

NMDA receptor gene variations as modifiers in Huntington disease: a replication study

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Carsten Saft, Jorgteplén, Stefan Wiczorek, G. Bernhard Landwehrmeyer, Raymund A.C. Roos, Justo Garcia de Yébenes, Matthias Dose, Sarah J Tabrizi, David Craufurd, the REGISTRY investigators of the European Huntington's Disease Network, Larissa Arning

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Abstract

Several candidate modifier genes which, in addition to the pathogenic CAG repeat expansion, influence the age at onset (AO) in Huntington disease (HD) have already been described. The aim of this study was to replicate association of variations in the N-methyl D-aspartate receptor subtype genes *GRIN2A* and *GRIN2B* in the “REGISTRY” cohort from the European Huntington Disease Network (EHDN). The analyses did replicate the association reported between the *GRIN2A* rs2650427 variation and AO in the entire cohort. Yet, when subjects were stratified by AO subtypes, we found nominally significant evidence for an association of the *GRIN2A* rs1969060 variation and the *GRIN2B* rs1806201 variation. These findings further implicate the N-methyl D-aspartate receptor subtype genes as loci containing variation associated with AO in HD.

Introduction

Huntington disease (HD) is an autosomal dominant neurodegenerative disorder characterised by motor disturbances, cognitive decline, and neuropsychiatric symptoms. It is caused by a CAG repeat expansion (>36 repeats) in exon 1 of the *HTT* gene. [1] The lengths of the expanded CAG tract is inversely related to the age at clinical onset of HD, accounting for more than half of the overall variance in age at onset (AO). [2] Despite this strong correlation, there remains considerable variation of over 40 years in AO in individuals with identical repeat lengths. Several candidate modifier genes of HD have already been described in independent studies. [3] [4] [5] [6] [7] [8] [9] In order to confirm the associations between modifier gene variations and AO, independent replication studies are compulsory. Here, we tested the primary hypothesis of an original study [4], that variations in the *NR2A* and *NR2B* glutamate receptor subunit genes (*GRIN2A*, *GRIN2B*) explain additional variance in AO for HD.

Methods

The study cohort comprised 1,211 individuals of European ancestry with HD collected by the EHDN “REGISTRY” study prior to October 14, 2008. “REGISTRY” is a multi-centre, multi-national observational study which aims to obtain natural history data on a wide spectrum of the European HD population (<http://www.euro-hd.net/html/registry>). [10] In order to test previously reported HD genetic modifiers in this cohort, HD patients with available data on age, sex, age at symptom onset, mutant CAG repeat size and body mass index (BMI) were included (initial $n = 1211$; $n = 1069$; 529 men and 540 women had a complete data set).

The expanded trinucleotide repeats ranged from 40 to 89 with a mean (\pm SD) of 45 ± 4.7 CAGs, and AO ranged from 6 to 74 years, with an onset (mean \pm SD) of 42 ± 11.8 years. AO was defined as the age at which, according to the rater, the first signs of HD appeared. Five hundred and thirty-eight patients first presented with motor disturbances (mean \pm SD motor AO = 43.4 ± 11.6 years), 241 with psychiatric problems (mean \pm SD psychiatric AO = 39.9 ± 10.8 years), and 112 with cognitive decline (mean \pm SD cognitive AO = 38.6 ± 13.1 years). For the remaining patients no specific symptoms were listed (mean \pm SD AO = 42.1 ± 11.8 years). Genotyping of three SNPs was conducted as described before. [4]

Results

None of the SNPs deviated from Hardy – Weinberg Equilibrium (HWE). Considering the earliest AO ($n = 1,069$), we did find evidence of association of the *GRIN2A* SNP rs2650427 (table 1). The R^2 statistic rose modestly (from 0.634 to 0.635) but significantly ($p = 0.028$) when *GRIN2A* genotypes were added to the regression model. The analysis did not, however, replicate the association reported between the SNP rs1969060 in intron 2 of the *GRIN2A* gene and SNP C2664T (rs1806201) in exon 12 of the *GRIN2B* gene (table 1); but when dividing the cohort according to the nature of the symptoms presented initially, both the *GRIN2B* C2664T and the *GRIN2A* rs1969060 polymorphisms explained a small but considerable amount of additional variance

in residual AO in the respective samples. Inclusion of the *GRIN2B* genotypes in the model for motor AO ($n = 538$) increased the R^2 statistic from 0.620 to 0.623 ($p=0.046$) and in the study of 241 patients with psychiatric AO, the R^2 statistic of the exponential regression rose from 0.515 to 0.523 with the *GRIN2A* rs1969060 genotypes included ($p=0.026$, table 1). Interestingly, the association of cognitive AO ($n = 112$) with the *GRIN2A* rs2650427 polymorphism shows the highest nominal significance as compared to the other models in the study (0.770 to 0.775, $p=0.014$). Yet, the results remain statistically significant when excluding the patients with CAGs over >70 ($n=4$).

Model	Genotypes	CAGmean \pm SD	earliest AO mean \pm SD	R ² *	P value
HD CAG 40-89 ($n=1069$)		44.97 \pm 4.7	41.87 \pm 11.8	0.634	<0.0005
+ <i>GRIN2B</i> C2664T (rs1806201)	CC ($n=560$)	44.94 \pm 4.8	42.13 \pm 12.1	0.634	0.541
	CT ($n=436$)	45.02 \pm 4.5	41.32 \pm 11.3	0.634	0.199
	TT ($n=73$)	44.86 \pm 4.6	43.14 \pm 11.9	0.634	0.196
	additive			0.634	0.973
+ <i>GRIN2A</i> rs1969060	TT ($n=745$)	44.83 \pm 4.5	42.00 \pm 11.9	0.634	0.160
	TC ($n=292$)	45.24 \pm 5.1	41.67 \pm 11.5	0.634	0.203
	CC ($n=32$)	45.75 \pm 4.2	40.66 \pm 11.5	0.634	0.645
	additive			0.634	0.172
+ <i>GRIN2A</i> rs2650427	CC ($n=374$)	44.99 \pm 4.0	41.40 \pm 11.9	0.634	0.125
	CT ($n=512$)	44.94 \pm 5.2	41.99 \pm 11.9	0.634	0.891
	TT ($n=183$)	42.51 \pm 4.2	43.14 \pm 10.9	0.635	0.031
	additive			0.635	0.028
Model	Genotypes	CAGmean \pm SD	motor AO mean \pm SD	R ² *	P value
HD CAG 40-77 ($n=538$)		44.72 \pm 4.0	43.39\pm11.6	0.620	<0.0005
+ <i>GRIN2B</i> C2664T (rs1806201)	CC ($n=274$)	44.52 \pm 3.8	44.41 \pm 11.8	0.622	0.099
	CT ($n=221$)	44.96 \pm 4.1	41.98 \pm 11.1	0.623	0.046
	TT ($n=43$)	44.77 \pm 4.9	44.07 \pm 12.4	0.620	0.560
	additive			0.621	0.296
+ <i>GRIN2A</i> rs1969060	TT ($n=373$)	44.51 \pm 3.6	43.79 \pm 11.5	0.620	0.824
	TC ($n=153$)	45.32 \pm 4.9	42.19 \pm 11.9	0.620	0.934
	CC ($n=12$)	43.75 \pm 2.5	46.25 \pm 9.5	0.620	0.658
	additive			0.620	0.744
+ <i>GRIN2A</i> rs2650427	CC ($n=181$)	44.15 \pm 3.8	41.99 \pm 11.8	0.620	0.362
	CT ($n=259$)	44.48 \pm 4.1	44.00 \pm 11.9	0.620	0.792
	TT ($n=98$)	44.60 \pm 4.2	44.34 \pm 10.4	0.621	0.143
	additive			0.621	0.158
Model	Genotypes	CAGmean \pm SD	psychiatric AO mean \pm SD	R ² *	P value
HD CAG 40-67 ($n=241$)		44.73 \pm 4.1	39.86\pm10.8	0.515	<0.0005
+ <i>GRIN2B</i> C2664T (rs1806201)	CC ($n=139$)	44.81 \pm 4.4	39.50 \pm 11.3	0.513	0.964
	CT ($n=90$)	44.74 \pm 3.8	39.79 \pm 10.5	0.514	0.607
	TT ($n=12$)	43.67 \pm 2.1	44.58 \pm 9.6	0.517	0.211
	additive			0.514	0.618
+ <i>GRIN2A</i> rs1969060	TT ($n=172$)	44.79 \pm 4.1	39.01 \pm 10.9	0.523	0.026
	TC ($n=63$)	44.01 \pm 3.7	42.78 \pm 9.8	0.523	0.033

	CC (n=6)	49.50±6.8	33.50±15.5	0.514	0.649
	additive			0.522	0.037
+ <i>GRIN2A</i> rs2650427	CC (n=83)	44.79±4.0	39.42±11.3	0.514	0.504
	CT (n=120)	44.24±3.8	40.90±10.5	0.514	0.702
	TT (n=38)	43.13±5.1	37.53±10.8	0.514	0.724
	additive			0.514	0.514
Model	Genotypes	CAGmean ± SD	cognitive AO mean ± SD	R ² *	P value
HD CAG 40-89 (n=112)		46.34±7.8	38.60±13.1	0.765	<0.0005
+ <i>GRIN2B</i> C2664T (rs1806201)	CC (n=54)	46.76±8.5	37.89±14.2	0.763	0.621
	CT (n=55)	45.74±7.1	39.73±11.9	0.763	0.530
	TT (n=3)	50.00±6.2	30.67±14.0	0.763	0.682
	additive			0.763	0.742
+ <i>GRIN2A</i> rs1969060	TT (n=74)	46.24±7.8	38.95±14.1	0.763	0.682
	TC (n=31)	46.74±8.5	37.68±11.4	0.763	0.799
	CC (n=7)	45.71±3.8	39.00±10.4	0.763	0.741
	additive			0.763	0.650
+ <i>GRIN2A</i> rs2650427	CC (n=40)	45.55±4.9	37.80±12.4	0.770	0.054
	CT (n=55)	47.67±10.0	36.87±13.2	0.763	0.742
	TT (n=17)	43.9±3.2	46.06±12.3	0.772	0.033
	additive			0.775	0.014

Table 1 The variability in AO attributable to the CAG repeat length was assessed by linear regression using the logarithmically transformed AO as the dependent variable and *GRIN* genotypes as independent variables. *R² illustrates the relative improvement of the regression model, when the genotypes are considered in addition to the CAG repeats.

In order to control the effect of sex-specific associations, we further analysed each combination of genotype with sex, but there was no trend towards significance. Moreover, on average, psychiatric and cognitive symptoms significantly predate clinical motor onset by 3.5 and 4.8 years ($p < 0.001$), thus confirming that affective and cognitive symptoms could be early manifestations of neuronal dysfunction.

Discussion

Of the three polymorphisms tested, *GRIN2A* rs2650427 showed the most consistent evidence of replication in the EHDN Registry study sample. This is in accordance with another replication study in the large set of kindreds from Venezuela, where *GRIN2A* variation also explained a small but considerable amount of additional variance in residual AO.[5]

Yet, the interpretation of the association of cognitive AO with the *GRIN2A* rs2650427 polymorphism should be considered with caution since the sample size of this subgroup (n=112) is too small to provide the statistical power required.

Unfortunately, none of the SNPs associated has been validated functionally and it is most likely that the polymorphisms analysed are not the functional variations, but represent markers in linkage disequilibrium with variations that modify the AO. Although, synonymous SNPs like *GRIN2B* rs1806201 might be pathogenetically relevant via influencing mRNA splicing, protein stability and structure.

The failure to replicate the sex-specific effect of rs1806201 suggests that the original observation may have been false positive, emphasizing the need for stringent statistical thresholds. On the other hand, since linkage disequilibrium is not uniform across populations, the mixed ancestry in the EHDN REGISTRY study sample could account for heterogeneous results. Inconsistent results may also occur because of difficulties in exact AO definitions. The data stresses the need for precise phenotyping in order to reduce heterogeneity, and to facilitate the discovery of clinically relevant biological pathways.

Although the associations replicated explain only a small fraction of the variance of AO, the observed correlations with HD phenotypes demonstrate that GRIN2A and GRIN2B remain promising candidate genes, worth to be studied further in more detail.

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Correspondence to Dr Larissa Arning, Ruhr-University, Department of Human Genetics, Universitätsstr. 150, MA5/39, 44801 Bochum, Germany, larissa.arning@rub.de

Competing interests

The authors have declared that no competing interests exist.

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Ethics approval

This study was conducted with the approval of the local ethics committee of the different clinical centres.

Expansion of Collaborator List

Investigators of the European Huntington's Disease Network

K Barth, Language coordinator

M Bascuñana Garde, Language coordinator

R Bos, Language coordinator

D Ecker, Language coordinator

OJ Handley, Language coordinator

N Heinonen, Language coordinator

C Held, Language coordinator

M Laurà, Language coordinator

A Martínez Descals, Language coordinator

T Mestre, Language coordinator

D Monza, Language coordinator

J Naji, Language coordinator

M Orth, Language coordinator

H Padieu, Language coordinator

S Pro Koivisto, Language coordinator

A Rialland, Language coordinator

P Sasinková, Language coordinator

P Trigo Cubillo, Language coordinator

M van Walsem, Language coordinator

M-N Witjes-Ané, Language coordinator
D Zielonka, Language coordinator
Raphael M. Bonelli, LKH Graz, Abteilung für Psychiatrie, Austria
Brigitte Herranhof, LKH Graz, Abteilung für Psychiatrie, Austria
Anna Hödl, LKH Graz, Abteilung für Psychiatrie, Austria
Hans-Peter Kapfhammer, LKH Graz, Abteilung für Psychiatrie, Austria
Michael Koppitz, LKH Graz, Abteilung für Psychiatrie, Austria
Markus Magnet, LKH Graz, Abteilung für Psychiatrie, Austria
Daniela Otti, LKH Graz, Abteilung für Psychiatrie, Austria
Annamaria Painold, LKH Graz, Abteilung für Psychiatrie, Austria
Karin Reisinge, LKH Graz, Abteilung für Psychiatrie, Austria
Florian Brugger, Universitätsklinik für Neurologie, Innsbruck, Austria
Caroline Hepperger, Universitätsklinik für Neurologie, Innsbruck, Austria
Anna Hotter, Universitätsklinik für Neurologie, Innsbruck, Austria
Philipp Mahlknecht, Universitätsklinik für Neurologie, Innsbruck, Austria
Michael Nocker, Universitätsklinik für Neurologie, Innsbruck, Austria
Klaus Seppi, Universitätsklinik für Neurologie, Innsbruck, Austria
Gregor Wenning, Universitätsklinik für Neurologie, Innsbruck, Austria
Pascale Ribaï, Institut de Pathologie et de Génétiqu, C
Christine Verellen-Dumoulin, Institut de Pathologie et de Génétiqu, Charleroi, Belgiu
Jiří Klempíř, Centrum extrapyramidových onemocnění, Prague, Czech Republic
Martin Kucharik, Centrum extrapyramidových onemocnění, Prague, Czech Republic
Jan Roth, Centrum extrapyramidových onemocnění, Prague, Czech Republic
Lis Hasholt, Hukommelsesklinikken, Rigshospitalet, Copehnhagen, Denmark
Lena E. Hjermind, Hukommelsesklinikken, Rigshospitalet, Copehnhagen, Denmark
Oda Jakobsen, Hukommelsesklinikken, Rigshospitalet, Copehnhagen, Denmark
Jørgen E Nielsen, Hukommelsesklinikken, Rigshospitalet, Copehnhagen, Denmark
Anne Nørremølle, Hukommelsesklinikken, Rigshospitalet, Copehnhagen, Denmark
Sven Asger Sørensen, Hukommelsesklinikken, Rigshospitalet, Copehnhagen, Denmark
Jette Stokholm, Hukommelsesklinikken, Rigshospitalet, Copehnhagen, Denmark
Heli Hiivola, Rehabilitation Centre Suvituuli, Turku-Suvituuli, Finland
Kirsti Martikainen, Rehabilitation Centre Suvituuli, Turku-Suvituuli, Finland
Katri Tuuha, Rehabilitation Centre Suvituuli, Turku-Suvituuli, Finland
Christoph Michael Kosinski, Universitätsklinikum Aachen, Neurologische Klinik, Germany
Daniela Probst, Universitätsklinikum Aachen, Neurologische Klinik, Germany
Christian Sass, Universitätsklinikum Aachen, Neurologische Klinik, Germany
Johannes Schiefer, Universitätsklinikum Aachen, Neurologische Klinik, Germany
Christiane Schlangen, Universitätsklinikum Aachen, Neurologische Klinik, Germany

Cornelius J. Werner, Universitätsklinikum Aachen, Neurologische Klinik, Germany

Herwig Lange, Reha Zentrum in Dinslaken im Gesundheitszentrums Lang, Dinslake, Germany

Matthias Löhle, Universitätsklinikum Carl Gustav Carus an der Technischen Universität Dresden, Klinik und Poliklinik für Neurologie, Dresden, Germany

Alexander Storch, Universitätsklinikum Carl Gustav Carus an der Technischen Universität Dresden, Klinik und Poliklinik für Neurologie, Dresden, Germany

Anett Wolz, Universitätsklinikum Carl Gustav Carus an der Technischen Universität Dresden, Klinik und Poliklinik für Neurologie, Dresden, Germany

Martin Wolz, Universitätsklinikum Carl Gustav Carus an der Technischen Universität Dresden, Klinik und Poliklinik für Neurologie, Dresden, Germany

Johann Lambeck, Universitätsklinik Freiburg, Neurologie, Freiburg, Germany

Birgit Zucker, Universitätsklinik Freiburg, Neurologie, Freiburg, Germany

Alexander Münchau, Universitätsklinikum Hamburg-Eppendorf, Klinik und Poliklinik für Neurologie, Hamburg, Germany

Lars Stubbe, Universitätsklinikum Hamburg-Eppendorf, Klinik und Poliklinik für Neurologie, Hamburg, Germany

Simone Zittel, Universitätsklinikum Hamburg-Eppendorf, Klinik und Poliklinik für Neurologie, Hamburg, Germany

Walburgis Heinicke, Psychatrium Heiligenhafen, Germany

Bernhard Longinus, Klinik für Psychiatrie und Psychotherapie Marburg-Süd, Germany

Alexander Peinemann, Huntington-Ambulanz im Neuro-Kopfzentrum – Klinikum rechts der Isar der Neurologischen Klinik und Poliklinik der Technischen Universität München, Germany

Michael Städtler, Huntington-Ambulanz im Neuro-Kopfzentrum – Klinikum rechts der Isar der Neurologischen Klinik und Poliklinik der Technischen Universität München, Germany

Adolf Weindl, Huntington-Ambulanz im Neuro-Kopfzentrum – Klinikum rechts der Isar der Neurologischen Klinik und Poliklinik der Technischen Universität München, Germany

Stefan Bohlen, Universitätsklinikum Münster, Klinik und Poliklinik für Neurologie, Münster, Germany

Herwig Lange, Universitätsklinikum Münster, Klinik und Poliklinik für Neurologie, Münster, Germany

Ralf Reilmann, Universitätsklinikum Münster, Klinik und Poliklinik für Neurologie, Münster, Germany

Antonie Beister, Isar-Amper-Klinikum – Klinik Taufkirchen (Vils), Germany

Matthias Dose, Isar-Amper-Klinikum – Klinik Taufkirchen (Vils), Germany

Kathrin Hammer, Isar-Amper-Klinikum – Klinik Taufkirchen (Vils), Germany

Gabriele Leythaeuser, Isar-Amper-Klinikum – Klinik Taufkirchen (Vils), Germany

Ralf Marquard, Isar-Amper-Klinikum – Klinik Taufkirchen (Vils), Germany

Tina Raab, Isar-Amper-Klinikum – Klinik Taufkirchen (Vils), Germany

Caroline Schrenk, Isar-Amper-Klinikum – Klinik Taufkirchen (Vils), Germany

Michele Schuierer, Isar-Amper-Klinikum – Klinik Taufkirchen (Vils), Germany

Alexandra Wiedemann, Isar-Amper-Klinikum – Klinik Taufkirchen (Vils), Germany

Antonie Beister, Taufkirchen, Germany

Matthias Dose, Taufkirchen, Germany

Kathrin Hammer, Taufkirchen, Germany

Gabriele Leythaeuser, Taufkirchen, Germany

Ralf Marquard, Taufkirchen, Germany

Tina Raab, Taufkirchen, Germany
Caroline Schrenk, Taufkirchen, Germany
Michele Schuierer, Taufkirchen, Germany
Alexandra Wiedemann, Taufkirchen, Germany
Daniel Ecker, Universitätsklinikum Ulm, Neurologie, Ulm, Germany
Carolin Eschenbach, Universitätsklinikum Ulm, Neurologie, Ulm, Germany
Bernhard Landwehrmeyer, Universitätsklinikum Ulm, Neurologie, Ulm, Germany
Franziska Lezius, Universitätsklinikum Ulm, Neurologie, Ulm, Germany
Michael Orth, Universitätsklinikum Ulm, Neurologie, Ulm, Germany
Sonja Trautmann, Universitätsklinikum Ulm, Neurologie, Ulm, Germany
Claudia Cormio, Dipartimento di Scienze Neurologiche e Psichiatriche Università di Bari, Italy
Olimpia Difruscolo, Dipartimento di Scienze Neurologiche e Psichiatriche Università di Bari, Italy
Marina de Tommaso, Dipartimento di Scienze Neurologiche e Psichiatriche Università di Bari, Italy
Vittorio Sciruicchio, Dipartimento di Scienze Neurologiche e Psichiatriche Università di Bari, Italy
Claudia Serpino, Dipartimento di Scienze Neurologiche e Psichiatriche Università di Bari, Italy
Elisabetta Bertini, Neurologia I- Unita' di Neurogenetica Dipartimento di Neurologia e Psichiatria, Università di Firenze, Italy
Claudia Mechi, Neurologia I- Unita' di Neurogenetica Dipartimento di Neurologia e Psichiatria, Università di Firenze, Italy
Marco Paganini, Neurologia I- Unita' di Neurogenetica Dipartimento di Neurologia e Psichiatria, Università di Firenze, Italy
Sivia Piacentini, Neurologia I- Unita' di Neurogenetica Dipartimento di Neurologia e Psichiatria, Università di Firenze, Italy
Maria Romoli, Neurologia I- Unita' di Neurogenetica Dipartimento di Neurologia e Psichiatria, Università di Firenze, Italy
Sandro Sorbi, Neurologia I- Unita' di Neurogenetica Dipartimento di Neurologia e Psichiatria, Università di Firenze, Italy
Giovanni Abbruzzese, Dipartimento di Neuroscienze, Oftalmologia e Genetica (DiNOG), Università di Genova, Italy
Emilio Di Maria, Dipartimento di Neuroscienze, Oftalmologia e Genetica (DiNOG), Università di Genova, Italy
Monica Bandettini di Poggio Giovanna Ferrandes, Dipartimento di Neuroscienze, Oftalmologia e Genetica (DiNOG), Università di Genova, Italy
Paola Mandich, Dipartimento di Neuroscienze, Oftalmologia e Genetica (DiNOG), Università di Genova, Italy
Roberta Marchese, Dipartimento di Neuroscienze, Oftalmologia e Genetica (DiNOG), Università di Genova, Italy
Alberto Albanese, Fondazione IRCCS Istituto Neurologico C. Besta, Milan, Italy
Stefano Di Donato, Fondazione IRCCS Istituto Neurologico C. Besta, Milan, Italy
Caterina Mariotti, Fondazione IRCCS Istituto Neurologico C. Besta, Milan, Italy
Paola Soliveri, Fondazione IRCCS Istituto Neurologico C. Besta, Milan, Italy
Cinzia Gellera, Fondazione IRCCS Istituto Neurologico C. Besta, Milan, Italy
Daniela Monza, Fondazione IRCCS Istituto Neurologico C. Besta, Milan, Italy
Chiara Tomasello, Fondazione IRCCS Istituto Neurologico C. Besta, Milan, Italy
Lorenzo Nanetti, Fondazione IRCCS Istituto Neurologico C. Besta, Milan, Italy
Di Maio Luigi, Azienda Ospedaliera Universitaria Federico II – Dipartimento di Scienze Neurologiche, Naples, Italy
Giuseppe De Michele, Azienda Ospedaliera Universitaria Federico II – Dipartimento di Scienze Neurologiche, Naples, Italy
Carlo Rinaldi, Azienda Ospedaliera Universitaria Federico II – Dipartimento di Scienze Neurologiche, Naples, Italy

Cinzia Russo, Azienda Ospedaliera Universitaria Federico II – Dipartimento di Scienze Neurologiche, Naples, Italy

Elena Salvatore, Azienda Ospedaliera Universitaria Federico II – Dipartimento di Scienze Neurologiche, Naples, Italy

Tecla Tucci, Azienda Ospedaliera Universitaria Federico II – Dipartimento di Scienze Neurologiche, Naples, Italy

Ferdinando Squitieri, Neurogenetics Unit – IRCCS Neuromed, Pozzilli , Italy

Tiziana Martino, Neurogenetics Unit – IRCCS Neuromed, Pozzilli , Italy

Sara Orobello, Neurogenetics Unit – IRCCS Neuromed, Pozzilli , Italy

Silvia Alberti, Neurogenetics Unit – IRCCS Neuromed, Pozzilli , Italy

Francesca De Gregorio, Neurogenetics Unit – IRCCS Neuromed, Pozzilli , Italy

Valentina Codella, Neurogenetics Unit – IRCCS Neuromed, Pozzilli , Italy

Nunzia De Nicola, Neurogenetics Unit – IRCCS Neuromed, Pozzilli , Italy

Vittorio Maglione, Neurogenetics Unit – IRCCS Neuromed, Pozzilli , Italy

Anna Rita Bentivoglio, Istituto di Neurobiologia e Medicina Molecolare CNR/ Istituto di Neurologia, Dipartimento di Neuroscienze/ CNR Istituto di Scienze e Tecnologie della Cognizione, Rome, Italy

Alfonso Fasano, Istituto di Neurobiologia e Medicina Molecolare CNR/ Istituto di Neurologia, Dipartimento di Neuroscienze/ CNR Istituto di Scienze e Tecnologie della Cognizione, Rome, Italy

Marina Frontali, Istituto di Neurobiologia e Medicina Molecolare CNR/ Istituto di Neurologia, Dipartimento di Neuroscienze/ CNR Istituto di Scienze e Tecnologie della Cognizione, Rome, Italy

Arianna Guidubaldi, Istituto di Neurobiologia e Medicina Molecolare CNR/ Istituto di Neurologia, Dipartimento di Neuroscienze/ CNR Istituto di Scienze e Tecnologie della Cognizione, Rome, Italy

Tamara Ialongo, Istituto di Neurobiologia e Medicina Molecolare CNR/ Istituto di Neurologia, Dipartimento di Neuroscienze/ CNR Istituto di Scienze e Tecnologie della Cognizione, Rome, Italy

Gioia Jacopini, Istituto di Neurobiologia e Medicina Molecolare CNR/ Istituto di Neurologia, Dipartimento di Neuroscienze/ CNR Istituto di Scienze e Tecnologie della Cognizione, Rome, Italy

Giovanna Loria, Istituto di Neurobiologia e Medicina Molecolare CNR/ Istituto di Neurologia, Dipartimento di Neuroscienze/ CNR Istituto di Scienze e Tecnologie della Cognizione, Rome, Italy

Carla Piano, Istituto di Neurobiologia e Medicina Molecolare CNR/ Istituto di Neurologia, Dipartimento di Neuroscienze/ CNR Istituto di Scienze e Tecnologie della Cognizione, Rome, Italy

Silvia Romano, Istituto di Neurobiologia e Medicina Molecolare CNR/ Istituto di Neurologia, Dipartimento di Neuroscienze/ CNR Istituto di Scienze e Tecnologie della Cognizione, Rome, Italy

Francesco Soleti, Istituto di Neurobiologia e Medicina Molecolare CNR/ Istituto di Neurologia, Dipartimento di Neuroscienze/ CNR Istituto di Scienze e Tecnologie della Cognizione, Rome, Italy

Maria Spadaro, Istituto di Neurobiologia e Medicina Molecolare CNR/ Istituto di Neurologia, Dipartimento di Neuroscienze/ CNR Istituto di Scienze e Tecnologie della Cognizione, Rome, Italy

Paola Zinzi , Istituto di Neurobiologia e Medicina Molecolare CNR/ Istituto di Neurologia, Dipartimento di Neuroscienze/ CNR Istituto di Scienze e Tecnologie della Cognizione, Rome, Italy

Arvid Heiberg, Rikshospitalet, Dept. of Medical Genetics, Oslo-RH, Norway

Marleen R van Walsem, Rikshospitalet, Dept. of Medical Genetics, Oslo-RH, Norway

Kathrine Bjørge, Ullevål University Hospital, Oslo, Norway

Madelein Fannemel, Ullevål University Hospital, Oslo, Norway

Per Gørvell, Ullevål University Hospital, Oslo, Norway

Lars Retterstøl, Ullevål University Hospital, Oslo, Norway

Inga Bjørnevoll, St. Olavs Hospital, Trondheim , Norway

Sigrud Botne Sando, St. Olavs Hospital, Trondheim , Norway
Jaroslaw Slawek, Specialistic Hospital, Gdansk Zasp, Gdansk, Poland
Witold Soltan, Specialistic Hospital, Gdansk Zasp, Gdansk, Poland
Emilia Sitek, Specialistic Hospital, Gdansk Zasp, Gdansk, Poland
Magdalena Boczarska-Jedynak, Silesian Medical University Katowice, Poland
Barbara Jasinska-Myga, Silesian Medical University Katowice, Poland
Gregorz Opala, Silesian Medical University Katowice, Poland
Andrzej Szczudlik, Krakowska Akademia Neurologii, Krakow, Poland
Monika Rudzińska, Krakowska Akademia Neurologii, Krakow, Poland
Magdalena Wójcik, Krakowska Akademia Neurologii, Krakow, Poland
Krzysztof Banaszekiewicz, Krakowska Akademia Neurologii, Krakow, Poland
Malgorzata Krawczyk, Krakowska Akademia Neurologii, Krakow, Poland
Daniel Zielonka, Medical University of Poznań, Poland
Jerzy Marcinkowski, Medical University of Poznań, Poland
Anna Ciesielska, Medical University of Poznań, Poland
Justyna Sempłowska, Medical University of Poznań, Poland
Anna Bryl, Medical University of Poznań, Poland
Aneta Klimberg, Medical University of Poznań, Poland
Piotr Janik, Medical University of Warsaw, Neurology, Warsaw-MU, Poland
Anna Kalbarczyk, Medical University of Warsaw, Neurology, Warsaw-MU, Poland
Hubert Kwiecinski, Medical University of Warsaw, Neurology, Warsaw-MU, Poland
Zygmunt Jamrozik, Medical University of Warsaw, Neurology, Warsaw-MU, Poland
Grzegorz Witkowski, Institute of Psychiatry and Neurology Dep. of Genetics, Dep. of Neurology, Warsaw-IPiN, Poland
Danuta Ryglewicz, Institute of Psychiatry and Neurology Dep. of Genetics, Dep. of Neurology, Warsaw-IPiN, Poland
Jakub Antczak, Institute of Psychiatry and Neurology Dep. of Genetics, Dep. of Neurology, Warsaw-IPiN, Poland
Maria Rakowicz, Institute of Psychiatry and Neurology Dep. of Genetics, Dep. of Neurology, Warsaw-IPiN, Poland
Katarzyna Jachinska, Institute of Psychiatry and Neurology Dep. of Genetics, Dep. of Neurology, Warsaw-IPiN, Poland
Elzbieta Zdzienicka, Institute of Psychiatry and Neurology Dep. of Genetics, Dep. of Neurology, Warsaw-IPiN, Poland
Przemyslaw Richter, Institute of Psychiatry and Neurology Dep. of Genetics, Dep. of Neurology, Warsaw-IPiN, Poland
Jacek Zaremba, Institute of Psychiatry and Neurology Dep. of Genetics, Dep. of Neurology, Warsaw-IPiN, Poland
Miguel Coelho, Neurological Clinical Research Unit, Institute of Molecular Medicine, Lisbon-Santa Maria, Portugal
Joaquim J Ferreira, Neurological Clinical Research Unit, Institute of Molecular Medicine, Lisbon-Santa Maria, Portugal
Tiago Mestre, Neurological Clinical Research Unit, Institute of Molecular Medicine, Lisbon-Santa Maria, Portugal
Mário M Rosa, Neurological Clinical Research Unit, Institute of Molecular Medicine, Lisbon-Santa Maria, Portugal
Anabela Valadas, Neurological Clinical Research Unit, Institute of Molecular Medicine, Lisbon-Santa Maria, Portugal
Miguel Gago, Hospital São João E.P.E., Porto-São João, Portugal
Carolina Garrett, Hospital São João E.P.E., Porto-São João, Portugal
Maria Rosalia Guerra, Hospital São João E.P.E., Porto-São João, Portugal

Francisco J Barrero, Hospital Universitario San Cecilio, Neurología, Granada, Spain
Blas Morales, Hospital Universitario San Cecilio, Neurología, Granada, Spain
José Luis López-Sendón Moreno, Hospital Universitario Ramón y Cajal, Neurología, Madrid, Spain
Esther Cubo, Servicio de Neurología Hospital General Yagüe, Burgos, Spain
Natividad Mariscal, Servicio de Neurología Hospital General Yagüe, Burgos, Spain
Jesús Sánchez, Servicio de Neurología Hospital General Yagüe, Burgos, Spain
Rocío García-Ramos García, Hospital Clínico Universitario San Carlos, Madrid-Clinico, Spain
Clara Villanueva, Hospital Clínico Universitario San Carlos, Madrid-Clinico, Spain
Purificacion Pin Quiroga, Hospital Clínico Universitario San Carlos, Madrid-Clinico, Spain
Mónica Bascuñana, Hospital Ramón y Cajal, Neurología, Madrid RYC, Spain
Patricia Trigo Cubillo, Hospital Ramón y Cajal, Neurología, Madrid RYC, Spain
Marta Fatàas, Hospital Ramón y Cajal, Neurología, Madrid RYC, Spain
José Luis López Moreno, Hospital Ramón y Cajal, Neurología, Madrid RYC, Spain
Guillermo García Ribas, Hospital Ramón y Cajal, Neurología, Madrid RYC, Spain
Christine Schwarz, Hospital Ramón y Cajal, Neurología, Madrid RYC, Spain
Justo García de Yébenes, Hospital Ramón y Cajal, Neurología, Madrid RYC, Spain
María José Saiz Artiga, Madrid-Fundación Jiménez Díaz, Madrid FJD, Spain
Asunción Martínez-Descals, Madrid-Fundación Jiménez Díaz, Madrid FJD, Spain
Pedro J García Ruíz, Madrid-Fundación Jiménez Díaz, Madrid FJD, Spain
Vicenta Sánchez, Madrid-Fundación Jiménez Díaz, Madrid FJD, Spain
Lorenza Fortuna Alcaraz, Hospital Universitario Virgen de la Arrixaca, Murcia, Spain
María Fuensanta Noguera Perea, Hospital Universitario Virgen de la Arrixaca, Murcia, Spain
María Martirio Antequera Torres, Hospital Universitario Virgen de la Arrixaca, Murcia, Spain
Laura Vivancos Moreau, Hospital Universitario Virgen de la Arrixaca, Murcia, Spain
Ana Rojo Sebastian, Barcelona-Hospital Mútua de Terrassa, Spain
Miquel Aguilar Barbera, Barcelona-Hospital Mútua de Terrassa, Spain
Dolors Badenes Guia, Barcelona-Hospital Mútua de Terrassa, Spain
Laura Casas Hernanz, Barcelona-Hospital Mútua de Terrassa, Spain
Gemma Tome Carruesco, Barcelona-Hospital Mútua de Terrassa, Spain
Esther Suarez San Martin, Barcelona-Hospital Mútua de Terrassa, Spain
Judit López Catena, Barcelona-Hospital Mútua de Terrassa, Spain
Jordi Bas, Hospital Universitari de Bellvitge, Barcelona-Bellvitge, Spain
Matilde Calopa, Hospital Universitari de Bellvitge, Barcelona-Bellvitge, Spain
Núria Busquets, Hospital Universitari de Bellvitge, Barcelona-Bellvitge, Spain
Penelope Navas Arques, Hospital Son Dureta, Palma, Spain
Aranzazú Gorospe, Hospital Son Dureta, Palma, Spain
Inés Legarda, Hospital Son Dureta, Palma, Spain
María José Torres Rodríguez, Hospital Son Dureta, Palma, Spain

Barbara Vives, Hospital Son Dureta, Palma, Spain
Fátima Carrillo, Hospital Virgen del Rocío, Sevilla, Spain
Pablo Mir, Hospital Virgen del Rocío, Sevilla, Spain
María José Lama Suarez, Hospital Virgen del Rocío, Sevilla, Spain
Ghada Loutfi, Norrlands Universitet Sjukhus, Department of Neurology, Umeå, Sweden
Eva-Lena Stattin, Norrlands Universitet Sjukhus, Department of Neurology, Umeå, Sweden
Laila Westman, Norrlands Universitet Sjukhus, Department of Neurology, Umeå, Sweden
Birgitta Wikström, Norrlands Universitet Sjukhus, Department of Neurology, Umeå, Sweden
Sven Pålhagen, Karolinska-University Hospital, Stockholm, Sweden
Elisabeth Björnsson, Karolinska-University Hospital, Stockholm, Sweden
Jean-Marc Burgunder, Neurologische Klinik des Inselspitals, Bern, Switzerland
Irene Romero, Zentrum für Bewegungsstörungen, Neurologische Klinik und Poliklinik, Bern, Switzerland
Michael Schüpbach, Zentrum für Bewegungsstörungen, Neurologische Klinik und Poliklinik, Bern, Switzerland
Sabine Weber Zaugg, Zentrum für Bewegungsstörungen, Neurologische Klinik und Poliklinik, Bern, Switzerland
Monique S.E. van Hout, Medisch Spectrum Twente, Enschede, The Netherlands
Jeroen P.P. van Vugt, Medisch Spectrum Twente, Enschede, The Netherlands
A. Marit de Weert, Medisch Spectrum Twente, Enschede, The Netherlands
J.J.W. Bolwijn, Polikliniek Neurologie, Groningen, The Netherlands
M. Dekker, Polikliniek Neurologie, Groningen, The Netherlands
K.L. Leenders, Polikliniek Neurologie, Groningen, The Netherlands
J.C.H. van Oostrom, Polikliniek Neurologie, Groningen, The Netherlands
Reineke Bos, Leiden University Medical Centre, Leiden, The Netherlands
Eve M. Dumas, Leiden University Medical Centre, Leiden, The Netherlands
Caroline K. Jurgens, Leiden University Medical Centre, Leiden, The Netherlands
Simon J. A. van den Bogaard, Leiden University Medical Centre, Leiden, The Netherlands
Raymund A.C. Roos, Leiden University Medical Centre, Leiden, The Netherlands
Marie-Noëlle Witjes-Ané, Leiden University Medical Centre, Leiden, The Netherlands
Berry Kremer, Universitair Medisch Centrum St. Radboud, Neurology, Nijmegen, The Netherlands
C.C.P. Verstappen, Universitair Medisch Centrum St. Radboud, Neurology, Nijmegen, The Netherlands
Jenny de Souza, The Barberrry Centre, Dept of Psychiatry, Birmingham, UK
Hugh Rickards, The Barberrry Centre, Dept of Psychiatry, Birmingham, UK
Jan Wright, The Barberrry Centre, Dept of Psychiatry, Birmingham, UK
Roger A. Barker, Cambridge Centre for Brain Repair, Forvie Site, Cambridge, UK
Kate Fisher, Cambridge Centre for Brain Repair, Forvie Site, Cambridge, UK
Anna Olivia Goyder Goodman, Cambridge Centre for Brain Repair, Forvie Site, Cambridge, UK
Susan Hill, Cambridge Centre for Brain Repair, Forvie Site, Cambridge, UK
Ann Kershaw, Cambridge Centre for Brain Repair, Forvie Site, Cambridge, UK
Sarah Mason, Cambridge Centre for Brain Repair, Forvie Site, Cambridge, UK

Nicole Paterson, Cambridge Centre for Brain Repair, Forvie Site, Cambridge, UK

Lucy Raymond, Cambridge Centre for Brain Repair, Forvie Site, Cambridge, UK

Johnathan Bisson, The Institute of Medical Genetics, University Hospital of Wales, Cardiff, UK

Monica Busse, The Institute of Medical Genetics, University Hospital of Wales, Cardiff, UK

Lynda Ellison-Rose, The Institute of Medical Genetics, University Hospital of Wales, Cardiff, UK

Olivia Handley, The Institute of Medical Genetics, University Hospital of Wales, Cardiff, UK

Sarah Hunt, The Institute of Medical Genetics, University Hospital of Wales, Cardiff, UK

Jenny Naji, The Institute of Medical Genetics, University Hospital of Wales, Cardiff, UK

Kathleen Price, The Institute of Medical Genetics, University Hospital of Wales, Cardiff, UK

Anne Rosser, The Institute of Medical Genetics, University Hospital of Wales, Cardiff, UK

Stephen Dunnett, The Institute of Medical Genetics, University Hospital of Wales, Cardiff, UK

Maureen Edwards, Molecular Medicine Centre, Western General Hospital, Department of Clinical Genetics, Edinburgh, UK

Paul A. De Sousa, Molecular Medicine Centre, Western General Hospital, Department of Clinical Genetics, Edinburgh, UK

Teresa Hughes (Scottish Huntington's Association), Molecular Medicine Centre, Western General Hospital, Department of Clinical Genetics, Edinburgh, UK

Marie McGill, Molecular Medicine Centre, Western General Hospital, Department of Clinical Genetics, Edinburgh, UK

Pauline Pearson, Molecular Medicine Centre, Western General Hospital, Department of Clinical Genetics, Edinburgh, UK

Mary Porteous, Molecular Medicine Centre, Western General Hospital, Department of Clinical Genetics, Edinburgh, UK

Paul Smith (Scottish Huntington's Association), Molecular Medicine Centre, Western General Hospital, Department of Clinical Genetics, Edinburgh, UK

Adam Zeman, Molecular Medicine Centre, Western General Hospital, Department of Clinical Genetics, Edinburgh, UK

Nicol Lambord, Heavitree Hospital, Exeter , UK

Julia Rankin, Heavitree Hospital, Exeter , UK

Liz Burrows, Department of Neurology Gloucestershire Royal Hospital, Gloucester, UK

Amy Fletcher, Department of Neurology Gloucestershire Royal Hospital, Gloucester, UK

Fiona Laver, Department of Neurology Gloucestershire Royal Hospital, Gloucester, UK

Mark Silva, Department of Neurology Gloucestershire Royal Hospital, Gloucester, UK

Aileen Thomson, Department of Neurology Gloucestershire Royal Hospital, Gloucester, UK

Thomasin Andrews, Guy's Hospital, London , UK

Andrew Dougherty, Guy's Hospital, London , UK

Fred Kavalier, Guy's Hospital, London , UK

Charlotte Golding, Guy's Hospital, London , UK

Alison Lashwood, Guy's Hospital, London , UK

Dene Robertson, Guy's Hospital, London , UK

Deborah Ruddy, Guy's Hospital, London , UK

Anna Whaite, Guy's Hospital, London , UK

Michael Patton, St. Georges-Hospital, London, UK

Maria Patterson, St. Georges-Hospital, London, UK

Colin Bourne, Leicestershire Partnership Trust, Mill Lodge, Leicester, UK
Carole Clayton, Leicestershire Partnership Trust, Mill Lodge, Leicester, UK
Heather Dipple, Leicestershire Partnership Trust, Mill Lodge, Leicester, UK
Jackie Clapton, Leicestershire Partnership Trust, Mill Lodge, Leicester, UK
Janet Grant, Leicestershire Partnership Trust, Mill Lodge, Leicester, UK
Diana Gross, Leicestershire Partnership Trust, Mill Lodge, Leicester, UK
Caroline Hallam, Leicestershire Partnership Trust, Mill Lodge, Leicester, UK
Julia Middleton, Leicestershire Partnership Trust, Mill Lodge, Leicester, UK
Ann Murch, Leicestershire Partnership Trust, Mill Lodge, Leicester, UK
Dawn Patino, Leicestershire Partnership Trust, Mill Lodge, Leicester, UK
Thomasin Andrews, The National Hospital for Neurology and Neurosurgery, London, UK
Stefania Bruno, The National Hospital for Neurology and Neurosurgery, London, UK
Elvina Chu, The National Hospital for Neurology and Neurosurgery, London, UK
Karen Doherty, The National Hospital for Neurology and Neurosurgery, London, UK
Nayana Lahiri, The National Hospital for Neurology and Neurosurgery, London, UK
Marianne Novak, The National Hospital for Neurology and Neurosurgery, London, UK
Aakta Patel, The National Hospital for Neurology and Neurosurgery, London, UK
Sarah Tabrizi, The National Hospital for Neurology and Neurosurgery, London, UK
Rachel Taylor, The National Hospital for Neurology and Neurosurgery, London, UK
Thomas Warner, The National Hospital for Neurology and Neurosurgery, London, UK
Edward Wild, The National Hospital for Neurology and Neurosurgery, London, UK
Natalie Arran, Genetic Medicine, University of Manchester, Manchester Academic Health Sciences Centre and Central Manchester University Hospitals NHS Foundation Trust, Manchester, UK
David Craufurd, Genetic Medicine, University of Manchester, Manchester Academic Health Sciences Centre and Central Manchester University Hospitals NHS Foundation Trust, Manchester, UK
Ruth Fullam, Genetic Medicine, University of Manchester, Manchester Academic Health Sciences Centre and Central Manchester University Hospitals NHS Foundation Trust, Manchester, UK
Liz Howard, Genetic Medicine, University of Manchester, Manchester Academic Health Sciences Centre and Central Manchester University Hospitals NHS Foundation Trust, Manchester, UK
Susan Huson, Genetic Medicine, University of Manchester, Manchester Academic Health Sciences Centre and Central Manchester University Hospitals NHS Foundation Trust, Manchester, UK
Lucy Partington-Jones, Genetic Medicine, University of Manchester, Manchester Academic Health Sciences Centre and Central Manchester University Hospitals NHS Foundation Trust, Manchester, UK
Nichola Verstraelen (formerly Ritchie), Genetic Medicine, University of Manchester, Manchester Academic Health Sciences Centre and Central Manchester University Hospitals NHS Foundation Trust, Manchester, UK
Julie Snowden, Genetic Medicine, University of Manchester, Manchester Academic Health Sciences Centre and Central Manchester University Hospitals NHS Foundation Trust, Manchester, UK
Andrea Sollom, Genetic Medicine, University of Manchester, Manchester Academic Health Sciences Centre and Central Manchester University Hospitals NHS Foundation Trust, Manchester, UK
Cheryl Stopford, Genetic Medicine, University of Manchester, Manchester Academic Health Sciences Centre and Central Manchester University Hospitals NHS Foundation Trust, Manchester, UK
Jennifer Thompson, Genetic Medicine, University of Manchester, Manchester Academic Health Sciences Centre and Central

Manchester University Hospitals NHS Foundation Trust, Manchester, UK

Leann Westmoreland, Genetic Medicine, University of Manchester, Manchester Academic Health Sciences Centre and Central Manchester University Hospitals NHS Foundation Trust, Manchester, UK

Andrea H Nemeth, Oxford Radcliffe Hospitals NHS Trust, Oxford, UK

Gill Siuda, Oxford Radcliffe Hospitals NHS Trust, Oxford, UK

Oliver Bandmann, The Royal Hallamshire Hospital, Sheffield, UK

Alyson Bradbury, The Royal Hallamshire Hospital, Sheffield, UK

Kay Fillingham, The Royal Hallamshire Hospital, Sheffield, UK

Isabella Foustanos, The Royal Hallamshire Hospital, Sheffield, UK

Katherine Tidswell, The Royal Hallamshire Hospital, Sheffield, UK

Oliver Quarrell, The Royal Hallamshire Hospital, Sheffield, UK

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