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Lecture description

The evolving landscape of genomic susceptibility to cancer

For many years the process of testing for genetic susceptibility to cancer was based on testing a limited number of patients for a limited number of genes. The limitations on patients was based on testing only those patients with a high likelihood of having genetic susceptibility to cancer (extensive family history, etc). The limitation on genes was imposed due to the cost of genetic testing and the uncertainty in evaluating genetic variants when found due to the lack of large population databases for comparisons. Over the last five years the cost of sequencing has plummeted and much larger databases of non-cancer patients who have undergone whole genome or whole exome sequencing (of all genes) are available. With these advances we are transitioning to doing comprehensive understanding of all cancer patients. These early studies have revealed surprising results including that approximately 10% of unselect adult or pediatric patients carry deleterious mutations in cancer susceptibility genes. We have also learned that our prior attempts to select which patients carry these mutations failed to identify about half of the patients with hereditary mutations. Thus, there is a significant need to adjust our approach and the way that we evaluate patients and the genomic data. We will discuss a number of these recent studies, some of the surprising results, e.g. adult breast cancer mutations in children with a variety of cancers and discuss the challenges interpreting many of these results.