Rare variants in SQSTM1 and VCP genes and risk of sporadic inclusion body myositis

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A B S T R A C T

Genetic factors have been suggested to be involved in the pathogenesis of sporadic inclusion body myositis (sIBM). Sequestosome 1 (SQSTM1) and valosin-containing protein (VCP) are 2 key genes associated with several neurodegenerative disorders but have yet to be thoroughly investigated in sIBM. A candidate gene analysis was conducted using whole-exome sequencing data from 181 sIBM patients, and whole-transcriptome expression analysis was performed in patients with genetic variants of interest. We identified 6 rare missense variants in the SQSTM1 and VCP in 7 sIBM patients (4.0%). Two variants, the SQSTM1 p.G194R and the VCP p.R159C, were significantly overrepresented in this sIBM cohort compared with controls. Five of these variants had been previously reported in patients with degenerative diseases. The messenger RNA levels of major histocompatibility complex genes were upregulated, this elevation being more pronounced in SQSTM1 patient group. We report for the first time potentially pathogenic SQSTM1 variants and expand the spectrum of VCP variants in sIBM. These data suggest that defects in

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1. Introduction

Sporadic inclusion body myositis (sIBM) is the most common myopathy among people aged >45 years, presenting a characteristic pattern of progressive muscle weakness and atrophy in both proximal and distal muscles, particularly in knee extensors and wrist and finger flexors (Machado et al., 2014). Muscle pathology in sIBM indicates a combination of inflammatory and degenerative features such as rimmed vacuoles, sarcoplasmic inclusions, and the deposition of degenerative proteins in affected muscle as pathologic hallmarks, which are features that differentiate sIBM from other muscle disorders (Machado et al., 2014). Electromyography shows a myopathic and neurogenic pattern in some sIBM patients (Lotz et al., 1989), which resembles some hereditary inclusion body myopathies (hIBMs) and motor neuron diseases (Dabby et al., 2001; Lotz et al., 1989). Genes have been identified as associated with hIBMs, and genetic susceptibility factors could also be involved in the pathogenesis of sIBM. In addition to the known hIBM genes, genes encoding for the proteins abnormally accumulated in sIBM muscle are of great interest (Gang et al., 2014), as many of these proteins, such as amyloid-β, hyperphosphorylated tau, p62, and transfactive response (TAR) DNA-binding protein-43 (TDP-43), have also been associated with neurodegenerative diseases including Alzheimer’s disease (AD), amyotrophic lateral sclerosis (ALS), and Parkinson’s disease. Furthermore, several studies have shown that the major histocompatibility complex (MHC)–related genes are dysregulated in sIBM (Gang et al., 2014). However, no genetic factors have yet been confirmed as associated with sIBM (Gang et al., 2014, 2015).

P62, also known as sequestosome 1 (SQSTM1), has been recognized as a strong biomarker in muscle with a high sensitivity and specificity for sIBM (Brady et al., 2014). Genetic variants in SQSTM1 had not been investigated in sIBM until a recent study using targeted next-generation sequencing in a group of 79 patients (Weihl et al., 2015). In that study, only a common SQSTM1 polymorphism was found, unlikely contributing to a rare disease. A recent study reported a splice donor variant in SQSTM1 in a family with an autosomal dominant distal myopathy and also in an unrelated patient with sporadic distal myopathy (Bucelli et al., 2015). In addition, mutations in SQSTM1 are well known to be associated with familial and/or sporadic Paget disease of bone, ALS, and frontotemporal dementia (FTD) (Fecto et al., 2011; Kwok et al., 2014; Laurin et al., 2002; Le Ber et al., 2013; Miller et al., 2015; Rubino et al., 2012). Mutations in valosin-containing protein (VCP) gene are known to cause an inherited form of IBM with Paget disease and frontotemporal dementia (IBMPFD) (Gidaro et al., 2008; Watts et al., 2004) and have also been reported in cases with ALS and FTD (Johnston et al., 2010; Koppers et al., 2012). Two missense mutations in VCP have been recently identified in 2 unrelated IBM patients, one with sIBM and another with family history for late-onset dementia (Weihl et al., 2015).

These findings, along with derervation in muscle electromyography of sIBM patients, suggest a possible genetic overlap between sporadic and IBM-like myopathies and also neurodegenerative diseases. To thoroughly investigate the contribution of SQSTM1 and VCP genes in sIBM, we investigated these 2 genes using whole-exome sequencing data from 181 sIBM patients, which was produced as a part of an International IBM Genetics Consortium.

2. Materials and methods

2.1. Subjects

This study is part of the International IBM Genetics Consortium, a Muscle Study Group–endorsed project, which currently has members from 17 specialized centers in 7 countries around the world. For this whole-exome sequencing Consortium study, DNA samples from a total number of 181 sIBM patients were collected from 11 centers. Patients diagnosed with sIBM had to have an sIBM diagnosis according to a muscle diseases expert and also had to fulfill the Griggs criteria (Griggs et al., 1995; Tawil and Griggs, 2002), the European Neuromuscular Center 2000 criteria (Badrising et al., 2000), or the MRC 2010 criteria (Hilton-Jones et al., 2010). Neuro-pathologically healthy controls (N = 235) aged >60 years were used as an internal aged control group to compare with our sIBM cohort. The study was approved by the National Research Ethics Service Committee London—Queen Square (research ethics committee reference: 12/LO/1557).

2.2. Genetic and bioinformatic analysis

Whole-exome sequencing data were generated for 181 sIBM DNA samples as previously described (Mencacci et al., 2015). In this study, we used a candidate gene approach on these whole-exome sequencing data to investigate variants in SQSTM1 and VCP genes. We excluded all synonymous variants, and all common variants with a population frequency >1% were identified in the 1000 Genomes project (www.1000genomes.org/), in the Exome Variant Server (EVS) database (evs.gs.washington.edu/EVS/), in the Exome Aggregation Consortium (ExAC) Browser (exac.broadinstitute.org/), and in the internal aged controls, as these variants less likely play a role in a rare disease. The filtered variants were confirmed by the conventional Sanger sequencing. The allele frequency of each variant found in sIBM was compared with the ExAC database using Fisher test. The pathogenicity of these variants was evaluated using the following in silico prediction tools: SIFT (Kumar et al., 2009), MutationTaster (Schwarz et al., 2014), and PolyPhen2 (Adzhubei et al., 2010). Genomic evolutionary rate profiling (GERP+) scores were used to estimate the conservation of each variant in multispecies alignments, with higher scores indicating the most conserved nucleotide positions (Davydov et al., 2010).

2.3. Messenger RNA expression and real-time quantitative polymerase chain reaction validation

Available flash frozen muscle biopsy tissues from 6 sIBM subjects with variants in SQSTM1 or VCP and 8 controls that were kindly provided by the MRC Sudden Death Brain and Tissue Bank in Edinburgh, UK, were used for the gene expression analysis. Total RNA was isolated from muscle tissue using the miRNeasy kit (Qiagen, Crawley, UK), and the concentration, purity, and integrity of each RNA sample were assessed as previously described (Trabzuni et al., 2011).

Whole-genome expression profiling was performed using the Illumina HumanHT-12 v4 Expression BeadChip (Illumina, Inc, USA) on 3 patients with SQSTM1 variants (cases 1, 3, and 4), 2 patients with VCP variants (cases 6 and 7), and 5 age- and gender-matched...
controls. Raw expression data were log2 transformed and quantile normalized, and differential expression analysis (patients with SQSTM1 variants vs. controls and all the patients vs. controls) was performed using the limma Bioconductor package (Ritchie et al., 2015). Genes were considered differentially expressed and used in further analysis, when false discovery rate–adjusted p value was <0.05 and absolute log2 fold change was >2.0. Functional enrichment analysis for Gene Ontology terms, KEGG (Kyoto Encyclopedia of Genes and Genomes) pathways, and Human Phenotype Ontology terms was performed using g:Profiler (bit.cs.ut.ee/gprofiler). Among the upregulated genes, 3 genes associated with inflammation markers (HLA-A, CD74, and HLA-DRA) were selected for validation using real-time quantitative polymerase chain reaction (RT-qPCR). Briefly, total RNA (600 ng) from the 6 cases and 8 controls was reverse transcribed into complementary DNA using random primers from High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems, USA). Three replicates per sample were assayed for each target gene using Fast SYBR Green PCR Kit (Applied Biosystems) and run in a QuantStudio 6 Flex Real-Time PCR System (Applied Biosystems). Details on primers and RT-qPCR conditions are available on request. Cyclophilin (PPIA) was selected as the reference gene. The 2–△ΔCt method (Schmittgen and Livak, 2008) was used for Ct normalization for each gene and determination of fold changes in gene expression between patients and controls. Mann-Whitney U test was performed to analyze the difference of relative gene expression between patient groups and controls. For all the analyses, p value <0.05 was considered statistically significant. Statistical analysis was performed using SPSS Statistics 22 (IBM, USA).

3. Results

From the entire cohort of 181 sIBM patients, 150 (82.9%) were Caucasians and 16 (8.8%) were from other ethnicities, including Asian Chinese, the Indian subcontinent, and Black Africans (ethnicity information was unavailable for 15 patients). The majority of sIBM patients were male (65.7%). Age of onset, which was recorded retrospectively, ranged from 31 to 85 years (mean 59.6 ± 9.6 years). The mean age of the 235 healthy aged controls was 79.1 ± 8.5 years, ranging from 60 to 102 years, and similarly to the sIBM cohort, the majority were also male (61.7%).

In this sIBM cohort, 4 rare missense variants in the SQSTM1 gene (ENST00000389805) were found in 4 patients (Table 1). Two rare missense variants in the VCP gene (ENST00000358901) were found in 3 sIBM patients. Of note, the frequency of the variants SQSTM1 p.G194R and VCP p.R159C was significantly higher in our sIBM cohort compared with the ExAC database (Fisher exact test, p = 0.018 and p = 5.288 × 10–3, respectively). These 2 variants were absent in the other population databases and in our aged control group. From the 6 rare variants we found, 4 (Table 1) had been previously reported in patients with ALS (Abramzon et al., 2012; Rubino et al., 2012). Among them, the SQSTM1 p.P392L is also known to be the most frequent SQSTM1 mutation in PDB (Laurin et al., 2002) and has also been reported in cases with FTD (Le Ber et al., 2013) and normal tension glaucoma (Scheetz et al., 2016), whereas VCP p.I27V and p.R159C have also been found in patients with IBM/FPD (Chan et al., 2012; Rohrer et al., 2011), and the VCP p.I27V has also been recently reported in one sIBM patient (Weihl et al., 2015). The SQSTM1 p.A117V was reported in one early-onset AD patient (Cuyvers et al., 2015). Variants found in sIBM patients were absent in our internal aged controls except SQSTM1 variants previously associated with ALS (p.P392L and p.K238E, Table 1).

Tables 2 and 3 summarize the demographic, clinical, and muscle biopsy characteristics of the patients carrying SQSTM1 and VCP variants. The 7 sIBM cases fulfilled the MRC 2010 diagnostic category of pathologically defined, clinically defined, or possible sIBM. There was also no family history of muscle diseases, and none of the 7 patients and their families showed evidence of bone or cognitive problems.

Fig. 2 illustrates the pathologic features of muscle biopsies observed in patients carrying variants in SQSTM1 only because of the availability of the biopsy images. P62-positive inclusions were found in 3 patients with SQSTM1. Patients with SQSTM1 variants showed a global upregulation of MHC-1 (diffuse pattern, Fig. 2G) compared with the healthy control (Fig. 2H).

To further understand molecular changes occurring in sIBM, particularly those related to the variants in SQSTM1 and VCP, we have performed whole-genome expression analysis. Most of the differential expressed genes were found comparing the SQSTM1 sIBM patient group with controls (Supplementary Tables 1 and 2), with 33 upregulated and 7 downregulated genes. The small number of available tissue samples (n = 2) from patients with VCP variants prevented statistical analysis of this sIBM patient group. The expression of SQSTM1 and VCP did not show significant differences between any patient group and controls, but a significant upregulation of MHC genes (class I [HLA-A] and class II [CD74 and HLA-DRA]) was seen in the group of patients carrying SQSTM1 variants (Supplementary Table 2). RT-qPCR analysis of those MHC genes validated their upregulation in
sIBM; this was particularly evident comparing the SQSTM1 group with the controls, with significant upregulation of all analyzed genes (Fig. 3). Functional enrichment analysis of upregulated genes in the SQSTM1 patient group showed a significant overrepresentation of several Gene Ontology terms related with immune response, MHC protein complex, and endosome vesicles and KEGG pathways mostly related to inflammatory, autoimmune, and infectious diseases (Supplementary Table 3). The small number of dysregulated genes found in the expression microarray analysis data prevented functional enrichment analysis for other comparison groups.

4. Discussion

Using whole-exome sequencing, we identified rare missense variants in the SQSTM1 and VCP genes in 7 sIBM cases. The frequency of patients with rare SQSTM1 and VCP variants in the sIBM cohort was 4.0%. Two independent cases have previously been reported with VCP variants (Weihl et al., 2015), but our study extends this finding in a larger cohort of sIBM patients. Regarding SQSTM1, this is to our knowledge the first report where possible pathogenic variants in this gene are observed in sIBM patients. The SQSTM1 gene encodes for sequestosome 1 and/or p62 (referred as p62 in the article), which is a multifunction protein participating in a number of different biological pathways (Komatsu et al., 2012), including the autophagy pathway and various transduction pathways such as nuclear factor-kappaB signaling and apoptosis. Mutations in SQSTM1 were first identified in PDB (Laurin et al., 2002), a chronic disease of bone that can cause skeletal deformity and fractures, and account for 25%–50% of familial and 5%–10% of sporadic PDB patients (Ralston and Layfield, 2012). In
addition, mutations in SQSTM1 are also known to contribute to 1%–3.5% of patients with ALS/FTD with or without familial history (Rubino et al., 2012), a similar frequency to the one we found in our sIBM cohort. Mutations in SQSTM1 are widespread along the gene (Fig. 1A), but the missense mutation p.P392L located in the C-terminal ubiquitin-associated domain, where most mutations lie in, is the most frequent SQSTM1 mutation in all the different clinical phenotypes (Fecto et al., 2011; Laurin et al., 2002). A mouse model with sqstm1 p.P394L mutation (Daroszewska et al., 2011), equivalent to SQSTM1 p.P392L in humans, developed a human PDB-like phenotype and showed dysregulation of autophagy and enhanced autophagosome formation. The SQSTM1 p.K238E has also been reported in one sporadic ALS (Rubino et al., 2012) and lies in a tumor necrosis factor receptor–associated factor 6 (TRAF6)–binding site—where p62 interacts with TRAF6, a critical component of the nuclear factor-kappaB pathway in response to multifactors, including proinflammatory cytokines (Fecto et al., 2011). The SQSTM1 p.G194R has not been observed in other diseases and was absent in our aged controls (Bersano et al., 2009). The SQSTM1 p.A117V is predicted as benign, it was absent in our aged controls, and it is worth mentioning that it has been found overrepresented in our sIBM cohort. Although the SQSTM1 p.A117V is predicted as benign, it was absent in our aged controls and recently was reported in a patient with early-onset AD (Cuyvers et al., 2015) and thus cannot be excluded as a risk factor for sIBM.

The VCP gene encodes for the ATPase valosin-containing protein, which plays a role in proteasomal degradation of misfolded proteins (Meyer and Weihl, 2014). VCP is also involved in critical signaling pathways, membrane fusion, cell cycle controls, and more importantly facilitating a cargo sorting via endosomal and/or autophagy pathway (Meyer and Weihl, 2014). Mutations in VCP are known to cause IBMFPD (Watts et al., 2004), Parkinson’s disease (Majounie et al., 2012), and are also associated with ALS with or without FTD (Johnson et al., 2010). The VCP p.L27V variant has been previously reported as potentially pathogenic (Majounie et al., 2012; Rohrer et al., 2011) and was recently found in another patient with sIBM (Weihl et al., 2015). Functional analysis of this variant showed an increase in p62 and LC3II protein levels (Weihl et al., 2015), suggesting it may cause disruption in autophagosome maturation (Ju et al., 2009). The VCP p.R159C found to be overrepresented in our sIBM cohort has been previously reported as pathogenic and associated with IBMFPD (Bersano et al., 2009) and sporadic ALS (Abramzon et al., 2012). Two additional mutations were also found at this amino acid residue in familial ALS (p.R159C) (Johnson et al., 2010) and IBMFPD (p.R159H) (Haubenberger et al., 2005). The VCP p.R159C lies within the highly conserved CDC48 domain of the protein (Fig. 1B), which is involved in ubiquitin-binding and protein–protein interaction, and a hotspot for VCP mutations (Bersano et al., 2009).

We reviewed the clinical and pathologic details of all sIBM patients with SQSTM1 and VCP variants and confirmed that none of them had developed symptoms of PDB, FTD, or ALS and none had family history of these diseases or family history of muscle weakness. VCP staining was not available for all the patients, but p62–protein-protein interaction, and a hotspot for VCP mutations (Bersano et al., 2009).

The expression levels of either SQSTM1 or VCP messenger RNA were not significantly altered in patients compared with controls, suggesting that the missense variants found in these patients did not alter the corresponding gene expression at the messenger RNA level. P62 and VCP aggregates in the muscle could be a result of increased protein stability, dysfunction of other factors along the proteasomal or lysosomal pathway, or both (Sandri, 2010).

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Fig. 2. Pathologic features observed in sporadic inclusion body myositis patients. There was variation in fiber size with endomysial inflammation, increased internal nucleation, and fiber regeneration (A, hematoxylin and eosin). Rimmed vacuoles were found in all cases (B, Gomori trichrome). The inflammatory infiltrate contains T lymphocytes (C, CD3). A ragged red fiber was observed in case 2 (D, Gomori trichrome). Cytochrome c oxidase negative fibers were identified (E, cytochrome oxidase and/or succinic dehydrogenase). P62 immunoreactive sarcoplasmic inclusions were identified (F) in addition to sparse intranuclear inclusions (arrow and inset). Major histocompatibility complex class I was diffusely increased in patients with sequestosome 1 (SQSTM1) variants (G) in comparison with a normal control (H). Scale bar represents 50 μm in A, C, G, and H; 25 μm in B, D, and F; and 10 μm in the inset in F. Panels A and G are from Case 1; panels B–F are from case 2.
Our findings suggest that variants in these genes constitute genetic susceptibility factors for sIBM and for other multisystem proteinopathy phenotypes. The findings from this study also expand the clinicopathologic spectrum of diseases associated with SQSTM1 and VCP genes, and the overlap between sIBM and IBMpFD, ALS, and/or FTD suggests that muscle and brain diseases share similar pathogenic pathways that may be important for further biomarkers, genes, and therapeutic target discovery. Further investigation of the sIBM whole-exome sequencing data is still ongoing and data from this international collaboration will likely reveal further findings.

**Disclosure statement**

Declaration of interests: All authors have no competing financial interests. Authors’ contributions: Qiang Gang contributed to sample collection, all the experimental work, data analysis, and drafting the first version of the manuscript; Conceição Bettencourt contributed to the experimental plans of microarray and RT-qPCR, preliminary analysis of microarray data, and statistical plan; Pedro M. Machado contributed to overall coordination of the study; namely worldwide sample collection and liaising with all the study collaborators; Conceição Bettencourt, Pedro M. Machado, and Henry Houlden also contributed to drafting the first version of the manuscript; Janice L. Holton contributed to the review and photography of the muscle biopsies; Alan M. Pittman and Deborah Hughes contributed to the generation of whole-exome sequencing data; Stefan Brady, Janice L. Holton, and Boel De Paepé contributed to immunotyping of muscle biopsies; and Andrew B. Singleton contributed to the exome data from control individuals. All the authors from International IBM Genetic Consortium and Muscle Study Group contributed to acquisition of clinical data and sample collection. Michael G. Hanna, Henry Houlden, and Pedro M. Machado are principal investigators of the International IBM Consortium Genetics Study. All the authors contributed to the critical revision of the manuscript and approved the final version.

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Appendix A Supplementary data

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