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Identification of copy number variations of chromosomes 7, 9 and 10 in human glioblastomas by SNP-arrays

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Glioblastomas (GBM) are the most frequent and malignant tumors of the central nervous system. Despite advances in treatment modalities, their prognosis remains dismal and a better knowledge at the molecular and genomic level is still required.

We have previously reported the cytogenetic heterogeneity of gliomas [1]. The aim of the present study was to identify genetically distinct subgroups of GBM, according to similar copy number (CN) profiles for chromosome 7, 9 and 10, and to establish the prognostic value of the different subsets. We also correlated those genetic subgroups with the clinical and biological features of the tumors.

Single-nucleotide polymorphism (SNP)-arrays (Affymetrix 500K) were performed in a group of 35 GBM, to screen for gains, losses, loss of heterozygosity (LOH) and CN neutral LOH (cnLOH).

We identified gains of chromosome 7 (97%) and deletions of chromosome 9 (60%) and chromosome 10 (83%), as the most frequent events in GBM. According to the CN variation observed in these chromosomes four subgroups were disclosed, revealing strong association with patients' overall survival. GBM with *EGFR* amplification showed longer survival times when compared to those with no amplification (p = 0.006), or to the other subgroups (p =0.0006).

In conclusion, our results support the concept that the characterization of genomic changes underlying GBM development, along with the recognition of genetic subsets within these tumors, may be useful to predict prognosis behaviour and to better stratify patients.

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1. Vital AL, Tabernero MD, Crespo I, Rebelo O, Tão H, Gomes F, Lopes MC, Orfao A: **Intratumoral patterns of clonal evolution in gliomas.** *Neurogenetics* 2010, **11**:227-39.

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