

A MITOCHONDRIAL ETIOLOGY OF PARKINSON'S DISEAS: EVIDENCE FROM MITOCHONDRIAL DNA HAPLOGROUP

Tsu-Kung Lin¹, Chia-Wei Liu¹, Shang-Te Chen¹, Yao-Chung Chuang¹, Mao-Meng Tiao², Pei-Wen Wang³, Shao-Wen Weng³, Jin-Bor Chen⁴, Jiin-Haur Chuang⁵

Departments of, Neurology¹, Pediatrics², Endocrinology³, Nephrology⁴, and Pediatric Surgery⁵, Chang Gung Memorial Hospital-Kaohsiung Medical Center, Taiwan.

Introduction:

There is increasing evidence that genetic variants of mitochondrial DNA (mtDNA) have an important role in the cause of idiopathic Parkinson's disease (PD). Although the relationship about the role of mtDNA variants in PD is still inconclusive, we argue here that this is attributable to the mtDNA haplogroup.

Methods:

To assess the possible contribution of mtDNA haplogroup-specific mutations to the occurrence of PD, we have therefore performed a large-scale association study on 1400 unrelated Taiwanese individuals, including 700 subjects with PD and 700 controls from the population. The genetic haplotypes were conducted by a Luminex100™ system.

Results:

The genotypes for 57 polymorphisms in the coding region of the mitochondrial genome were determined, and the haplotypes were classified into 18 major haplogroups, i.e., A, B4, B5, C, D4, D5, E, F1, F2-4, G, M7b, M7c, M8, M9, M10-12, N9, Y and Z. Multivariate logistic regression analysis revealed that the haplogroup B5 was significantly associated with resistance against PD with an odds ratio of 0.567 (95%CI 0.361-0.892, $P = 0.017$). The haplogroup N9 was noted to be associated with increased incidence of PD with an odds ratio of 1.77 (95%CI 1.008-3.11, $P = 0.05$) which reached marginal statistical significance.

Conclusion:

Our data imply that specific mtDNA mutations/lineages appear to have a significant effect on a predisposition to PD in the Taiwanese population. However, the precise mechanism behind this reduced risk remains to be established.