Cancer Genomics: Chapter 21. Neuroblastoma

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Neuroblastoma is one of the most common childhood tumors and has a remarkably diverse pattern of presentation and clinical behavior. Current management approaches rely on risk stratification using clinical, pathological and, increasingly, genetic factors. This chapter explores the current state of knowledge of the genetic factors behind neuroblastoma and discusses how these may impact on treatment. Both segmental chromosomal abnormalities (including loss of 1p or 11q, or gain of 17q) and changes in individual genes (such as MYCN amplification, mutations in ALK and ATRX) have been implicated in neuroblastoma pathogenesis. Recent whole-genome approaches have identified multiple genetic variants (involving LMO1, BARD1, LIN28B, NBPF23 and others) that may predispose to neuroblastoma, while germline mutations in ALK and PHOX2B are associated with rare familial cases of neuroblastoma. The roles of mRNA gene expression profiling, microRNAs that regulate protein translation from mRNA and epigenetic modifications (such as DNA methylation) in neuroblastoma are also discussed. Incorporation of subsets of these genomic factors into risk stratification will ultimately lead to more personalized treatment for neuroblastoma patients.

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