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Science

Parkinson's disease (PD) is the most common neurodegenerative movement disorder in the world. The clinical features of this disease are caused by an unexplained loss of the nigrostriatal dopaminergic neurons that are important for controlling voluntary movements. Recent studies have identified genes that are mutated in families with PD, and the functional characterization of these PD-related genes has provided important clues on the potential pathobiological mechanisms leading to disease. Mutations in *LRRK2* have been recognized as the major prevalent genetic cause of familial and sporadic PD. Not much is known about the function of this protein, but strong evidences point its kinase activity as crucial for LRRK2-driven toxicity. Therefore, the identification and characterization of the substrates of LRRK2 are needed, and the aim of this project is to tackle this issue by using relevant cell and animal models available, in combination with a set of optimized biochemical protocols. This will shed new insights on the biological and pathological function of the protein and it will be essential for assay development and further progress in the screening of novel neuroprotective drugs targeting LRRK2.