The first-ever CNV analysis in Latin American Parkinson's disease patients

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5. Rationale: Identification of copy number variants (CNVs) in Parkinson's disease (PD) patients has not been investigated well enough, especially in non-European populations. Despite the fact that the incidence of PD has been found highest among Hispanics (16.6 per 100,000), little is known about the frequency and characteristics of CNVs in Latino PD patients.

Methods

We selected 1,504 patients from the Latin American Research Consortium on the Genetics of PD (LARGE-PD), including samples from Brazil, Colombia, Peru, Uruguay, and Chile. We genotyped 1,779,819 single nucleotide polymorphisms (SNPs) using the Illumina Multi-Ethnic Global Array. The final dataset after quality control included 1,412 samples with 767 cases and 645 controls. CNVs were called using PennCNV and annotated with both known PD and dementia-related genes, and with RefSeq genes.

Results

CNV burden analysis including all CNVs showed no difference between PD patients vs controls (OR: 0.9, 95% CI: 0.8 – 1.2), whereas burden with only known PD genes showed that PD patients had significantly more CNVs in known PD genes compared to controls ($p < 0.001$, OR: 2.9, 95% CI: 1.7 -5.1). When we focused on likely pathogenic CNVs that are larger than > 1Mb, we detected 66 CNVs in PD patients vs 28 in controls ($p < 0.001$, 95 % CI: 1.5 - 3.8).

Summary

Here we present the first-ever CNV analysis in Latin American PD patients. We found that PD patients are enriched with large and rare CNVs as well as CNVs affecting known PD genes. In sum, our work will provide a new perspective for understanding the genetic architecture and

differences in these underrepresented populations. Expanding the diversity of genetic associations will make tailored treatments based on genetic profiles available to this type of patients.