Undergraduate Research Symposium May 19, 2017 Mary Gates Hall

Online Proceedings

POSTER SESSION 2

Commons West, Easel 22

1:00 PM to 2:30 PM

Proteomic Profiling of Patient-Derived Retinal Pigment Epithelium in Sorsby Fundus Dystrophy

Thomas H Khuu, Sophomore, Biochemistry
Mary Gates Scholar
Mentor: Jennifer Chao, Ophthalmology

Sorsby Fundus Dystrophy (SFD) is a rare autosomal-dominant macular dystrophy that causes central vision loss in early adulthood due to mutations in the *TIMP3* gene, yet its pathogenesis remains unclear. SFD is clinically similar to age-related macular degeneration (AMD), the leading cause of vision loss in older persons in the United States. Preliminary data revealed structural and functional differences between retinal pigment epithelial (RPE) cells differentiated from SFD patient-derived induced pluripotent stem cells (iPSC) and control iPSC-derived RPE cells. In contrast to control iPSC-derived RPE, SFD RPE does not accumulate any detectable extracellular matrix (ECM) and demonstrates a 40-fold increase in the level of intracellular hydroxyproline, a collagen degradation product whose increased expression adversely impacts SFD RPE metabolism and increases its susceptibility to oxidative damage. We wanted to determine whether differential protein expression between SFD and control RPE cells could elucidate the mechanisms behind these changes. A shotgun proteomics approach using isobaric Tag for Relative and Absolute Quantification (iTRAQ) identified peptide sequences present in these cells, and proteins were identified based on these sequences. Proteins with a twofold increase or decrease between cell types were noted, which included glutathione-s-transferases, gamma-glutamyl transferase 5, and chitinase-3-like 1. I am confirming these results through Western Blot and will analyze them by protein network analysis to determine their relevance to the disease model based on previously obtained metabolic data. The results from this experiment will help reveal the mechanisms behind SFD pathogenesis and potentially identify targets for disease treatment.

Molecular Diagnostic of Post-Surgical Endophthalmitis

Bryan Yue, Senior, Computer Science, Biochemistry
Mentor: Cecilia Lee, Ophthalmology

Post-surgical endophthalmitis is a serious vision-threatening inflammation following any ocular procedure. Detection of endophthalmitis with culture has been traditionally used; however, endophthalmitis caused by viruses are overlooked. In a 1995 Endophthalmitis Vitrectomy Study by RK Forster, 33% of patient samples were culture negative. This represents a significant portion of patients who could have had endophthalmitis due to viruses. Using alternative techniques, we can characterize viral pathogens found in post-surgical endophthalmitis with qPCR (quantitative polymerase chain reaction) and polymerase chain reaction (PCR). qPCR quantifies the number of viral DNA strands whereas PCR indicates presence or absence of the viral DNA. This allows doctors to treat more patients which would have been previously thought to not have endophthalmitis. Patients diagnosed with endophthalmitis following intraocular procedures were recruited from Wills Eye Hospital and University of Washington from Sept 1st , 2014 to Dec 31st , 2015. All patients underwent vitreous or aqueous tap. The specimens were sent for microbial culture. Following DNA extraction, qPCR for Torque Teno Virus (TTV), Merkel Cell Polyomavirus (MCV), and actin were performed in all samples. qPCR results were verified via PCR and gel electrophoresis. A total of 29 samples were collected (12 culture-positive [41.38%], 17 culture-negative [58.62%]). Overall, 18 (62.07%) samples were positive for TTV and 15 (51.72%) for MCV. The presence of TTV or MCV was not associated with culture positivity by Fisher's exact test. Viral DNA sequences are unexpectedly common in endophthalmitis. The role of these viruses in this disease process remains unclear.

POSTER SESSION 4

Balcony, Easel 101

4:00 PM to 6:00 PM