Case Study: PROTEOMICS - MASS SPECTROMETRY 2

Research Question

Our aim was to gain insights into the fundamental biology of how we recycle/remove waste material in the eye. This 'waste removal and recycling' process known as outer segment phagocytosis (OSP) is relevant to genetic and age-related forms of blindness. In particular, defects to our gene of interest (*rab28*) are known to result in dysfunctional OSP. Our goal was to understand changes in the zebrafish eye due to loss of Rab28 that are likely to explain how this results in inherited human blindness.

Our Approach

We used mass spectrometry to evaluate the proteomic profile of *rab28* KO zebrafish eyes and wildtype zebrafish eyes at daily peaks and troughs of the waste removal process. Proteomic analysis demonstrates loss of zebrafish Rab28 leads to reduced levels of phototransduction cascade components and core ciliary trafficking proteins, in addition to known OSP regulators. As we have uncovered potential regulators of the OSP process, we now hope to conduct further research into the pathways of recycling/removing waste material in the eye.

Resulting Publication: Moran AL, Carter SP, Kaylor JJ, et al. Dawn and dusk peaks of outer segment phagocytosis, and visual cycle function require Rab28. FASEB J. 2022;36:e22309. doi:10.1096/fj.202101897R

Expertise:

We offer the dedicated strategic support of our expert team, both before mass spectrometry (sample preparation and separation) and after (data analysis, bioinformatics) to enable our research and commercial partners to take full advantage of their results.

Testimonial

"In this, and similar projects, the capacity to efficiently and effectively conduct proteomic profiling with the core facility, led to fundamental new discoveries into the molecular processes of photoreceptor outer segment phagocytosis. This was key to the resulting high impact publication, a PhD thesis and will support several follow-on projects".

'The support provided by Eugene Dillon and the wider Proteomics team has been of huge benefit to my PhD project. The team's assistance and intellectual input has led to the development and optimisation of protocols for large-scale protein analysis in both cell culture and zebrafish models, which can now be applied to ongoing and future projects".

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