Conclusions: Our study suggested that gene polymorphisms of TNFα -1031, IL-6-174 and IL-1beta may be linked with PD risk. However, large well-designed studies will be essential to authenticate our findings.

P 5.015.
ALPHA-SYNUCLEIN MUTATIONS IN PARKINSON DISEASE IN THE KAZAKH POPULATION

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Introduction: The accumulation of aggregated proteins in the brain is common across several neurodegenerative disorders. In Parkinson's disease (PD), the protein α-synuclein (α-SYN) is the major component of aggregates known as Lewy bodies. There are several pathogenic mutations in α-SYN gene that are associated with familial forms of PD. We assessed autosomal dominant α-synuclein missense mutations such as Ala53Thr, Gly51Asp and Glu46Lys in the Kazakh population.
Objectives: We conducted a clinical and genetic study of the 34 PD patients in Almaty, Kazakhstan.
Methods: We assessed 34 patients that fulfilled IDC-10 criteria for early-onset (<50 years old) with a rapidly progressive form of PD. The patients had moderate L-dopa response, particularly at the initial stages; some suffered from severe insomnia, constipation as well as cognitive impairment and psychiatric symptoms, such as depression and hallucinations. Genomic DNA was extracted from peripheral blood lymphocytes using standard protocols (ThermoScientific, Genomic DNA Purification Kit#K0512). PCR was performed by using reported primers (primers taken at the web-site www.neurology.org). Restriction Fragment Length Polymorphism Analysis was used for the identification of the mutations. All patients signed the written consent.
Results: Ala53Thr, Gly51Asp and Glu46Lys were not found in our 34 screened PD Kazakh patients.
Conclusions: The point mutations in α-synuclein gene can lead to α-synuclein aggregation in different brain regions leading to parkinsonian syndrome with varying degree of cognitive dysfunction. We assessed 34 Kazakh PD patients with early onset PD clinical phenotype, but Ala5Thr, Gly51Asp, Glu46Lys mutations were not detected.

P 5.016.
POLYMORPHISMS OF DOPAMINE RECEPTOR GENES ARE ASSOCIATED TO INCREASED RISK OF VISUAL HALLUCINATIONS IN ITALIAN PARKINSON'S DISEASE PATIENTS

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Objectives: To determine whether single nucleotide polymorphisms (SNPs) of dopamine receptor (DRD) genes are associated with visual hallucinations (VHs) in Italian Parkinson's disease (PD) patients. VHs are a frequent and important non-motor complication of PD. VHs are associated to a negative prognosis, in terms of both morbidity and mortality. Variations in DRD genes may have a role in predisposing to VHs, since previous studies showed an association between DRD variations and Alzheimer's disease with psychosis, as well as schizophrenia and bipolar disorder (1,2). A previous study on DRD variations in PD subjects with and without VHs, showed no statistically significant association (3).
Methods: Case-control study of 84 PD subjects, 42 with and 42 without VHs matched for age, gender, disease duration and dopaminergic medication. Genomic DNA was analyzed by polymerase chain reaction for SNPs in both D1 (DRD1 A48G and C62T, DRD5 T798C) and D2-like receptor genes (DRD2 G2137A and C957T, DRD3 G25A and G712C, DRD4 C616G and nR VNTR 48 bp). Genotype distributions and allele frequencies were compared between groups.
Results: Allelic frequencies did not deviate from Hardy-Weinberg equilibrium. We found that patients with, compared to those without VHs, had a statistically increased frequency of the following alleles: allele G at DRD1 A48G (OR 3.7; P = 0.0075), allele T at DRD1 C62T (OR 10.7; P = 0.0001) and allele T at DRD2 C957T (OR 3.4, P = 0.0286). No significant association with VHs was found for the other DRD SNPs. On a functional level, D1 and D2 receptor systems have opposite effects on cAMP, with the former increasing and the latter decreasing its production. Notably, DRD1 62T is known to increase gene expression, whereas DRD2 957T decreases mRNA stability, and those two effects point to a synergistic over-activation of the D1 signaling pathway.
Conclusions: Our study shows that PD patients with VHs display higher frequency of DRD SNPs that are known to increase cAMP intercellular levels. Our data are in line with robust associations published in psychiatric conditions, such as nicotine and alcohol dependence, bipolar disorder and psychoses (2). On a clinical level, our findings may provide valuable information for personalizing pharmacological therapy in PD patients.
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P 5.017.
EVALUATION OF CLINICAL PHENOTYPES ASSOCIATED WITH CYTOGENETIC EFFECTS AND METHYLENETETRAHYDROFOLATE REDUCTASE (MTHFR) GENE POLYMORPHISMS IN PARKINSON DISEASE IN COIMBATORE REGION, SOUTH INDIA

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Objectives: The present study aims to investigate the clinical phenotypic and behavioural studies on Parkinson's disease (PD) patients. Chromosomal analysis in PD patients by using GTG banding and the MTHFR gene polymorphisms (A1298C and C677T) were investigated using PCR-RFLP method. In addition, the study aims to understand whether the biomarkers play a vital role in clinical outcome of PD.
Methods: In order to investigate the possible cytogenetic damage and genotypic analysis in PD patients, 12 PD patients and equal numbers of controls were recruited.
Results: The present study analyzed the percentage of chromosomal aberrations (CA) found in PD individuals such as deletion, duplication, translocations Gaps, di-centric and ring chromosomes. There were significant differences found in the cytogenetic variables in the frequency of CA in PD patients and controls. The genotypic pattern of MTHFR gene was different among the distributions of the A1298C and C677T alleles in the PD patients and the controls (p=0.001).
Conclusion: From this pilot investigation, it can be concluded that population-based epidemiologic studies may lean-to important new beam on how we comprehend PD, its natural history, its treatment, and its consequences.

P 5.018.
A MOLECULAR AND GENETIC BASIS STUDY IN POLG MUTATION OF MTDNA IN PARKINSON PATIENTS IN SOUTH INDIAN POPULATION

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