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DETERMINING THE STABILITY OF THE BOWEN-CONRADI SYNDROME PROTEIN EMG1

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Background:

The ribosomal RNA small subunit methyltransferase Emg1 plays a crucial role in the assembly of the small subunit (SSU) of the ribosome. A mutation in Emg1 has been identified as the key factor causing Bowen-Conradi Syndrome (BCS), a rare genetic disease affecting Hutterite communities of Canadian prairie regions. While the mutation itself has been identified, the molecular consequences of the amino acid substitution has yet to be determined.

Objective:

To characterize the stability of the Emg1 BCS mutant in comparison to the WT protein while simultaneously investigating the mutational molecular interactions causing any destabilization effects within the protein.

Methods:

All methods use a yeast model system of BCS in which the endogenous chromosomal protein can be genetically depleted and WT, BCS, and other Emg1 variants are epitope-tagged and constitutively expressed from a plasmid. We used a cycloheximide chase assay to determine the stability of the BCS protein relative to its WT counterpart. The mutational molecular interactions were investigated using site directed mutagenesis in order to introduce different amino acids into the yeast Emg1 protein which were then expressed within yeast cells. The mutated cells will be further assessed using a series of growth curves and dot plates.

Results:

We find that WT Emg1 levels exhibit only a minor decrease over the course of the cycloheximide assay. However, BCS Emg1 levels begin at a lower abundance in comparison to the WT and then exhibit a rapid decay during the time course of the assay.

Conclusion:

The rapid degradation of BCS Emg1 in the cycloheximide assay confirms for the first time that the BCS mutation causes a destabilization of Emg1 protein as part of the molecular pathogenesis of BCS. We expect the outcome of the mutational analysis to give us structural and functional insight as to why the destabilization occurs.