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A translational approach for epigenetic regulation of tumor suppressor genes and microRNAs in malignant plural mesothelioma (MPM)

Yuen Yee Cheng
Asbestos Disease Research Institute, Australia

Malignant Plural Mesothelioma (MPM) is an aggressive cancer caused by asbestos explore. Due to heavy use of asbestos as building material in the pass and long latency of MPM, predict the number of cases will max out during the 2020s and 2030s. Despite the combination of cisplatin/gemcitabine treatment, there is currently no treatment option for MPM with median survival of 9-12 months. Treatment options for MPM are mainly palliative in nature as most patients will be confined with recurrence of the disease and resistance of chemotherapy. It is urgently needed to discover treatment options for MPM. Using microRNA microarray study, we found down-regulation of microRNA is a common event in MPM. The re-introduction of potential tumor suppressor microRNA in MPM led to suppression of tumor cell growth *in vitro* and *in vivo*. Our contribution of microRNA study led to the world's first clinical trial of microRNA replacement in MPM. We have further discovered the down regulation of microRNAs are a result of DNA hypermethylation of their host gene promoter region. We have planned multidiscipline studies including epigenetic regulation in MPM to understand the fundamental biology of MPM in discovering newer treatment options. Dr. Cheng is currently the lead guest editor of the special issue "Epigenetic Biomarkers in Cancer" to recruit high standard research publications in these areas which ultimately may contribute to newer diagnostic tools for MPM.