Novel Recruitment Strategy to Enrich for LRRK2 Mutation Carriers

Tatiana Foroud, PhD1, Danielle Smith, BS1, Jacqueline Jackson, BS1, Jennifer Verbrugge, MS1, Cheryl Halter, MS1, Leah Wetherill, MS1, Katherine Sims, MD2, Winnie Xin, PhD3, Vanessa Arnedo, MPH3, Shirley Lasch, MBA4 and Kenneth Marek, MD4.

Medical and Molecular Genetics, Indiana University School of Medicine, Indianapolis, IN, United States; 1Massachusetts General Hospital, Boston, MA, United States; 2Michael J. Fox Foundation, New York, NY, United States and 3Institute for Neurodegenerative Disorders, New Haven, CT, United States.

In summary, we used an internet-based approach to screen large numbers of individuals to identify those with risk factors increasing the likelihood that they carried a mutation contributing to PD susceptibility. This was a highly efficient approach that in only 6 months yielded >100 individuals whose DNA was sequenced. A similar approach could be implemented to other policy makers to identify individuals for clinical trials, biomarker analyses and other types of research studies.

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Figure 1: Web-based recruitment

Table 1: Response for 42 individual with LRRK2 2019G mutation testing results

Table 2: Summary and demographic information for individuals completing the Indiana University Widespread Recruitment Initiative (WRI) screen by state (n=2399)

PPMI Study Design

PPMI is an observational international multi-center study with a goal of recruiting 250 PD patients with and without family history, 250 GBA mutation carriers, 250 LRRK2 mutation carriers, 100 prodromal PD, 70 SWEDD individuals, and 200 age and gender matched healthy controls. Subjects will be followed for 3 to 5 years. The PPMI study is a two phase design: 1) Development of PD progression markers that could be utilized to accelerate research on disease modifying therapies; and 2) strategy for comprehensive biomarker acquisition including CSF has been developed as part of the Parkinson’s Progression Markers Initiative (PPMI) study.

Methods

• Individuals with and without PD of AJ ancestry were recruited and consented through an internet based study website developed as part of the Parkinson’s Progression Markers Initiative (PPMI) study.
• Participants were screened through the Michael J. Fox Foundation (MJFF) website and those with risk factors were referred to the Indiana University (IU) Parkinson’s Progression Markers Initiative (WRI) study where they completed the consenting process. Those who qualified were sent a saliva kit for LRRK2 genetic testing. Individuals with previous LRRK2 testing provided their report for review and confirmation of results. Figure 1: An algorithm was applied to a series of screening questions to identify individuals at increased risk to carry the LRRK2 2019G mutation. Figure 2: Algorithms (1) screening question. A total of 976 individuals completed the initial screening. 741 qualified for LRRK2 mutation testing and 670 were tested. Results were available for 642 individuals. 72 individuals carried at least one LRRK2 G2019S mutation; 38 with PD (12.5%) and 34 without (10.1%). Among 64 individuals with previous testing, 30 individuals were found to carry the LRRK2 G2019S mutation upon review of their reports. Figure 6: Table 2

Conclusion

In summary, we used an internet-based approach to screen large numbers of individuals to identify those with risk factors increasing the likelihood that they carried a mutation contributing to PD susceptibility. This was a highly efficient approach that in only 6 months yielded >100 individuals whose DNA was sequenced. A similar approach could be implemented to other policy makers to identify individuals for clinical trials, biomarker analyses and other types of research studies.

References