Microarray analysis of polysome associated mRNAs from a human glioblastoma reveals intratumoral heterogeneity.

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Glioblastoma is among the most aggressive tumor type and less responsive to chemotherapeutic agents, thus a better understanding of the behavior of these tumors may help to develop new treatments for this disease. Currently, many genome-wide projects attempt to define general patterns of gene expression based on deep sequencing or microarray data from total mRNA populations. However, this approach provides little information about the molecular mediators of tumor biology, because the expression levels of mRNAs do not necessarily reflect the levels of proteins. The identification of mRNAs target of translational alterations in tumors can show gene expression profiles that better reflect the population of proteins. In this work we were able to identified mRNAs differentially translated in a large human glioblastomas that presented histologically different parts. The sample was divided in 8 pieces that were classified as high or low grade based on histological characteristics. Actively translating ribosomes and their associated mRNAs were isolated biochemically through a polysomal profile. mRNA was then extracted from polysomal fractions, and submitted to a microarray analysis. By comparing high vs low grade tumor pieces, we were able to identify more differentially translated genes than differentially expressed genes. These results were validated by Real-Time PCR. Among the differentially translated mRNAs, there are many related to proliferation, development and cancer. The technic of isolating mRNA engaged in translation can be used to identify biomarkers of tumor progression, leading to new therapeutic approaches. Ethical approval: 1775/13.
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