INTRODUCTION

Parkinson’s disease (PD) is a neurodegenerative disorder characterised by the loss of dopaminergic neurons in the mesencephalon. The diagnosis of PD is usually made when patients first notice symptoms of motor dysfunction (bradykinesia, tremor and rigidity) that are related to loss of the dopaminergic innervation in the striatum. However, the dopaminergic deficiency in the mesencephalon remains clinically silent until the concentration of dopamine has decreased by 60–80% in the striatum, and until 30–40% loss of dopaminergic neurons has been reached (1–7). Compensatory mechanisms may thus be involved to explain this delay in the occurrence of motor symptoms.

In the central nervous system, two main enzymes, the monoamine oxidase B (MAOB) and the catechol-O-methyltransferase (COMT) metabolise dopamine. The human COMT gene (OMIM 116790) is localised on chromosome 22q11.2. The distribution of COMT activity in the population and in families indicates that it is regulated by a single autosomal locus with two codominant alleles. The substitution of valine (Val) by methionine (Met) at codon 158 (Val158Met) in the membrane-bound isoform, corresponding to codon 108 in the soluble form, results in a trimodal distribution of high, low and intermediate enzymatic activity. COMT activity is threefold to fourfold higher in the liver and red blood cells of 158Val patients than in those with the 158Met variant. There are ethnic differences in the distribution of the Val158Met genotype. About 25% of the Caucasian population is homozygous for the low activity variant (Val/Val) and 50% has the intermediate activity variant (Val/Met). The Val158Met COMT polymorphism is a modifier of the age at onset (AAO) in Parkinson’s disease (PD). The rs4680 was genotyped in a total of 16 609 subjects from European and North American origin (5886 patients with PD and 10 723 healthy controls). The multivariate analysis for comparing PD and control groups was based on a stepwise logistic regression, with gender, age and cohort origin included in the initial model. The multivariate analysis of the AAO was a mixed linear model, with COMT genotype and gender considered as fixed effects and cohort and cohort-gender interaction as random effects. COMT genotype was coded as a quantitative variable, assuming a codominant genetic effect. The distribution of the COMT polymorphism was not significantly different in patients and controls (p=0.22). The Val allele had a significant effect on the AAO with a younger AAO in patients with the Val/Val (57.1±13.9, p=0.03) than the Val/Met (57.4±13.9) and the Met/Met genotypes (58.3±13.5). The difference was greater in men (1.9 years between Val/Val and Met/Met, p=0.007) than in women (0.2 years, p=0.81). Thus, the Val158Met COMT polymorphism is not associated with PD in the Caucasian population but acts as a modifier of the AAO in PD with a sexual dimorphism: the Val allele is associated with a younger AAO in men with idiopathic PD.

ABSTRACT

The catechol-O-methyltransferase (COMT) is one of the main enzymes that metabolise dopamine in the brain. The Val158Met polymorphism in the COMT gene (rs4680) causes a trimodal distribution of high (Val/Val), intermediate (Val/Met) and low (Met/Met) enzyme activity. We tested whether the Val158Met polymorphism is a modifier of the age at onset (AAO) in Parkinson’s disease (PD). The rs4680 was genotyped in a total of 16 609 subjects from five independent cohorts of European and North American origin (5886 patients with PD and 10 723 healthy controls). The multivariate analysis for comparing PD and control groups was based on a stepwise logistic regression, with gender, age and cohort origin included in the initial model. The multivariate analysis of the AAO was a mixed linear model, with COMT genotype and gender considered as fixed effects and cohort and cohort-gender interaction as random effects. COMT genotype was coded as a quantitative variable, assuming a codominant genetic effect. The distribution of the COMT polymorphism was not significantly different in patients and controls (p=0.22). The Val allele had a significant effect on the AAO with a younger AAO in patients with the Val/Val (57.1±13.9, p=0.03) than the Val/Met (57.4±13.9) and the Met/Met genotypes (58.3±13.5). The difference was greater in men (1.9 years between Val/Val and Met/Met, p=0.007) than in women (0.2 years, p=0.81). Thus, the Val158Met COMT polymorphism is not associated with PD in the Caucasian population but acts as a modifier of the AAO in PD with a sexual dimorphism: the Val allele is associated with a younger AAO in men with idiopathic PD.

but little is known about its effect on motor symptoms. In the present study, we hypothesise that COMT activity might modulate the age at onset (AAO) of motor symptoms in PD by modifying the bioavailability of the remaining endogenous dopamine in the striatum. Using the COMT Val158/108Met polymorphism as a surrogate marker of enzyme activity, we performed an association study in 16,609 patients and controls of European and North American origin.

PATIENTS AND METHODS

French samples
Subjects with PD (n=1031) were recruited through the French network for the study of Parkinson’s disease genetics associating 15 university hospitals across France. All patients were of European origin. Definite and probable PD was defined according to the UK Parkinson’s Disease Society Brain Bank (UKPDSBB).12 The healthy controls (n=2061) of the French sample came from either the French Three-City (3C) cohort (n=1933)13 or the Parkinson’s disease genetics network (n=128). The participants of the 3C cohort were non-institutionalised subjects over 65 years of age, randomly selected from the electoral rolls of three French cities. The control subjects were matched for gender with patients with PD.

German samples
The German samples consisted of three independent cohorts (Kiel, Lübeck and Tübingen). Patients with PD (n=648) and healthy controls (n=688) from the Kiel sample were from the Population Based Assessment of Genetic Risk Factors for PD study performed in northern Germany in cooperation with the Populationsgenetik (POPGEN) biobank.14 All participating patients with PD were diagnosed by board certified neurologists according to the UKPDSBB Criteria.12 Controls (n=688), also obtained by POPGEN, were matched to the cases by gender and geographical origin and were screened to confirm the absence of PD. The Lübeck sample consisted of 525 cases and 223 healthy controls collected in specialised outpatient clinics. All patients underwent a detailed neurological examination by a movement disorder specialist and the diagnosis of PD was established clinically according to the UKPDSBB.12 The controls underwent the same neurological examination as the patients. The PD cases (n=662) for the Tübingen cohort were collected by movement disorders specialists at the Universities of Munich and Tübingen, according to the UKPDSBB.12 Sample collection from controls (n=767) was performed as part of the Prospective validation of risk markers for the development of idiopathic Parkinson’s disease (Idiopathic Parkinson Kohorte Syndroms, PRIPS) study in Tübingen.

International Parkinson’s Disease Genomics Consortium
Genome-wide association studies-based data from three contributing cohorts from the International Parkinson’s Disease Genomics Consortium was used in this study and have been described in detail elsewhere.15 16 This includes 937 cases of PD and 3033 controls from the US samples from the National Institute on Aging cohort, 744 cases and 2019 controls from the Dutch cohort, and 1648 cases and 2699 controls from the UK cohort.17–19 All these studies were carried out in accordance with the Declaration of Helsinki and the rules for clinical good practice. All participants gave their informed consent. The local Ethical Committees approved the studies.

AAO definition
AAO was systematically determined at the time of inclusion by a retrospective interview. The AAO was defined as the first PD-related motor symptom (akinesia, tremor or rigidity) experienced by the patient for the French, Lübeck and Tübingen cohorts, and by the age at which PD was first diagnosed for the Kiel sample and the International Parkinson’s Disease Genomics Consortium cohorts.

Genotyping
The COMT polymorphism G185A (rs4680) was analysed by an allelic discrimination Taqman assay (Applied Biosystems PRISM 7900 sequence detection system, Applied Biosystems, Foster City, USA) for the German samples or extracted from DNA array studies as described elsewhere.15 16 20–24

Statistical analysis
Descriptive statistics used numbers and percentages as qualitative variables and means and SDs as quantitative variables.

Relationships between qualitative variables were tested using χ² tests and comparisons between means of quantitative variables were performed using Student t tests for two groups and unbalanced analysis of variance (ANOVA) for more than two groups. The multivariate analysis for comparing PD and control groups was based on a stepwise logistic regression, with all variables included in the initial model and variables statistically significant with p<0.05 by the Wald test retained in the final model. The multivariate analysis of the AAO was first based on a mixed linear model, with the COMT genotype and gender considered as fixed effects and cohort and cohort-gender interaction considered as random effects. In a second step, two distinct models were fitted, one for men and one for women, with the COMT genotype as the fixed effect and the cohort as the random effect. In all mixed linear models, the COMT genotype was coded as a quantitative variable, namely as the number of ‘L’ alleles. Hardy-Weinberg equilibrium was tested using χ² tests in each sample. All tests were two-sided, with a p value of 0.05 considered statistically significant. Computations were performed using the SAS V9 statistical package.

RESULTS

Characteristics of patients and controls
A total of 17,665 subjects were available (6177 patients with PD and 11,488 controls). Due to insufficient DNA quantity or quality or missing clinical information 1056 specimens were excluded for further analysis. Finally, 16,609 subjects were genotyped for the rs4680 polymorphism and included in the analysis (5886 patients with PD and 10,723 healthy controls).

Table 1 Characteristics of subjects

<table>
<thead>
<tr>
<th></th>
<th>Controls</th>
<th>PD</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sex</td>
<td>Age at inclusion</td>
<td>AAO</td>
</tr>
<tr>
<td></td>
<td>n</td>
<td>Sex ratio</td>
</tr>
<tr>
<td>All</td>
<td>5886</td>
<td>1.5</td>
</tr>
<tr>
<td>US</td>
<td>937</td>
<td>1.5</td>
</tr>
<tr>
<td>UK</td>
<td>1648</td>
<td>1.4</td>
</tr>
<tr>
<td>NL</td>
<td>744</td>
<td>1.8</td>
</tr>
<tr>
<td>France</td>
<td>1031</td>
<td>1.3</td>
</tr>
<tr>
<td>Germany</td>
<td>1526</td>
<td>1.5</td>
</tr>
</tbody>
</table>

AAO, age at onset; n, number of subjects; NL, Netherlands; Sex ratio, male/female; PD, Parkinson’s disease; US, North-American.
The characteristics of subjects in the five cohorts are summarised in table 1. The mean AAO for patients with PD was 57.6±13.8 years. Cohorts of patients with PD were significantly different in terms of AAO (p<0.001) and sex ratio (p=0.04). The mean AAO was also significantly different between gender (male 57.1±13.7, female 58.3±13.9, p=0.001). Subsequent analyses thus included gender and cohorts in the multivariate model.

**DISCUSSION**

This is the largest study in which the COMT polymorphism rs4680 (Val158Met) was genotyped in PD in 16 609 patients and controls from different European and North American samples. We show that the rs4680 polymorphism is a genetic modifier of the AAO in patients with idiopathic PD. Our results suggest a codominant effect of the COMT Val158Met polymorphism resulting in a modification of the AAO by 1.2 years between extreme genotypes (Val/Val and Met/Met). This effect was significant in men but not in women with a 1.9 years difference between extreme genotypes in men. This modifying effect was not associated with an increased risk of PD associated with the Val158Met polymorphism. This result confirms, in a larger cohort, the absence of association between this polymorphism and PD risk in the Caucasian population. In the French and US samples we revealed a significant earlier AAO associated with the Val/Val genotypes. In the remaining samples from Germany, the Netherlands and the UK no significant result has been shown. A possible explanation might be that these samples were underpowered.

The effect of the COMT Val158Met polymorphism on AAO might be explained by a difference of metabolism of the endogenous dopamine in the striatum at disease onset. Indeed, patients carrying the Val158 allele (Val/Val and Val/Met) may have a reduced dopamine bioavailability because of a higher enzyme activity leading to earlier motor symptoms. Conversely, poor metabolisers (Met/Met) may have a greater dopamine bioavailability delaying their motor symptoms. The inverse U curve effect of dopamine concentration in the frontal cortex was elegantly validated in studies of working memory in healthy controls and schizophrenic patients demonstrating that the Val158Met COMT polymorphism has indeed functional consequences on brain function. In PD, studies on the impact of the Val158Met polymorphism on non-motor symptoms have produced conflicting results. No evidence was found for an association between the Val158Met genotype and daytime sleepiness or on neuropsychological measures of attention and executive function. Other studies showed that the genotype directly affects executive function in early stage PD, Val/Val patients have less frontoparietal activation on fMRI and better performance on executive tasks. A pharmacogenetic study showed that the COMT polymorphism determines the acute response to entacapone, although the motor response to levodopa alone was not modified by the COMT polymorphism. These results collectively show that the COMT polymorphism modifies the PD phenotype. Considering its frequency, it might have to be taken into account in the clinical management of patients with PD.

An interesting result in our study was the gender difference of the COMT genotype effect on AAO. The AAO was not significantly different in women whereas it was 1.9 years earlier in men with an earlier AAO for those carrying the Val158 allele, corresponding to the high enzyme activity (table 3, p=0.04). The multivariate analysis confirmed the significant association of the AAO with the COMT polymorphism when cohorts and gender were included in the model (p=0.03). The difference of AAO was 1.2 years earlier for patients with the Val/Val genotype compared with patients with the Met/Met genotype (57.1±13.9 vs 58.3±13.5, p=0.017). Interestingly, this difference was higher in male patients (56.0±14.1 for Val/Val compared with 57.9±13.6 for Met/Met, p=0.007) than in female patients (58.6±13.4 for Val/Val compared with 58.8±13.3 for Met/Met, p=0.81) (table 3).

**Table 2** Distribution of the COMT Val158Met polymorphism in PD and controls

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Total (n)</th>
<th>Control (n)</th>
<th>PD (n)</th>
<th>p Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Val/Val</td>
<td>23.7 (3945)</td>
<td>23.6 (2526)</td>
<td>24.1 (1417)</td>
<td>0.22</td>
</tr>
<tr>
<td>Val/Met</td>
<td>49.5 (8214)</td>
<td>49.5 (5303)</td>
<td>49.5 (2911)</td>
<td>0.22</td>
</tr>
<tr>
<td>Met/Met</td>
<td>26.8 (4452)</td>
<td>27.0 (2894)</td>
<td>26.5 (1558)</td>
<td>0.22</td>
</tr>
</tbody>
</table>

Val/Val: homozygous for the Val158 allele; Val/Met: heterozygous; Met/Met: homozygous for the Met158 allele. p Value: multivariate analysis (see material and methods).

**Table 3** Age at onset in patients with PD according to COMT Val158Met genotype

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Univariate p value</th>
<th>Multivariate p value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Met/Met</td>
<td>0.026**</td>
<td></td>
</tr>
<tr>
<td>Val/Met</td>
<td>0.007**</td>
<td></td>
</tr>
<tr>
<td>Val/Val</td>
<td>0.81**</td>
<td></td>
</tr>
</tbody>
</table>

*Multivariate model including cohorts and gender as covaractors. **Multivariate model including cohorts as covaractor.

COMT, catechol-O-methyltransferase; PD, Parkinson’s disease.
with the Val/Val genotype compared with the Met/Met genotype. A sexually dimorphic autosomal genetic association of the COMT gene has been well recognised in psychiatric disorders but has not yet been described in PD. One of the best-replicated findings was the association of low enzymatic activity with obsessive-compulsive disorder in men, but not in women. In postmortem studies, the dorsolateral prefrontal cortex of women had lower COMT activity than men. Further evidence for gender differences comes from COMT knockout mice (COMT−/−). In this model dopamine levels in the frontal cortex are significantly increased in male COMT−/− mice compared with wild-type mice, but not in female COMT−/− mice. Sex hormones, especially oestrogen, probably contribute to explain gender differences. Oestrogens inhibit COMT mRNA expression in cells expressing oestrogen receptors. However the oestrogen hypothesis might only be a part of the explanation of the gender dimorphism in our study because (1) oestrogen levels fall in postmenopausal women, the age at which PD commonly occurs and (2) in mid-age men the COMT protein and activity levels rise considerably, despite steady oestradiol levels within this period. Bearing this in mind further pathophysiological mechanism could be responsible for the sexual dimorphism like additional gene implication or epigenetic regulation. A candidate gene involved in gender differences could be the monoamine oxidase B (MAOB; OMIM 309860), an X linked gene, which also participates in dopamine metabolism. The MAOB brain activity increases with age and its activity is regulated by epigenetic factors. Different SNPs of the MAOB and the combination of genotypes at risk for the MAOB and the COMT gene were suspected to be associated with PD. Interestingly, one MAOB SNP (rs1799836) was available in French patients with PD (n=992). In this subset, no significant association was found between AAO and this MAOB SNP either alone or in combination with the COMT rs4680 (data not shown).

Our study may have some limitations although statistical biases were carefully avoided by performing multivariate analyses adjusting for cohort origin and gender. Because non-motor—and non-dopaminergic symptoms—may precede motor symptoms in PD, disease onset might not adequately reflect dopaminergic denervation in the striatum that might be modified by the COMT. Finally, other environmental modifiers, like tobacco, are also likely to contribute to the development of PD symptoms but environmental factors were not available in our dataset. Genetic forms of PD as well as genetic susceptibility factors such as mutations in the galactocerebrosidase gene were not systematically screened. Indeed, an association between heterozygous galactocerebrosidase gene mutation and the AAO has been suspected in PD. Future studies must integrate the effects of environmental and genetic factors, including the COMT polymorphism, that could affect the bioavailability of dopamine in general, and especially in individuals at risk for PD.

In conclusion, our data indicate that the COMT polymorphism rs4680 (Val158Met) is a genetic modifier of AAO in patients with PD, with a higher effect in male patients than in female patients. This may be important for future diagnostic and therapeutic strategies.

Author affiliations
1INSERM, UMR_5975, CR-ICM, Paris, France
2UPMC University Paris 06, UMR_5975, CR-ICM, Pitié-Salpêtrière Hospital, Paris, France
3CNRS UMR 7225, CR-ICM, Pitié-Salpêtrière Hospital, Paris, France
4Assistance Publique Hôpitaux de Paris, Département de Génétique et Cytogénétique, Hôpital de la Pitié-Salpêtrière, Paris, France
5INSERM, CIC-9503, Hôpital de la Pitié-Salpêtrière, Paris, France
6Assistance Publique Hôpitaux de Paris, Department of Neurology, Hôpital de la Pitié-Salpêtrière, Paris, France
7Department of Neurology, University Hospital Würzburg, Würzburg, Germany
8Assistance Publique Hôpitaux de Paris, Department of Biostatistics, Hôpital de la Pitié-Salpêtrière, Paris, France
9Laboratory of Neurogenetics, National Institute on Aging, National Institutes of Health, Bethesda Maryland, USA
10INSERM U1043, CPTI, Toulouse, France
11Paul Sabater University, Toulouse, France
12Department of Molecular Neuroscience, UCL Institute of Neurology, London, UK
13Department of Clinical Genetics Section of Medical Genomics, VU Medical Center, Amsterdam, Netherlands
14Institute of Experimental Medicine, Christian-Albrechts University, Kiel, Germany
15Assistance Publique Hôpitaux de Paris, Department of Pharmacology, Hôpital de la Pitié-Salpêtrière, Paris, France
16Faculté de Médecine de Toulouse, Université de Toulouse, France
18Department of Neurodegenerative Diseases, Hertie-Institute for Clinical Brain Research, University of Tübingen, Tübingen, Germany
19Department of Neurology, UKS-H, Campus Kiel; Christian-Albrechts-University, Kiel, Germany
20Department of Neurology, ULS-H, Campus Kiel; Christian-Albrechts-University, Kiel, Germany
21Hôpital Gabriel Montpied, CHU de Grenoble, Department of Neurology, Clermont-Ferrand, France
22CHU de Grenoble, Department of Neurology, Grenoble, France
23CHU de Nantes, Centre d’Investigation Clinique, Nantes, France
24Hôpital Haut-Lévêque, Department of Neurology, Pessac, France
25INSERM, U744, Lille, France
26Institut Pasteur de Lille, Lille, France
27Université Lille-Nord de France, Lille, France
28Université Pierre et Marie Curie—Paris 6, CNRS 7225 CRICM, ER4-UPMC Modélisation en recherche clinique, Hôpital Pitié-Salpêtrière, Paris, France
29INSERM UMR_S975, Neuroepidemiologie, Paris, France
30INSERM U897, Université Bordeaux Ségalen, Bordeaux, France
31“Movement Disorders and Basal Ganglia: Pathophysiology and experimental Therapeutics”, INSERM, UMR_S975, Paris, France

Acknowledgements We thank all study participants for their cooperation. The technical assistance of the DNA and cell bank of the Federative Institute for Neuroscience is gratefully acknowledged and the authors wish to thank Dr Merle Ruberg for critical review of the manuscript. We also thank the members of the French 3C Consortium: Annick Alpérovitch, Claudine Ber, Christophe Tzourio and Philippe Amouyel for allowing us to use part of the 3C cohort. This study was supported by grants from the German Federal Ministry of Education and Research (BMBF 01GR0468. CK is a recipient of a career development award from the Hermann and Lilly Schilling Foundation. The US work was supported in part by the Intramural Research Programs of the National Institute on Aging project numbers 201 AG000949-02. Portions of this study used the high-performance computational capabilities of the Biowulf Linux cluster at the National Institutes of Health, Bethesda, Md. (http://biowulf.nih.gov).

Collaborators The French Parkinson’s Disease Genetics Study Group includes, Y Agid: AP-HP, Hôpital de la Pitié-Salpêtrière, Department of Neurology, 75013 Paris, France; M Arheim: AP-HP, Hôpital de la Pitié-Salpêtrière, Département de Génétique et Cytogénétique, Centre de Génétique Moléculaire et Chromosomique, 75013 Paris, France; A-M Bonnet: AP-HP, Hôpital de la Pitié-Salpêtrière, Département de Neurologie, 75013 Paris, France; M Borg: Service de Neurologie, Hôpital Pasteur, Nice, France; A. Brice: AP-HP, Hôpital de la Pitié-Salpêtrière, Département de Neurologie, 75013 Paris, France; AP-HP, Hôpital de la Pitié-Salpêtrière, Département de Génétique et Cytogénétique, Centre de Génétique Moléculaire et Chromosomique, 75013 Paris, France; E Broussolle: University of Lyon; Hospices Civils de Lyon, Neurological Hospital, Lyon, France; J-C Corvol: INSERM, Centre d’Investigation Clinique CIC-9503, Hôpital de la Pitié-Salpêtrière, Paris, France; Ph. Damier: CHU Nantes, CIC0004, Department of Neurology, Nantes, France; +A. Destée: Université Lille-Nord de France, CHRU de Lille, Neurologie, Hôpital Roger Salengro, Lille Cedex, France; A Durr: AP-HP, Hôpital de la Pitié-Salpêtrière, Département de Génétique et Cytogénétique, Centre de Génétique Moléculaire et Chromosomique, 75013 Paris, France; F Durif: Hôpital Gabriel Montpied, Department of Neurology, Clermont-Ferrand, France; S Klebe: AP-HP, Hôpital de la Pitié-Salpêtrière, Département de Génétique et Cytogénétique, Centre de Génétique Moléculaire et Chromosomique, 75013 Paris, France; E Lohmann: AP-HP, Hôpital de...
Movement disorders

Birmingham NHS Foundation Trust, Birmingham B15 2TH; Ese Mundanohuo: Neurogenetics Unit, UCL Institute of Neurology/National Hospital for Neurology and Neurosurgery, Queen Square, London, UK; Sean O’Sullivan: Queen Square Brain Bank for Neurological Disorders, Institute of Neurology, University College London, London, UK; Jason Lowe, FRCP, FMedSci, MRC Centre for Neurodegenerative Disease Research, University of Cambridge, UK; Cardiff, UK; Richard Pearson: Wellcome Trust Centre for Human Genetics, Roosevelt Drive, Oxford OX3 7UL, UK; Joel S Perlmutter: Department of Psychiatry, Department of Neurology, Washington University School of Medicine, St. Louis, Missouri, USA; Hjörvar Pétursson: deCODE genetics, Sturlugata 8, IS-101 Reykjavik, Iceland, Department of Medical Genetics, University of Iceland, Reykjavik, Iceland; Matti Pitirinen: Wellcome Trust Centre for Human Genetics, Roosevelt Drive, Oxford OX3 7UL, UK; Pierre Pollak: Service de Neurologie, CHU de Grenoble, Grenoble, France; Bart Post: Department of Neurology, Radboud University Nijmegen Medical Centre, Nijmegen, The Netherlands; Simon Potter: Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK; Bernard Ravina: Translational Neurology, Biogen Idec, 14 Cambridge Center, Bio 6, Cambridge, Massachusetts, USA; Tamas Revesz: Queen Square Brain Bank for Neurological Disorders, Institute of Neurology, University College London, London, UK; Olaf Riess: Department of Medical Genetics, Institute of Human Genetics, University of Tübingen, Tübingen, Germany; Fernando Rivadeneira: Department of Epidemiology, Erasmus University Medical Center, Rotterdam, The Netherlands, Department of Internal Medicine, Erasmus Medical Center, Rotterdam, The Netherlands; Patrick Roland: Department of Clinical Genetics, Sector of Medical Genomics, VU University Medical Centre, Amsterdam, The Netherlands; Mina Ryten: Department of Molecular Neurosciences, UCL Institute of Neurology, Queen Square, London, WC1N 3BG; Stephen Sawcer: University of Cambridge, Department of Clinical Neurosciences, Addenbrooke’s hospital, Hills Road, Cambridge, CB2 0QQ, UK; Anthony Schapira: Department of Clinical Neurosciences, UCL Institute of Neurology, Royal Free Hospital, Rowland Hill St, London NW3 2QG, UK; Jan Scheffer: Department of Human Genetics, Radboud University Nijmegen Medical Centre, Nijmegen, The Netherlands; Karen Shaw: Queen Square Brain Bank for Neurological Disorders, Institute of Neurology, University College London, London, UK; Ira Shoulson: Department of Neurology, University of Rochester, Rochester, New York 14620, USA; Ellen Sidransky: Section on Molecular Neurogenetics, Genetic Medicine Branch, NIGMS, National Institutes of Health, Bethesda, Maryland, USA; Rohan de Silva: Department of Molecular Neurosciences, UCL Institute of Neurology, Queen Square, London, WC1N 3BG; Colin Smith: Department of Pathology, Wilkie Building, Tavistock Place, Edinburgh, EH8 9AG; Chris CA Spencer: Wellcome Trust Centre for Human Genetics, Roosevelt Drive, Oxford OX3 7UL, UK; Heirinn StafanSSon: deCODE genetics, Sturlugata 8, IS-101 Reykjavik, Iceland; Stacy Steinberg: deCODE genetics, Sturlugata 8, IS-101 Reykjavik, Iceland; Joanna D Stockton: School of Clinical and Experimental Medicine, University of Birmingham, Edgbaston, Birmingham B15 2TT; Amy Strange: Wellcome Trust Centre for Human Genetics, Roosevelt Drive, Oxford OX3 7UL, UK; Zhan Su: Wellcome Trust Centre for Human Genetics, Roosevelt Drive, Oxford OX3 7UL, UK; Kevin Talbot: Department of Oxford, Department of Clinical Neurology, John Radcliffe Hospital, Oxford OX3 9DU, UK; Ciarán Talbot: Oxford Centre for Biomedical Research Department of Clinical Neurology, Sunnyvale, California, USA; Awaze Tashakkori-Ghanbaria: Welcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK; François Tison: Service de Neurologie, Hôpital Haut-Lévêque, Pessac, France; John Hardy: Department of Molecular Neuroscience, UCL Institute of Neurology, Queen Square, London, WC1N 3BG; Peter Heutink: Department of Clinical Neurogenetics, Section of Medical Genomics, VU University Medical Centre, Amsterdam, The Netherlands; Alexis Brice: INSERM, UMR_S975 (Formerly UMR_S679), Paris, France; Pierre et Marie Curie-Paris, Centre de Recherche de l’Institut du Cerveau et de la Moelle épinière, UMR_S975, Paris, France, CNRS, UMR 7225, Paris, France, AP-HP, Pitié-Salpêtrière Hospital, Department of Genetics and Cytogenetics, Paris, France; Thomas Gasser: Department for Neurodegenerative Diseases, Hertie Institute for Clinical Brain Research, University of Tübingen, and DZNE, German Center for Neurodegenerative Diseases, Tübingen, Germany; Nicholas W Wood: UCL Genetics Institute, Gower House, Edgbaston, Birmingham B15 2TT; Andrew B Singleton: Laboratory of Neurogenetics, National Institute on Aging, National Institutes of Health, Bethesda, MD 20892, USA.

Contributors 5K drafting/revising the manuscript, study concept or design, analysis or interpretation of data, acquisition of data. JLG drafting/revising the manuscript, study concept or design, analysis or interpretation of data. KAM drafting/revising the manuscript, study concept or design, analysis or interpretation of data, acquisition of data. JCC drafting/revising the manuscript, study concept or design, analysis or interpretation of data, acquisition of data. JSS drafting/revising the manuscript and interpretation of data. RC revising the manuscript and analysis or interpretation of data. AB drafting/revising the manuscript, study concept or design, analysis or interpretation of data, acquisition of data. WC drafting/revising the manuscript, study concept or design, analysis or interpretation of data, acquisition of data. JSS was responsible for the preparation and sample collection of the Ki67 sample. CK and JH were responsible for the patient characterisation and sample collection of the Ki67 sample. GC and JH were responsible for the patient characterisation and sample collection of the International Parkinson’s Disease Genomics Consortium. SK, JCC, AB, SL, MS, MM, FD, PP, FT, AD and MV were responsible for the patient characterisation and sample collection of the French sample. PA, JCL and CT were responsible for the SC sample collection. FCB, KT assisted in experimental design and execution. All authors critically reviewed the manuscript.

Funding IPDGC: This US work was supported in part by the Intramural Research Programs of the National Institute on Aging, National Institutes of Health, National Human Genome Research Institute, National Institutes of Health, Department of Health and Human Services; project numbers Z01 AG000949-02 and Z01-ES01986. In addition to this study was supported by the US Department of Defense, award number W81XWH-09-2-0128. Funding to support collection of a portion of the samples was obtained from the National Institutes of Health (grants NS057105 and RO294992), the American Parkinson Disease Association (APDA), Barnes Jewish Hospital Foundation and the Greater St Louis Chapter of the APDA. This work was supported in part by the Wellcome Trust/MRC Joint Call in Neurodegeneration award (WT089698B) to the UK Parkinson’s Disease Consortium (UKPDC) whose members are from the UCL Institute of Neurology, the University of Sheffield and the MRC Protein Phosphorylation and Regulation Centre, University of Dundee. Additionally part of the study was undertaken at UCL/UCL using funding through a Department of Health NIHR Biomedical Research Centre. This work was also supported by Parkinson’s UK (Grants B047 and J-0804) and the Medical Research Council (G0700943). Genotyping of UK replication cases on Immunoscp was included as part of the Wellcome Trust Case Control Consortium 2 project which is funded by the Wellcome Trust (084575/B/08/Z and 084575/208/Z), and is partly supported by a Wolfson-Royal Society Merit Award. The UK gene expression work was supported in part by the UK Medical Research Council (G0901254) to researchers based in the UCL Institute of Neurology and King’s College London. JH receives support from the Reta Lila Weston Trust for Medical Research. This work was also supported by the Landspitali University Hospital Research Fund (S.Sv.), the Icelandic Research Council (S.Sv.), the European Community Framework Programme 7, People programme, (APP) on novel genetic and phenotypic markers of Parkinson’s disease and Essential Tremor (Mark MD), contract no PIAP-PA-2008-230596 Mark MD. (H Petursson, J Holton). The KORA research platform (KORA): Cooperative Research in the Region of Augsburg; http://www.gsf.de/KORA) was initiated and financed by the ForschungszentrumUlmUmwelt and Gesundheit (GSF), which is funded by the German Federal Ministry of Education and Research (BMBF). The study was additionally funded by the National German Genome Network (NGFNplus #01GSO8134; German Ministry for Education and Research) and in addition by the German Federal Ministry of Education and Research (BMBF) NGFN (1G04R048) and in the frame of ERA-NET NEURON (1G09W080). This work was also supported by the Helmholtz Alliance Mental Health in an Ageing Society (HelMA, HA-215) funded by the Initiative and Networking Fund of the Helmholtz Association. The French GWAS can work was supported by the French National Agency of Research (http://www-agence-nationale-recherche.fr, ANR-08-MNP-012) and by the National Research Funding Agency (ANR-08-NEUR-004-01) in ERA-NET NEURON framework (http://www.neuron-eranet.eu). We also want to thank the Hersenstichting Nederland (http://www.hersenstichting.nl), the Neuroscience Campus Amsterdam and the section of CEA, the French National Agency of Research, which has been responsible for the support of the IPDGC program.
Medical genomics, the Prinse Beatrix Fonds (http://www.prinsebeatrixfonds.nl) for sponsoring this work. This study utilised the high-performance computational capabilities of the Biowulf Linux cluster at the National Institutes of Health, Bethesda, Md. (http://biowulf.nih.gov). DNA panels and samples from the NINDS Human Genetic Resource Center DNA and Cell Line Repository (http://orf.princetonnj.org/whsnets)) were used in this study, as well as clinical data. The submitters that contributed samples are acknowledged in detailed descriptions of each panel (http://tcf.coriell.org/sections/Collections/NINDS/?SetId=10). The authors thank The French Parkinson’s Disease Genetics Study Group: Y Agid, M Anheim, A-M Bonnet, M Borg, A Brice, E Broussolle, J-C Corvol, Ph Damier, A Destée, A Duf, F Durif, S Ducasse, E Lohmann, C Martinez, P Pollak, O Rascol, F Tison, C Tou揉et, C M Vėrė, F Viallet and M Vidalenkov. The authors thank the members of the French 3C consortium: Drs Annick Alperschwitz, Claudine Berr, Christophe Tzourio and Jean-Charles Lambert for giving us the possibility to use part of the 3C cohort; and Drs M Lathrop and D Zelenika for their support in generating the genome-wide molecular data. The UK brain samples for the gene expression studies were obtained from the MRC Sudden Death Brain Bank in Edinburgh. This study makes use of GWA data generated by the Wellcome Trust Case-Control consortium 2 (WTCCC2) on UK PD cases and on UK controls from the 1958 Birth Cohort (S8BC) and National Blood Service (NBS). UK population control data was made available through WTCCC1. We thank Jeffrey Barrett for assistance with the design of the Immunochip.

Competing interests None.

Ethics approval Local ethics committees.

Disclosure Dr Klebe received funding from the Deutsche Forschungsgemeinschaft (DFG) (DFG KI 1433/2-1). He received royalties from Thieme publishers. Dr Golmard reports no disclosures. Dr Nalls reports no disclosures. Dr Martinez reports no disclosures. Prof Singleton reports no disclosures. Dr Bras reports no disclosures. Prof. Hardy consults for Esai Pharmaceuticals. Dr Javier Simon-Sanchez reports no disclosures. Dr Peter Heutink reports no disclosures. Dr Kato reports no disclosures. Drs M Lathrop and D Zelenika for their support in generating the genome-wide association and population-based linkage analyses. Drs M Lathrop and D Zelenika for their support in generating the genome-wide association and population-based linkage analyses.

Provenance and peer review Not commissioned; externally peer reviewed.

Open Access This is an Open Access article distributed in accordance with the Creative Commons Attribution Non Commercial (CC BY-NC 3.0) licence, which permits others to distribute, remix, adapt, build upon this work non-commercially, and license their derivative works on different terms, provided the original work is properly cited and the use is non-commercial. See: http://creativecommons.org/licenses/by-nc/3.0/

REFERENCES


