Genetic Variability in Pesticide-Related Parkinson's Disease: Insights from European and Admixed American Populations

Póster

Genética Humana/Médica

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Gene-pesticide exposure interactions (GPEI) may explain a significant proportion of Parkinson's disease (PD) risk and severity. In Chile, exposure to pesticides is associated with increased odds of developing PD, indicating that pesticide exposure plays a key role in PD etiology in our population. The genetic basis of GPEI leading to PD may differ among populations of different ancestral origin. In this study, we compared GPEI allele frequencies between European (EUR) and Admixed American (AMR) populations to assess genetic differences in PD susceptibility to pesticide exposure. Using PubMed and Web of Science databases, we identified 52 variants in 13 observational studies. We assessed variant frequencies in EUR (n = 41,901) and AMR (n = 3,564) from the GP2 release 10 dataset. 5 SNPs in NFE2L2, PON1, OGG1,

PINK1 and BCHE (rs1803274) presented an absolute frequency difference (ΔAF) over 0.1. Regression models adjusted for age, sex, and genetic variability identified two GPEI variants associated with PD risk: HLA-DRA rs3129882 in EUR (aOR [CI95]: 1.05 [1.015, 1.084]) and AMR (aOR [CI95]: 1.13 [1.008, 1.27]) with a ΔAF: 0.0336; and ACBC1 rs1045642 only in AMR population (aOR [CI95]: 1.15 [1.021, 1.293]) with a ΔAF: 0.068. Regarding clinical features, BCHE rs1803274 was associated with Age at Onset and UPDRS III. Altogether, these results suggest differences between populations in key GPEI genes associated with PD risk, severity and progression. Further studies incorporating environmental exposure and lifestyle factors would deepen our understanding of GPEI.

Palabras Clave

(1) Pesticide Exposure, (2) Latino Population, (3) Ancestry.

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