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

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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 PPP2RD5 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 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 hypertelorism, and downslanting 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 PPP2R5D-encoded B56δ regulatory subunit, with the same E198K mutation present in 5 individuals. Five patients had mutations in the PPP2R1A-encoded scaffolding Aα subunit, with the same R182W mutation in 3 individuals. Some Aα 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 Aα 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.

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Authorship note: Gunnar Houge and Dorien Haesen contributed equally to this work.

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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 *A*-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 (supplementary material available online with this article; doi:10.1172/JCI79860DS1). 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 10⁻⁶⁵ (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 gastrostomy. 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 *PPP2R5D* 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), who learned to walk between 1½ and 2¼ years of age 6–7 years. The exceptions were the 4 patients with E200K, P201R, or W207R *PPP2R5D* 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, see Table 2), and he was the only *PPP2R5D* case that was microcephalic. In the other *PPP2R5D* cases, head circumferences were from upper-normal range to pronounced macrocephaly, and in the latter cases, hydrocephalus was suspected. In contrast, most *PPP2R1A* cases were normocephalic or microcephalic, and hydrocephalus was initially suspected in only one case (Table 3). In all these patients, the corpus callosum was absent or almost absent, a feature that distinguished *PPP2R1A* cases from *PPP2R5D* cases. In contrast, facial features were overlapping (Figure 1): A hypotonic and sometimes also elongated face with tented upper lip, mild hypertelorism with downslanting palpebral fissures, and frontal bossing in the *PPP2R5D* cases.

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,

### 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>
<tr>
<td>1</td>
<td>PPP2R5D</td>
<td>chr6:g.42974253C&gt;T</td>
<td>c.157C&gt;T</td>
<td>p.Pro53Ser</td>
</tr>
<tr>
<td>2–7</td>
<td>PPP2R5D</td>
<td>chr6:g.42975003G&gt;A</td>
<td>c.592G&gt;A</td>
<td>p.Glu198Lys</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.Glu200Lys</td>
</tr>
<tr>
<td>10</td>
<td>PPP2R5D</td>
<td>chr6:g.42975013G&gt;C</td>
<td>c.602G&gt;C</td>
<td>p.Pro204Arg</td>
</tr>
<tr>
<td>11</td>
<td>PPP2R5D</td>
<td>chr6:g.42975030T&gt;A</td>
<td>c.619T&gt;A</td>
<td>p.Trp207Arg</td>
</tr>
<tr>
<td>12</td>
<td>PPP2R1A</td>
<td>chr19:g.52715971C&gt;T</td>
<td>c.536C&gt;T</td>
<td>p.Pro179Leu</td>
</tr>
<tr>
<td>13–15</td>
<td>PPP2R1A</td>
<td>chr19:g.52715979C&gt;T</td>
<td>c.544C&gt;T</td>
<td>p.Arg182Trp</td>
</tr>
<tr>
<td>16</td>
<td>PPP2R1A</td>
<td>chr19:g.52716229G&gt;A</td>
<td>c.773G&gt;A</td>
<td>p.Arg258His</td>
</tr>
</tbody>
</table>

*aGenomic positions are according to Build37/hg19. *b* cDNA reference sequences: NM_006245.2 for *PPP2R5D* and NM_014225.5 for *PPP2R1A.*
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 B56δ 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 B55α (also called B) family members tested (isoforms B55α and B55β), as well as to the B56δ-specific N-terminal domain.

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Table 2. Clinical features in cases with de novo PPP2R5D missense mutations

<table>
<thead>
<tr>
<th>Case</th>
<th>Mutation</th>
<th>Age of examination</th>
<th>Sex</th>
<th>Delivery</th>
<th>Birth weight</th>
<th>Hypotonia</th>
<th>Walked unsupported</th>
<th>Ataxic gait</th>
<th>Language</th>
<th>Epilepsy</th>
<th>EEG</th>
<th>ID/DD</th>
<th>Hypoglycemia</th>
<th>Fatigue</th>
<th>Narrow palate</th>
<th>Scoliosis</th>
<th>Other findings</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>P53S</td>
<td>53 yr</td>
<td>Male</td>
<td>Normal</td>
<td>Normal</td>
<td>Not reported</td>
<td>9 yr</td>
<td>No</td>
<td>No words</td>
<td>No</td>
<td>No</td>
<td>Severe</td>
<td>Abnormal</td>
<td>Present</td>
<td>Narrow palate</td>
<td>Present</td>
<td>Abnormal</td>
</tr>
<tr>
<td>2</td>
<td>E198K</td>
<td>5 yr</td>
<td>Female</td>
<td>Normal</td>
<td>Normal</td>
<td>Present</td>
<td>6 yr</td>
<td>Yes</td>
<td>3–4 words</td>
<td>No words</td>
<td>No</td>
<td>Severe</td>
<td>Normal</td>
<td>Yes</td>
<td>Narrow palate</td>
<td>Present</td>
<td>Abnormal</td>
</tr>
<tr>
<td>3</td>
<td>E198K</td>
<td>11 yr</td>
<td>Male</td>
<td>Emergency C/S</td>
<td>Normal</td>
<td>Present</td>
<td>Not so far</td>
<td>Yes</td>
<td>No words</td>
<td>No</td>
<td>No</td>
<td>Severe</td>
<td>Normal</td>
<td>Yes</td>
<td>Narrow palate</td>
<td>Present</td>
<td>Abnormal</td>
</tr>
<tr>
<td>4</td>
<td>E198K</td>
<td>10 yr</td>
<td>Male</td>
<td>Emergency C/S</td>
<td>Normal</td>
<td>Present</td>
<td>Not so far</td>
<td>Yes</td>
<td>No words</td>
<td>No</td>
<td>No</td>
<td>Severe</td>
<td>Normal</td>
<td>Yes</td>
<td>Narrow palate</td>
<td>Present</td>
<td>Abnormal</td>
</tr>
<tr>
<td>5</td>
<td>E198K</td>
<td>15 yr</td>
<td>Male</td>
<td>Normal</td>
<td>Normal</td>
<td>Present</td>
<td>6 yr</td>
<td>Yes</td>
<td>No words</td>
<td>No</td>
<td>No</td>
<td>Severe</td>
<td>Normal</td>
<td>Yes</td>
<td>Narrow palate</td>
<td>Present</td>
<td>Abnormal</td>
</tr>
<tr>
<td>6</td>
<td>E198K</td>
<td>13 yr</td>
<td>Male</td>
<td>Normal</td>
<td>Normal</td>
<td>Present</td>
<td>Not so far</td>
<td>Yes</td>
<td>No words</td>
<td>No</td>
<td>No</td>
<td>Severe</td>
<td>Normal</td>
<td>Yes</td>
<td>Narrow palate</td>
<td>Present</td>
<td>Abnormal</td>
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<tr>
<td>7</td>
<td>E198K</td>
<td>2 yr</td>
<td>Female</td>
<td>Normal</td>
<td>Normal</td>
<td>Present</td>
<td>7 yr</td>
<td>Yes</td>
<td>No words</td>
<td>No</td>
<td>No</td>
<td>Severe</td>
<td>Normal</td>
<td>Yes</td>
<td>Narrow palate</td>
<td>Present</td>
<td>Abnormal</td>
</tr>
<tr>
<td>8</td>
<td>E198K</td>
<td>20 yr</td>
<td>Male</td>
<td>Normal</td>
<td>Normal</td>
<td>Present</td>
<td>Not so far</td>
<td>Yes</td>
<td>No words</td>
<td>Yes, poor intelligibility</td>
<td>No</td>
<td>Severe</td>
<td>Normal</td>
<td>Yes</td>
<td>Narrow palate</td>
<td>Present</td>
<td>Abnormal</td>
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<tr>
<td>9</td>
<td>E200K</td>
<td>4 yr</td>
<td>Male</td>
<td>C/S</td>
<td>Normal</td>
<td>Present</td>
<td>1½ yr</td>
<td>No</td>
<td>No words</td>
<td>No</td>
<td>No</td>
<td>Severe</td>
<td>Normal</td>
<td>Yes</td>
<td>Narrow palate</td>
<td>Present</td>
<td>Abnormal</td>
</tr>
<tr>
<td>10</td>
<td>E200K</td>
<td>3 yr</td>
<td>Male</td>
<td>Breech</td>
<td>Normal</td>
<td>Present</td>
<td>2½ yr</td>
<td>No</td>
<td>No words</td>
<td>No</td>
<td>No</td>
<td>Severe</td>
<td>Normal</td>
<td>Yes</td>
<td>Narrow palate</td>
<td>Present</td>
<td>Abnormal</td>
</tr>
<tr>
<td>11</td>
<td>P201R</td>
<td>9 yr</td>
<td>Female</td>
<td>Normal</td>
<td>Normal</td>
<td>Present</td>
<td>1½ yr</td>
<td>No</td>
<td>No words</td>
<td>No</td>
<td>No</td>
<td>Severe</td>
<td>Normal</td>
<td>Yes</td>
<td>Narrow palate</td>
<td>Present</td>
<td>Abnormal</td>
</tr>
</tbody>
</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.

for Au-P179L, provided that C binding would be lost or diminished in the B56δ-Aα mutant complex. To provide direct evidence that mutant Au 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-Aα (WT) complex (as expected from normal holoenzyme formation), it was barely detectable in the B56δ-Aα-P179L complex, indicating that mutant Au-P179L may bind B56δ but not C. In contrast, the B56δ-Aα-R182W and B56δ-Aα-R258H1 complexes did not bind C at all. However, measurements of specific PP2A activity in these samples showed a decrease in phosphatase activity for all Au mutants compared with WT (Figure 4C), suggesting that the C subunit present in these B56δ-mutant A-C complexes is catalytically impaired.

Because previous reports had indicated increased B56δ subunit degradation upon gradual reduction of A subunit levels (8, 9), we examined the stability of our mutant subunits, since unstable mutant proteins would preclude the interpretation of our functional data. In line with our hypothesis, we did not experience any problems expressing ID-associated B56δ subunits in cells. Furthermore, protein-synthesis–blocking experiments showed that the ID-associated B56δ (P53S, E198K) or Au (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 Au-mutants, and B56δ binding Au-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 *PPP2R5D* and *PPP2R1A* mutations disrupt B56δ-dependent dephosphorylation dynamics and link PP2A dysfunction to congenital brain dysfunction.

In general, the Aa 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, B55δ, B56α, B56y, and B56ε) for these Aa mutants (Figure 3B). The Aa 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 *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.

*PPP2R5D* 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 *PPP2R5D* 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 *PPP2R5D* case with short stature (highlighted in white) are displayed with amino acid numbering according to B56δ. Note that the E198 residue directly contacts the C subunit. Color code: C subunit, blue; A subunit, yellow; B56δ, red. The structure was analyzed and visualized with Molsoft MolBrowser 3.7. (B) Cellular binding assays of ID-associated B56δ mutants and endogenous A and C subunits. EGFP-tagged WT B56δ, 5 ID-associated B56δ mutants (P53S, E198K, E200K, P201R, and W207R), or EGFP alone (−) were ectopically expressed in HEK293 cells. Following EGFP trapping, the presence of endogenous A and C subunits in the trapped complexes was examined by immunoblotting (IB). After quantification of the band intensities with ImageJ software, the ratios between EGFP and C signals—and between EGFP and A signals—were determined and calculated relative to B56δ WT control. Mean values and a representative image of 4 independent experiments are shown (1-way multiple-comparisons ANOVA; *P < 0.05, **P < 0.01).
Table 3. Clinical features in cases with de novo PPP2R1A missense mutations

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<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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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).
A

IB: HA (Aα)

IB: B56δ

IB: B56δ Lysates

IB: B55α Lysates

B

IB: HA (Aα)

IB: B56δ

IB: C

C

IB: C

Figure 4. Analysis of Aα mutant complexes. (A) Endogenous B subunit binding assays: HA-tagged WT Aα, Aα mutants (P179L, R182W, and R258H), or an empty HA-vector (−) were transfected into HEK293 cells. Following anti-HA immunoprecipitation, presence of endogenous B56δ and B55α subunits in the immunoprecipitates was examined by immunoblotting (IB). (B) Formation of B56δ-(mutant Aα)-C complexes: HEK293 cells stably expressing EGFP-TEV-B56δ were transfected with HA-Aα, HA-Aα mutants, or empty HA-vector (−). Following EGFP-trapping and cleavage of the trapped complexes with TEV protease, the eluates were subjected to HA immunoprecipitation and the immunoprecipitates analyzed by IB with anti-HA, anti-C, and anti-B56δ antibodies. After quantification of the band intensities (ImageJ), the ratios between C and HA signals were determined and calculated relative to WT Aα control (set to 100% in each IP-on-IP experiment). Mean values and a representative image of 4 independent experiments are shown (1-way multiple-comparisons ANOVA; *P < 0.05). (C) PP2A activity measurements in B56δ-(mutant Aα)-C complexes. The pmol number of released phosphate from K-R-pT-I-R-R phosphopeptide (350 μM) was determined by Malachite Green for each B56δ-(mutant Aα)-C complex (retrieved as in B). To obtain specific C activities, this number was divided by the amount of C in the respective samples, as determined by IB and following quantification by ImageJ software. All specific activities were eventually recalculated relative to WT Aα control (set to 100%). Mean values and one representative image of 3 independent experiments are shown (1-way multiple-comparisons ANOVA; **P < 0.01).

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 B56δdeltopathies) 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 PI3K signaling cascade — such as GSK-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 PPP2RSD and PPP2RIA 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.
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. Cases 1 and 11 have been previously published as part of studies showing the power and impact of next-generation sequencing–based (NGS-based) technologies in a clinical diagnostic setting without clinical details on the patients’ phenotypes or functional evaluation of the mutations (43, 44).

The 7 United Kingdom patients (cases 3–5, 10, and 12–14 in Tables 2 and 3) were recruited to the DDD study by the United Kingdom National Health Service or the Republic of Ireland Regional Genetics Service (3). Recruitment criteria were patients with neuromotor developmental disorders and/or congenital anomalies, abnormal growth parameters, dysmorphic features, and unusual behavior. DNA samples from patients and parents were analyzed by the Wellcome Trust Sanger Institute using high-resolution microarray analysis (array-CGH and SNP-genotyping) to investigate copy number variations (CNVs) in the child, and exome sequencing to investigate single nucleotide polymorphisms (SNPs) and small insertions/deletions (indels). Putative de novo 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).

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-C1) eukaryotic expression vectors, respectively. The different PPI2A 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 GFP-trap-A beads (ChromoTek GmbH) on a rotating wheel. The beads were washed 4 times with 0.3 mL of wash buffer.

For GST pulldown, cell lysates were incubated at 4°C for 1 hour with NENT 100 buffer (20 mM Tris-HCl pH 7.4, 1 mM EDTA, 0.1% Nonidet P-40, 25% glycerol, and 100 mM NaCl) containing 1 mg/mL bovine serum albumin and 25 μL glutathione-Sepharose beads (GE Healthcare) on a rotating wheel. The beads were washed 2 times with 0.3 mL of NENT 300, containing 300 mM NaCl.

For HA immunoprecipitation, the lysates were precleared with Protein A-Sepharose beads (GE Healthcare) for 1 hour, and incubated on a rotating wheel at 4°C for 2 hours with 1 μg HA antibody (Sigma-Aldrich) in TBS/1% Nonidet P-40. Protein A-Sepharose beads were added for 1 hour, and beads were washed 2 times in NENT 100 and 2 times in TBS/0.1% Nonidet P-40. Alternatively, 25 μL HA-agarose beads (Sigma-Aldrich) were directly added to the lysates and incubated on a rotating wheel in 500 μL TBS/0.1% Nonidet P-40 for 1.5 hours at 4°C. Beads were washed 4 times in TBS/0.1% Nonidet P-40.

In all cases, bound proteins were eluted by the addition of NuPAGE sample buffer (Invitrogen) and boiling. The eluted proteins were subsequently analyzed by SDS-PAGE on 4%-12% (wt/vol) Bis-Tris gels (Bio-Rad) and Western blotting. The membranes were blocked in 5% milk solution in TBS/0.1% Tween 20 for 1 hour at room temperature and subsequently incubated with the primary antibody overnight at 4°C. The following primary antibodies were used: mouse monoclonal anti-GST (Sigma-Aldrich), anti-HA (Sigma-Aldrich), anti-GFP (Corning), anti-PP2A-A subunit (supplied by S. Dilworth, Middlesex University, London, United Kingdom), anti-PP2A-C subunit (BD Biosciences); and rabbit polyclonal anti-B55α (Cell Signaling Technology), and anti-B56δ (20). After washing in TBS/0.1% Tween 20, the membranes were incubated at room temperature for 1 hour with horseradish peroxidase–conjugated secondary antibodies (Dako) and developed using a Pierce enhanced chemiluminescence detection system (Thermo Fisher Scientific). All densitometric quantifications were done with ImageJ software.

For the IP-on-IP approach, 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-pT-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. Picomolar 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-Aα (WT), HA-Aα-R182W, or HA-Aα-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 <10–6 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 (10–6)9, or <10 –54, 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 × 10–3, 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

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20. Martens E, et al. Genome organisation, chromo-
somal localisation tissue distribution and develop-


27. Ahn JH, McAvoY T, Rakhilin SV, Nishii A, Green-


