Analysis of DNM3 and VAMP4 as genetic modifiers of LRRK2 Parkinson’s disease

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The data published in this manuscript have not been published elsewhere except where indicated (novel data are combined with 2 previously published studies) in meta-analysis.

All authors have reviewed and approved this manuscript for submission.

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**ABSTRACT**

The **LRRK2** gene has rare (p.G2019S) and common risk variants for Parkinson’s disease (PD). **DNM3** has previously been reported as a genetic modifier of the age at onset in PD patients carrying the **LRRK2** p.G2019S mutation. We analyzed this effect in a new cohort of **LRRK2** p.G2019S heterozygotes (n = 724) and meta-analyzed our data with previously published data (n = 754). **VAMP4** is in close proximity to **DNM3**, and was associated with PD in a recent study, so it is possible that variants in this gene may be important. We also analyzed the effect of **VAMP4** rs11578699 on **LRRK2** penetrance. Our analysis of **DNM3** in previously unpublished data does not show an effect on age at onset in **LRRK2** p.G2019S carriers; however, the inter-study heterogeneity may indicate ethnic or population-specific effects of **DNM3**. There was also evidence for linkage disequilibrium between **DNM3** and **VAMP4**. Analysis of sporadic patients stratified by the risk variant **LRRK2** rs10878226 indicates a possible interaction between common variation in **LRRK2** and **VAMP4** in disease risk.

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**1. Introduction**

The p.G2019S coding variant in the **LRRK2** (leucine-rich repeat kinase 2) gene is the commonest high penetrance mutation causing parkinsonism. The mutation occurs in 1%–40% of Parkinson’s disease (PD) cases, varying by ethnicity (Healy et al., 2008). **LRRK2** parkinsonism is broadly similar to “idiopathic” disease in clinical manifestations and age at onset (AAO), generating interest in its potential as a therapeutic target with broader application to PD (Maio et al., 2018). Genome-wide association studies (GWAS) show that common variation in **LRRK2** is also a risk factor for sporadic PD (Mat et al., 2012; Ross et al., 2011).

There is a wide range in PD AAO among p.G2019S carriers. It has been reported that the PD AAO of **LRRK2** p.G2019S carriers is modified by the DYNAMIN-3 (**DNM3**) rs2421947 variant; **GC** rs2421947 heterozygotes have been reported to have a median disease onset 12.5 years younger than other p.G2019S carriers (Trinh et al., 2016). **DNM3** is a microtubule-associated protein that is able to bind and hydrolyze guanosine triphosphate and is involved in producing microtubule bundles. The mechanism through which it may impact PD AAO for **LRRK2** patients is not understood. In a cohort from Spain the median onset was 3 years younger in patients with the **G** allele, though this was not significant (Fernandez-Santiago et al., 2018). There was no effect of **DNM3** on PD AAO in individuals carrying **LRRK2** risk alleles (Foo et al., 2019).

In the largest GWAS meta-analysis of idiopathic PD (iPD) the nearby **VAMP4** (vesicle-associated membrane protein 4) rs11578699, located 113,325 bp from **DNM3** rs2421947, is associated with PD, raising the possibility that the **DNM3** effect may be due to linkage disequilibrium with **VAMP4** (Nalls et al., 2019). It has been suggested that **VAMP4** may be involved in PD through the endocytic membrane trafficking pathway.

We sought to replicate the **DNM3** discovery finding, to determine whether the association varies with ethnicity and whether linkage disequilibrium with **VAMP4** is relevant. We analyzed a multi-ethnic cohort of **LRRK2** p.G2019S carriers and a larger cohort of European patients with and without the **LRRK2** common risk allele.

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**2. Methods**

**2.1. Data collection**

**2.1.1. Patient cohorts**

**LRRK2** p.G2019S heterozygote participants were identified from cohorts in the International Parkinson’s Disease Genomics Consortium (IPDGC) and other collaborative centers. Data from 724 **LRRK2** p.G2019S heterozygote participants were contributed by the National Institute of Health, University College London, McGill University (samples were collected in Columbia University and Sheba Medical Center), Sorbonne University (in collaboration with Habib Bourguiba Hospital, Sfax, Tunisia, and Bilda Hospital, Bilda, Algeria), National Institute of Neurological Disorders and Stroke and the University of Tübingen. Data from 2 published studies analyzing **DNM3** rs2421947 and **LRRK2** p.G2019S parkinsonism with AAO was also included comprising an additional 754 participants (Fernandez-Santiago et al., 2018; Trinh et al., 2016). All studies willing to participate and currently holding minimum required data for **LRRK2** p.G2019S carriers were included: PD onset age or sampling age for asymptomatic carriers; and **DNM3** rs2421947 or a high r2 (measure of linkage disequilibrium [LD]) proxy single nucleotide polymorphism. Where these studies had also genotyped **VAMP4** rs11578699 or a high r2 proxy, these data were also included in the analysis of the **VAMP4** gene (n = 786). Patients with PD without a known Mendelian or high-risk genetic cause of disease were collated from the UK-wide Tracking Parkinson’s study (Malek et al., 2015) and from IPDGC datasets. Summary statistics for **DNM3** rs2421947 and **VAMP4** rs11578699 were obtained from the most recent large-scale PD GWAS (Nalls et al., 2019) and PD AAO GWAS (Blauwendraat et al., 2019).

**2.1.2. Standard protocol approvals, registrations, and patient consents**

All studies were approved by each respective Institutional Ethics Review Committee and all participants provided written informed consent. All studies were carried out in accordance with the Declaration of Helsinki.

Research ethics approval for the Tracking Parkinson’s study was provided by West of Scotland Research Ethics Service (reference 11/AL/0163). The study is registered with ClinicalTrials.gov under the identifier NCT02881099. Research ethics approval for the Parkinson’s Families Project was provided by the London Camden and King’s Cross ethics committee (reference 15/LO/0097) and the Health Research Authority. The Study is registered with ClinicalTrials.gov under the identifier NCT01276108. The local Research Ethics Board number for samples processed at McGill University is IRB00010120, and the approved project identifier is 2017-2944, valid until December 2019, to be renewed then. The local Institutional Review Board approval for samples from Columbia University is AAAF3108. Ethical approval from 2 of the studies is published (Fernandez-Santiago et al., 2018; Trinh et al., 2016).
2.2. Genetic analyses

Genotyping was performed on different platforms (NeuroChip array, NeuroX array, TaqMan assays, Infinium OmniExpress-24, and Illumina HumanCore Exome array) at participating centers. The LRRK2 p.G2019S mutation was directly genotyped. Sanger sequence or KASPar (“Competitive” allele-specific polymerase chain reaction) verification of the DNM3 rs2421947 variant was carried out on data subsets at study-specific centers. Where the variant DNM3 rs2421947 was imputed, only $r^2$ values above 0.85 were used, and only $r^2$ values above 0.75 were used for VAMP4 rs11578699 (Table e1), as the $r^2$ quality of available data for variant VAMP4 rs11578699 was lower. In total, 1478 LRRK2 p.G2019S carriers were identified across study cohorts. In addition, 2052 samples from patients with iPD from the Tracking Parkinson’s disease study passed quality control and had no identified genetic cause of disease (Malek et al., 2015). Ninety-six patients with PD were excluded due to missing AAO data; therefore 1956 patients with PD and without LRRK2 p.G2019S were included in further analysis. Summary statistics and patient data from the most recent PD GWAS (Blauwendraat et al., 2019; Nalls et al., 2019). The gnomAD database features unrelated individuals sequenced as part of disease-specific and population-based genetic studies. Individuals affected by severe pediatric disease and their first-degree relatives have not been included.

2.3. Statistical analyses

Data from the studies were pooled and principal component analysis was used to define ethnicity, where available. Within the Ashkenazi Jewish (AJ), European, and North African analyses ethnic outliers were excluded. We calculated Hardy-Weinberg equilibrium for VAMP4 rs11578699 and DNM3 rs2421947 in p.G2019S carriers. Quality control Hardy-Weinberg equilibrium for iPD and controls is summarized in the recent large-scale PD GWAS. We assessed linkage disequilibrium (LD) measures $r^2$ and $D’$ between DNM3 rs2421947 and VAMP4 rs11578699 in different populations to evaluate the possibility that an extended haplotype block might explain the relationship between DNM3 and LRRK2 (Table e2). The allele-based Fisher’s exact test was used to compare DNM3 rs2421947 and VAMP4 rs11578699 minor allele frequencies between LRRK2 p.G2019S heterozygotes of different ethnic backgrounds and with iPD (Table 1). Student’s t-tests and analysis of variance were used to assess differences in AAO by genotype (Table 2). We then analyzed the effect of DNM3 rs2421947 (Fig. 1) on AAO in iPD in the Tracking Parkinson’s dataset using linear regression of AAO, and Kaplan-Meier survival analysis. Next, we analyzed patients with LRRK2 p.G2019S of AJ, North African, and European ethnicity using linear regression of AAO with available covariates of sex, ethnicity, relatedness, and study center of origin (Fig. 2). AAO was regressed by DNM3 rs2421947 genotypes, and separately for rs11578699 VAMP4 genotypes. We meta-analyzed DNM3 rs2421947 data from all previously unpublished datasets using linear regression models (Fig. 2B). We pooled these data with previously published data and meta-analyzed again with the same methods (Fig. 2C and D). We then analyzed the effect of VAMP4 rs11578699 on AAO in iPD carrying the LRRK2 rs10878226 variant. LRRK2 rs10878226 has also been implicated in PD risk (odds ratio 1.20, 95% confidence interval [CI] 1.08–1.33, $p = 6.3 \times 10^{-4}$, $n = 6129$) (Mata et al., 2012).

2.4. Gene expression

Gene expression profiles of DNM3 rs2421947 and VAMP4 rs11578699 were assessed using publicly available Web-based resources: BRAINEAC.v2 (www.braineac.org) (Ramasamy et al., 2014); GTEx (www.gtexportal.org); and Allen Brain Atlas (www.brainmap.org) (Hawrylycz et al., 2012), and evaluated based on the significance level required for inclusion in colocalization (COLOC) analysis (Appendix e-1).

2.5. Data availability statement

The majority of anonymized data not published in full here will be shared by request from any qualified investigator, with the exception of a subset of data from the latest IPDGC GWAS which cannot be shared for legal or ethical reasons.

3. Results

DNM3 did not influence AAO in all PD patients from the Tracking Parkinson’s cohort (GG vs. CC and CG carriers: beta = -0.02, $p = 0.97$, $n = 1956$). This is consistent with the latest PD AAO GWAS (p = 0.39, effect = -0.01, standard error [se] = 0.13). The Kaplan-Meier method was used for visualizing risk across DNM3 rs2421947

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**Table 1**

<table>
<thead>
<tr>
<th></th>
<th>gnomAD(^a)</th>
<th>p.G2019S PD(^b)</th>
<th>p.G2019S asymptomatic(^c)</th>
<th>Idiopathic PD</th>
<th>Total(^d)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>DNM3</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ashkenazi</td>
<td>0.47 (n = 145)</td>
<td>0.41 (n = 146)</td>
<td>0.79 (n = 7)</td>
<td>N/A</td>
<td>0.45 (n = 298)</td>
</tr>
<tr>
<td>African/North African</td>
<td>0.42 (n = 4348)</td>
<td>0.39 (n = 480)</td>
<td>N/A</td>
<td>N/A</td>
<td>0.42 (n = 4829)</td>
</tr>
<tr>
<td>From Spain/Latino</td>
<td>0.41 (n = 424)</td>
<td>0.49 (n = 195)</td>
<td>0.49 (n = 117)</td>
<td>N/A</td>
<td>0.44 (n = 736)</td>
</tr>
<tr>
<td>European (non-Finnish)</td>
<td>0.41 (n = 7700)</td>
<td>0.47 (n = 483)</td>
<td>0.68 (n = 50)</td>
<td>0.44 (n = 14,508)</td>
<td>0.43 (n = 22,734)</td>
</tr>
<tr>
<td><strong>VAMP4</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ashkenazi</td>
<td>0.20 (n = 138)</td>
<td>0.27 (n = 24)</td>
<td>0.5 (n = 8)</td>
<td>N/A</td>
<td>0.22 (n = 170)</td>
</tr>
<tr>
<td>African/North African</td>
<td>0.18 (n = 3979)</td>
<td>0.26 (n = 484)</td>
<td>N/A</td>
<td>N/A</td>
<td>0.19 (n = 4463)</td>
</tr>
<tr>
<td>From Spain/Latino</td>
<td>0.16 (n = 393)</td>
<td>N/A</td>
<td>N/A</td>
<td>N/A</td>
<td>0.16 (n = 393)</td>
</tr>
<tr>
<td>European (non-Finnish)</td>
<td>0.19 (n = 6994)</td>
<td>0.20 (n = 248)</td>
<td>0.18 (n = 22)</td>
<td>0.19 (n = 21,242)</td>
<td>0.19 (n = 21,242)</td>
</tr>
<tr>
<td>Total</td>
<td>0.18 (n = 11,504)</td>
<td>0.23 (n = 752)</td>
<td>0.27 (n = 30)</td>
<td>0.19 (n = 21,242)</td>
<td>N/A</td>
</tr>
</tbody>
</table>

**Key:** DNM3, Dynamin 3; LRRK2, leucine-rich repeat kinase 2; N/A, not available; PD, Parkinson’s disease; VAMP4, vesicle-associated membrane protein 4.

\(^a\) The gnomAD database features unrelated individuals sequenced as part of disease-specific and population-based genetic studies. Individuals affected by severe pediatric disease and their first-degree relatives have not been included.

\(^b\) LRRK2 p.G2019S parkinsonism.

\(^c\) LRRK2 p.G2019S asymptomatic carriers.

\(^d\) This series includes ethnicity subcategories: Estonian, other non-Finnish European, Northwestern European, and Southern European.


\(^f\) All samples from the following categories were combined: gnomAD, idiopathic PD, LRRK2 p.G2019S patients, and asymptomatic carriers.
Table 2

Age at onset by genotype in LRRK2 p.G2019S carriers in this study

<table>
<thead>
<tr>
<th>Population series</th>
<th>Mean age at onset (SD)</th>
<th>ANOVA p value</th>
<th>GG vs. CG p value</th>
<th>CG vs. CC p value</th>
<th>GG vs. CC p value</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>GG</td>
<td>CG</td>
<td>CC</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ashkenazi Jewish</td>
<td>57.20 (8.96)</td>
<td>60.11 (12.21)</td>
<td>58.41 (8.01)</td>
<td>0.34</td>
<td>0.13</td>
</tr>
<tr>
<td>North African</td>
<td>52.64 (11.21)</td>
<td>51.95 (11.99)</td>
<td>54.27 (11.05)</td>
<td>0.49</td>
<td>0.65</td>
</tr>
<tr>
<td>European*</td>
<td>63.26 (12.14)</td>
<td>61.20 (12.45)</td>
<td>62.17 (13.48)</td>
<td>0.52</td>
<td>0.24</td>
</tr>
<tr>
<td>Combined</td>
<td>57.11 (12.02)</td>
<td>57.44 (12.93)</td>
<td>58.59 (12.30)</td>
<td>0.55</td>
<td>0.76</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Population series</th>
<th>Mean age at onset (SD)</th>
<th>ANOVA p value</th>
<th>CC vs. TC p value</th>
<th>TC vs. TT p value</th>
<th>CC vs. TT p value</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>CC</td>
<td>TC</td>
<td>TT</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ashkenazi Jewish</td>
<td>63.92 (9.57)</td>
<td>57.45 (11.93)</td>
<td>57.00 (N/A)</td>
<td>0.91</td>
<td>N/A</td>
</tr>
<tr>
<td>North African</td>
<td>54.38 (11.89)</td>
<td>53.35 (11.58)</td>
<td>55.22 (11.48)</td>
<td>0.55</td>
<td>0.36</td>
</tr>
<tr>
<td>European*</td>
<td>62.44 (12.38)</td>
<td>63.89 (12.21)</td>
<td>61.33 (13.75)</td>
<td>0.66</td>
<td>0.41</td>
</tr>
<tr>
<td>Combined</td>
<td>57.39 (12.61)</td>
<td>56.41 (12.62)</td>
<td>56.76 (12.10)</td>
<td>0.60</td>
<td>0.32</td>
</tr>
</tbody>
</table>

Combined subgroup mean and standard deviation age at onset in years of LRRK2 p.G2019S parkinsonism for DNM3 rs2421947 and VAMP4 rs11578699 genotypes; one-way ANOVA between DNM3 rs2421947 and VAMP4 rs11578699 genotypes; Student’s t-test between genotype.

Key: ANOVA, analysis of variance; DNM3, Dynamin 3; LRRK2, leucine-rich repeat kinase 2; N/A, not available; VAMP4, vesicle-associated membrane protein 4.

a Uncorrected.

b The following population series subgroups were from combined European unspecific and British.

c The following population series subgroups were from combined Ashkenazi Jewish, North African, European unspecific, and British.

effects for iPD (Fig. 1A), and LRRK2 p.G2019S carriers (Fig. 1B–D). The same method was also used to visualize risk for VAMP4 rs11578699 genotypes in individuals with LRRK2 p.G2019S (Fig. 1E and F).

We carried out a multi-ethnic meta-analysis of newly contributed data of DN3M rs2421947 GG versus CC and CC genotypes for iPD (Fig. 1A) and LRRK2 p.G2019S patients (Fig. 1B–D). Meta-analyses of DN3M rs2421947 GG versus CC and CC genotypes of novel data from this manuscript from 724 LRRK2 p.G2019S carriers; (C, D) MTA analyses of DN3M rs2421947 GG versus CC and CC genotypes from 1478 LRRK2 p.G2019S carriers including 754 previously published; (E, F) MTA analyses of CC versus TT and TC. Percentage contribution and numbers of individuals included in each analysis are indicated. Analyses are carried out on ethnicity subgroups: Ashkenazi Jewish (Summary: AJ), European (Summary: EU), and North African (Summary: NA). Abbreviations: DN3M, Dynamin 3; LRRK2, leucine-rich repeat kinase 2; VAMP4, vesicle-associated membrane protein 4.

Using Cox proportional survival analysis, we studied the discovery data and subsequent cohorts separately (GG vs. CC and CG as described previously). There was a strong association between rs2421947 and PD AAO in discovery data (hazard ratio [HR] 1.59, 95% CI 1.28–1.97, \( p < 0.001 \)). This was also present through AAO linear regression analysis (beta = -4.93, \( p = 0.00019 \)). The association was absent in our replication data (HR 1.09, 95% CI 0.95–1.26, \( p = 0.22 \)). We meta-analyzed the samples studied in this paper with the discovery data (Fig. 2).

Finally, we investigated the possibility that there might be an interaction between the GWAS defined common LRRK2 risk allele (rs10878226) and VAMP4. We analyzed 4882 cases with PD carrying the LRRK2 risk variant minor allele using linear regression of AAO, and plotting of the Kaplan-Meier curve, as shown in Fig. 3. TT versus TC and CC VAMP4 rs11578699 genotype was nominally significantly associated with AAO risk in this cohort (beta = 1.68, se = 0.81, p = 0.037, \( n = 4882 \)). VAMP4 rs11578699 was not significantly associated with AAO risk in IPD cases without the LRRK2 rs10878226 risk variant (beta = -0.28, se = 0.48, p = 0.56, \( n = 14,970 \)). Fewer patients with PD had been genotyped for DN3M rs2421947 in the PD GWAS cohort (Table 1), though for DN3M rs2421947 was not associated with AAO risk in IPD cases with the LRRK2 rs10878226 risk variant (beta = 0.045, se = 0.53, p = 0.93, \( n = 3300 \)) nor without (beta = 0.21, se = 0.31, p = 0.69, \( n = 9822 \)).

4. Discussion

We have analyzed the effect of DN3M rs2421947 on AAO in LRRK2 p.G2019S parkinsonism.
We have not replicated the association between DNM3 and LRRK2 p.G2019S AAO in this study or in meta-analysis with all available data. In the original discovery analysis, there was a difference of 12.5 years between DNM3 rs2421947 GG and CC genotypes (meta-analysis HR 1.61, 95% CI 1.15–2.27, p = 0.02). In our data the AAO difference between GG and CC genotypes was 1.4 years, which was not significant. Using AAO regression, meta-analysis of independent sample series in newly genotyped samples did not identify a significant difference in AAO between genotypes (beta = 1.19, p = 0.55, n = 708). Similarly, when discovery and replication data were analyzed together there was no significant effect of DNM3 rs2421947 on AAO (beta = 2.21, p = 0.083, n = 1304). However, there was significant heterogeneity in replication and combined DNM3 regression meta-analyses.

In “sporadic” PD, consistent with the recent AAO GWAS (Ross et al., 2011), our study indicated that DNM3 rs2421947 does not affect AAO in non-p.G2019S disease.

We did not identify LD between DNM3 and VAMP4, nor an independent effect of VAMP4 on LRRK2 penetrance. Analysis of carriers of a common LRRK2 risk single nucleotide polymorphism provided nominally significant support for a potential interaction between VAMP4 and LRRK2, which requires replication in larger sample sizes. Gene expression analysis indicated that VAMP4 rs11578699 is an expression quantitative trait loci for VAMP4 expression.

One possibility for the lack of replication of DNM3 modification of p.G2019S AAO is that heterogeneity in the sample may limit the observed effect in the meta-analysis; this has previously led to non-replication in independent samples in GWAS (Dunckley et al., 2007; Fernandez-Santiago et al., 2011). Significant heterogeneity was observed in the linear regression meta-analysis of replication and combined data in this study, which may be explained by ethnicity effects. The effect of DNM3 may vary between ethnicities or be population specific, and the strongest effects were seen in AJ p.G2019S carriers although not reaching significance (Fig. 2). Further studies in larger numbers of AJ and Arab patients are needed.

Due to its role in innate immunity LRRK2 may have been under different selective pressures in human evolution, relating to differences in environmental pathogens. Interestingly, LRRK2 p.G2019S penetrance varies across ethnic groups. Hentati et al. (2014) have reported a later AAO in LRRK2 p.G2019S carriers from Norway compared to Tunisian patients. Later AAO penetrance for AJ PD p.G2019S carriers compared to non-Jewish carriers has been indicated previously through plotting of estimated cumulative risk, though this was not significant; penetrance was 42.5%
rs10878226, which is associated with PD (combined odds ratio 1.20, LRRK2 an independent marker of PD risk. Around a quarter (24.6%) of allele frequencies in this study suggest that this is unlikely to primarily relate to VAMP4 and DNM3. However, there may be other rare variant effects that will emerge with fine mapping of this region.

The LRRK2 common risk variant analysis is of interest; the variant is not a proxy for p.G2019S in Europeans, so this represents an independent marker of PD risk. Around a quarter (24.6%) of sporadic PD cases carry the common LRRK2 risk variant rs10878226, which is associated with PD (combined odds ratio 1.20, 95% CI 1.08–1.33, p = 6.3 × 10⁻⁴, n = 6129) (Mata et al., 2012). Our common LRRK2 variant analysis indicates a possible interaction between common variation in LRRK2 and VAMP4, which requires further study. VAMP4 and LRRK2 are both involved in synaptic vesicle dynamics, which has relevance to the etiology of PD. Underscoring this possibility, analysis of VAMP4 and DNM3 expression indicated that both are highly expressed in the brain, though these are not in LD and likely represent independent signals.

Modifiers of the penetrance of LRRK2 p.G2019S are likely to be therapeutic targets and may be important in genetic counseling. Our large study aggregating new and previously published data has indicated significant heterogeneity across studies. We have not replicated the original discovery of an interaction between DNM3 and LRRK2 p.G2019S. Further genome-wide studies in different populations are needed, to resolve the determinants of the variable penetrance seen in individuals with p.G2019S.

Disclosure statement

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at https://doi.org/10.1016/j.neurobiolaging.2020.07.002.

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