Leucine rich repeat kinase 2 (LRRK2) GLY2019SER mutation is absent in a second cohort of Nigerian Africans with Parkinson disease

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Abstract

To date the LRRK2 p.G2019S mutation remains the most common genetic cause of Parkinson disease (PD) worldwide. It accounts for up to 6% of familial and approximately 1.5% of sporadic cases. LRRK2 has a kinase enzymatic domain which provides an attractive potential target for drug therapies and LRRK2 kinase inhibitors are in development. Prevalence of the p.G2019S has a variable ethnic and geographic distribution, the highest reported among Ashkenazi Jews (30% in patients with familial PD, 14% in sporadic PD, 2.0% in controls) and North African Berbers (37% in patients with familial PD, 41% in sporadic PD, and 1% in controls). Little is known about the frequency of the LRRK2 p.G2019S among populations in sub-Saharan Africa. Our group and others previously reported that the p.G2019S is absent in a small cohort of Nigerian PD patients and controls. Here we used Kompetitive Allele Specific PCR (KASP) assay to screen for the p.G2019S in a larger cohort of Black African PD patients (n = 126) and healthy controls (n = 54) from Nigeria. Our analysis confirmed that all patients and controls are negative for the p.G2019S mutation. This report provides further evidence that the LRRK2 p.G2019S is not implicated in PD in black populations from Nigeria and support the notion that p.G2019S mutation originated after the early human dispersal from sub-Saharan Africa. Further studies using larger cohorts and advance sequencing technology are required to underpin the genetic causes of PD in this region.

Introduction

Mutations in the leucine-rich repeat kinase 2 (*LRRK2*) gene, initially described in 2004, are the most prevalent genetic cause of Parkinson disease (PD), and have been associated with both familial and sporadic cases of PD in some populations.[1,2] Although at least seven distinct

pathogenic mutations in *LRRK2* have been proven to cause PD, there is considerable population variability in the frequencies of these mutations.[3] The most common is the LRRK2 p. G2019S substitution, with a global frequency of 1% in sporadic PD and up to 5% in familial PD.[4] The highest frequencies of LRRK2 p.G2019S mutations are reported from the North African Berber and Arab populations, where it is present in 30–42% of familial PD, 30–39% of apparently sporadic PD, and 0–2.2% of healthy controls.[5]

The interest in exploring genetic underpinnings of PD extend beyond elucidating pathogenetic mechanisms, to ultimately manipulating the knowledge to derive viable disease modifying and therapeutic targets. Following evidence of gain-of-function increase in LRRK2 kinase activity in mutation carriers, promising pre-clinical studies have already demonstrated neuroprotective properties of LRRK2 kinase inhibitors, including reduced alpha-synuclein aggregation, reduced dopaminergic neurodegeneration, and reduced microglial and macrophage activation.[6] Considering the enormous potential future application to LRRK2 p.G2019S – related PD, determining the relevance in diverse populations is imperative.

Although comprehensively studied in numerous European and North American populations, studies on the frequency of LRRK2 p.G2019S in sub-Saharan Africa have been scarce. A previous report from our Nigerian African population including 57 sporadic PD patients and 51 healthy controls did not identify LRRK2 p.G2019S mutations in either PD cases or controls. [7] In this study we aimed at exploring a larger cohort of PD cases and healthy controls from a Black African Nigerian background for the LRRK2 p.G2019S mutation to further clarify the role of this mutation in PD in sub-Saharan Africans.

Materials and methods

Participant recruitment, diagnostic ascertainment and clinical evaluation

PD cases (n = 126) were recruited from the Movement Disorders Clinic of the Lagos University Teaching Hospital, Idi Araba, Lagos State, Nigeria in the period between February 2016 and May 2017. The International Parkinson Disease and Movement Disorder Society (IPMDS) clinical diagnostic criteria were applied in this study, and cases meeting the diagnostic criteria for both clinically established PD and probable PD were included.[8] Hoehn and Yahr stage was as per the IPMDS revised Unified Parkinson Disease Rating Scale.[9] Case ascertainment was rigorous and based on agreement by two movement disorders specialists. Both sporadic and familial PD cases were included. Persons with a presumed secondary cause or red flags suggestive of other hereditary or degenerative Parkinsonism were excluded from the study. The protocol included information on demographic characteristics, age at onset of initial motor symptom of PD, and family history of tremor or parkinsonism in a first degree relative. Age at onset was defined by the age (years) at onset of the earliest motor symptom of PD. Controls (n = 54) were population-based unrelated volunteers recruited via advertisement in the neighbouring communities, and were age ± 3 years and gender-matched, otherwise neurologically healthy, and without any clinical evidence of medical illness (as determined by history and a medical and neurological clinical examination).

This study was approved by the Health Research Ethics Committee of the Lagos University Teaching Hospital, Idi Araba, Lagos (Ethics approval # ADM/DCST/HREC/366) and University College London and the National Hospital for Neurology and Neurosurgery, London (Ethics approval # 07/Q0512/26). In accordance with the protocol, written informed consent was obtained from all participants, and included permission to re-contact for future studies. Clinical data from hard-copy case record forms were logged into a secure database. All data was de-identified to protect confidentiality, and assigned a unique study code and given a unique laboratory code. Clinical variables were analysed using the IBM Statistical Package for

Social Sciences (SPSS) version 21. Chi-square test and analysis of variance test were used to compare categorical parameters and age respectively between PD cases and controls. Normality of distribution of continuous variables was tested using the Kolmogorov-Smirnov test. Age at onset of PD, age at study, and duration of PD were non-normally distributed, and are presented as median and interquartile range. Level of significance was set at a p value <0.05.

DNA extraction and LRRK2 p.G2019S genotyping

Whole blood (20 mls) was collected into EDTA Vacutainer bottles using standard protocols. Samples were stored at minus 80˚C in the Central Research Laboratory of the College of Medicine, University of Lagos, until sample shipment to the designated extraction laboratory. Genomic DNA was extracted using the standard diagnostic laboratory protocols. DNA concentration was measured with a NanoDrop Spectrophotometer (Thermo Scientific, Waltham, MA, USA). Genotyping was performed using Kompetitive Allele Specific PCR genotyping assay (KASP, LGC Genomics, Herts, United Kingdom [UK]). KASP assay is based on competitive allele-specific PCR and it enables bi-allelic scoring of single nucleotide polymorphisms (SNPs) and insertions and deletions (Indels) at specific loci (https://www.lgcgroup.com/kasp/). KASP was chosen because of its reported efficiency and accuracy in detecting p.G2019S genotypes in previous studies [10]. The SNP of interest p.G2019S (rs34637584) and a 50 base-pairs (bp) sequence surrounding the SNP were annotated using ENSEMBL genome browser and were submitted to LGC Genomics website via their SNP submission template. Allele specific primers cassettes (two forward fluorescence labelled primers) and one common reverse primer were designed using KASP on Demand (KOD) service. Assay was validated by manufacturer using DNA samples with known genotype (positive controls) and empty wells (negative controls) prior to running patients and control samples. The validated assay showed distinct genotype clusters and consistently high call rates (Fig 1A). PD and control samples were then diluted to a uniform concentration, and the equivalent of 50 ng DNA in 5 ul from each sample were arranged in 96-well plates and submitted to LGC for genotyping. No template controls (NTCs) were included in each plate to enable the detection of contamination or non-specific amplification. PCR was performed as per manufacturer protocol (https://www. lgcgroup.com/LGCGroup/media/PDFs/Products/Genotyping/KASP-genotyping-chemistry-User-guide.pdf?ext=.pdf). Briefly, 5 ul of KASP universal master Mix and 0.14 ul of the three
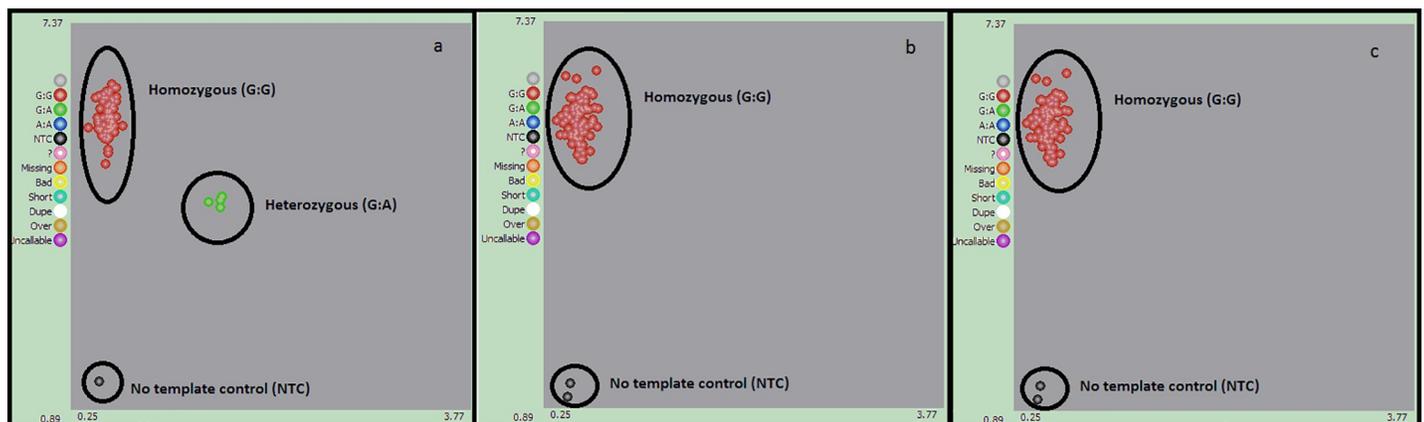

Fig 1. KASP assay cluster plots of the p.G2019S (rs34637584). Genotypes cluster are visualised using SNP Viewer software. Samples marked red are p.G2019S homozygous (G:G), those marked green are p.G2019S heterozygous (G:A) and those marked black are non-template control (NTC). Plot (1-a) shows two distinctive clusters: the red cluster obtained from samples known to be homozygous (G;G) and the green cluster obtained from samples known to be heterozygous (G:A). Those samples with known genotypes were used to validate the assay prior to running the test samples. No known p.G2019S homozygous (A:A) sample was available to be included. Plots(1-b) and (1-c) show the data from the Nigerian cohort. All PD patients and controls are homozygous for the normal p.G2019S allele (G:G).

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primers mix were added to each well. PCR was performed using Hydrocycler water bath-based thermal cycler as follow: 94˚C for 15 min, then 10 cycles of 94˚C for 20 s, 61˚C for 1 min, followed by 26 cycles of 94˚C for 20 s and 1 min at 55˚C. Genotyping plates were read using BMG PHERAStar plate reader (BioTek Instruments, Inc) and visually inspected to insure PCR reaction has reached endpoint and tight genotyping clusters have been obtained. Genotypes were called using Kraken software (LGC Genomics Ltd) and double-checked manually. Results were visualized with SNP Viewer software (version 1.99, Hoddesdon, UK). Genotypes were examined for deviation from Hardy-Weinberg equilibrium using Chi-square test.

Results

Baseline clinical characteristics of PD cases and controls

The baseline characteristics of the PD cases and controls are shown in Table 1. The study included 126 PD cases and 54 controls with comparable mean ages (years) at the time of the study (61.9 ± 9.9 and 64.6 ± 8.7 respectively) (ANOVA; p = 0.14). The median age at onset of PD was 59.0 years, while median duration of PD was 48 months. A family history of parkinsonism or tremor was reported only in first degree relatives, and was present in 20 (15.9%) of the PD and none of the controls (as this was an exclusion criterion for controls).

LRRK2 G2019S mutation analysis in PD cases and controls

The LRRK2 p.G2019S mutation was absent in all subjects. All 126 PD patients and 54 controls were homozygous for the p.G2019S (GG) normal allele (Fig 1B and 1C). Allelic frequencies for p.G2019S (rs34637584) SNP were in Hardy-Weinberg equilibrium (P = 1). KASP assay performed very well. 100% call rates was achieved with clear genotyping clusters and no ambiguous calls.

Discussion

The data from this second cohort of PD from Nigeria corroborate the conclusions from our earlier publication that the commonest pathogenic mutation in LRRK2 (itself the commonest genetic cause of both familial and sporadic PD), the p.G2019S mutation, observed in several

Table 1. Clinical characteristics of Parkinson disease cohort.

Characteristic	Parkinson disease n = 126	Controls n = 54	Statistics [p value]
Gender distribution, *n [%]* *Male* *Female*	93 [73.8] 33 [26.2]	34 [63.0] 20 [37.0]	0.14
Age at study, *years* [mean ± SD [range]]	61.9 ± 9.9 [36–81]	64.6 ± 8.7 [41–80]	0.09
Age at onset, *years**	59.0 [13]		
Young onset [≤ 50 years at onset], *n [%]*	34 [27.0]		
Young onset [≤ 40 years at onset], *n [%]*	8 [6.4]		
Duration of PD, *months**	48.0 [36]		
Family history of tremor or parkinsonism, *n [%]*	20 [15.9]	0 [0%]	
Hoehn and Yahr stage at study [median [range]]	2.0 [1–5]		

Footnote:

*Age at onset and duration of PD presented as median and interquartile range.

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different populations, is not a frequent cause of PD in Nigeria. [7] This is similar to the view from other studies in the black populations of sub-Saharan Africa, and in contrast to the data from Northern African Arab and Berber populations. In a small cohort study from Zambia (east Africa), the p.G2019S mutation was absent in 39 PD patients [11], as was the observation in another group of 54 PD patients and 46 controls from Ghana (west Africa).[12] In a study of 205 South African PD patients from varied backgrounds (42% Caucasian, 31% Afrikaner, 17% mixed ancestry, 8% Black and 2% Indian), LRRK2 p.G2019S mutation was not found in Afrikaner and Black South African patients. Only 2% of patients (three Caucasian and one patient of mixed ancestry) were found to be carriers [13]. All patients shared a common ances-tor with the other haplotype 1-associated families reported worldwide.[14] This ethnic and geographical disparity is not peculiar to the African continent, and has been reported world-wide. [15] For example, Papapetropoulos *et al* explored the frequency of the G2019S LRRK2 mutation in southern Europe to determine if it was uniformly common, and found no patients with the mutation in mainland Greece, despite the close proximity to other European regions with high prevalence of LRRK2 mutations. [16] The disparity has been attributed to the LRRK2 p.G2019S gene mutation being a result of mutational events in a common ancestral founder, at least one of which occurred in the Near East about 4000 years ago.[17–18] The genetic architecture of black sub-Saharan Africans is evidently different from that of other populations within Africa (particularly North Africa), and also of other continents.

Unfortunately the genetic contributors to PD in black sub-Saharan Africans remain unknown. Very limited number of reports are available from this region. This study is the sec-ond report from Nigeria and—according to our knowledge- only one report is available from Ghana, one from Zambia and only a handful from South Africa (correct as at October 2018). [19] Majority of the previous studies are characterized by small sample size and mixed ances-tries, particularly the South African cohorts. In addition almost all these studies used a candi-date gene approach and until now no Genome Wide Association Study (GWAS) or next generation sequencing data is available. No pathogenic mutations were identified so far in most of the screened candidate genes including SNCA, DJ-1, UCH-L1, ATP13A2, EIF4G1, and VPS35. Inconclusive data are available on the role of parkin and PINK1 in young onset and familial PD cases in the region. [19]

Our findings, together with those of other researchers from sub-Saharan Africa lead us to reiterate the strong need to continue to explore the genetic underpinnings of apparently spo-radic and inherited PD in persons of black African ancestry. This will necessitate incorporating larger cohorts to ensure that studies are sufficiently powered to reveal any significant genetic traits when contrasted with otherwise healthy controls. Furthermore, such studies should pref-erably employ advanced high throughput genetic technologies (such as whole genome and whole exome sequencing) to identify SNPs and other molecular targets associated with PD, and improve the likelihood that the complex underpinnings of the genetic component of PD in sub-Saharan Africa are unravelled. This is particularly important to ensure that downstream applications of the results of genomics studies, such as genetic test batteries developed for PD in the future, will have improved yield, and genetic counselling will be developed with con-tent relevant to the sub-Saharan African population. In addition, such data will provide a basis for expanding our understanding of the genetics mechanisms contributing to PD in our population.

Our study utilized a rigorous clinical and laboratory methodology for case ascertainment and genotyping respectively. Diagnosis of PD was based on the IPMDS criteria, and all cases also fulfilled the UKPD Brain Bank criteria, verified in person by two neurologists specializing in movement disorders. With respect to the genotyping, the KASP is considered to be a reliable and more cost-effective genotyping assay for p.G2019S screening than multiplex methods,

with the added advantage of being time-effective.[20] We acknowledge the limitation of not testing other known mutations on the LRRK2 gene (such as R1441C/G/H), largely on account of funding limitations at this time. With the advantage of our established repository and ongoing recruitments, future studies are planned to expand the testing to include a larger sample size screen for other PD related gene mutations.

We conclude that the contribution of genetics to the causation of PD in sub-Saharan Africa remains unclear and largely unexplored. The region offers the unique advantage of having the greatest diversity of polymorphisms than any other world region, and this can be explored through adequately funded collaborative studies.

Supporting information

S1 File. Minimal data set for LRRK2 G2019S mutation screening in Nigerian cohort.
(XLSX)

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