



Cancer Genomics: Chapter 20. Genomic Basis of Pediatric Lymphomas

Nathanael G. Bailey, Thomas Gross, Megan S. Lim

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Lymphomas account for approximately 10% of childhood malignancies. Pediatric lymphomas are typically aggressive: lymphoblastic lymphoma, Burkitt lymphoma (BL), diffuse large B-cell lymphoma (DLBCL), and anaplastic large cell lymphoma (ALCL) are among the most common pediatric lymphoma subtypes. The genetic basis of these neoplasms is beginning to be understood. Lymphoblastic lymphomas arise through a variety of genetic pathways, dependent upon B- or T-progenitor origin. Aggressive B-cell lymphomas (BL and DLBCL) commonly arise secondary to errors that occur during physiologic B-cell development. BL is characterized by MYC translocation with an immunoglobulin locus enhancer. This lesion may also be present in DLBCL, particularly in children, but DLBCLs often have mutations of a variety of other genes, such as BCL6. DLBCL may be separated into germinal center B-cell-like (GCB) and activated B-cell-like groups. Pediatric DLBCL are more commonly in the GCB category than are adult DLBCL. Adult DLBCL has a tendency toward increased genomic complexity compared with pediatric DLBCL. ALCL is a T-cell lymphoma that is typically characterized by ALK fusions, most commonly with NPM. Genomic profiling has identified areas of recurrent genetic gains and losses in ALCL. Understanding the underlying genetic basis of lymphoma provides hope for the development of more targeted therapies for this group of diseases. However, further investigation of the lymphoma genome is necessary, particularly in pediatric patients.

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