

Abstract

To ascertain the genetic basis of pediatric Burkitt lymphoma (pBL), we performed clinical-grade next-generation sequencing of 182 cancer-related genes on 29 formalin-fixed, paraffin embedded primary pBL samples. Ninety percent of cases had at least one mutation or genetic alteration, most commonly involving MYC and TP53. EBV(-) cases were more likely than EBV(+) cases to have multiple mutations ($P < .0001$). Alterations in tumor-related genes not previously described in BL were identified. Truncating mutations in ARID1A, a member of the SWI/SNF nucleosome remodeling complex, were seen in 17% of cases. MCL1 pathway alterations were found in 22% of cases and confirmed in an expanded panel. Other clinically relevant genomic alterations were found in 20% of cases. Our data suggest the roles of MCL1 and ARID1A in BL pathogenesis and demonstrate that comprehensive genomic profiling may identify additional treatment options in refractory disease