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## PROFILING OF MIRNAS EXPRESSION IN PEDIATRIC BRAIN TUMORS

**Marwa Tantawy, Mariam G Elzayat, Dina Yehia and Hala Taha**

Children's Cancer Hospital, Egypt

**Introduction:** The understanding of pediatric CNS tumors biology is essential in the development of disease stratification and in development of less toxic therapeutic agents as well as finding novel markers for early diagnosis. MicroRNAs are short 18–25 nucleotide small non-coding RNA molecules regulate gene expression. Recent studies showed that miRNAs play a significant role in brain tumor biology and may up-regulated or down-regulated in malignancies, which referred their oncogenic or tumor suppressor effect. MiRNA expression patterns have been linked to clinical outcomes, tumor regulation; such as tumor progression, cell growth, cell death and metastasis. The identification of tumor specific miRNA signatures may assist in future in the discovery of new biomarkers with diagnostic and prognostic utility. The main objective of the present study is to detect the expression of different miRNAs in different subtypes of pediatric CNS tumors to distinguish between them in discovering biomarkers for early detection in addition to develop novel therapies.

**Methods:** The expression level of 82 miRNAs were detected in 120 cases of pediatric CNS tumors from fixed formalin paraffin embedded tissues (FFPE), divided into four subtypes including; low grade glioma, high grade glioma, ependymoma, and medulloblastoma using quantitative real time PCR (qRT-PCR).

**Results:** Analysis of qRT-PCR data showed significant differences in miRNA expression between tumor subtypes with P value < 0.05 and Low expression of (miR-221, miR-9, and miR-181c/d) and over expression of miR-101, miR-222, miR-139, miR-1827 and miR-34c) in medulloblastoma patients compared to other subtypes. Low expression of miR-10a and overexpression in (miR-10b, and miR-29a) in Ependymoma patients compared to other subtypes. Low expression of miR-26a and over expression in (miR-19a/b, miR-24, miR-27a, miR- 584 and miR-527) in low grade glioma patients compared to other subtypes.

**Conclusion:** Micro RNAs are differentially expressed between different subtypes of pediatric CNS tumors suggesting that they may play a significant role in diagnosis to distinguish between different subtypes. A greater understanding of aberrant miRNA expression in pediatric brain tumors may support in the development of novel therapies. In addition, the characterization of tumor specific miRNA signatures may play an important role in the discovery of biomarkers with diagnostic or prognostic utility.

## BIOGRAPHY

Marwa Tantawy from Pathology Department, Children's Cancer Hospital in Egypt. She completed her PhD in Ain Shams University in 2016 and her masters in Immunology and Parasitology at Cairo University in 2009.

[marwa.tantawy@57357.org](mailto:marwa.tantawy@57357.org)