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Cytogenomic and epigenomic profiles of glioma stem cell lines

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Cancer is a disease based on several levels of genomic alterations, such as DNA mutations, chromosomal aberrations, copy number alterations (CNAs) and epigenomic changes. Glioblastoma multiforme (GBM) is a grade IV astrocytoma with a 12-15 month of median survival. GBM heterogeneity is mirrored by the presence of distinct sub-populations of cells showing different tumorigenic capabilities: glioma stem cells (GSCs) are believed to be the real driving force of tumor initiation, progression and relapse. Multiple level of genomic disruption are instrumental to cancer development, therefore the study of the genome alterations in GSC lines through a multilevel approach is mandatory to understand GBM pathogenesis. In this study we performed a genome wide-analysis on three GSC lines through a genomic and epigenomic analysis. CNAs were identified, by means of array comparative genomic hybridization (aCGH, Human Genome CGH microarray kit 44K, Agilent Technologies), whereas methylation profiles were assessed using ChIP on chip technology, a technique that combines chromatin immunoprecipitation (ChIP) with microarray technology (Agilent Technologies). The bioinformatic analysis evaluated both the biological functions and the pathway influenced by specific genes identified through the genome-wide analysis. Genes found in previously undescribed CNAs or sharing the same methylation pattern at promoter region showed involvement in cancer mechanism, cell cycle regulation, central nervous system differentiation and pathways related to stemness maintenance. This approach might enable the detection of genetic markers specific of the GBM stem subpopulation and may provide a valuable useful tool for diagnostic classification, prognostic assessment and development of new targeted therapies.

Biography

Simona Baronchelli is a PhD student in Neuroscience at University of Milan-Bicocca, Italy. She achieved her Master degree in Medical Biotechnology from the same university in 2008. She is engaged in Medical Genetics and the two main subjects of investigation are the evaluation of omics landscapes of glioma stem cell lines and the study of cytogenetic abnormalities in premature ovarian failure. She is the author of several abstracts presented to national and international congress and three papers published on peer-reviewed journals.