Variant recurrence confirms the existence of a FBXO31-related spastic-dystonic cerebral palsy syndrome

Ivana Dzinovic1, Matej Škorvánek2,3, Petra Pavelekova2,3, Chen Zhao1, Boris Keren4, Sandra Whalen5, Somayeh Bakhtiar5,6,7, Sheng Chih Jin5, Michael C. Krue6,7, Robert Jech9, Juliane Winkelmann1,10,11,12 & Michael Zech1,10

1Institute of Neurogenomics, Helmholtz Zentrum München, Munich, Germany
2Department of Neurology, P.J. Safarik University, Kosice, Slovak Republic
3Department of Neurology, University Hospital of L. Pasteur, Kosice, Slovak Republic
4Department of Genetics, Pitié-Salpêtrière Hospital, APHP. Sorbonne Université, Paris, France
5UF de Génétique Clinique et Centre de Référence Anomalies du Développement et Syndromes Malformatifs, APHP. Sorbonne Université, Hôpital Armand Trousseau, Paris, France
6Pediatric Movement Disorders Program, Division of Pediatric Neurology, Barrow Neurological Institute, Phoenix Children’s Hospital, Phoenix, Arizona
7Departments of Child Health, Neurology, and Cellular & Molecular Medicine, and Program in Genetics, University of Arizona College of Medicine-Phoenix, Phoenix, Arizona
8Department of Genetics, Washington University School of Medicine, St Louis, Missouri
9Department of Neurology, Charles University, 1st Faculty of Medicine, General University Hospital, Prague, Czech Republic
10Institute of Human Genetics, Technical University of Munich, Munich, Germany
11Lehrstuhl für Neurogenetik, Technische Universität München, Munich, Germany
12Munich Cluster for Systems Neurology, SyNergy, Munich, Germany

Correspondence
Michael Zech, Institute of Neurogenomics, Helmholtz Zentrum München, Deutsches Forschungszentrum für Gesundheit und Umwelt (GmbH), Ingolstädter Landstraße 1, 85764 Neuherberg, Germany. Tel: 0049-89-3187-1884; Fax: 0049-89-3187-3297; E-mail: michael.zech@mri.tum.de

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Abstract
The role of genetics in the causation of cerebral palsy has become the focus of many studies aiming to unravel the heterogeneous etiology behind this frequent neurodevelopmental disorder. A recent paper reported two unrelated children with a clinical diagnosis of cerebral palsy, who carried the same de novo c.1000G > A (p.Asp334Asn) variant in FBXO31, encoding a widely studied tumor suppressor not previously implicated in monogenic disease. We now identified a third individual with the recurrent FBXO31 de novo missense variant, featuring a spastic-dystonic phenotype. Our data confirm a link between variant FBXO31 and an autosomal dominant neurodevelopmental disorder characterized by prominent motor dysfunction.
Introduction

Cerebral palsy (CP) represents a major neurodevelopmental disorder (NDD) with an estimated prevalence of 2-3 per 1000 live births.\(^1,2\) The clinical presentation is heterogeneous and the defining features comprise disorders of movement and posture, usually described as non-progressive, but prone to change throughout the course of disease.\(^3\) The motor disorder arises in early infancy and persist until the end of life, often accompanied by additional features such as developmental delay, intellectual disability (ID), and speech impairment.\(^4\) The etiologic implication of environmental factors has been investigated extensively, whereas genetic contributions to CP have only begun to be elucidated.\(^5\)

Two recent large-scale whole-exome sequencing (WES) studies described patients with CP who harbored causative variants in known NDD-associated genes as well as in genes not previously linked to human Mendelian disorders.\(^6,7\) Jin and colleagues\(^5\) identified two unrelated CP-affected individuals with an identical de novo missense variant (c.1000G > A, p. Asp334Asn) in \(FBXO31\), encoding F-box only protein 31 (FBXO31), a molecule for which a relationship to disease had only been known from cancer research.\(^7\) The features shared by both subjects included spasticity, ID, speech deficits, and behavioral abnormalities.\(^5\) Herein, we report on the identification of the recurrent \(FBXO31\) c.1000G > A (p. Asp334Asn) variant in a patient with a complex movement-disorder syndrome, providing the first independent replication of the involvement of a specific de novo \(FBXO31\) mutation in a human NDD. Additionally, we present a comparison of phenotype abnormalities observed in all three \(FBXO31\)-mutated individuals, contributing information for a better understanding of this newly identified monogenic condition.

Methods

The proband presented here was identified as part of a cohort of ~950 whole-exome-sequenced individuals with various types of dystonic disorders. Clinical evaluation was performed at the Department of Neurology, University Hospital of L. Pasteur, Kosice, Slovakia. Prior to the collection of clinical information and data from genomic testing, written informed consent was obtained from the proband’s legal representatives (parents). The case study was carried out in accordance with the Declaration of Helsinki and under protocols approved by respective ethical committees. For the family trio, WES was conducted at the sequencing core of Helmholtz Center Munich using previously published methods.\(^6\) Briefly, exome capture was performed using Agilent SureSelect v6 reagents and exome libraries were subjected to paired-end sequencing on an Illumina HiSeq4000. Sequence-data processing was done with a validated in-house pipeline, implementing Burrows-Wheeler-Aligner, SAMtools, ExomeDepth, and custom scripts. An average of 96-fold to 114-fold coverage was obtained for the three exomes, with 97%-98% of the target nucleotides covered ≥20-fold. Variants were annotated with gene, transcript, functional class, population frequency, deleteriousness predictions, and ClinVar entry. The proband’s entire WES data set was searched for pathogenic or likely pathogenic variants\(^8\) in reported disorder-associated genes, as described.\(^6\) For the identification of de novo alleles, variants were called in all three samples simultaneously, and de novo events were detected by bioinformatics subtraction analysis.\(^6,9\)

Results

Case presentation

We report the case of a 9-year-old boy demonstrating a complex, non-progressive movement-disorder syndrome dominated by spasticity and dystonia (Table 1). The proband was born at term per caesarian section after an uneventful pregnancy. He was the first child of unrelated, healthy parents of Slovakian descent. Family history was unremarkable. There were no postpartum complications and no congenital anomalies. During the first months of life, he presented with muscular hypotonia and delayed acquisition of developmental milestones. He rolled over at the age of 6 months, but did not come to sit until 9 months. He walked with support at 20 months. He spoke in single words at the age of 12 months, but lost the ability to speak at 18 months. Neuropediatric assessment at the age of 2 years documented a conversion to limb spasticity from hypotonia, more pronounced in the lower extremities. In addition, involuntary abnormal twisting and postural abnormalities affecting all four limbs and occasionally the trunk were noted. A working clinical diagnosis of spastic-dystonic CP was established. Over the following 7 years, there was no significant worsening of tone and movement abnormalities, but the proband required assistance with activities of daily living due to severe physical disability. He could not walk longer distances without bilateral support and he displayed reduced manual dexterity. He was able to follow two-step commands, but had no expressive language. Examined elsewhere, he was diagnosed with an intellectual disability. Because of his motor and speech impairments, he has never been able to engage in active play with his peers. At the latest neurological evaluation (age 9 years), he was alert, interactive with eye contact, but he did not vocalize or
verbalize. He had generalized dystonia involving his arms, legs, and trunk, as well as signs of pyramidal tract dysfunction including spasticity (more severely affecting the legs than the arms), hyperreflexia, and clonus in both legs. Mobility was impaired, with an unsteady spastic-dystonic gait. His intellectual development was estimated as moderately compromised, although formal IQ testing had not been performed. No distinctive craniofacial features or physical defects were documented.

Diagnostic evaluations

Routine laboratory tests were non-diagnostic, although slightly elevated levels of lactate in blood and urine were documented once. A series of metabolic studies were unrevealing. On brain MRI (age 3 years), there was reduced white-matter volume in the parietal and occipital lobes bilaterally, along with an aspect of global white-matter dysmyelination. After targeted molecular investigations had failed to provide an etiologic diagnosis, the proband and his parents underwent trio-WES in a research context. The analysis revealed that the proband was heterozygous for a \( FBXO31 \) c.1000G > A (p. Asp334Asn) missense substitution, which had occurred de novo. This variant, absent from control databases (gnomAD, in-house exomes), has been described recently in two individuals with an NDD diagnosed as spastic diplegic CP.\(^5\) The variant affected a conserved residue\(^1^0\) within a functionally important domain of the encoded protein, involved in the interaction with \( FBXO31 \)'s substrate cyclin-D1 (Fig. 1A and B).\(^5,11\) According to the guidelines of the American-College-of-Medical-Genetics-and-Genomics,\(^8\) the variant was classified as “pathogenic”. No other potentially disease-relevant variants were observed in the proband’s WES data.

**Comparative phenotypic analysis**

A clinical overview of the proband presented here and the individuals reported by Jin et al.\(^5\) is given in Table 1. The three cases shared a presentation of motor and/or speech delay, and all had ID that varied from mild to moderate. Additional consistent features included profound abnormalities of speech and muscle tone. The latter comprised spasticity (as seen in all three patients), predominantly affecting the lower limbs and leading to a diagnosis of CP in each subject,\(^5\) as well as dystonia (observed in the herein reported case). Other neurological and non-neurological manifestations such as congenital malformations, behavioral issues, minor dysmorphia, and neuroanatomical alterations occurred in two or only one of the subjects.

**Discussion**

\( FBXO31 \) encodes a 539 amino-acid protein containing an N-terminal F-box domain and a C-terminal substrate-
recognition domain (Fig. 1A).11 FBXO31 is a component of a SKP1-cullin-F-box (SCF)-type ubiquitin ligase, a ubiquitously expressed complex involved in proteasome-dependent degradation of various regulatory proteins such as cyclin-D1 (Fig. 1A and B).11,12 Deregulation of SCF complexes and their subunits has been linked to diverse human pathologies including monogenic disorders.13 For instance, within the class of FBXO (F-box-only) proteins, FBXO11 has been associated with an autosomal dominant NDD (MIM:618089).14 Moreover, biallelic variants in FBXO7 cause Parkinson’s disease-15 (MIM:260300),15,16 linking the occurrence of movement disorder symptoms to FBXO gene perturbation.

A disease-relevant role of FBXO31 has been initially studied in the context of oncogenesis, where the protein was postulated to act as a potent tumor suppressor.7 More recent research suggests that FBXO31 is also indispensable for the normal function of the nervous system, impacting neural network formation and synaptic strength.17 Although the mechanistic basis for how mutation of FBXO31 leads to an NDD remains an area of investigation, Jin et al.5 have shown that c.1000G > A (p. Asp334Asn) produced decreased levels of FBXO31’s substrate cyclin-D1 in patient-derived cells, consistent with a gain-of-function effect. We have now identified a third individual with the c.1000G > A (p. Asp334Asn) variant, displaying phenotype characteristics closely resembling those of the originally described cases.5 Emerging hallmarks of FBXO31-related disease seem to include a delay in psychomotor development, dysfunction of both pyramidal and extrapyramidal systems (as evidenced by the manifestation of spasticity and dystonia), impairments in expressive and receptive language, and ID. Notably, a diagnostic label of CP had been given to all three FBXO31-mutated individuals.

### Table 1. FBXO31-related disease - Genetic findings and clinical features of the present proband and two cases reported by Jin et al.5

| Present proband | F2181 | F6991 |
|-----------------|-------|-------|
| Age at last assessment | 9 years | 9 years | 10 years |
| Gender | Male | Female | Male |
| Genomic variant (GRCh37/hg19) | Chr16:87367889C > T | Chr16:87367889C > T | Chr16:87367889C > T |
| FBXO31 cDNA change (NM_024735.5) | c.1000G > A | c.1000G > A | c.1000G > A |
| FBXO31 protein change (NP_079011.3) | p. Asp334Asn | p. Asp334Asn | p. Asp334Asn |
| Zygosity | Heterozygous | Heterozygous | Heterozygous |
| Inheritance | de novo | de novo | de novo |
| Family history | Negative | Negative | Negative |
| Prenatal findings | No | Decreased fetal movements, mild intrauterine growth restriction | Decreased fetal movements, mild intrauterine growth restriction |
| Gestational age at birth (weeks) | In term (38) | In term (40) | In term (N/A) |
| Malformations at birth | No | Cleft palate, intestinal malrotation, and midgut volvulus requiring small bowel resection | No |
| Developmental delay | Yes (global) | Yes (global) | Yes (global) |
| Hypotonia | Yes (neonatal) | Yes (neonatal) | Yes (neonatal) |
| Intellectual disability | Yes (moderate) | Yes (mild) | Yes (moderate) |
| Speech impairment | Loss of speech at the age of 1.5 years, receptive language disorder | Dysarthria, mixed receptive/expressive language disorder | Speech not fully acquired, receptive language disorder |
| Behavioral abnormalities | No | Attention deficit hyperactivity disorder | Attention deficit hyperactivity disorder |
| Movement disorder | Generalized dystonia, limb spasticity (lower limbs > upper limbs) | Lower-limb spasticity | Lower-limb spasticity |
| Diagnosis of cerebral palsy (CP) | Yes (spastic-dystonic CP) | Yes (spastic diplegic CP) | Yes (spastic diplegic CP) |
| Loss of independent ambulation | No | No | No |
| Brain magnetic resonance imaging | Bilateral occipital and parietal white-matter volume reduction, irregular white-matter dysmyelination | Normal | Mild ventricular dilatation, thin corpus callosum |
| Dysmorphic signs | No | Esotropia | Strabismus |

N/A, not available.

1Labeled as in Jin et al.5

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finding supports the recent idea that monogenic defects represent important contributors to the pathogenesis of CP and CP-like syndromes. The proportion of patients diagnosed with CP whose conditions are attributable to FBXO31 variants remains to be determined. In addition, further studies are required to clarify whether monoallelic FBXO31 variants other than c.1000G > A (p. Asp334Asn) are disease-causing.

Collectively, this report confirms that a recurrent missense variant in FBXO31 causes a novel neurodevelopmental syndrome. The occurrence of de novo FBXO31 mutation should be considered in patients with CP and spastic-dystonic disorders for which no alternative cause is found.

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Conflicts of Interest
The authors declare that they have no conflict of interest.

Author Contributions
I.D. contributed to data acquisition and analysis and drafted a significant portion of the manuscript. P.P., C.Z., B.K., S.W., S.B., S.C.J., and M.C.K. contributed to data acquisition and analysis. M.S., R.J., and J.W. contributed to design and conception of the study and data acquisition and analysis. M.Z. contributed with design and conception of the study, data acquisition and analysis, supervised the study, and drafted a significant portion of the manuscript. All authors performed a critical review of the manuscript.

References
1. Christensen D, Van Naarden BK, Doernberg NS, et al. Prevalence of cerebral palsy, co-occurring autism spectrum disorders, and motor functioning - Autism and Developmental Disabilities Monitoring Network, USA, 2008. Dev Med Child Neurol 2014;56:59–65.
2. Oskoui M, Coutinho F, Dykeman J, et al. An update on the prevalence of cerebral palsy: a systematic review and meta-analysis. Dev Med Child Neurol 2013;55:509–519.
3. Sadowska M, Sarecka-Hujar B, Kopyta I. Cerebral palsy: current opinions on definition, epidemiology, risk factors, classification and treatment options. Neuropsychiatr Dis Treat 2020;16:1505–1518.
4. Korzeniewski SJ, Slaughter J, Lenski M, et al. The complex aetiology of cerebral palsy. Nat Rev Neurol 2018;14:528–543.
5. Jin SC, Lewis SA, Bakhtiari S, et al. Mutations disrupting neuritogenesis genes confer risk for cerebral palsy. Nat Genet 2020;52:1046–1056.
6. Zech M, Jech R, Boesch S, et al. Monogenic variants in dystonia: an exome-wide sequencing study. Lancet Neurol 2020;19:908–918.
7. Tan Y, Liu D, Gong J, et al. The role of F-box only protein 31 in cancer. Oncol Lett 2018;15:4047–4052.
8. Richards S, Aziz N, Bale S, et al. Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology, Genet Med 2015;17:405–424.
9. Zech M, Lam DD, Weber S, et al. A unique de novo gain-of-function variant in CAMK4 associated with intellectual disability and hyperkinetic movement disorder. Cold Spring Harb Mol Case Stud 2018;4(6):a003293.
10. Wiel L, Baakman C, Gilissen D, et al. MetaDome: pathogenicity analysis of genetic variants through aggregation of homologous human protein domains. Hum Mutat 2019;40:1030–1038.
11. Li Y, Jin K, Bunker E, et al. Structural basis of the phosphorylation-independent recognition of cyclin D1 by the SCF(FBXO31) ubiquitin ligase. Proc Natl Acad Sci USA 2018;115:319–324.
12. Deshaies RJ, Joazeiro CA. RING domain E3 ubiquitin ligases. Annu Rev Biochem 2009;78:399–434.
13. Skaar JR, Pagan JK, Pagano M. SCF ubiquitin ligase-targeted therapies. Nat Rev Drug Discov 2014;13:889–903.
14. Gregor A, Sadleir LG, Asadollahi R, et al. De novo variants in the F-box protein FBXO11 in 20 individuals with a variable neurodevelopmental disorder. Am J Hum Genet 2018;103:305–316.
15. Shojaei S, Sina F, Banihosseini SS, et al. Genome-wide linkage analysis of a Parkinsonian-pyramidal syndrome pedigree by 500 K SNP arrays. Am J Hum Genet 2008;82:1375–1384.
16. Di Fonzo A, Dekker MC, Montagna P, et al. FBXO7 mutations cause autosomal recessive, early-onset parkinsonian-pyramidal syndrome. Neurology 2009;72:240–245.
17. Vadhvani M, Schwedhelm-Domeyer N, Mukherjee C, Stegmüller J. The centrosomal E3 ubiquitin ligase FBXO31-SCF regulates neuronal morphogenesis and migration. PLoS One 2013;8:e57530.