AARN annual meeting 2018
ABTA Grant Opportunities

**Basic Research Fellowship**
Two-year, $100,000 mentored grants supporting postdoctoral fellows who conduct laboratory or field-based research projects that focus on brain tumors.

**Discovery Grant**
One-year, $50,000 grants for high risk, high impact research with the potential to change current diagnostic or treatment models.

**Medical Student Summer Fellowship**
Three-month, $3,000 grants awarded to medical students who wish to spend a summer conducting brain tumor research with esteemed scientist mentors.

**Research Collaboration Grant**
Two-year, $200,000 grants for multi-investigator and multi-institutional brain tumor collaborative research projects. Intended to promote team science, streamlining and accelerating research progress.
Exchanging ideas and building relationships….

for better science, treatments, and care
how to read a scientific poster
TARGETED NEXT-GENERATION SEQUENCING PANEL (GLIOSEQ) PROVIDES COMPREHENSIVE GENETIC PROFILING OF CENTRAL NERVOUS SYSTEM TUMORS


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BACKGROUND

• Identification of genetic changes in CNS tumors is important for the appropriate clinical management of patients.
• Targeted panel-based next-generation sequencing (NGS) can be used for detection of several types of genetic alterations, in a fast, cost-effective manner.
• Several general cancer-themed targeted NGS panels are commercially available, although none of them is designed to specifically target alterations important for pediatric and adult CNS tumors.

METHODS

• We designed the GlioSeq NGS panel using custom AmpliSeq primers (Life Technologies).
• The panel for DNA variant analysis consists of 396 amplicons in 2 primer pools. It covers 1147 brain-related genes, including grade II-IV gliomas, medulloblastomas, and meningiomas.
• NGS was performed using small amounts of DNA (20 ng) and RNA (10 ng) from FFPE resected tissue specimens or small snap-frozen brain biopsies.
• Several general cancer-themed targeted NGS panels are commercially available, although none of them is designed to specifically target alterations important for pediatric and adult CNS tumors.

RESULTS

• The output data was analyzed with Torrent Suite Variant Caller (Life Technologies) and in-house developed bioinformatics pipelines. Alterations were confirmed using conventional techniques.
• The panel detects mutations, gene fusions, and copy number changes among 30 high-yield genes in pediatric and adult brain tumors, including grade II-IV gliomas, medulloblastomas, and meningiomas.
• NGS approaches often identify unexpected alterations that greatly impact the care of brain tumor patients.

CONCLUSIONS

• GlioSeq accurately and sensitively detects a wide range of genetic alterations in a single workflow.
• NGS approaches often identify unexpected alterations that greatly impact the care of brain tumor patients. CH was supported by a National Institutes of Health K08 CA155764-01A1 and NS059038-04. This work was supported by a joint program of the National Institutes of Health of the United States and the Ministry of Health of the Russian Federation. Grant No. 2016-00257-

REFERENCE

If you can't explain it simply, you don't understand it well enough.

Albert Einstein