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Unassigned abstracts

HPA axis dysfunction in psychiatry: Genetic background

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HPA axis dysfunction is a key neurobiological finding in major depression (MDD) and in a number of other stress related psychiatric disorders. Hyperdrive of corticotropin releasing hormone (CRH) is at the core of HPA axis dysregulation in MDD. The liability to develop CRH hyperdrive is a complex trait, partially determined by genetic factors. A main functional candidate gene for the regulation of the HPA axis is the gene encoding for the glucocorticoid receptor (GR). Transgenic mice with functional GR gene impairment show profound behavioral changes and elevated plasma corticotropin responses to stress. In humans, several GR polymorphisms were shown to influence HPA axis function. Recently, our group published a positive association finding between polymorphisms in the 5' region of the GR gene and recurrent MDD in two separate populations (1).

The action of the glucocorticoid receptor is tightly regulated by a number of co-chaperones. Binder et al. (2) found significant associations of response to antidepressants and polymorphisms in the FKBP5 gene, a glucocorticoid receptor–regulating co-chaperone of hsp-90.

Several other candidate genes are of interest, such as the CRH receptor 1 and CRH receptor 2 genes, the CRH binding protein gene (3), the AVP receptor gene and the mineralocorticoid receptor gene. These and other genetic determinants of HPA axis function, from our own studies and from the literature, will be discussed.

References

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Transmission diseqilibrium of chromosome 22q11-13 marks in Chinese Han mixed pedigrees of schizophrenia and mood disorder

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Background: Several genome-wide linkage scans have reported that chromosome 22q11-13 might contain susceptibility loci for both schizophrenia and mood disorder.

Methods: We genotyped 44 Chinese Han family trios with mixed family history of schizophrenia and mood disorder with 11 DNA microsatellite markers on chromosome 22q11-13. These markers spanned 56.55 cM on 22q11-13 with mean intervals of 5.66 cM and average heterozygosity 0.71.The transmission disequilibrium test (TDT) was used to search for susceptibility loci to schizophrenia and mood disorder.

Results: Including all family trios regardless of proband diagnosis, we found six markers associated with susceptibility to psychotic disorders., including D22S420 ($\chi2$=4.76, df=1, P=0.029) %3001D22S277 ($\chi2$=5.44, df=1, P=0.020)%3001D22s315 (allele 5, $\chi2$=7.00, df=1, P=0.008; allele 7, $\chi2$=-4.83, df=1, P=0.028; allele 11, $\chi2$=4.00, df=1, P=0.046)%3001D22S274 (allele 7, $\chi2$=-5.40, df=1, P=0.020; allele 10, $\chi2$=6.23 df=1, P=0.013) %3001D22S1160 ($\chi2$=-4, df=1, P=0.046) and D22S1161 ($\chi2$=5.14, df=1, P=0.023). When grouped separately into schizophrenia and mood disorder according to proband diagnosis, four markers D22S420($\chi2$=7.36, df=1, P=0.007) %3001D22S315 (allele 5, $\chi2$=4., df=1, P=0.046; allele 7, $\chi2$=-8.89, df=1, P=0.003)%3001D22S1161($\chi2$=6.23, df=1, P=0.013) and D22S280 ($\chi2$=4, df=1, P=0.046) were significantly associated with schizophrenia, but were not significantly associated with mood disorder, D22S274(allele 7, $\chi2$=5., df=1, P=0.025; allele 10, $\chi2$=6, df=1, P=0.014) were significantly associated with mood disorder only, and D22S277($\chi2$=4, df=1, P=0.046) was associated with both schizophrenia and mood disorder.

Conclusions: These results indicate that chromosome 22q11-13 contains the susceptibility loci to schizophrenia and mood disorder, and that overlapping regions may be shared by these disorders.

Attitudes of nurses towards schizophrenia

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Objectives: According to the recent literature, stigma connected to schizophrenia has a negative impact on the commencement, process and the outcome of the treatment. The aim of this study was to investigate the attitude of nurses from our local community towards schizophrenia.

Methods: This study engaged 166 nurses (8 male, 158 female) employed at the Clinical Hospital in Osijek and the Primary Medical Care in Osjecko-baranjska County. The subjects have filled out the