STUDY OF GENETIC VARIABILITY IN A NOVEL PARKINSON DISEASE GENE: EIF4G1

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Introduction: Farrer and colleagues recently reported mutations in eIF4G1 in one family with a phenotype of typical PD. Linkage was ascribed to a region at chromosome 3q26-28 containing approximately 159 genes. Sequencing analysis found only one novel coding variant in the eIF4G1 gene (p.R1205H) segregating with disease. Screening of large PD cohort found this mutation in 9 individuals and absent in 4000 controls (allele freq=0.2%) and another novel missense mutation (p.A502V) in three PD individuals and absent in controls. Linkage was not replicated in any other PD family.

Aims: The aim of our study is to investigate the coding variability in the eIF4G1 gene around the two novel mutations found in the PD patients.

Methods: PCR and sequencing analysis of the exons containing mutations in cohort of about 50 familial PD patients and also in a cohort of 130 unrelated African individuals (from the Centre d’Etude du Polymorphisme Humain).

Results: We failed to identify any mutation in the familial cases. We identified seven coding variants in the African cohort, three of which are novel coding changes predicted to be benign, and have an allele frequency of about 1%.

Conclusions: Given the frequency of the three novel changes found in the African cohort, we presume they are benign.