Discovery of New Genetic Mutations in Uveal Melanoma Patients by Analyzing Nitrogenous Base Pair Anomalies

Nanda, Hersh (School: BASIS Chandler)

The purpose of this research is to investigate which genetic mutations are responsible for Uveal Melanoma (UM), a rare subtype of melanoma but the most frequent primary cancer of the eye. Genome data of UM patients was obtained from U.S. National Institute of Health's (NIH) National Library of Medicine. Data was obtained from samples that were surgically collected from eye enucleations or resected from liver metastases. The DNA sequence from the cancerous cells was compared to a reference DNA sequence (from normal tissue pairs) to identify any nucleotide base pair mismatches. The locus of each mutation was noted to determine what genes were mutated. Pareto analysis of cross-patient data was performed to identify chromosomes with most genetic mutations and recurrent genetic mutations across patients. Gene functions of mutated genes were studied to investigate possible causal links to cancer, such as anomalies in genes that coded for proteins with a known role in tumor repression. A total of seven recurrent and 107 non-recurrent genetic mutations were discovered, with most mutations occurring in chromosomes 3 and 23. Recurrent mutations varied from 8.7% to 17.39% occurrence in the UM patient sample. The recurring genetic mutations were: ALG1L2, DMD, IL1RAPL2, KIAA0825, LOC440040, NXF2, and PHYHD1. These mutations are newly discovered and not reported in published literature. The research revealed UM is a heterogenous disease with homozygous mutations and is a recessive disorder. The research has wider significance because the seven recurrent mutations discovered may cause other cancers, but future research is needed.