Characterization of a novel magnesium gene by next generation sequencing: Unraveling the mysterious role of FAM111a in Kenney-Caffey syndrome

Clinical relevance

Patients with Kenney-Caffey syndrome suffer from a rare disease that is characterized by a proportionate short stature, skeletal abnormalities and a severe primary hypomagnesemia paired with a secondary hypocalcemia and hypoparathyroidism. The causative gene in these patients is FAM111a, a protein residing in the nucleus, which has been linked to DNA replication. However the actual function of this protein and how it affects ion transport remains elusive. Since we have no idea how FAM111a might affect the transport of ions like Mg^{2+} and Ca^{2+}.
We devised a two-pronged strategy to elucidate its function. In one, we performed a GFP-pulldown of FAM111a and subsequent mass spectrometry to figure out its interaction partners. In the other we performed a RNA-sequencing experiment in kidney cells were we knocked down FAM111a to find out how FAM111a has an effect on gene transcription and consequently which genes are affected.

Aim

The goal of this project is therefore to validate potential targets from both the GFP-pulldown and RNA-sequencing experiments and perform additional follow-up experiments to further elucidate the role of FAM111a in renal ion transport.

The student will be involved in:

- Analysis of complex “big” data sets (RNA-seq)
- Validating candidate genes from the FAM111a GFP-pulldown by co-immunoprecipitation
- Knocking down FAM111a in a renal cell line to investigate expression differences of candidate genes.
- Perform follow-up experiments based on the nature of the candidate genes in various renal cell lines.

The student will learn these techniques:

- GFP-pulldown experiments
- Cell culture
- RT-qPCR
- Co-immunoprecipitation
- siRNA mediated knockdown in immortalized cell lines
- Molecular cloning
- Western blotting

Contact

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