Statement of purpose

My name is Hsiao-Chu Hsu, and I am from Taiwan. After completing my master’s degree in 2010, I came to Florida with my husband who works as a graduate assistant in RSMAS, University of Miami. I was offered a job as a research assistant in Altor Bioscience Corporation in Miramar for three years. I worked in GLP (Good Laboratory Practice) and QC (Quality Control) lab which is responsible for drug validation, stability, and testing new drug functions on the enrolled patients. I was trained in the labs to abide by strict procedures and a timely manner on conducting projects and documentation. Furthermore, the company’s discovery on novel drugs got me interested in research, where I occasionally worked with research scientists to perform mice tissue dissection.

At graduate level, I majored in molecular Biology field by performing experiments utilizing zebrafish as animal model. My research focused on the role of endoderm in the interrenal tissue (analogous as adrenal cortex in human) development in the zebrafish. By examine endodermless mutant, *cos32*, which has been reported to show apparently defeats in heart, vasculature and pronephric duct. Therefore, it has been postulated that the endoderm might provide signals that guide the morphogenesis of certain mesoderm tissues. The result showed the central migration of interrenal tissue and its associated midtrunk venous endothelium were disrupted in *cas* mutants and morphants. When rescuing the endoderm by knockdown of *osr1* (*odd skipped related 1*) expression in *cas*, central migration defects of interrenal tissue and midtrunk venous endothelium were both recovered. In addition, the extracelluar matrix protein Fibronectin, which was defective in *cas*, did not seem to be required for the interrenal migration. These data shows that the endoderm might pattern the morphology of endothelium, which in turn would attract interrenal cells and guide their migration to the midline.

my major concern is to better understand the mechanism of gene function associated with cancer diseases

While I was preparing for graduate school application this year, I took an EDX (Free online courses from the world’s best universities) course of Quantitative Biology workshop, which brought about my interest on computational data analysis on genomic sequences and experimental data (cell expression) by primary programming such as Matlab, Python and R. After six weeks of challenging hard work, I finally finished and passed the course as a final 82 grade (passable score is 70). This experience encouraged me to gain more solid knowledge on quantitative and programming applied in biomedical field. Today, we are in the era of post-genomics, which we can study genetic disease or cancer by comparing variance between patients and health population with Whole Genome Sequencing (WGS) or Single Nucleotide Polymorphism (SNP) in efficiency to discover pathogenic genes.

In addition, we can examine more deep study on function of human- analogous genes or even human lethal gene targeting in model animals that complete genome sequences have been published. Therefore, we can gain better idea of treatment or drug discovery for genetic heritable or cancer patients. In order to further the depth of research,

, I will focus on three aspects: 1. Statistical and quantitative analysis of genomic data, such as microarray data and next generation sequencing data 2. Study of gene expression of differences between populations, associated genomic variants to disease with dataset 3. Comparative genomics between human and model organisms in gene identification.

After three years working in a biopharmaceutical company, I find myself in the need of much more resource and time to develop a good research. Thus, I am eager to enroll in PHD program. I believe that genetic and genomics research will bring human beings a better personal medicine treatment and solve orphan genetic disease. My dream is to dedicate myself on biomedical study for human’s health welfare. Hope I can get an opportunity to get into this program.