

Pediatric Low-Grade Glioma Classification

Pediatric Low-Grade Gliomas (PLGGs) display heterogeneity regarding morphology, genomic drivers and clinical outcomes.

They constitute the largest, yet clinically and (molecular-) a histologically heterogeneous group of **pediatric brain tumors** of **WHO grade I** and II occurring throughout all **pediatric** age groups and at all **central nervous system** (CNS) sites. The **tumors** are characterized by a slow growth rate and may show periods of growth arrest ¹⁾.

Pediatric low-grade gliomas were shown to be characterized by an **array** of distinct molecular aberrations. The **CIMPACT-4** consensus proposed pediatric **low-grade gliomas** of the diffuse type to be characterized by distinct molecular changes rather than distinct histological features.

Fukuoka et al. described a small series of pediatric **oligodendroglioma**-like tumors with **BRAF V600E** mutations. Interestingly, they exhibited molecular changes usually associated with adult **high-grade gliomas**: chromosome instability, **chromosome 7** gains, and **chromosome 10** loss, but had an indolent **natural history** ^{2) 3)}.

Genetic abnormalities

Mobark et al. profiled a targeted panel of cancer-related genes in 37 Saudi Arabian patients with pLGGs to identify genetic abnormalities that can inform prognostic and therapeutic decision-making. They detected genetic alterations (GAs) in 97% (36/37) of cases, averaging 2.51 single nucleotide variations (SNVs) and 0.91 gene fusions per patient. The KIAA1549-BRAF fusion was the most common alteration (21/37 patients) followed by AFAP1-NTRK2 (2/37) and TBLXR-PI3KCA (2/37) fusions that were observed at much lower frequencies. The most frequently mutated genes were NOTCH1-3 (7/37), ATM (4/37), RAD51C (3/37), RNF43 (3/37), SLX4 (3/37) and NF1 (3/37). Interestingly, they identified a **GOPC-ROS1** fusion in an 8-year-old patient whose tumor lacked BRAF alterations and histologically classified as low-grade glioma. The patient underwent gross total resection (GTR). The patient is currently disease-free. To the author's knowledge, this is the first report of GOPC-ROS1 fusion in PLGG. Taken together, they revealed the genetic characteristics of pLGG patients can enhance diagnostics and therapeutic decisions. In addition, we identified a GOPC-ROS1 fusion that may be a biomarker for pLGG ⁴⁾.

Pediatric **low-grade gliomas** (PLGGs) are commonly associated with **BRAF** gene fusions that aberrantly activate the mitogen-activated protein kinase (**MAPK**) signaling pathway.

This has led to PLGG clinical trials utilizing **RAF**- and **MAPK** pathway-targeted therapeutics. Whole-genome profiling of PLGGs has also identified rare gene fusions involving another **RAF** isoform, **CRAF/RAF1**, in PLGGs and cancers occurring in adults. Whereas BRAF fusions primarily dysregulate MAPK signaling, the CRAF fusions QKI-RAF1 and SRGAP3-RAF1 aberrantly activate both the MAPK and phosphoinositide-3 kinase/mammalian target of rapamycin (**PI3K/mTOR**) signaling pathways. Although ATP-competitive, first-generation RAF inhibitors (vemurafenib/PLX4720, RAFi) cause paradoxical activation of the MAPK pathway in BRAF-fusion tumors, inhibition can be achieved with 'paradox breaker' RAFi, such as **PLX8394**.

Jain et al. report that, unlike BRAF fusions, CRAF fusions are unresponsive to both generations of RAFi, vemurafenib and PLX8394, highlighting a distinct responsiveness of CRAF fusions to clinically relevant RAFi. Whereas PLX8394 decreased BRAF-fusion dimerization, CRAF-fusion dimerization is unaffected primarily because of robust protein-protein interactions mediated by the N-terminal non-kinase fusion partner, such as QKI. The pan-RAF dimer inhibitor, LY3009120, could suppress CRAF-fusion oncogenicity by inhibiting dimer-mediated signaling. In addition, as CRAF fusions activate both the MAPK and PI3K/mTOR signaling pathways, we identify combinatorial inhibition of the MAPK/mTOR pathway as a potential therapeutic strategy for CRAF-fusion-driven tumors. Overall, we define a mechanistic distinction between PLGG-associated BRAF- and CRAF/RAF1 fusions in response to RAFi, highlighting the importance of molecularly classifying PLGG patients for targeted therapy. Furthermore, this study uncovers an important contribution of the non-kinase fusion partner to oncogenesis and potential therapeutic strategies against PLGG-associated CRAF fusions and possibly pan-cancer CRAF fusions ⁵⁾.

References

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