A genome-wide association study in multiple system atrophy

OPEN

ABSTRACT

Objective: To identify genetic variants that play a role in the pathogenesis of multiple system atrophy (MSA), we undertook a genome-wide association study (GWAS).

Methods: We performed a GWAS with >5 million genotyped and imputed single nucleotide polymorphisms (SNPs) in 918 patients with MSA of European ancestry and 3,864 controls. MSA cases were collected from North American and European centers, one third of which were neuropathologically confirmed.

Results: We found no significant loci after stringent multiple testing correction. A number of regions emerged as potentially interesting for follow-up at \( p < 1 \times 10^{-6} \), including SNPs in the genes FBXO47, ELOVL7, EDN1, and MAPT. Contrary to previous reports, we found no association of the genes SNCA and COQ2 with MSA.

Conclusions: We present a GWAS in MSA. We have identified several potentially interesting gene loci, including the MAPT locus, whose significance will have to be evaluated in a larger sample set. Common genetic variation in SNCA and COQ2 does not seem to be associated with MSA. In the future, additional samples of well-characterized patients with MSA will need to be collected to perform a larger MSA GWAS, but this initial study forms the basis for these next steps. Neurology® 2016;87:1591-1598

GLOSSARY

GWAS = genome-wide association study; MAF = minor allele frequency; MSA = multiple system atrophy; OR = odds ratio; PD = Parkinson disease; SNP = single nucleotide polymorphism.

Multiple system atrophy (MSA) is an adult-onset neurodegenerative disorder of unknown cause. Clinical features include parkinsonism, cerebellar ataxia, pyramidal signs, and dysautonomia. MSA typically presents as a sporadic disease, although rare reports of familial occurrences have been described,\(^1\)–\(^3\) and there is a greater risk of parkinsonian disorders in relatives of patients with MSA.\(^4\)

The pathogenesis of MSA is largely unknown. Identification of \( \alpha \)-synuclein-positive glial cytoplasmic inclusions as a neuropathologic hallmark provided the first clue that abnormal protein accumulation is involved in the development of MSA.\(^5\) Furthermore, it suggested a link to other neurodegenerative diseases that are characterized by \( \alpha \)-synuclein deposition, commonly referred to as synucleinopathies. These include Parkinson disease (PD), MSA, dementia with Lewy bodies, pure autonomic failure, and neurodegeneration with brain iron accumulation type I.\(^6\)

Additional evidence in support of shared pathogenic mechanisms among synucleinopathies was suggested by recent genetic findings demonstrating that variants at the SNCA locus, coding for the deposited \( \alpha \)-synuclein protein, are associated with increased risk for PD and MSA.\(^7\)–\(^8\) In addition, the (MAPT) H1 haplotype has been associated with MSA.\(^7\)\(^8\) More recently, the COQ2 gene was reported to harbor mutations in familial MSA cases from Japan.\(^10\) However, follow-up studies in non-Asian ethnic cohorts were unable to replicate this finding.\(^11\)–\(^12\) Thus, many prior observations require further evaluation.

Authors’ affiliations are listed at the end of the article.

CONFLICT OF INTEREST Go to Neurology.org for full disclosures. Funding information and disclosures deemed relevant by the authors, if any, are provided at the end of the article. The Article Processing Charge was paid by Wellcome Trust.

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To investigate whether common genetic risk factors play a role in MSA, we performed a genome-wide association study (GWAS) including 918 patients with MSA and 3,864 controls.

METHODS Study design. We performed a multicenter GWAS with patients with MSA of European ancestry and regionally matched controls. Collection sites for this study included brain banks and clinical centers in Germany, Austria, Netherlands, Denmark, the United Kingdom, Italy, Portugal, Spain, and the United States (table e-1 at Neurology.org). Since patients were recruited in different geographic regions across Europe and the United States, we matched cases with regional controls. Genotype data of healthy individuals from previous GWAS were obtained from Germany, the United Kingdom, the United States, and Italy. The MSA cases were grouped into 4 geographic regions and each case was matched with 4 controls from the same geographic region: UK and Irish MSA cases were matched with UK controls; Northern European MSA cases from Germany, Netherlands, Belgium, Austria, Denmark, and Sweden were matched with German controls; Southern European cases from Italy and Spain were matched with Italian controls; American MSA cases were matched with American controls. Matching was carried out using multidimensional scaling based on the first 2-component vectors for each subpopulation, derived from common variants assayed in both cases and controls (minor allele frequency [MAF] > 0.05). A flowchart of studied populations and quality control steps is shown in figure e-1.

Study participants. DNA samples from a total of 1,030 patients with MSA were collected for this study (details for each population are shown in table 1, demographics are listed in table e-2). Patients were clinically diagnosed with possible or probable MSA (n = 699) by movement disorder specialists, or pathologically with definite MSA (n = 331) by neuropathologists according to Gilman criteria.16 For controls, we used genotype data from 3,864 previously published neurologically normal individuals from the United Kingdom (n = 936 samples), Germany (n = 944 samples), United States (n = 794 samples), and Italy (n = 1,190 samples) (table 1). All controls were genotyped on Illumina Bead-Chips (Illumina, San Diego, CA, USA). Details about sample collection and genotyping procedures in control cohorts have been described elsewhere.17-19

Standard protocol approvals, registrations, and patient consents. The appropriate institutional review boards approved the study, and written informed consent was obtained for each participant.

Genotyping. Samples from 1,030 MSA cases were genotyped on 1 of 3 Illumina genotyping BeadChips (Human610-Qud v1, Human660W-Qud v1, or HumanOmniExpress-12 v3). Control samples were genotyped on the following BeadChips: UK WTCCC on Illumina Human1.2M-DuoCustom BeadChip; US, German, and Italian controls on Illumina BeadChips 550K version 1 chips or version 3.7,4,6 These chip versions have 343,783 unique single nucleotide polymorphisms (SNPs) in common, and only shared SNPs were used for downstream analyses.

Statistical analysis. Genotype calling. For each of the 3 genotyping platforms, raw data were imported to GenomeStudio (v2010.1, genotyping module v1.6.3, Illumina) and genotype calls were recalculated using a no-call threshold of <0.15.

Quality control. For quality control, we excluded samples with a genotyping call rate <95%, duplicate samples, cryptically related individuals (pi-hat threshold >0.2), individuals in whom the reported sex did not match the genotypic sex, and individuals with non-European ancestry as determined by multiple dimensional scaling analysis (samples deviating >6 SDs from the CEU/TSI population were excluded; see figure e-2). Next, we excluded SNPs with inaccurate cluster separation (cluster separation score <0.3), SNPs that were not shared among all 3 genotyping chip versions, and SNPs with an individual SNP call rate <95%.

Following this step, we excluded SNPs with missingness by haplotype or phenotype that exceeded a significance of p < 0.0001 or a significant deviation from Hardy-Weinberg equilibrium with a p value < 0.00001. Of the remaining SNPs, only those with a MAF >0.01 were used for downstream analyses.

Power calculations and heritability analysis. Power calculations were performed for a GWAS testing 918 cases and 3,864 controls under a log-additive and a recessive model (QUANTO software v1.2.3). A minor allele frequency >1% and a 2-sided α = 5 × 10⁻⁸ were assumed. Under the log-additive model (figure e-3A), power analysis for this study indicated greater than 80% power to detect associated loci with an odds ratio greater than 1.8 at risk allele frequencies between 7% and 87%. We recently also performed a heritability analysis based on our GWAS data demonstrating that the heritability for MSA due to common coding variants is estimated to be between 2.1% and 6.7%.17

Genotype imputation. About 4,903,804 SNPs were imputed based on haplotype reference data from the 1000 Genomes project (1000genomes.org/; December 2010 version). These data were derived from studying the genomic sequence of 104 participants of European ancestry. Imputations were performed for each of the 4 cohorts separately using MACH software as described elsewhere (version 1.0.16).18,19 SNPs with an MAF <0.3 and MAF <0.01 were excluded from further analysis as imputed genotypes below this threshold are likely to be of poor quality.

Association tests. Due to the relatively diverse ancestries of European and US cohorts included in this study, we used principal component vectors 1 to 10 from a multidimensional scaling analysis generated in PLINK as covariates to adjust for possible population substructure in the logistic regression model used for the GWAS (figure e-4). The genomic inflation factor was.

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Table 1 Samples included

<table>
<thead>
<tr>
<th>Cohorts</th>
<th>No. of participants</th>
<th>% Female</th>
<th>Definite/clinically diagnosed</th>
</tr>
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<tr>
<td>United Kingdom</td>
<td>282</td>
<td>36.8</td>
<td>161/121</td>
</tr>
<tr>
<td>United States</td>
<td>148</td>
<td>47.6</td>
<td>126/22</td>
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<tr>
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<td>344</td>
<td>52.5</td>
<td>29/315</td>
</tr>
<tr>
<td>Italy/Spain/Portugal</td>
<td>256</td>
<td>53.5</td>
<td>15/241</td>
</tr>
<tr>
<td>Total</td>
<td>1,030</td>
<td>47.8</td>
<td>331/699</td>
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<tr>
<td>United Kingdom</td>
<td>936</td>
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<td>Germany</td>
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<tr>
<td>Total</td>
<td>3,864</td>
<td>52.2</td>
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</tr>
</tbody>
</table>

Abbreviation: NA = not applicable.
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RESULTS

SNCA SNP genotyping using a restriction enzyme assay.

Results

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Analysis of brain tissue quantitative trait loci.

Figure 1

Manhattan plot showing association results in multiple system atrophy

\( \lambda = 1.057 \). For each SNP, \( p \) values and odds ratios under the additive models were calculated using Mach2dat software. Only SNPs exceeding the conservative Bonferroni threshold for multiple testing (\( p < 5 \times 10^{-8} \)) were considered genome-wide significant. We also performed a subanalysis for association in pathologically confirmed MSA cases (\( n = 295 \) cases after quality control) vs 3,864 controls. The genomic inflation factor in this subgroup was \( \lambda = 1.024 \).

SNCA SNP genotyping using a restriction enzyme assay.

SNP rs11931074, located downstream of the SNCA gene, was re-genotyped using a restriction enzyme assay. Primers were designed to amplify the SNP and surrounding region. Restriction enzyme BsrI (New England Biolabs, Ipswich, MA) was used to cut the PCR product. The major allele was cut, whereas the minor allele remained uncut. Disease association was tested with a \( \chi^2 \) test.

Analysis of brain tissue quantitative trait loci.

For SNPs of interest, we attempted to infer functional consequences in frontal cortex and cerebellar tissue samples from neurologically normal individuals that were assayed for both genome-wide methylation and expression levels. These analyses may shed light on potential disease mechanisms for follow-up in future studies. We tested \( \text{cis} \) associations (any methylation or expression probes \( \pm 1 \) Mb from each SNP) in each of the datasets.

RESULTS

Genotyping, imputation, and quality control.

After quality control procedures, the total study consisted of 918 cases and 3,864 controls. Of the MSA cases, 291 had a pathologically confirmed diagnosis. Loci with the lowest \( p \) values (\( p < 5 \times 10^{-8} \)) in each of the datasets were tested for association. Instead, the allele frequency was calculated postimputation samples run on this array (\( n = 703 \)) and consequently was not in the dataset of genotyped SNPs in common. Therefore, we lack evidence that common genetic variation in the \( \text{COQ2} \) locus plays a major role in MSA risk in the European/Northern American population.

SNCA rs11931074 SNP genotyping.

SNP rs11931074 in the SNCA locus (or rs3822086, which is in close linkage disequilibrium) has been linked to MSA in several smaller studies. This SNP is not represented on the OmniExpress Bead arrays; hence, it was not genotyped in any samples run on this array (\( n = 703 \)) and consequently was not in the dataset of genotyped SNPs in common. Instead, the allele frequency was calculated postimputation, demonstrating that it was neither significantly associated in the entire dataset (\( p \) value = 0.4722) nor in the subgroup of definite MSA cases (\( p \) value = 0.4407). We
Results for association tests in multiple system atrophy cases vs controls are shown. MAPT refers to effect allele.

Abbreviations: OR = odds ratio; UTR = untranslated region.
Results for association tests in multiple system atrophy cases vs controls are shown.
*First allele refers to effect allele.

MAPT is not the closest gene in this locus but due to its known role in other neurodegenerative diseases the most likely candidate.

Analysis of brain tissue quantitative trait loci in candidate loci. Twenty-one out of 24 SNPs of interest (p value < 1 × 10^{-7}) passed quality control in the mRNA expression datasets, and 23 SNPs of interest passed quality control in the CpG methylation datasets. We tested multiple probes per SNP in each set of analyses. A total of 168 unique SNP–probe pairs were tested in the frontal cortex mRNA expression dataset, 165 pairs in the cerebellar mRNA expression dataset, and 391 pairs in the frontal cortex and cerebellar CpG methylation dataset. Associations were tested using linear regression adjusting for appropriate covariates and resulting p values were adjusted based on the false-discovery rate correction as previously described. After correcting for multiple testing, we found 8 significant associations between SNPs of interest and either CpG methylation or mRNA expression.
MAPT locus. Furthermore, MSA was also previously found to be associated with the MAPT H1 haplotype in a small cohort of American MSA cases. These results, however, will need to be verified in a larger MSA cohort.

Located on chromosome 6, EDN1 is part of the endothelin gene family, which functions in the maintenance of vascular tone. Studies have demonstrated the presence of endothelin peptides in nonvascular structures including epithelial cells, glia, and neurons. Given the phenotype of autonomic dysfunction or failure in patients with MSA, one may hypothesize that such pathophysiology may be associated with variation in EDN1.

ELOVL7, originating on chromosome 5, is involved in transferase activity. Chiefly, transferase is a condensing enzyme that acts as a catalyst for the synthesis of saturated and polyunsaturated very long chain fatty acids.

FBXO47 has a known association with papillary renal cell carcinoma. Located on chromosome 17, FBXO47 promotes protein ubiquitination and degradation via phosphorylation, which are critical mechanisms in many neurodegenerative diseases. This locus could provide an important mechanism to MSA pathology in light of the oligodendroglial α-synuclein burden, but requires further study to draw any conclusions.

Common variation in the COQ2 gene (recently found to be mutated in familial and sporadic probable MSA cases in Japan) did not show a significant association in the MSA GWAS data. This suggests that common genetic variation in this gene does not play a major role in disease pathogenesis in patients with MSA of European descent.

We were unable to replicate the previously reported association of variants at the SNCA—A Korean study was also unable to reproduce the association indicating possible differences between populations or an actual null result. The previously associated SNP rs11931074 has considerable variation in frequency among different populations. The reported risk allele has a frequency of about 7%—8% in our different European controls and in the European HapMap data. In contrast, the same allele is much more abundant in Asian and African populations (e.g., 58% in Japanese and 68% in Yorubans). Our study attempts to account for both interpopulation and intrapopulation heterogeneity through principal component analysis, and interpopulation heterogeneity of SNCA is a plausible explanation for the previous findings.

The quantitative trait analysis data suggest a complex risk locus on chromosome 17. This includes several SNPs in the region associated with multiple expression or methylation effects. Several of these genes are involved in pathways potentially relevant to MSA pathology; namely, the ribosylation protein (ARL17A), the ribosome protein (RPL19), and the proteasome protein (PSMB3).

The disease pathology of several neurodegenerative disorders illustrates a common theme of disrupted proteasomal protein clearance and degradation. Notably, PSMB3 may be involved in trinucleotide repeat expansion—a phenomenon seen in several

<table>
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<th>Table 3</th>
<th>Results from the SNCA SNP rs11931074 restriction enzyme assay</th>
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Abbreviations: MAF = minor allele frequency, MSA = multiple system atrophy.
hereditary neurologic disorders (in particular autosomal dominant ataxias)—and it may be driving the trinucleotide expansion process. Supporting this hypothesis, there is considerable clinical overlap between MSA and several hereditary ataxias. Similarly, ribosomal dysfunction with aberrant protein synthesis may promote neurodegeneration. Interest-

ingly, no alteration in expression of MAPT—the most obvious candidate gene in the chromosome 17 locus—was found. All but one associated QTL in MSA were in cerebellar tissue (table e-4). Since the cerebellum is among the most disturbed brain regions in MSA, differences in expression in this region are consistent with an etiologic role in MSA.

There are a number of limitations to this study. First, although this represents by far the largest collection of MSA samples to date, the number of MSA cases is still relatively small for a GWAS. GWAS are designed to identify disease variants of relatively high frequency (MAF >1%) in a population operating under the common disease/common variant hypothesis. In PD, most identified risk factors have an odds ratio (OR) between 0.8 and 1.5. Similarly, in Alzheimer disease—apart from APOE (OR ~4)—common genetic risk factors have low ORs ranging from 0.8 to 1.2. In these diseases, successful identification of significant loci was only feasible with considerably larger sample sizes than our study. However, with our current number we can reasonably exclude the existence of common risk alleles of large effect. A second limitation is the use of population control cohorts rather than age-matched controls, which increases the chance for population heterogeneity. We applied stringent corrections, including principal components from multidimensional scaling as covariates in our statistical model to address this concern. Third, the misdiagnosis rate of clinically ascertained patients, in particular those in early disease stages, can be as high as 38%. We addressed this concern by including a large number of pathology-confirmed cases (~one-third of all patients in this study). The inclusion of pathology-confirmed cases is particularly important for future follow-up studies in MSA.

Finally, a major challenge is that currently no additional large cohorts of MSA cases with a similar genetic background are available. A comparison of European and non-European cohorts may be informative with regard to interpopulation heterogeneity.

None of the studied variants were statistically significant after appropriate correction for multiple testing. However, we identified 4 promising loci that could reveal important insight into the disease pathways of MSA. Increasing the sample size of our GWAS will be key to the successful confirmation of these candidate loci and the identification of other risk genes.

AUTHOR AFFILIATIONS
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cences, INSERM and University Hospital of Toulouse, Faculty of Medicine; Centre de Référence Atrophie Multisystématisée (W.G.M.), CHU de Bordeaux, Poitou; and Université de Bordeaux (W.G.M.), Institut des Maladies Neurogénétiques, UMR 5293, Bordeaux, France.

AUTHOR CONTRIBUTIONS

ACKNOWLEDGMENT
DNA and brain samples: The authors used DNA samples and phenotype data from the NINDS Human Genetics Resource Center DNA and Cell Line Repository at Coriell (Newark, NJ; ccr.coriell.org/ninds), and thank the patients and the submitters who contributed samples to this repository. Human tissue was obtained from the Queen Square Brain Bank (London, UK); Klinik für Neurologie (A.S.), Universitätsgesellschaft der Johann-Wolfgang-Goethe Universität Frankfurt, Germany; Laboratory of Neurogenetics, National Institute on Aging (S.W.S., M.A.N., M.F., T.R.P., B.J.T., A.B.S.), and Neurodegenerative Diseases Research Unit, National Institute of Neurological Disorders and Stroke (S.W.S.), National Institutes of Health, Bethesda, MD; Department of Neurobiology (M.T.P.), University of Bordeaux, Pessac; and Université de Bordeaux (W.G.M.), Institut des Maladies Neurogénétiques, UMR 5293, Bordeaux, France.
Newcastle Brain Tissue Resource at Newcastle University (Newcastle, UK); the Manchester Brain Bank at the University of Manchester (Manchester, UK); Jacksonville Brain Bank for Alzheimer’s, Parkinson’s, and Related Disorders at the Mayo Clinic (Jacksonville, FL); the NICHD Brain and Tissue Bank for Developmental Disorders at the University of Maryland (Baltimore, MD); the New York Brain Bank of the Taub Institute at Columbia University (New York, NY); the Human Brain and Spinal Fluid Resource Center (Los Angeles, CA); the Miami Brain Bank (Miami, FL); the Center for Neurodegenerative Disease Research at the University of Pennsylvania (Philadelphia, PA); the Harvard Brain Bank (Boston, MA); the Emory University Alzheimer’s Disease Research Center Brain Bank (Atlanta, GA); Neurobiobank München at the Ludwig-Maximilians-Universität (Munich, Germany); Brain Bank Center Würzburg (Würzburg, Germany); the Netherlands Brain Bank at the Netherlands Institute for Neuroscience (Amsterdam, Netherlands); and the Neurological Tissue Bank at the University of Barcelona (Barcelona, Spain). The Italian samples were obtained from the Parkinson Institute Biobank (parkinsonbiobank.com), member of the Telethon Network of Genetic Biobank (project n. GTBi2001) funded by TELETHON Italy, and supported by “Fondazione Guglielmo e Francesca Guzzoni per il Motivo di Parkinson.”

STUDY FUNDING
No targeted funding reported.

DISCLOSURE
A. Sailer was supported in part by the Intramural Research Program of the National Institutes of Health (National Institute of Neurological Disorders and Stroke, National Institute on Aging; project number: Z01 AG000949). She also received funding support from the Multiple System Atrophy Trust, the Medical Research Council UK, and Wellcome Trust. S. Schötz was supported in part by the Intramural Research Program of the National Institutes of Health (National Institute of Neurological Disorders and Stroke, National Institute on Aging; project number: Z01 AG000949). She also received a R25 career development grant by the National Institute of Neurological Disorders and Stroke (grant number: R25 NS06729) and a Rapid Response Innovation Award by the Michael J. Fox Foundation. M. Nalb was supported in part by the Intramural Research Program of the National Institutes of Health (National Institute on Aging; project number: Z01 AG000949). C. Schulte reports no disclosures relevant to the manuscript. M. Federoff was supported in part by the Intramural Research Program of the National Institutes of Health (National Institute on Aging; project number: Z01 AG000949). A. Less received funding support from the Multiple System Atrophy Trust, the Medical Research Council UK, Wellcome Trust, and the Reta Lila Weston Institute for Neurological Studies. O. Ross, D. Dickson, K. Mok, N. Menegacci, L. Schottlaender, and V. Chelbin report no disclosures relevant to the manuscript. H. Ling receives funding from a CBDS Solutions Research Grant and is employed by Reta Lila Weston Institute for Neurological Studies. S. O’Sullivan reports no disclosures relevant to the manuscript. N. Wood received funding support from the Multiple System Atrophy Trust, the Medical Research Council UK, Wellcome Trust, the Reta Lila Weston Institute for Neurological Studies, B. Traynor was supported in part by the Intramural Research Program of the National Institutes of Health (National Institute on Aging; project number: Z01 AG000949). L. Ferrari was supported in part by the Intramural Research Program of the National Institutes of Health (National Institute of Neurological Disorders and Stroke, National Institute on Aging; project number: Z01 AG000949). H. Federoff reports no disclosures relevant to the manuscript. T. Miyhe reports no disclosures relevant to the manuscript. H. Morris reports grants from Parkinson’s UK and Medical Research Council UK during the conduct of the study and grants from Welsh Assembly Government, personal fees from Teva, personal fees from Ab scrip, personal fees from UCB, personal fees from Boehringer-Ingelheim, personal fees from GSK, nonfinancial support from Teva, grants from Ipsen Fund, nonfinancial support from Medtronic, grants from MNDA, grants from PSP Association, grants from CBDS Solutions, grants from Drake Foundation, and personal fees from Azorda, outside the submitted work; in addition, Dr. Morris has a patent related to CSORF72. H. R. M. is a co-applicant on a patent application related to CSORF72: Method for diagnosing a neurodegenerative disease (PCT/ GB2012/052140 pending). G. Deuschl, N. Quinn, W. Prowse report no disclosures relevant to the manuscript. W. Oertel has served as a consultant for Mundipharma, Novartis, and UCB Pharma; on advisory boards for Boehringer Ingelheim, Merck, Sharp & Dohme, Medtronic, Mundipharma, Neurona, Novartis, UCB Pharma, and Teva; and received honoraria for presenting lectures from Abbvie, Desitin, Boehringer Ingelheim, Mundipharma, Novartis, Orion Pharma, Schwarz Pharma Neuroscience/UCB, and Teva. He has received scientific grants from the German Ministry of Education and Health, the German Research Foundation, the Michael J. Fox Foundation, the National Institutes of Health (National Institute on Aging; project number: Z01 AG000949), the Multiple System Atrophy Trust, the European Commission, the Medical Research Council UK, and Wellcome Trust; and received research support from the Parkinson Disease Foundation, the Michael J. Fox Foundation, and the Reta Lila Weston Institute for Neurological Studies. J. Hardy received funding support from the Multiple System Atrophy Trust, the Medical Research Council UK, Wellcome Trust, and the Reta Lila Weston Institute for Neurological Studies. J. Delattre is a member of the Telethon Network of Genetic Biobank (project n. GTBi2001) funded by TELETHON Italy, and supported by “Gruppo di studio per il Morbo di Parkinson.”

Received January 17, 2016. Accepted in final form June 15, 2016.

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3. Wullner U, Diakon, K. Mok, N. Menegacci, L. Schottlaender, and V. Chelbin report no disclosures relevant to the manuscript. H. Ling receives funding from a CBDS Solutions Research Grant and is employed by Reta Lila Weston Institute for Neurological Studies. S. O’Sullivan reports no disclosures relevant to the manuscript. N. Wood received funding support from the Multiple System Atrophy Trust, the Medical Research Council UK, Wellcome Trust, the Reta Lila Weston Institute for Neurological Studies. B. Traynor was supported in part by the Intramural Research Program of the National Institutes of Health (National Institute on Aging; project number: Z01 AG000949). L. Ferrari was supported in part by the Intramural Research Program of the National Institutes of Health (National Institute of Neurological Disorders and Stroke, National Institute on Aging; project number: Z01 AG000949). H. Federoff reports no disclosures relevant to the manuscript. T. Miyhe reports no disclosures relevant to the manuscript. H. Morris reports grants from Parkinson’s UK and Medical Research Council UK during the conduct of the study and grants from Welsh Assembly Government, personal fees from Teva, personal fees from Ab scrip, personal fees from UCB, personal fees from Boehringer-Ingelheim, personal fees from GSK, nonfinancial support from Teva, grants from Ipsen Fund, nonfinancial support from Medtronic, grants from MNDA, grants from PSP Association, grants from CBDS Solutions, grants from Drake Foundation, and personal fees from Azorda, outside the submitted work; in addition, Dr. Morris has a patent related to CSORF72. H. R. M. is a co-applicant on a patent application related to CSORF72: Method for diagnosing a neurodegenerative disease (PCT/GB2012/052140 pending). G. Deuschl, N. Quinn, W. Prowse report no disclosures relevant to the manuscript. W. Oertel has served as a consultant for Mundipharma, Novartis, and UCB Pharma; on advisory boards for Boehringer Ingelheim, Merck, Sharp & Dohme, Medtronic, Mundipharma, Neurona, Novartis, Orion Pharma, Schwarz Pharma Neuroscience/UCB, and Teva. He has received scientific grants from the German Ministry of Education and Health, the German Research Foundation, the Michael J. Fox Foundation, the National Institutes of Health (National Institute on Aging; project number: Z01 AG000949), the Multiple System Atrophy Trust, the Medical Research Council UK, and Wellcome Trust; and received research support from the Parkinson Disease Foundation, the Michael J. Fox Foundation, and the Reta Lila Weston Institute for Neurological Studies. J. Hardy received funding support from the Multiple System Atrophy Trust, the Medical Research Council UK, Wellcome Trust, and the Reta Lila Weston Institute for Neurological Studies. J. Delattre is a member of the Telethon Network of Genetic Biobank (project n. GTBi2001) funded by TELETHON Italy, and supported by “Gruppo di studio per il Morbo di Parkinson.”

Neurology 87 October 11, 2016

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A genome-wide association study in multiple system atrophy
Anna Sailer, Sonja W. Scholz, Michael A. Nalls, et al.
Neurology 2016;87;1591-1598 Published Online before print September 14, 2016
DOI 10.1212/WNL.0000000000003221

This information is current as of September 14, 2016