Molecular Genomics in Malignant Mesothelioma
Dr Lu Shir Kiong
The Brunei Cancer Centre, Jerudong, Brunei Darussalam BG3122

Cancers result from an accumulation of genetic aberrations that are either acquired or inborn. Technologies have been developed to determine the molecular profile of cancer that may have implications for clinical care. Advances in sequencing technologies such as next generation sequencing and array-based approaches have revealed the genetic landscape, including driver genes in a wide range of cancers. These have already translated into better understanding of the biological behaviour of several cancer types to improve diagnosis, prognosis and treatment. Malignant pleural mesothelioma (MPM) is a rare and aggressive type of cancer related to asbestos exposure. The treatment options are limited and response to standard chemotherapy regime is poor. Current understanding of the genetic makeup of this deadly disease is still lacking. Thus, the aim of my research was to gain further insights into the pathogenesis of MPM by exploring the tumour mutational and transcriptional profiles. The results showed MPM is a complex disease with heterogeneous molecular aberrations. By combining findings from both transcriptome and exome analyses, we identified alterations in genes involved in common signalling pathways, such as WNT and MAPK. These may have important roles in driving MPM carcinogenesis with therapeutic implications and require further explorations.