B56δ-related protein phosphatase 2A dysfunction identified in patients with intellectual disability

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Here we report inherited dysregulation of protein phosphatase activity as a cause of intellectual disability (ID). De novo missense mutations in 2 subunits of serine/threonine (Ser/Thr) protein phosphatase 2A (PP2A) were identified in 16 individuals with mild to severe ID, long-lasting hypotonia, epileptic susceptibility, frontal bossing, mild hypotelorism, and downsloping palpebral fissures. PP2A comprises catalytic (C), scaffolding (A), and regulatory (B) subunits that determine subcellular anchoring, substrate specificity, and physiological function. Ten patients had mutations within a highly conserved acidic loop of the PPP2RSD-encoded B56δ regulatory subunit, with the same E198K mutation present in 6 individuals. Five patients had mutations in the PPP2RIA-encoded scaffolding Au subunit, with the same R182W mutation in 3 individuals. Some Au cases presented with large ventricles, causing macrocephaly and hydrocephalus suspicion, and all cases exhibited partial or complete corpus callosum agenesis. Functional evaluation revealed that mutant A and B subunits were stable and uncoupled from phosphatase activity. Mutant B56δ was A and C binding–deficient, while mutant Au subunits bound B56δ well but were unable to bind C or bound a catalytically impaired C, suggesting a dominant-negative effect where mutant subunits hinder dephosphorylation of B56δ-anchored substrates. Moreover, mutant subunit overexpression resulted in hyperphosphorylation of GSK3β, a B56δ-regulated substrate. This effect was in line with clinical observations, supporting a correlation between the ID degree and biochemical disturbance.

Introduction

Unlike protein kinases, mutations in serine/threonine (Ser/Thr) protein phosphatases have not commonly been associated with disorders of human development. There are 2 major Ser/Thr protein phosphatase families in the cell: protein phosphatase 1 (PP1) and protein phosphatase 2A (PP2A), together accounting for more than 90% of all phospho-Ser/Thr dephosphorylations. PP2A consists of a catalytic subunit (C), a substrate binding regulatory subunit (B), and a scaffolding subunit (A) that links B and C. Unlike the generally expressed A and C subunits, there is a plethora of B subunits with different expression patterns (1). The differential substrate preferences of the nearly 100 different PP2A holoenzymes that, in theory, can be formed by 2 C isoforms, 2 A isoforms, and at least 23 types of B subunits is largely unknown (2), particularly within the context of a whole organism. Apparently, PP2A-dependent protein dephosphorylation has a potential for regulation that may be just as fine-tuned as protein phosphorylation. Unlike protein phosphorylation, associations between mutations in PP2A subunits and genetic diseases or syndromes have not been described until recently, when 4 de novo PPP2RSD and 3 de novo PPP2RIA mutations were found among the first 1,133 parent-child trios sequenced in the United Kingdom Deciphering Developmental Disorders project (3).

Here, we add clinical descriptions and functional data to the DDD findings and present 9 additional cases with de novo PP2A subunit mutations; 7 in PPP2RSD, encoding the regulatory B56δ subunit, and 2 in PPP2RIA, encoding the scaffolding Au subunit.
Taken together, of the 11 mutations in PPP2R5D, 6 mutations and 2 mutations were identical; 3 of the 5 mutations in PPP2R1A were also identical. All Aα mutations and all but one of the B56δ mutations had the potential to hinder access of catalytically competent C subunits to B56δ-regulated substrates, suggesting a common dominant-negative disease mechanism mainly affecting B56δ-regulated Ser/Thr dephosphorylation.

## Results

In cases with intellectual disability (ID) of unknown etiology, parent-child trio exome sequencing was performed to find de novo and recessive mutations that could explain the condition. De novo missense mutations in 2 subunits of the Ser/Thr phosphatase PP2A were identified in 16 individuals from the United Kingdom (7 cases), the Netherlands (7 cases), Israel (1 case), and Norway (1 case).

The 7 United Kingdom cases were found among 1,133 chromosomally normal parent-child trios (3). This suggests that the prevalence of PP2A subunit mutations in the moderate-to-severe ID group without pathogenic copy number aberrations is around 0.6%. In the United Kingdom, this was part of the large DDD project (http://www.ddduk.org); in other cases, this was done as part of routine diagnostics. In 11 cases, de novo missense mutations in PPP2R5D, encoding the regulatory B56δ PP2A subunit, were found. In 5 other cases, a de novo missense mutation in PPP2R1A, encoding the scaffolding Aα subunit of PP2A, was found. Six mutations and 2 mutations in PPP2R5D were identical, and 3 PPP2R1A mutations were identical. Details on all mutations can be found in Table 1. Other trio exome sequencing results indicating a de novo change of possible relevance or a recessive condition of potential interest can be found in Supplemental Table 1 (supplemental material available online with this article; doi:10.1172/JCI79860DSI). In 10 cases, such findings were made, but based on bioinformatic evaluation of the variants and the clinical features of the patients, all but one of these findings could easily be excluded as causative factors for the phenotype. The exception was case 15, which had heterozygosity for a TMEM67 splice mutation and a few signs that were compatible with a ciliopathy (e.g., unilateral postaxial polydactyly). However, this could also be a random finding, since a second TMEM67 mutation was not found upon Sanger sequencing. In addition, detecting the same de novo missense mutations in patients with identical clinical features is, in itself, evidence in support of causality, especially when supported by functional data (see below). As a crude estimation, the likelihood of finding 10 de novo missense mutations in the same 9–amino acid stretch of B56δ by chance should be less than 10⁻⁶⁰ (see Statistics).

The clinical features of the 11 PPP2R5D cases and the 5 PPP2R1A cases are summarized in Tables 2 and 3, respectively. Despite mutations occurring in 2 different PP2A subunit genes with different biochemical functions (regulatory and scaffolding), there are clinical similarities between the cases. All patients were born after a normal pregnancy, and 15/16 cases had birth weights within normal range. In 2 cases, breech deliveries were reported, and in 2 other cases, emergency cesarean sections had to be performed. After birth, ID and hypotonia were common features in all cases. Despite pronounced and long-lasting hypotonia, feeding difficulties were usually not a major problem, and only one case had gastrosomy. In 12/16 cases, the degree of ID was severe, and this correlated with very late independent walking, usually around age 6–7 years. The exceptions were the 4 patients with E200K, P201R, or W207R mutations (see below for functional explanation), who learned to walk between 1½ and 2¼ years of age and had mild/moderate ID (Table 2). These 4 cases were also the only ones with language development beyond a few words. Seven out of 16 patients had epilepsy, including one of the mild ID cases. Only one patient had short stature (case 1 with a P53S mutation), head circumferences of routine diagnostics. In 11 cases, de novo missense mutations in PPP2R5D, encoding the regulatory B56δ PP2A subunit, were found. In 5 other cases, a de novo missense mutation in PPP2R1A, encoding the scaffolding Aα subunit of PP2A, was found. Six mutations and 2 mutations in PPP2R5D were identical, and 3 PPP2R1A mutations were identical. Details on all mutations can be found in Table 1. Other trio exome sequencing results indicating a de novo change of possible relevance or a recessive condition of potential interest can be found in Supplemental Table 1 (supplemental material available online with this article; doi:10.1172/JCI79860DSI). In 10 cases, such findings were made, but based on bioinformatic evaluation of the variants and the clinical features of the patients, all but one of these findings could easily be excluded as causative factors for the phenotype. The exception was case 15, which had heterozygosity for a TMEM67 splice mutation and a few signs that were compatible with a ciliopathy (e.g., unilateral postaxial polydactyly). However, this could also be a random finding, since a second TMEM67 mutation was not found upon Sanger sequencing. In addition, detecting the same de novo missense mutations in patients with identical clinical features is, in itself, evidence in support of causality, especially when supported by functional data (see below). As a crude estimation, the likelihood of finding 10 de novo missense mutations in the same 9–amino acid stretch of B56δ by chance should be less than 10⁻⁶⁰ (see Statistics).

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The finding of recurrent and clustered de novo missense mutations in 2 PP2A subunit genes (PPP2R5D and PPP2R1A) suggested a dominant-negative– or gain-of-function–related disease mechanism, rather than haploinsufficiency or loss-of-function. All but one of the PPP2R5D mutations (E198K, E200K, P201R, W207R, and E200K) were identical, and 3 mutations in PPP2R5D encoding the scaffolding Aα subunit of PP2A were found. Six mutations in PPP2R5D and one in PPP2R1A were identical; 3 of the 5 mutations in PPP2R1A, 6 mutations in PPP2R5D and all but one of the B56δ mutations had the potential to hinder access of catalytically competent C subunits to B56δ-regulated substrates, suggesting a common dominant-negative disease mechanism mainly affecting B56δ-regulated Ser/Thr dephosphorylation.

## Table 1. De novo mutation details and the corresponding cases

<table>
<thead>
<tr>
<th>Cases</th>
<th>Gene</th>
<th>Genomic change</th>
<th>cDNA change</th>
<th>Protein change</th>
</tr>
</thead>
<tbody>
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<td>PPP2R5D</td>
<td>chr6:g.42974253T&gt;A</td>
<td>c.157C&gt;T</td>
<td>p.Trp207Arg</td>
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<tr>
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<td>PPP2R5D</td>
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<td>c.592G&gt;A</td>
<td>p.Glu200Lys</td>
</tr>
<tr>
<td>8–9</td>
<td>PPP2R5D</td>
<td>chr6:g.42975009G&gt;A</td>
<td>c.598G&gt;A</td>
<td>p.Pro201Arg</td>
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<td>c.602C&gt;G</td>
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<td>c.610T&gt;A</td>
<td>p.His204Arg</td>
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<tr>
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<td>c.536C&gt;T</td>
<td>p.Pro179Leu</td>
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<td>13–15</td>
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<td>p.Arg182Trp</td>
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<td>c.773C&gt;A</td>
<td>p.Arg258His</td>
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*Genomic positions are according to Build37/hg19. cDNA reference sequences: NM_006245.2 for PPP2R1A and NM_014225.5 for PPP2R1A.*
further strengthening our working hypothesis that a charge change in the acidic B56δ loop could be pathogenic.

Our cellular binding assays with Glutathione S-Transferase–tagged (GST-tagged) B subunits and HemAgglutinin-tagged (HA-tagged) WT or mutant Aα subunits revealed that all 3 PPP2R1A mutations also affected PP2A holoenzyme formation (Figure 3). Surprisingly, interaction with the C subunit was hindered, despite the Aα mutations being in HEAT domains predicted to interact with B (Figure 3A). The mutations’ effect on B subunit binding was complex (Figure 3B). All Aα mutants lacked significant binding to the B55α (also called B) family members tested (isoforms B55α and B55β), as well as to the B56 (also called B’ or PR61) family members tested (B56α and B56γ). On the other hand, binding to B56δ was almost entirely retained, whereas B56ε bound significantly less. For PR72, a member of the B’’ family of PP2A regulatory subunits, binding was retained to Aα-P179L but was completely lost to the Aα-R182W and Aα-R258H mutants (Figure 3B). These (mutant) Aα binding characteristics were confirmed for endogenous B55α and B56δ subunits, for which good-quality, isoform-specific antibodies are available (Figure 4A). These data could be compatible with a dominant-negative effect on, notably, B56δ for all Aα mutants, and on PR72

and W207R) clustered in a highly conserved acidic loop that faces the A and C subunits (4–6). This acidic surface corresponds to the extended loop between α-helices 3 and 4 of HEAT domain 2 in the crystal structure of the highly related B56γ isoform (Figure 2A). Only the P53S mutation (case 1 in Table 2) localized outside this loop, i.e., in the B56δ-specific N-terminal domain.

To investigate if the PPP2R5D missense mutations affected subunit interactions, a human embryonic kidney cell line — HEK293 cells, a well-known model from previous PP2A subunit interaction studies (7) — was transfected with EGFP-tagged WT or mutant B56δ subunits in order to study subunit interactions. All ID-associated B56δ mutants except P53S showed deficient holoenzyme formation, i.e., A- or C-to-B56δ association (Figure 2B). To check if others had discovered missense variants in the same acidic B56δ loop, Broad institute’s ExAC browser (http://exac.broadinstitute.org/) was consulted. Only 2 other missense variants (P196L and P201S) were reported. Interestingly, the latter variant was in the same residue as the de novo mutation (P201R) in case 10, although the amino acid change was different. Unlike P201R, we found that P201S failed to show any significant A or C binding defects (Supplemental Figure 1), further strengthening our working hypothesis that a charge change in the acidic B56δ loop could be pathogenic.

Our cellular binding assays with Glutathione S-Transferase–tagged (GST-tagged) B subunits and HemAgglutinin-tagged (HA-tagged) WT or mutant Aα subunits revealed that all 3 PPP2R1A mutations also affected PP2A holoenzyme formation (Figure 3). Surprisingly, interaction with the C subunit was hindered, despite the Aα mutations being in HEAT domains predicted to interact with B (Figure 3A). The mutations’ effect on B subunit binding was complex (Figure 3B). All Aα mutants lacked significant binding to the B55 (also called B) family members tested (isoforms B55α and B55β), as well as to the B56 (also called B’ or PR61) family members tested (B56α and B56γ). On the other hand, binding to B56δ was almost entirely retained, whereas B56ε bound significantly less. For PR72, a member of the B’’ family of PP2A regulatory subunits, binding was retained to Aα-P179L but was completely lost to the Aα-R182W and Aα-R258H mutants (Figure 3B). These (mutant) Aα binding characteristics were confirmed for endogenous B55α and B56δ subunits, for which good-quality, isoform-specific antibodies are available (Figure 4A). These data could be compatible with a dominant-negative effect on, notably, B56δ for all Aα mutants, and on PR72
Table 2. Clinical features in cases with de novo PPP2R5D missense mutations

<table>
<thead>
<tr>
<th>Mutation</th>
<th>Case 1</th>
<th>Case 2</th>
<th>Case 3</th>
<th>Case 4</th>
<th>Case 5</th>
<th>Case 6</th>
<th>Case 7</th>
<th>Case 8</th>
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<td>10 yr</td>
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<td>2 yr</td>
<td>20 yr</td>
<td>4 yr</td>
<td>3 yr</td>
<td>9 yr</td>
</tr>
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<td>Normal</td>
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<td>Emergency C/S</td>
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<td>Amniotic rupture</td>
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<td>5th</td>
<td>25th</td>
<td>20 cm &lt; 3rd</td>
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<td>Head circumference</td>
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<td>5 cm &gt; 97th at age 3½ yr</td>
<td>50th</td>
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<td>Other findings</td>
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<td>Hypoglycemia</td>
<td>Abnormal fat oxidation</td>
<td>Bilateral 6th nerve palsies</td>
<td>Narrow palate</td>
<td>Mild 2/3 and 3/4 finger syndactyly</td>
<td>Scoliosis</td>
<td>Neonatal nonepileptic myoclonus</td>
<td>Fatigue</td>
<td>Ptosis</td>
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</table>

Height, head circumference, and weight are measured relative to centiles (the 3rd and 97th centile correspond to ± 2 SD). Abbreviations: ID/DD, intellectual disability/developmental delay; y, years; -, unknown or not done; SGA, small for gestational age; C/S, cesarean section; CC, corpus callosum.

Discussion

The presented work demonstrates that de novo missense mutations in genes encoding PP2A subunits may cause syndromic ID — and for Aα-P179L, provided that C binding would be lost or diminished in the B56α-Aα mutant complex. To provide direct evidence that mutant Aα can complex with B56δ without C, we expressed HA-Aα mutants or HA-Aα (WT) in HEK293 cells stably expressing EGFP-TEV-B56δ (WT) and analyzed the presence of endogenous C in anti-HA immunoprecipitates from the tobacco etch virus–cleaved (TEV-cleaved) eluates of GFP-trapped B56δ (Figure 4B). While C subunit was clearly present in B56δ (WT) complex (as expected from normal holoenzyme formation), it was barely detectable in the B56δ (P179L, P53S, E198K) or Aα (P179L, R182W) mutants tested appeared more long-lived than the WT subunits in our assay (Supplemental Figure 2).

Taken together, for all but one (P53S in PPP2R5D) of the de novo mutations identified, our biochemical data are consistent with a common defect in PP2A-B56δ–dependent dephosphorylation. A-C binding–defective B56δ mutants, or C binding–but not B56δ binding-defective Aα-mutants, and B56δ binding Aα-mutants harboring a catalytically impaired C subunit, may all block dephosphorylation of PP2A-B56δ–specific substrates and interfere with phosphorylation–dephosphorylation dynamics in the brain. In line with this hypothesis, overexpression of the E198K B56δ mutant or the R182W Aα mutant in HEK293 cells resulted in increased phosphorylation of GSK-3β Ser9, an established PP2A-B56δ substrate in this cell line (Figure 5 and ref. 10).

Discussion

The presented work demonstrates that de novo missense mutations in genes encoding PP2A subunits may cause syndromic ID — and
probably also nonsyndromic ID, since the facial dysmorphism in these cases is subtle (Figure 1). The \textit{PPP2R2D} and \textit{PPP2R1A} mutations disrupt B56δ-dependent dephosphorylation dynamics and link PP2A dysfunction to congenital brain dysfunction.

In general, the Aα cases were more severely affected than the B56δ cases. All had severe ID, absent speech, diminished brain growth, and partial or complete agenesis of the corpus callosum (Table 3). This is in line with the expected greater difficulty to compensate for a general scaffolding (A) subunit dysfunction than a specific regulatory (B) subunit dysfunction, as reflected by our biochemical data showing additional loss or reduction of holoenzyme assembly of many different PP2A complexes (B55α, B55β, B56α, B56γ, and B56δ) for these Aα mutants (Figure 3B).

The Aα scaffolding subunit is highly flexible, composed of 15 tandem repeat HEAT motifs (11) that mediate interactions with a regulatory B subunit (HEAT repeats 1-8) and the C subunit (HEAT repeats 11-15)(4, 5, 12, 13). Two ID-associated \textit{PPP2R1A} mutations (P179L and R182W) cluster in HEAT domain 5 of Aα, and one (R258H) occurs in HEAT domain 7; these mutations are involved in contacts with subunits of all B families (4, 5, 12, 13). However, for these mutations, loss-of-function might be less critical than substrate protection and altered phosphorylation dynamics; hence, the retained binding to PR72 for Aα-P179L could have additional functional consequences due to sequestration of PR72 in a complex deficient in C subunit binding or with decreased specific activity of C.

Besides its scaffolding function, Aα is a major player in the biogenesis of active PP2A holoenzymes (14). This highly regulated but incompletely understood process does not only involve simple trimeric assembly of the A, B, and C subunits, but it also involves several activation steps of the C subunit, which is de novo translated as an inactive enzyme (15). It has been suggested that some of these activation steps require or are facilitated by the A subunit (16, 17), explaining why A-subunit mutations may affect the specific activity of the associated C subunit, as observed here within the B56δ-(mutant A)-C complexes (Figure 4C). Additional activity measurements performed directly in anti-HA immunoprecipitates of HA-tagged (mutated) A subunits seem to further confirm this hypothesis (Supplemental Figure 3). Hence, it can be further rationalized why mutations in the A subunit have a much more severe effect on the PP2A system as a whole, as opposed to mutations in B56δ, which affect a single PP2A holoenzyme complex.

\textit{PPP2R2D} encodes the longest isoform of the B’ family of PP2A regulatory subunits and harbors unique N- and C-terminal extensions, which are predicted to be important for substrate recognition and/or subcellular targeting (18). Ten out of 11 \textit{PPP2R2D} mutations were located in a conserved acidic loop of B56δ needed for holoenzyme formation (Table 1), and all mutations introduced a positively charged residue (either arginine or lysine). Only one mutation (P53S) was atypical, and this case also had a different clinical picture: it was the only \textit{PPP2R2D} case with short stature in Table 2. In theory, P53S in the B56δ-specific N-terminal domain might change the PP2A-B56δ interaction with relevant substrates or introduce a new phosphorylation site that affects regulation by protein kinases. Such changes could easily have a gain-of-function or dominant-negative effect.

We also observed a correlation between the degree of biochemical disturbance and clinical severity. Among the \textit{PPP2R2D} cases (Table 2), the 6 patients with E198K mutations were the most severely affected, in line with a near absence of A and C subunit binding. The least-affected individuals were the E200K mutations, both with mild ID correlating with some residual A and C subunit binding (Figure 2B). Notably, E198 is the only one of the 5 mutated residues that directly interacts with the catalytic subunit (Figure 2A and refs. 4-6). Additionally, since all B subunits,
except B56δ and PR72, have been shown to make stabilizing contacts with the C subunit tail (5, 19). PR72, in HEK293 cells (Figure 5), but also with subcellular δ mutants may still form complexes with B56δ, and thereby with control of localized anchoring of PP2A via B56δ subunits may not only interfere in a dominant manner with B56δ, and indirectly by PP2A-B56δ–dependent activation through Thr-75 dephosphorylation (24). B56δ has several sites for PKA phosphorylation that activate PP2A-B56δ phosphatase activity (24, 29).

...for GSK-3α activity (31) of tyrosine hydroxylase, the rate-limiting enzyme in catecholamine synthesis. Which of these candidate substrates will be further determined in appropriate cellular and animal models.

...functions (25) — and lack of nuclear PP2A-B56δ targeting has consequences for regulation of localized signaling. One example could be the signaling complex scaffolded by the neural variant of the cAMP-dependent PKA anchoring protein mAKAP, that binds B56δ and several other phosphatases (PP1, PP2B) and kinases (PKA, PDK1, RSK3, ERK5) (26, 27). Dephosphorylation of PP2A-B56δ substrates may also be hindered, e.g., the transcription factor and PKA-substrate HAND (28), the neural cyclin-dependent kinase 5 (CDK5) activator CDK5R1 (21), and DARPP-32 (24, 25). PKA activates DARPP-32 directly by Thr-34 phosphorylation and indirectly by PP2A-B56δ–dependent activation through Thr-75 dephosphorylation (24). B56δ has several sites for PKA phosphorylation that activate PP2A-B56δ phosphatase activity (24, 29). Moreover, PKA-activated PP2A-B56δ–dependent dephosphorylation of another DARPP-32 phosphorylation site (Ser-97) induces nuclear import — mediating dopamine-dependent epigenetic functions (25) — and lack of nuclear PP2A-B56δ targeting has been associated with juvenile myoclonic epilepsy (30). There is also evidence that PP2A-B56δ regulates both expression (30) and activity (31) of tyrosine hydroxylase, the rate-limiting enzyme in catecholamine synthesis. Which of these candidate substrates will eventually be of pathologic relevance in our ID patients remains to be further determined in appropriate cellular and animal models.

A model for a common dominant-negative effect of mutant B56δ and Aα subunits is depicted in Figure 6. This model explains why all our biochemical findings are compatible with B56δ-dependent PP2A dysregulation. Our model is also supported by a recent paper showing that Aα can form a tight complex in vitro with members of the B1” subunit family, including PR72, in

Table 3. Clinical features in cases with de novo PPP2R1A missense mutations

<table>
<thead>
<tr>
<th>Mutation</th>
<th>Case 12</th>
<th>Case 13</th>
<th>Case 14</th>
<th>Case 15</th>
<th>Case 16</th>
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<tbody>
<tr>
<td>Age of examination</td>
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<td>4 yr</td>
<td>11 yr</td>
<td>1 yr</td>
<td>5 yr</td>
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<td>Male</td>
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<td>Normal</td>
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<td>Normal</td>
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<td>Normal</td>
<td>Normal</td>
<td>Normal</td>
</tr>
<tr>
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<td>Present</td>
<td>Present</td>
<td>Present</td>
<td>Present</td>
</tr>
<tr>
<td>Walked unsupported</td>
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<td>Not so far</td>
<td>Not so far</td>
<td>Not so far</td>
<td>3 yr</td>
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<td>Severe</td>
<td>Severe</td>
<td>Severe</td>
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<tr>
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<td>&lt;97th</td>
<td>50th</td>
<td>75th</td>
<td>90th</td>
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<td>98th &gt; 75th</td>
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<td>97th</td>
<td>10th</td>
<td>16th</td>
<td>97th</td>
</tr>
<tr>
<td>Brain MRI</td>
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<td>CC hypoplasia</td>
<td>CC hypoplasia</td>
<td>CC agenesis</td>
<td>Delayed myelisation</td>
</tr>
<tr>
<td>Other findings</td>
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<td>Scoliosis</td>
<td>Scoliosis Hip dysplasia</td>
<td>Hypermobility</td>
<td>Physically strong</td>
</tr>
</tbody>
</table>

Height, head circumference, and weight are given relative to centiles (the 3rd and 97th centile correspond to ± 2 SD). Abbreviations: y, years; CC, corpus callosum; C/S, cesarean section; –, unknown or not done.
Figure 3. Binding of mutant and WT Aα to C and B subunits. (A) PP2A-C subunit binding assays: HA-tagged WT Aα, 3 ID-associated Aα mutants (P179L, R182W, and R258H), or an empty HA-vector (−) were transfected into HEK293 cells. Following anti-HA immunoprecipitation, the presence of endogenous C subunit in the immunoprecipitates was examined by immunoblotting (IB). After quantification of the band intensities with ImageJ software, the ratios between HA and C signals were determined and calculated relative to WT Aα control. Mean values and a representative image of 3 independent experiments are shown (1-way multiple-comparisons ANOVA, **P < 0.01). (B) PP2A B subunit binding assays: Several GST-tagged B subunits, belonging to 3 different families (B55 or B, B56 or B′, and B′) or GST alone (−) were coexpressed in HEK293 cells with HA-tagged WT Aα, or ID-associated Aα-P179L, R182W, and R258H mutants. The presence of HA-Aα (WT or mutant) in the complete lysates and the isolated GST pulldown complexes was determined by IB. After quantification of the band intensities with ImageJ software, the ratios between GST and HA signals were determined and calculated relative to WT Aα control (which were set to 100% for each B-type subunit pulldown). Mean values and a representative image of 3 independent experiments are shown (1-way multiple-comparisons ANOVA; *P < 0.05, **P < 0.01, ***P < 0.001).
the absence of the C subunit (32). It may be of interest to study if fingolimod (FTY720), a PP2A activator and immunosuppressant that is licensed for treatment of multiple sclerosis (33–35), or if fingolimod (FTY720), a PP2A activator and immunosuppres-

the most prevalent mutations. A growth advantage may also explain mutation recurrence if these de novo mutations turn out to be solely paternal (40). Since 88% of the cancer-associated Aα mutations are of the missense-variant, a dominant-negative effect also in cancer promotion is likely. None of our patients have been diagnosed with or treated for cancer. The cancer risk might not be increased, in line with what is usually the case for congenital gain-of-function mutations in other cancer-related pathways like the RAS/MAPK pathway or the PI3K/akt cascade. Only further patients and patient follow-ups will answer this question, but a major cancer risk seems unlikely.

The tumor-suppressor effect of PP2A may operate by KRAS/MAPK cascade inhibition, KRAS/ARF/TP53 cascade inhibition, or PI3K/akt/TP53 cascade inhibition (33). Somatic mosaic activation of the PI3K/akt cascade causes the megalencephaly-capillary malformation-polymicrogyria (MCAP) and megalencephaly-polymicrogyria-polydactyly-hydrocephalus (MPPH) group of overgrowth syndromes (41).

These patients have variable ID, a tendency to develop hydrocephalus and epilepsy, and dysmorphic facial features, including frontal bossing with hypotonia, tented upper lip, and deep-set eyes. The latter features are shared with several of our patients (Figure 1). It is therefore relevant to consider B56δ-dependent PP2A dysregulation syndrome (which we propose to be designated B56δeltopathies) among the differential diagnoses to the MCAP/MPPH group of syndromes, at least in some cases. It is conceivable that the B56δ mutations may affect only a subgroup of PP2A substrates located distally in the PIK3 signaling cascade — such as OSK-3β Ser9, a well-established Akt phosphorylation site — since the proximal steps do not appear to be subject to B56δ-dependent dephosphorylation (42).

In summary, we have demonstrated that de novo missense mutations in the PPP2R3D and PPP2R1A genes encoding PP2A subunits represent a new mechanism for ID, due to disrupted B56δ-dependent dephosphorylation dynamics and PP2A dysfunction.

Methods

Case detection. There were 7 Dutch patients (from RUMC: cases 1, 8–9, and 11; from UMC Utrecht: cases 7, 15, and 16). Six of these cases were identified through routine diagnostic exome sequencing.

For future evaluation of de novo mutation origin (paternal or maternal) (37), it is of interest that all 3 PPP2R1A mutations also are found in the Sanger Institute’s Catalogue of Somatic Mutations in Cancer (the COSMIC database; http://cancer.sanger.ac.uk/cosmic), mainly in endometrial and ovarian cancers (38, 39). Aα P179L/P179R, R182W, and R258H are by far
Variations (CNVs) in the child, and exome sequencing to investigate single nucleotide polymorphisms (SNPs) and small insertions/deletions (indels). Putative de novo sequence variants were validated using targeted Sanger sequencing of blood-sample DNA. All genomic variants were annotated with the most severe consequence predicted by Ensembl Variant Effect Predictor (VEP) (45) and their minor allele frequencies observed in diverse population samples. Likely, diagnostic variants were fed back to referring clinical geneticists for validation and discussion with the family via the patient’s record in Database of Chromosomal Imbalance and Phenotype in Humans Using Ensembl Resources (DECIPHER; Ensembl) (46), where they can be viewed in an interactive genome browser. Full genomic datasets were also deposited under accession number EGAS00001000775 in the European Genome-Phenome Archive (www.ebi.ac.uk/ega).

The de novo PPP2R5D mutations in the Norwegian (case 2) and Israeli (case 6) patients were identified by exome sequencing of parent-child trios in a diagnostic setting. Only the PPP2R5D variant remained as true de novo after filtering and verification by Sanger sequencing of blood DNA, and no pathogenic copy number changes were detected by a high-resolution copy number array. Biochemical investigations. To study the functional consequences of the de novo missense mutations, WT Aα and B56δ (isoform 1) cDNAs were cloned into HA-tag (pMB001) and EGFP-tag (pEGFP-P-C1) eukaryotic expression vectors, respectively. The different PI2A B-subunit cDNAs were in a GST-tag eukaryotic expression vector, as described (19). PCR-based site-directed mutagenesis (Stratagene) was performed directly in the pMB001 or pEGFP vectors with proof-
All mutations were confirmed by sequencing (LGC Limited). Thereafter, HEK293 cells (ATCC) were transfected with PEI transfection reagents according to standard protocol. Forty-eight hours after transfection, cells were rinsed with PBS, lysed in 200 μL NET buffer (50 mM Tris pH 7.4, 150 mM NaCl, 15 mM EDTA, and 1% Nonidet P-40) containing protease and phosphatase inhibitor cocktail (Roche Applied Science), and centrifuged for 15 minutes at 13,000 g. In case phosphatase activity needed to be measured, phosphatase inhibitors were omitted from the lysis buffer.

For EGFP trapping, cell lysates were incubated at 4°C for 1 hour with wash buffer (10 mM Tris-HCl pH 7.5, 0.5 mM EDTA, and 150 mM NaCl) and 15 μL of NET-100 buffer (20 mM Tris HCl pH 7.4, 1 mM EDTA, and 1% Nonidet P-40) containing protease and phosphatase inhibitor cocktail (Roche Applied Science), and centrifuged for 15 minutes at 13,000 g. In case phosphatase activity needed to be measured, phosphatase inhibitors were omitted from the lysis buffer.

For GST pulldown, cell lysates were incubated at 4°C for 1 hour with NET-100 buffer (20 mM Tris-HCl pH 7.4, 1 mM EDTA, and 1% Nonidet P-40, 25% glycerol, and 100 mM NaCl) containing 1 mg/mL bovine serum albumin and 2 μL glutathione-Sepharose beads (GE Healthcare) on a rotating wheel. The beads were washed 4 times with 0.3 mL of wash buffer.

For HA immunoprecipitation, the lysates were precleared with Protein A-Sepharose beads (GE Healthcare) for 1 hour, and incubated overnight at 4°C with 0.2 mL of NET-100 buffer (20 mM Tris-HCl pH 7.4, 1 mM EDTA, and 1% Nonidet P-40) containing a polyclonal population of HEK293 cells stably expressing EGFP-TEV-B56δ was used (selected with 2 μg/mL puromycin). The EGFP-TEV expression vector was a gift of E. Heroes (KU Leuven, Leuven, Belgium). Forty-eight hours after transfection with HA-Au (pMB001) or HA-mutant Au (pMB001), EGFP trapping was performed, and the trapped complexes were incubated overnight at 4°C with 0.2 μg/μL of recombinant TEV protease in TEV cleavage buffer (TBS, 1 mM DTT, 0.5 mM EDTA). Following addition of EDTA (1 mM), PMSF (1 mM), and TLCK (1 mM), the TEV eluates were subjected to HA immunoprecipitation with HA-agarose beads and the washed immunoprecipitates were analyzed by immunoblotting with anti-HA, anti–PP2A-C, and anti-B56δ antibodies (20, 21).

For PP2A activity measurements, the HA-agarose beads were washed once more with 20 mM Tris-HCl pH 7.4 plus 1 mM DTT, and finally resuspended in 60 μL enzyme dilution buffer (catalog 20-169, Millipore). All assays were performed with 20 μL of this phosphatase suspension and 4.5 μL of 2 mM stock of K-R-ppT-I-R-R phosphopeptide (catalog 12-219, Millipore) for 10–60 minutes at 30°C (still in the linear range of the assay). The released free phosphate was determined by the addition of malachite green solution (10/1 mix of solution A [catalog 20-105, Millipore] and solution B [catalog 20-104, Millipore]). After 15 min incubation at room temperature, absorbance at 630 nm was measured in a multi-channel spectrophotometer. Pico- molar amounts of phosphate released were calculated by comparison with a standard curve of known KH2PO4 concentrations, as outlined in the manufacturer’s instructions (Ser/Thr Phosphatase Assay Kit 1, Millipore). Specific phosphatase activity was obtained by correcting
these absolute values for amount of C present in the samples, as determined by immunoblotting with anti-C antibodies and quantification of the signals by ImageJ software.

For protein-stability analysis, HEK293 cells were transfected with EGFP-B56 (WT); with EGFP-B56-P53S or EGFP-B56-E198K mutants (pEGFP-C1); or with HA-αs (WT), HA-αs-R182W, or HA-αs-P179L mutants (pMB001), one 10 cm plate per plasmid. Twenty-four hours after transfection, each 10-cm plate was split over 6 wells on a 6-well plate, in which eventually 50 µM cycloheximide (CHX, Sigma-Aldrich) was added per well to block translation. Following incubation with CHX for different time points (0, 10, and 24 hours), whole-cell lysates were prepared in NET lysis buffer and further analyzed by immunoblotting with anti-vinculin mouse monoclonals (Sigma-Aldrich), anti-HA, or anti-GFP antibodies. Band intensities were quantified using ImageJ software.

Statistics. Statistical analysis of biochemical data was done with 1-way multiple-comparisons ANOVA, and P < 0.05 was considered to be significant.

The calculation of the chance likelihood for finding 10 de novo mutations in the same 9–amino acid stretch of B56δ was based on the following assumptions: The target size is <10<sup>-6</sup> of the total ORF size, the number of random missense changes per generation is on average 1, and the index is removed from the equation. This gives a chance likelihood of less than (10<sup>-6</sup>)<sup>9</sup>, or <10<sup>-54</sup>, not taking the lack of similar variants in ExAC into account. The chance of finding a similar variant in the whole ID dataset by chance is about 2 × 10<sup>-5</sup>, assuming that about 2,000 ID cases were tested. In that case, the phenotype should also be random, and this was not the case.

Study approval. The DDD study has UK Research Ethics Committee (REC) approval (10/H0305/83, granted by the Cambridge South REC, and GEN/284/12 granted by the Republic of Ireland REC). In other cases, ascertainment of patients was part of the clinical routine. All patients’ families have consented to publication of clinical findings. Written informed consent was also obtained for publication of all facial photographs presented in Figure 1.

Acknowledgments

The DDD study presents independent research commissioned by the Health Innovation Challenge Fund (HICF-1009-003), a parallel funding partnership between the Wellcome Trust and the Department of Health, and the Wellcome Trust Sanger Institute (WT098051). For details on the members of the study, see Supplemental Table 3. The views expressed in this publication are those of the author(s) and not necessarily those of the Wellcome Trust or the Department of Health. The research team acknowledges the support of the NIH Research, through the Comprehensive Clinical Research Network. Concerning the biochemical studies, we thank S. Dilworth for the gift of monoclonal PP2A-A subunit antibody and E. Heroes for the TEV-EGFP eukaryotic expression vector. Funding was provided by the UK Leuven Research Fund (OT/13/094 to V. Janssens), the Research Foundation Flanders (G.0582.11 to V. Janssens), and the IAP program of the Belgian federal government (P7/13 to V. Janssens). D. Haesen received a fellowship of the Flemish Agency for Innovation by Science and Technology (IW-T). A. Hoischen was supported by the Netherlands Organization for Health Research and Development (ZonMW 916-12-095). G. Houge was supported by HelseVest grant 911744.

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