I received my Ph.D in Experimental Pathology from The University of Texas Medical Branch in Galveston (UTMB) in the area of blood-brain barrier structure and function, and stayed here as a postdoctoral fellow currently working on blood-brain barrier injury in viral encephalitis. Since my early graduate training I have participated in brain tumor diagnostic sessions and conferences, and recently I created a database of the clinical cases of brain tumors for the Neuropathology section. I also helped to develop a new brain cancer research initiative for gliomas, the most common primary brain tumors, at UTMB.

The ASIP 2009 Summer Academy training course provided advanced knowledge in cancer pathobiology, genetics, pharmacogenomics and current therapy. In this course I learned that carcinogenesis is a multistage process in which permanent genetic changes are introduced. Frequently, multiple mutations are involved in a single type of cancer, and patients with the same morphologic diagnosis may not have the same mutations. Cells with these mutations either gain functions in activating cell proliferation or lose functions in suppressing cell death. As a result, tumors grow out of control and may further metastasize to local adjacent tissues or to remote organs. Knowing which genes are mutated in cancers would greatly facilitate drug development and selection of treatments.

I am aiming to apply the knowledge I gained from the course to explore techniques and funding opportunities in brain tumor basic and clinical research. The

current standard diagnosis of gliomas largely relies on cancer cell growth patterns, morphology, and cellular and proliferation markers. There are very limited genetic tests available. I would like to use the database I created to correlate information about pathologic features, treatments and post-treatment follow up. Using available tissue from paraffin blocks, I will propose to analyze genes suspected to be mutated in these cancers using methods such as fluorescent in situ hybridization and tissue array, and correlate the findings with diagnoses and clinical outcomes. I am also proposing to collect fresh tissue from newly diagnosed gliomas to further study gene expression and mutations using techniques for which paraffin-embedded samples are not suitable. The long-term goal of this project is to develop rapid and reliable diagnostic methods to determine gene alterations in gliomas, and eventually other types of brain tumors, for efficient targeted therapy and better drug development.