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Identification of a common deletion region in 10q26 associated with human gliomas

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Gliomas are the most frequent primary tumours of the central nervous system and several types of gliomas are histopathologically recognized. Loss of the whole chromosome 10, or part of it, is the most prevalent genetic abnormality in astrocytic tumours, particularly in glioblastomas, in which it is observed in up to 80% of all cases [1]. In an attempt to localize a common region of loss in these tumours, we carried out an allelotyping analysis of 25 glioblastomas multiforme, 6 astrocytomas, 4 oligodendrogliomas and 2 ependymomas using highly polymorphic DNA markers, located in the q26 region of chromosome 10. Two meningioma samples have also been analysed. Loss of heterozygosity was found in 76% (19/25) of the glioblastomas, 50% (3/6) of the astrocytomas, 50% (2/4) of the oligodendrogliomas and 100% (2/2) of the ependymomas. None of the two meningiomas showed evidence of loss in this region. The allelotyping results revealed a minimal common region of loss, bordered by the D10S1236 and D10S186 markers, spanning 8.88 Mb, which may be a possible location for a tumour suppressor gene involved in human glioma progression. This region may also be associated to glioma tumorigenesis, since it also appears deleted in early stage gliomas. The fact that microsatellite instability (MSI) screening of gliomas has rendered only one positive sample shows that there is little evidence of MSI for one of the analysed markers, suggesting that this is not a significant event in the tumorigenesis of these malignancies.

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