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Research Article

An identification of stem cell-resembling gene expression profiles in high-grade astrocytomas[†]

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KEYWORDS

microarray • neural stem cells • gliomas • gene expression profile • cancer stem cells

ABSTRACT

High-grade astrocytomas are among the most intractable types of cancers and are often fatal. Previous studies have suggested that high-grade astrocytomas may adopt the self-renewal and migration properties of neural stem cells (NSCs) to proliferate and spread by expressing the stem cell-specific genes. However, despite a few common molecules being documented, the molecular basis underlying these similarities remains largely unknown. To have a better understanding of the stem cell characteristics of high-grade astrocytomas, we performed the study to identify the stem cell-resembling gene expression profile in high-grade astrocytomas. cDNA microarray analysis was used to detect the differentially expressed genes of isolated human high-grade astrocytomas versus their peritumoral tissue counterparts, and the identification of stem cell-resembling genes was approached by comparing the high-grade astrocytomas-specific gene expression profile with that of NSCs identified by our previous study and other groups. We identified more than 200 high-grade astrocytomas-specific genes in this study, and near 10% genes or gene families of them exhibited similar up or down expression patterns as in NSCs. Further analysis indicated that these genes were actively involved in cell proliferation, adhesion, migration, and metastasis. This study revealed a list of stem cell-specific genes in high-grade astrocytomas, which was likely to have critical roles in determining the “stem” characteristics of high-grade astrocytomas. © 2008 Wiley-Liss, Inc.

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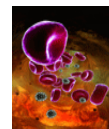
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