

Wed, 2 Mar 2016, 11:57 SGT - Singapore Markets close in 5 hrs and 9 mins

MedGenome's OncoMD Helps Analyze Genetic Alterations in Mesothelioma



Press Release: MedGenome – [10 hours ago](#)

FOSTER CITY , California, March 1, 2016 /PRNewswire/ --

A comprehensive genomics study has used MedGenome's [OncoMD knowledge base](#) to identify cancer relevant alterations in Mesothelioma, a deadly cancer.

(Logo: <http://photos.prnewswire.com/prnh/20160112/784044>)

Mesothelioma is a relatively rare cancer with a five year survival rate between five and ten percent. The global death due to Mesothelioma is estimated to be ~43,000 per year. The disease is associated with exposure to asbestos, which is still used in many countries, including China, India, Brazil, Russia and others. A comprehensive genomics study led by Dr. Sekar Seshagiri PhD, Principal Scientist and Associate Director, Genentech and Dr. Raphael Bueno MD, Chief of the Division of Thoracic Surgery and co-director of the Lung Center Brigham Women's Hospital identified ~2700 protein-altering mutation from ~200 tumor samples. The results from this study are published this week in *Nature Genetics*.

Tumor accumulates mutations as they evolve, but many of the observed mutations are collateral "passenger" events and a small number are meaningful "driver" events. Being able to sort the signal (driver) from noise (passenger) is not a trivial task. "MedGenome's OncoMD structured knowledge base can help stratify the mutations into potential drivers and passengers" said Dr. Amit Chaudhuri, Vice President Research and a co-author on the mesothelioma study. He further added "Identifying driver events will enable development of targeted therapies, and where such therapies already exist, you can match the patient with the right drug. It's the holy grail of personalized precision medicine."

OncoMD is a curated knowledge base of over 1.9 million cancer mutations captured from over 7000 peer reviewed publications. It has the largest collection of cancer exomes, greater than 17,000, combining data from TCGA, ICGC and other published cancer studies. Cancer mutations are annotated for their biological relevance, drug sensitivity and as targets of investigational drugs in clinical trials, providing a rich context to understand and interpret genetic alterations in cancer.

OncoMD is available for free to the academic community for research use. OncoMD can be accessed at <http://oncomd.medgenome.com/OncoMDLite>.