells grown at 30℃ and 35℃. However, cells grown at 22℃ show normal protein levels of BCS variant EMG1. This suggests a temperature dependent instability of the BCS variant. In a cyclohexamide chase assay, we observe a significantly lower half-life of BCS variant EMG1 compared to wild-type. In a trypsin sensitivity assay, we observe that wild-type EMG1 is very stable whereas BCS variant EMG1 is rapidly degraded.

Conclusion

From this data, we conclude that BCS is due in part to local or global protein unfolding of EMG1 which decreases the protein’s stability and abundance. Further studies will examine the ubiquitination levels of the wild-type and BCS variant EMG1.

Authors

- For each author, please click "**[+] Add Item**" and provide the author's information

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