Kit Sing Au, PhD, is an Assistant Professor the Division of Medical Genetics within the Department of Pediatrics at the University of Texas Medical School at Houston (UTMSH) and he joined the faculty in August 1999. Dr. Au is the Director of the Genetic Laboratory for the Tuberous Sclerosis Complex (TSC) Center. He is also a co-investigator (co-I) and the Director of the Genetic Core for the Tuberous Sclerosis Complex Autism Center of Excellence project.

Dr. Au and Dr. Hope Northrup are research partners for over 20 years focusing on two human genetic diseases involving the central nervous system: TSC and myelomeningocele (MM). These projects involve discovery of disease genes and variants, gene function study and genotype-phenotype correlation.

Tuberous Sclerosis Complex: TSC is a dominantly inherited disease with affected individual having multiple organ hamartomas, hamartias and neuro-psychiatric deficits. Mutation in either TSC1 or TSC2 causes TSC in ~85% of patients. TSC1 and TSC2 together regulate mTOR signaling to modulate cell growth and cell proliferation. Of more than 400 TSC patients examined at UTMSH, ~15% have no mutation identified (NMI) in the TSC1 and TSC2. Recently, we have applied a whole exome sequencing (WES) approach to evaluate mutations in additional genes that may cause TSC among the NMI patients.

Interestingly, clinical symptoms vary widely among TSC patients. Currently, Dr. Au is PI and Dr. Northrup is co-I on a project with the Van Andell Institute in Michigan using WES to search for gene mutations that modify the TSC neurological phenotype.

Myelomeningocele: The second project in the laboratory is to identify genes contributing to MM development. MM is the most severe form of open neural tube defects (NTDs) compatible with survival. Affected individuals live with various physical and/or intellectual disabilities. MM affects ~1 in 2,500 live births in the United States.

Genetic and environmental factors together contribute to MM risk. Our group has shown multiple folate metabolizing genes associated with MM providing the genetic basis for epidemiologic studies showing pre-conception usage of folic acid reduces NTDs incidence. We recently reported glucose metabolism genes associated with MM lending the first genetic evidence for glucose derangements to be an important risk factor for MM.

After many years of research experience on MM, Drs. Au and Northrup hypothesize that the genetic architecture of MM is comprised of novel and/or de novo variants in MM associated genes and in additional genes not yet associated with MM. Dr. Au is PI and Drs. Northrup, James Hixson and Alanna Morrison co-I in a recently submitted NIH R01 grant utilizing WES to test this hypothesis. The grant has received a priority score of 7%.