Young Researchers Forum posters

YRP.01
Neurological signs in schizophrenia: trait markers of brain dysfunction

C. Arango. *Spain*

No abstract was available at the time of printing.

YRP.02
Speech processing cortical representation: invariance in left superior temporal sulcus and variability in Broca's area

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Background: In a previous PET study contrasting French to Tamil stories (1), we demonstrated the involvement during speech processing of both the superior and middle temporal gyri together with the left inferior frontal gyrus (LIFG). In the present study, FMRI was used to obtain a more accurate definition of the involved areas, and to evaluate their variability with respect to handedness.

Methods: 18 healthy male subjects (Edimburgh score range −100 +100) including 7 right-handers (score > 60) were submitted to both 3D high resolution T1 and BOLD acquisitions (1.5-T GE Signa). A block design alternating 30-s duration periods of auditory Tamil and French stories was repeated 4 times. We computed on the French–Tamil contrast both a group conjunction analysis [to uncover activations present in all subjects and anatomically congruent] and individual analyses [to investigate inter-individual variability]. The statistical threshold was set at $p<0.05$ (corrected for multiple comparisons). Final smoothness was 7mm in each direction. Anatomical localization of functional activations was performed on the mean T1 MRI image of the 18 subjects.

Results: *Conjunction analysis* showed a string of activations along the left superior temporal sulcus (t1) and the presence of homologous, although of smaller amplitude, right hemisphere clusters. However, in contrast with our previous results, no activation was found in the LIFG. Rather, *individual analyses* showed activations in LIFG in 12 subjects and in 4 additional subjects when lowering the threshold at the level set for individual contrast in the conjunction analysis ($p = 0.84$, corrected for multiple comparisons).

Discussion: This study shows an anatomical congruence of the temporal activations following the mean t1 anatomical path, and reveals a brain functional invariant since its implication was independent of handedness. This high-order integrative area thus demonstrates a striking low anatomo-functional variability, pointing towards the existence of a strong genetic component in its implementation. On the opposite, the anatomo-functional variability observed in the LIFG is consistent with studies showing large variability in the cytoarchitectonic fields of this cortical area.

(1) Mazoyer, B. *et al* (1993) *J. Cog. Neurosci.* 5, 467–479.
(2) Amunt 1999 *J. Comp. Neurol.* 412: 319–341.

YRP.03
Genotyping Reelin in multiple affected families with schizophrenia: a suitable marker for the vulnerability to develop schizophrenia?

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Recently we could replicate the finding of disturbed neuronal migration in the entorhinal cortex of schizophrenic patients. Neuronal migration is mainly genetically controlled and the Reelin-Dab1 cascade forms a central pathway for directing the migrating neurons. In addition there is increasing evidence that Reelin is reduced in the cortex of patients suffering from schizophrenia. Therefore we have analysed 7 different SNPs situated in coding (2) and non-coding regions (5), as well as one polymorphic triplet repeat located in 5′ untranslated regions of the Reelin gene in 35 Schizophrenic patients, 85 of their relatives and 45 control subjects. Parallel to that on MRI-scans the gyrification index (GI) in 140 of the 155 cases was determined. Schizophrenic ($p<0.0001$) and non-schizophrenic ($p<0.001$) family members showed significantly disturbed frontal gyrification compared to control subjects, while the non-schizophrenic family members revealed a gyrification pattern in between the other two groups. Such an intermediate phenotype and the high degree of heretability of the gyrification index qualifies it as a endophenotypic marker, which is thought be a good link from the phenotype to the susceptibility genes in schizophrenia. The attempt is made to connect the Reelin genotype with the gyrification index.

YRP.04
Introducing a new recruitment design for genetic association studies in opioid dependence

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Objective: In a modified case-control association study we tested the assumption that two polymorphisms ($A_{118}G$ in exon 1 and IVS2+31 in intron 2) of the human μ-opioid receptor gene (OPRM1) confer susceptibility to opioid dependence.

Methods: In contrast to classical case-control studies both groups, opioid dependent cases and non-opioid dependent controls were recruited from individuals who have had access to drugs and were in prison for illegal possessment of drugs.

Results: For both allelic variants of OPRM1 under study we did not find evidence for association with opioid dependence.

Conclusions: Despite this negative association result we think that this new recruitment method introduced here, is useful since it offers a more adequate matching for case-control association studies of opioid dependence.

YRP.05
In opioid dependence

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No abstract was available at the time of printing.

https://doi.org/10.1016/S0924-9338(02)80941-5 Published online by Cambridge University Press