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### ► To cite this version:

Celia Kun-Rodrigues, Owen A Ross, Tatiana Orme, Claire Shepherd, Laura Parkkinen, et al.. Analysis of C9orf72 repeat expansions in a large international cohort of dementia with Lewy bodies. *Neurobiology of Aging*, 2017, 49, pp.214.e13-214.e15. 10.1016/j.neurobiolaging.2016.08.023 . hal-04590470

HAL Id: hal-04590470

<https://hal.sorbonne-universite.fr/hal-04590470>

Submitted on 28 May 2024

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## Author manuscript

*Neurobiol Aging.* Author manuscript; available in PMC 2018 January 01.

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Published in final edited form as:

*Neurobiol Aging.* 2017 January ; 49: 214.e13–214.e15. doi:10.1016/j.neurobiolaging.2016.08.023.

## Analysis of C9orf72 repeat expansions in a large international cohort of dementia with Lewy bodies

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### Abstract

*C9orf72* repeat expansions are a common cause of amyotrophic lateral sclerosis and frontotemporal dementia. To date, no large-scale study of dementia with Lewy bodies (DLB) has been undertaken to assess the role of *C9orf72* repeat expansions in the disease. Here, we investigated the prevalence of *C9orf72* repeat expansions in a large cohort of DLB cases and identified no pathogenic repeat expansions in neuropathologically or clinically defined cases, showing that *C9orf72* repeat expansions are not causally associated with DLB.

### Keywords

*C9orf72*; Dementia with Lewy bodies (DLB); Genetic screen

### 1. Introduction

Hexanucleotide repeat expansions (HREs) in a noncoding region of *C9orf72* are recognized as the most common genetic cause of familial and sporadic amyotrophic lateral sclerosis, frontotemporal dementia (FTD), amyotrophic lateral sclerosis-FTD, and Huntington disease phenocopies (Beck et al., 2013; Boeve et al., 2012; Hensman Moss et al., 2014; Majounie et al., 2012c; Simon-Sanchez et al., 2012; van der Zee et al., 2013).

A normal repeat expansion shows 1 to 23 GGGGCC repeats located between exons 1a and 1b of *C9orf72* (DeJesus-Hernandez et al., 2011; Renton et al., 2011). HREs identified in several neurodegenerative syndromes were found to range from 500 to 4400 repeats, but on a repeat-primed polymerase chain reaction (PCR), more than 32 repeats are often considered a pathogenic genotype (Beck et al., 2013).

*C9orf72* HREs have been identified in nonmotor neurodegenerative phenotypes including Alzheimer's disease (AD) at frequencies of ~1% (Beck et al., 2013; Harms et al., 2013; Kohli et al., 2013; Majounie et al., 2012b), although conflicting reports exist in the literature (Rollinson et al., 2012; Xi et al., 2012).

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#### Disclosure statement

Ronald C. Petersen reports consultancies with Roche, Inc, Merck, Inc, Genentech, Inc, Biogen, Inc, and Eli Lilly. Brad F. Boeve reports GE Healthcare, FORUM Pharmaceuticals, and C2N Diagnostics as research support and advisory board member of the Tau Consortium. The remaining authors report no competing interests.

Dementia with Lewy bodies (DLB) accounts for 15%–25% of all dementia cases (Heidebrink, 2002). Its core features encompass cognitive impairment, fluctuating attention, parkinsonism, and recurrent visual hallucinations (Weisman and McKeith, 2007).

Neuropathological diagnosis of DLB is achieved when the presence of Lewy bodies is confirmed in the cortex and the brainstem (McKeith et al., 2005). Little is known about the genetics of DLB, although molecular studies seem to point toward genetic overlaps with other neurodegenerative diseases, mainly with AD and Parkinson's disease (PD) (Bras et al., 2014; Guerreiro et al., 2016; Keogh et al., 2016; Meeus et al., 2012).

So far, the *C9orf72* repeat expansion has only been genotyped in small cohorts of ~100 DLB cases or less (Geiger et al., 2016; Lesage et al., 2013; Robinson et al., 2014; Snowden et al., 2012; Yeh et al., 2013). We have recently shown in a large cohort that *C9orf72* repeat expansions are not a common cause of DLB in pathologically diagnosed cases (Guerreiro et al., 2015). Here, we expand on these findings using a cohort of 1524 DLB cases.

## 2. Material and methods

Samples consisted of an international cohort of 1398 neuropathologically diagnosed DLB cases and 126 clinically diagnosed DLB cases (Supplementary Table 1). DNA was extracted from brain tissue for the neuropathologically diagnosed samples and from blood for the clinical diagnosed samples using standard procedures. We performed repeat-primed PCR according to Renton et al. (2011). Genotypes were assessed using Peak Scanner v2.0 (Applied Biosystems) with repeat expansions displaying a characteristic saw tooth pattern with a 6 base pair periodicity on analysis.

## 3. Results

Repeat mean number was 5.17 ( $\pm 4.30$  standard deviation) ranging from 1 to 58. All except 5 samples presented less than 23 repeats in the repeat-primed PCR (Supplementary Fig. 1). Two neuropathologically diagnosed DLB samples showed 32 repeats and 1 showed 33 repeats; and 2 clinically diagnosed samples exhibited 33 and 58 repeats. These last 2 samples had been previously analyzed as part of the cohort published by Snowden et al. (2012).

## 4. Discussion

This is the first study genotyping the *C9orf72* HREs in a large cohort of mainly neuropathologically diagnosed DLB samples. Within the neuropathologically defined DLB cases, we did not find any HREs above the typical threshold for pathogenicity (~32 repeats). This is concordant with previous studies that found no repeat expansions in 34 clinically diagnosed cases of a Taiwanese cohort or in 111 pathological DLB cases (Geiger et al., 2016; Yeh et al., 2013). Snowden et al. (2012) found 2 cases with HREs greater than 30 repeats in a study that was comprised of 102 “probable DLB” blood samples. When the same group restricted their analysis to include only pathologically diagnosed samples, no pathogenic repeat expansions were identified (Robinson et al., 2014).

DLB is considered to be part of a spectrum between AD and PD (Weisman and McKeith, 2007) where large *C9orf72*HREs are not frequent. In AD, it was suggested that pathogenic repeat expansions may only be associated with late onset AD (Kohli et al., 2013) or that amnesic FTD (which is easily misdiagnosed as AD) could be responsible for the low frequencies observed for AD (Majounie et al., 2012b). In PD, there is no evidence for a role of *C9orf72* pathogenic repeat expansions (Majounie et al., 2012a; Xi et al., 2012).

Clinical symptoms in DLB can vary substantially from patient to patient and some can even overlap with less typical forms of FTD (Claassen et al., 2008), which could account for the pathogenic repeat expansions found in misdiagnosed DLB clinical cases. Furthermore, recent data suggest that the threshold for pathogenicity of HREs should be higher than the initially proposed 30 repeats (Xi et al., 2015).

In our cohort of neuropathologically diagnosed DLB samples, we found 3 cases with likely benign 32 and 33 repeats. Excluding the clinically diagnosed cases, we found no evidence of pathogenic repeat expansions. Even including the clinically diagnosed cohort, no extended repeat expansions were identified; with the longest allele exhibiting 58 repeats.

Our study shows that *C9orf72* pathogenic repeat expansions are not a common cause of DLB.

## Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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## Acknowledgments

This work was supported in part by the National Institutes of Neurological Disease and Stroke. Jose Bras and Rita Guerreiro are supported by fellowships from the Alzheimer's Society. Tatiana Orme is supported by a scholarship from the Lewy Body Society. For the neuropathologically confirmed samples from Australia, tissues were received from the Sydney Brain Bank, which is supported by Neuroscience Research Australia and the University of New South Wales. This study was also partially funded by the Wellcome Trust, Medical Research Council, Canadian Institutes of Health Research, and Ontario Research Fund. The Nottingham Genetics Group is supported by ARUK and The Big Lottery Fund. The effort from Columbia University was supported by the Taub Institute, the Panasci Fund, the Parkinson's Disease Foundation, and NIH grants NS060113 (Dr Clark), P50AG008702 (P.I. Scott Small), P50NS038370 (P.I.R. Burke), and ULI1TR000040 (P.I.H. Ginsberg). Dr Ross is supported by the Michael J. Fox Foundation for Parkinson's Research, NINDS R01# NS078086. The Mayo Clinic Jacksonville is a Morris K. Udall Parkinson's Disease Research Center of Excellence (NINDS P50 #NS072187) and is supported by The Little Family Foundation and by the Mangurian Foundation Program for Lewy Body Dementia research and the Alzheimer Disease Research Center (P50 AG016547). The work from the Mayo Clinic Rochester is supported by the National Institute on Aging (P50 AG016574 and U01 AG006786). This work has received support from The Queen Square Brain Bank at the UCL Institute of Neurology; where Dr Lashley is funded by an ARUK senior fellowship. Some of the tissue samples studied were provided by the MRC London Neurodegenerative Diseases Brain Bank and the Brains for Dementia Research project (funded by Alzheimer's Society and ARUK). This research was supported in part by both the NIHR UCLH Biomedical Research Centre and the Queen Square Dementia Biomedical Research Unit. This work was supported in part by the Intramural Research Program of the National Institute on Aging, National Institutes of Health, Department of Health and Human Services; project AG000951-12. The University of Pennsylvania case collection is funded by the Penn Alzheimer's Disease Core Center (AG10124) and the Penn Morris K. Udall Parkinson's Disease Research Center (NS053488). The authors would like to thank the Exome Aggregation Consortium and the groups that provided exome variant data for comparison. A full list of contributing groups can be found at <http://exac.broadinstitute.org/about>. Tissue samples from UCSD are supported by NIH grant AG05131. The authors thank the brain bank GIE NeuroCEB, the French program "Investissements d'avenir" (ANR-10-IAIHU-06). Dr Tienari and Dr Mallykangas are supported by the Helsinki University Central Hospital, the Folkhälsan Research Foundation and the Finnish Academy. This work was in part supported by the Canadian Consortium on Neurodegeneration in Aging (ER).

## Appendix A. Supplementary data

Supplementary data related to this article can be found at <http://dx.doi.org/10.1016/j.neurobiolaging.2016.08.023>.

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