

first exon, which is the promoter region for type II and is far upstream from the exons of all other isoforms.^{11,12} The functional allele contributing to the increased risk for schizophrenia has not been identified in NRG-1, nor is there evidence that any of the associated variations would impact gene expression or function. As two single SNPs associated with schizophrenia were located around the promoter region of NRG-1 and the first exon of GGF, these SNPs might regulate the expression levels of NRG-1 isoforms and/or isoform-isoform ratios. However, no obvious allele effects of these SNPs on NRG-1 expression patterns were observed in this small sample. The estimated relative risks of each of these markers alone were less than that of the seven-marker core haplotype.^{11,12} Taken together, these two SNPs do not appear to be functional alleles, at least in terms of the regulation of NRG-1 expression in human DLPFC. However, the possible relative decrease in type II expression may be regulated by an as yet unidentified allele in linkage disequilibrium with the associated haplotype.

Our findings offer preliminary evidence that abnormal expression of NRG-1 isoforms in DLPFC may be related to the pathophysiology of schizophrenia, but the evidence is weak. The biologic implications of our results are unknown, but they are at least conceptually consistent with evidence that schizophrenia involves genetic abnormalities in developmental/plasticity-related processes.^{51,52} Additional studies are needed to characterize NRG-1 expression in schizophrenia, including slide-based mRNA analyses, protein analyses, neuroleptics effects, diagnostic specificity, and further exploration of genotype based variation.

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