Variants at 8q24.21 have been shown to be associated with glioma development. By means of tag SNP genotyping and imputation, pooled next-generation sequencing using long-range PCR and subsequent validation SNP genotyping, we identified seven low-frequency SNPs at 8q24.21 that were strongly associated with glioma risk (P=1×10(-25) to 1×10(-14)). The most strongly associated SNP, rs55705857, remained highly significant after individual adjustment for the other top six SNPs and two previously published SNPs. After stratifying by histological and tumor genetic subtype, the most significant associations of rs55705857 were with oligodendroglial tumors and gliomas with mutant IDH1 or IDH2 (odds ratio (OR)=5.1, P=1.1×10(-31) and OR=4.8, P=6.6×10(-22), respectively). Strong associations were observed for astrocytomas with mutated IDH1 or IDH2 (grades 2-4) (OR=5.16-6.66, P=4.7×10(-12) to 2.2×10(-8)) but not for astrocytomas with wild-type IDH1 and IDH2 (smallest P=0.26). The conserved sequence block that includes rs55705857 is consistently modeled as a microRNA [1].

Findings suggest a possible participation of rs891835, rs6470745, and rs55705857 as risk factors to develop glioma [2].

Tumor DNA may approximate genotype at the rs55705857 locus. Hummel et al., confirmed this locus confers an increased risk of all cancers and especially of oligodendroglioma. No increased cancer or brain tumor risk is seen in family members of individuals without the high-risk G allele [3].

Some studies have linked oligodendroglioma with a viral cause. A 2009 Oxford Neurosymposium study illustrated a 69% correlation between NJDS gene mutation and the tumor initiation shown by Kevin Smith. A single case report has linked oligodendroglioma to irradiation of pituitary neuroendocrine tumor.

1)
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