



Applicant

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Project Title

Predicting clinical manifestations of Parkinson's Disease using polygenic risk scores

Project Summary

People living with Parkinson's disease experience a variety of symptoms including problems with movement, memory, and concentration. In a recent study, 90 genetic variants were associated with the development of Parkinson's disease, some linked to specific symptoms. It is unknown, however, whether having multiple gene variants can predict what symptoms will occur. Using an individual's genetic information, the genetic risk for Parkinson's disease can be found for this individual. We will calculate the genetic risk for Parkinson's disease in CLSA comprehensive cohort participants and examine whether we can use this genetic risk to predict common symptoms of Parkinson's disease. The purpose of this study is to find out if we can predict the symptoms that individuals with Parkinson's disease will have by using their genetic information. If we could do that, it might also be possible to identify molecular pathways that could be of interest as potential targets for new treatment.

Keywords

Parkinson's disease, neuroepidemiology, genetics