APPLICATION OF AUTOMATED SYSTEMS FOR ANALYZING PEDIATRIC BRAIN TUMORS: MORPHOLOGY, IHC, AND GENETICS

Tashmatov Suxrob Abdurashidovich[1]
Magrupov Baxodir Asadullayevich[2]
"National Children's Medical Center" Children's Neurosurgery Department, Parkent Street, 294, Tashkent, Uzbekistan, 1001711[1]
Center for the Development of Professional Qualification of Medical Workers, Department of Pathological Anatomy and Forensic Medicine[2]
https://doi.org/10.5281/zenodo.15475661

Abstract

This study presents the first experience in Uzbekistan using automated platforms to analyze pediatric brain tumors through a combination of histological, immunohistochemical (IHC), and genetic methods. Tissue samples from 98 children (aged 1–17 years) were examined using automated systems (Leica Bond-Max, Ventana Benchmark Ultra). Key markers such as Ki-67, GFAP, OLIG2, Synaptophysin, IDH1, and BRAF V600E were assessed. The integration of digital microscopy, IHC, and PCR-based molecular diagnostics improved diagnostic accuracy and allowed for the identification of biological behavior and prognosis. The study demonstrates the efficiency and reproducibility of automated analysis in pediatric neuro-oncology practice.

Keywords: pediatric brain tumors, automated systems, IHC, molecular markers, Ki-67, IDH1, BRAF, digital pathology, diagnosis.

Relevance

Brain tumors are the most common solid tumors in children and account for a significant portion of pediatric cancer mortality. Accurate diagnosis and classification are crucial for treatment planning and prognosis. Traditional histology often falls short in characterizing tumors with complex or ambiguous features. Recent advances in digital pathology and automated analysis platforms have enabled more standardized and objective evaluation. In Uzbekistan, there is limited experience using integrated diagnostic systems for pediatric neuro-oncology. The introduction of automated systems such as Leica Bond-Max and Ventana Benchmark Ultra offers high-throughput, reproducible assessment of immunohistochemical markers and molecular alterations. This approach minimizes human error, reduces variability, and accelerates workflow. Furthermore, molecular profiling of IDH1, BRAF V600E, and Ki-67 provides critical prognostic and therapeutic information. Implementing such systems into clinical practice in Uzbekistan can modernize the diagnostic process, improve accuracy, and facilitate targeted therapy decisions for children with central nervous system tumors.

Objective:

To evaluate the effectiveness of automated systems in analyzing histological, immunohistochemical, and genetic features of pediatric brain tumors for improving diagnostic precision and treatment planning.

Materials and Methods

The study included tumor samples from 98 pediatric patients aged 1 to 17 years, treated at the National Children's Medical Center between 2021 and 2024. Tissue sections were fixed in formalin, embedded in paraffin, and stained with H&E. Immunohistochemistry was

performed using Leica Bond-Max and Ventana Benchmark Ultra platforms to assess Ki-67, GFAP, OLIG2, Synaptophysin. Genetic analysis of IDH1 and BRAF V600E mutations was conducted using PCR and Sanger sequencing. Digital imaging and automated quantification tools were used for interpretation. Statistical analysis was performed using SPSS and GraphPad Prism to evaluate correlations between histological types and molecular profiles.

Results

Among the 98 analyzed tumors, astrocytomas accounted for 49%, medulloblastomas for 22%, and ependymomas for 16%. High Ki-67 index (>20%) was seen in 34% of cases, primarily in medulloblastomas and high-grade gliomas. Positive GFAP and OLIG2 expression was confirmed in most glial tumors. IDH1 mutations were found in 9% of samples, mostly in diffuse gliomas, while BRAF V600E mutations were detected in 13%, mainly in pilocytic astrocytomas. Automated quantification showed consistent and reproducible results. The use of automated systems significantly reduced analysis time and improved marker detection sensitivity, providing a strong basis for molecular classification and personalized treatment.

Conclusion

The integration of automated platforms into the analysis of pediatric brain tumors enhances diagnostic accuracy, efficiency, and reproducibility. Combining histological assessment with immunohistochemistry and molecular profiling on automated systems enables comprehensive tumor characterization. This approach allows early identification of high-risk tumors and molecular subtypes, guiding therapy choices. In the context of Uzbekistan's developing healthcare infrastructure, implementing automated diagnostic tools represents a significant advancement toward modern, personalized pediatric neuro-oncology. The study highlights the practical value of technology-driven diagnostics in routine clinical workflows and supports wider adoption of digital and molecular pathology in resource-limited settings.

References:
Используемая литература:
Foydalanilgan adabiyotlar:

1. Khamdamov B. Z., Umarov B. Y. COMBINED LOCAL TREATMENT OF LONG-TERM NON-HEALING WOUNDS://Collection of abstracts of the scientific and practical conference «Current Problems of Surgical Soft Tissue Infections»(2024), Tashkent, October 28 //JOURNAL OF EDUCATION AND SCIENTIFIC MEDICINE. – 2024. – Т. 1. – №. 5. – С. 7-8.
2. Умаров Б. Я., Мемиров Б. М., Латыпова З. Г. ВЛИЯНИЕ САНИТАРНО-ГИГИЕНИЧЕСКИХ УСЛОВИЙ ПРОЖИВАНИЯ НАСЕЛЕНИЯ И КАЧЕСТВА ВОДОПРОВОДНОЙ ВОДЫ НА ЗАБОЛЕВАЕМОСТЬ ОСТРЫМИ КИШЕЧНЫМИ ИНФЕКЦИЯМИ //Гигиена и санитария. – 1991. – №. 1. – С. 29-30.
3. Umarov B. Y. THE NATURE OF NECROBIOTIC PROCESSES OF LONG-TERM NON-HEALING WOUNDS://Collection of abstracts of the scientific and practical conference «Current Problems of Surgical Soft Tissue Infections»(2024), Tashkent, October 28 //JOURNAL OF EDUCATION AND SCIENTIFIC MEDICINE. – 2024. – Т. 1. – №. 5. – С. 9-10.