The prognostic significance of molecular alterations in pediatric gliomas of central nervous system

Abstract

The purpose of this dissertation is to delve into the molecular and genetic underpinnings of low-grade gliomas in children, focusing on a cohort treated over the past two decades. It aims to correlate these findings with the clinical course and outcomes of the disease. The study was conducted through a collaborative effort between the Clinic of Pediatric Hematology and Oncology and the Laboratory of Molecular Pathology at the Charles University, highlighting the significance of a multidisciplinary approach in diagnosing.

This work highlights the importance of diagnosis as a synthesis of insights from various disciplines, underscoring the significance of molecular-genetic factors in the prognosis and treatment of low-grade gliomas in children. Through a detailed study involving methods such as PCR, Sanger sequencing, RNA panel sequencing, MLPA, and DNA methylation profiling, key genetic alterations were identified, including frequent *BRAF* fusions and mutations, changes in *FGFR* genes, and alterations in *MYB/MYBL* genes, among others.

The study revealed the diverse molecular landscape of pediatric low-grade gliomas, emphasizing the need for integrated diagnostics in determining the appropriate management and therapeutic strategies for this patient group. The research underscores the critical role of comprehensive molecular-genetic analysis in enhancing the understanding and treatment of pediatric low-grade gliomas.

Key words: pediatric low grade gliomas, DNA methylation, RNA sequencing, survival analysis