Mutations specific to the Rac-GEF domain of TRIO cause intellectual disability and microcephaly

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<td>microcephaly, Rac, TRIO, Db1, Rho GTPase</td>
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INTRODUCTION

Neurodevelopmental delay is genetically heterogenous and affects between 1% and 3% of the general population.[1] The utilisation of next generation genomic techniques such as Whole Exome Sequencing (WES) has facilitated the identification of numerous novel pathogenic variants implicated in the evolution of neurodevelopmental pathology.[2] One such gene on chromosome 5, TRIO, has recently been identified as a candidate for human neurodevelopmental delay.[3]

Neurodevelopment is a complex process requiring coordinated axonal guidance and neuronal migration to facilitate the delivery of neurons from the neuroepithelium to their synaptic target.[4,5] This process is driven by specific molecular cues which regulate the neuronal growth cone, residing at the tip of the axon.[5,6] Motility of the growth cone is, in part, regulated through remodelling of the actin cytoskeleton.[7,8]

Members of the Rho GTPase family are key modulators of cytoskeletal dynamics.[9,10] They play an essential role in neurodevelopment through the control of actin cytoskeleton dynamics, including motility of the growth cone.[11] Rho GTPases are activated by guanine nucleotide exchange factors (GEFs). TRIO encodes a guanine nucleotide exchange factor expressed ubiquitously in many tissues, including the central nervous system (CNS).[4,12] It is highly expressed in many areas of the developing brain including the cerebellum, cortex, hippocampi and thalami.[9,12] Interestingly, TRIO can be alternatively spliced, and as a result, can encode several isoforms whose expression is nervous-system specific.[9,13] Trio is thought to be one of the major regulators of neuronal development by controlling actin cytoskeleton remodelling through the activation of the GTPase Rac1.[14] The importance of Trio in neuronal development is further emphasised by the fact that total knock-out or specific deletion of TRIO in the mouse nervous system is embryonically lethal; embryos display defects in brain organisation and reduced brain size.[4,15] Deletion of TRIO, specifically in the hippocampus and in the cortex during early embryogenesis, results in aberrant organisation of these structures, impairing the learning ability of these mice.[12]

Our findings consolidate and extend the human phenotype recently reported by Ba et al.[3] Through the application of parent/offspring WES analysis, we report three children from across the UK with microcephaly and neurodevelopmental delay who harbour de novo missense mutations in TRIO. We also report a family with TRIO mutations that segregate autosomal dominantly. We show for the first time that TRIO mutations identified in patients affect Trio function and consequently could be responsible for the phenotype observed.

METHODS

Patients 1, 2 and 3 were assessed at the Wessex Clinical Genetics Service (Figure 1). Exome sequencing of patients 2 and 3 was performed on DNA extracted from whole blood. Sequencing and
analysis were undertaken as previously described;[16] all variant positions reported are defined on GRCh37 (hg19) and TRIO transcript NM_007118. To validate the sample provenance, a parallel SNP panel was applied to confirm data identity.[17]

Patients 4, 5 and 6 were referred to regional Clinical Genetics services across the UK, where they were recruited to the Deciphering Developmental Disorders (DDD) study (http://www.ddduk.org). DDD has so far investigated over 4000 children with severe, undiagnosed developmental delay, and their parents, using a combination of genome-wide assays to detect all major classes of genetic variation in the protein-coding portion of the genome. Clinical information and phenotypes have been recorded using the Human Phenotype Ontology via a secure web portal within the DECIPHER database.[18,19] DNA samples from patients and their parents were analysed by the Wellcome Trust Sanger Institute using high-resolution microarray analysis (array-comparative genomic hybridisation (CGH) and SNP-genotyping) to investigate copy number variants (CNVs) in the affected child, and exome sequencing to investigate single nucleotide variants (SNVs) and small insertions/deletions (indels). Putative de novo sequence variants were validated using targeted Sanger sequencing. The population prevalence (minor allele frequency) of each variant in nearly 15 000 samples from diverse populations was recorded, and the effect of each genomic variant was predicted using the Ensembl Variant Effect Predictor.[20] Likely diagnostic variants in known developmental disorder genes were fed back to the referring clinical geneticists for external Sanger validation and discussion with the family via the patient's record in DECIPHER, where they can be viewed in an interactive genome browser. Full genomic datasets were also deposited in the European Genome–Phenome Archive (http://www.ebi.ac.uk/ega).

Functional analysis to assess input of variants was undertaken. TRIO point mutants were generated by introducing a point mutant in the wild-type (wt) form of GFP-tagged Trio using the Quick change site-directed mutagenesis kit (Stratagene). The Rac1-GTP pull-down assay was performed using the Cdc42/Rac1-interactive binding (CRIB) domain of PAK1 as described.[6] Total HEK293T lysates and corresponding pull-downs retained on GST-Sepharose beads were processed for Western blotting using the Rac1 (BD) and GFP (Clinisciences) antibodies.

RESULTS

Patients 1, 2 and 3

Patient 1 (see Figure 1) was whole exome sequenced and a frameshift deletion (p.Gln1489Argfs*11) in TRIO was identified, which was paternally inherited. This variant is predicted to cause nonsense-mediated decay of the transcript, and thus prevent expression of this allele.[21] She was last assessed at the age of 17 months and was displaying signs of mild developmental delay; she sat unsupported at 9 months and walked unaided at 17 months. First words were spoken at 17 months and there was
evidence of mild delay in expression and comprehension. She is a fussy eater and has dietetic input to
to increase calorific intake. There were some subtle behavioural signs including poor attention. She is
microcephalic with a head circumference five standard deviations below the mean. Dysmorphic
features included a short nose, long philtrum, thin upper lip, epicanthic folds, 2/3 toe syndactyly and
an almost absent 5th toe nail. She has right radial aplasia, a rudimentary thumb and absent first
metacarpal. She was found to have multiple cardiac septal defects at birth; at the age of three she has
two small apical muscular ventricular septal defects and a patent foramen ovale, none of which are of
concern clinically. The pregnancy was complicated by pre-existing maternal type II diabetes mellitus,
which required insulin therapy. She also has a 15q11.2 microdeletion.

Patient 2 is the father of patient 1 and was genotyped using traditional Sanger methods. He harbours
the same deletion in TRIO in addition to the same 15q11.2 microdeletion. He displayed mild learning
difficulties in childhood and attended a specialist school. He is microcephalic with an occipital frontal
circumference (OFC) 3 standard deviations below the mean. Other dysmorphic features include a
straight nose, small jaw, pointed features, low anterior hair line, flattened thenar eminence, tapering
digits, fifth finger clinodactyly and dental delay including absence or failed eruption of the lower
central incisors and all four lateral molars.

Patient 3 is the uncle of patient 1 and brother of patient 2, who underwent whole exome sequencing.
He harbours the same deletion in TRIO in addition to a pathogenic variant in KCNJ2. He has learning
difficulties and is microcephalic with a head circumference 5 standard deviations below the mean. He
has similar dysmorphic features to his brother including a straight nose, small jaw, low anterior hair
line, pointed features and short and tapering fingers. He has a structurally normal heart but
experiences ventricular ectopic beats which may be attributable to his co-existing variant in
KCNJ2.[22] Similarly to his brother, he too has dental abnormalities with absence of any upper or
lower lateral incisors.

Patient 4

Patient 4 has a de novo missense mutation in TRIO (p.Arg1428Gln). She was last assessed at the age
of 16 years, when she had evident global developmental delay. From a gross motor perspective, she
sat unsupported at 10 months and walked at 22 months. It was not possible to elucidate the age of her
first words, however at the age of 16 years, although talkative, she remains unable to read or write. No
feeding difficulties have been reported. This individual has numerous behavioural difficulties
including stereotypies and obsessive compulsive traits. There was previous concern about aggressive
and disruptive behaviour which has now resolved. She is microcephalic with an OFC 5.41 standard
deviations below the mean. Some dysmorphism was noted including congenital ptosis, upslanting
palpebral fissures, large fleshy ears and 5th finger clinodactyly. Neurological features include
insensitivity to pain and urinary incontinence.
Patient 5

Patient 5 was last assessed at the age of 8 years. She has a de novo missense mutation in TRIO (p.Pro1461Thr). She has global developmental delay and is microcephalic with an OFC 5 standard deviations below the mean. She sat unsupported at 11 months and walked unaided at 2½ -3 years. Her first words were spoken between 4 and 5 years. Early feeding difficulties were reported including a poor suck, impaired bottle feeding and failure to thrive. Behavioural features include attention deficit hyperactivity disorder and poor sleep.

Patient 6

Patient 6 has a de novo missense mutation in TRIO (p.Asn1080Ile) and she was last assessed at the age of 9 years. She has global developmental delay, most notably affecting gross motor and language development. She sat unsupported at 11 months and walked unaided at 4-5 years. She has no verbal communication and utilises Makaton. She is still in nappies. There were some early feeding difficulties requiring gastrostomy; these have now resolved, although she remains with a thin body habitus. She has behavioural features that include hand stereotypies and aggressive episodes; she bites herself and can attack her younger brother. Head circumference is within the normal range. She has facial features that resemble Angelman-like facies with plagiocephaly. Neurological features include nocturnal tonic clonic seizures, and a wide-based and ataxic gait.

TRIO mutations

The six patients presented in this study have mutations in TRIO, a gene containing 57 exons that encodes a distinct member of the Dbl family of GEFs, displaying strong conservation across evolution.[12] Alternative splicing of TRIO results in isoforms that harbour either one or both of the highly conserved DH-PH domains. Out of the six Trio isoforms, five contain the first DH-PH domain. Following stimuli from growth factor or cytokine receptors, each PH domain downstream of a DH domain uniquely targets a specific intracellular Rho-GDP complex and facilitates catalytic exchange of GDP for GTP. DH1-PH1 domains specifically activate RhoG and Rac1.

We set out to test whether the mutations identified in Trio could impact on its function and consequently contribute to the phenotypes observed in the six patients. The RhoGEF Trio is a major regulator of neuronal development, mainly through its activation of Rac1. Patients 1, 2 and 3 share a frameshift mutation (p.Q1489fs*) resulting in a truncated Trio protein (Figure 3); it would be expected that this truncated transcript would be degraded by nonsense-mediated decay, resulting in the production of negligible protein product. Patients 4, 5 and 6 harbour de novo missense mutations. Interestingly, among the four mutations identified, three lie within the GEFD1 domain, responsible for Rac1 activation (p.R1428Q, p.P1461T and p.Q1489fs*) (Figure 3C). Furthermore, the mutations affect highly conserved residues, since both R1428 and P1461 are present in Trio from invertebrates.
to mammals (Figure 4B). They lie respectively within the alpha-5 and alpha-6 helices of the DH domain, which have been shown to interact with the target GTPase and occur at the protein-protein interface (Figure 4A). The truncated mutant of Trio, p.Q1489fs*, is missing the PH1 domain, which is shown to be required for efficient GDP/GTP exchange.[23] In contrast to the other 5 patients, individual 6 has a missense mutation (p.N1080I) within a spectrin repeat (Figure 3C).

We tested whether the mutations identified in our 6 patients affected Trio-mediated Rac1 activation (Figures 3D and 3E). We introduced four mutations individually into the Trio cDNA and expressed wt or mutant GFP-tagged Trio proteins in HEK293T cells. Rac1-GTP pull down experiments were performed using the Cdc42/Rac1-interactive binding (CRIB) domain of PAK1. As expected, Rac1-GTP was efficiently pulled down from cells expressing wt Trio. In contrast, the pull down of active Rac1 from cells expressing the Trio p.R1428Q, p.P1461T or the truncated mutant p.Q1489fs* was strongly reduced, albeit to a lesser extent than the fully dead GEF mutant used as a negative control (Q1427A/L1435E).[24]. The results obtained with the two point mutants in the GEFD1 domain are therefore consistent with a crucial function of these two residues in Rac1 activation. The p.N1080I mutant (in individual 6) did not affect Trio-mediated Rac1 activation. Taken together, our results reveal that in five out of six patients harbouring a mutation in the Trio gene, Rac1 activation is strongly reduced, demonstrating that Trio function is affected in these patients.

DISCUSSION

TRIO is highly expressed in the developing brain; rat models show transcripts present in all major brain areas postnatally.[9,25] TRIO and its orthologues play a fundamental role in mammalian neuronal development, with mutations implicated in impaired neuronal migration, whereby abnormal function results in global brain reduction and aberrant structural developmental of the hippocampus, cerebellum and cortex.[4,15] Complete knockout mice are embryonically lethal; they have smaller brains and aberrant organisation in the hippocampus and hindbrain.[4,12,15] A mouse model recently reported with a Trio knockout specific to the hippocampus and brain cortex addressed the role of Trio in postnatal brain development, concluding that Trio regulates the neuronal development of the hippocampus and affects the learning ability and intelligence of adult mice.[12]

Five of the six patients we report, share a core phenotype comprising intellectual disability (ID), behavioural difficulties, subtle dysmorphism and microcephaly. This presentation aligns with the phenotype recently presented by Ba et al.,[3] who screened 2 300 ID cases and identified four truncating mutations in TRIO. Similarly, they described skeletal anomalies, short stature, feeding difficulties and facial asymmetry. Perhaps most strikingly however, are the similarities of the digital dysmorpology, most notably phalyngeal hypoplasia, swollen proximal interphalangeal joints (PIP) joints and tapering fingers shared between their study and our findings. The microcephalic presentation is likely to be primary in nature, in which the skull is small because the underlying brain...
is small. Noteworthy, the microcephaly we describe is more severe than in the individuals reported by Ba et al.[3], whom all harboured loss of function mutations. Of interest, we showed that microcephaly was present in individuals who harboured mutations in the GEFD1 domain affecting Rac1 activation by Trio. Since Trio function in the nervous system is mainly mediated by Rac1 activation, we can propose from these data that alteration of Rac1 activation by Trio variants is associated with microcephaly. Furthermore, we have recently shown that Trio is implicated in cell division by counteracting the effect of MgcRacGAP on Rac1 during cytokinesis.[26] Interestingly, many genes associated with cell cycle regulation have been found to be mutated in different forms of microcephaly.[27,28] Therefore, the microcephaly phenotype observed in patients with TRIO mutations could also originate from a cell cycle defect.

In contrast to patients 1 - 5, one individual in our study (individual 6) is somewhat of a phenotypic outlier; although she has ID, behavioural difficulties and dysmorphism, she is the only patient we report without microcephaly and whom has seizures, complete speech failure and plagiocephaly. Unlike individuals 1 – 5 whom have mutations affecting the PH-DH1 domain, individual 6 has a missense mutation which affects a spectrin repeat and was functionally shown not to affect Trio-mediated Rac1 activation (Figure 3). Spectrin repeats are important for Trio function as they bind many Trio regulators, such as NAV1, DISC1 and KidIns220.[14,29] Therefore, we can hypothesise that the mutant Trio, p.N1080I, is mediated by a pathway independent of Rac1 activation, and could impair the binding of Trio to its interactors, potentially leading to protein mislocalisation.

TRIO is expressed in many tissue types, however its role outside of the central nervous system remains to be fully elucidated. Interpretation of a truly specific TRIO phenotype is confounded by additional findings; notably a 15q11.2 microdeletion in patients 1 and 2 and a pathogenic KCNJ2 variant in patient 3. Mutations in KCNJ2 have been associated with Anderson-Tawil syndrome, short QT and familial atrial fibrillation,[22,30] likely explaining the ventricular ectopic beats seen in individual 3. It is also of note that individual 1 has right radial aplasia and ventricular septal defects, which may be secondary to an in utero environment complicated by maternal type II diabetes.[31]

Two of our probands displayed additional neurological signs including seizures, ataxia and pain insensitivity, and three of the probands had feeding difficulties. Furthermore, the intellectual disability reported was variable. The phenotypic variability could be related to the differing variant types (loss of function versus missense) and the importance of mutations affecting different exon positions within the DH-PH1 domain and their consequent effect on protein function. Of particular interest, there was little difference in phenotypic severity between individuals harbouring loss of function mutations versus missense mutations that did not significantly alter protein length, nor in the biological disruption of Trio mediated Rac1 activity.

CONCLUSIONS
We are the first study to describe pathogenic missense mutations in TRIO and a TRIO syndrome that segregates in an autosomal dominant pattern. Our findings corroborate and extrapolate previous literature; we show that mutations in TRIO affecting the RhoGEF1 domain cause a phenotype comprising microcephaly, intellectual disability, behavioural difficulties and dysmorphism with specific digital features. We functionally prove that genotypic, patient-specific TRIO mutants cause protein dysfunction modulated through reduced Rac1 activity, and that microcephaly was only present in individuals who harboured mutations in the GEFD1 domain. It now remains to be established whether the phenotypic contribution of TRIO variants in patients are attributable to the function of Trio in cell division and/or neuronal differentiation.

Table 1. Clinical Phenotype

<table>
<thead>
<tr>
<th>Phenotype</th>
<th>Patient 1 (Proband)</th>
<th>Patient 2 (Father)</th>
<th>Patient 3 (Paternal Uncle)</th>
<th>Patient 4</th>
<th>Patient 5</th>
<th>Patient 6</th>
</tr>
</thead>
</table>

(+): present; (-): absent; AD: autosomal dominant; ADHD: attention deficit hyperactivity disorder; DM: diabetes mellitus; F: female; M: male; NR: recorded but absent; PFO: patent foramen ovale; PIP: proximal interphalangeal; RBBB: right bundle branch block; sd: standard deviations; VSD: ventricle septal defect
<table>
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<tr>
<th>Background</th>
<th>TRIO Mutation</th>
<th>Frameshift</th>
<th>Frameshift</th>
<th>Frameshift</th>
<th>Missense</th>
<th>Missense</th>
<th>Missense</th>
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<tr>
<td>Coding Change</td>
<td>c.4466delA</td>
<td>c.4466delA</td>
<td>c.4466delA</td>
<td>c.4283 G&gt;A</td>
<td>c.4381 C&gt;A</td>
<td>c.3239 A&gt;T</td>
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<tr>
<td>Exon</td>
<td>Exon 30</td>
<td>Exon 30</td>
<td>Exon 30</td>
<td>Exon 28</td>
<td>Exon 29</td>
<td>Exon 19</td>
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<tr>
<td>Domain affected</td>
<td>DH1</td>
<td>DH1</td>
<td>DH1</td>
<td>DH1</td>
<td>DH1</td>
<td>Spectrin repeat</td>
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</tr>
<tr>
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<td>Novel</td>
<td>Novel</td>
<td>Novel</td>
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<td>Inherited</td>
<td>Inherited</td>
<td>Inherited</td>
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<td>M</td>
<td>M</td>
<td>F</td>
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<tr>
<td>Gestational Age (weeks)</td>
<td>38</td>
<td>-</td>
<td>-</td>
<td>41</td>
<td>38</td>
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<th>Development</th>
<th>Age at Last Assessment</th>
<th>17 months</th>
<th>36 years</th>
<th>10 years</th>
<th>16 years</th>
<th>8 years</th>
<th>9 years</th>
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<tbody>
<tr>
<td>Early Milestones</td>
<td>1st Smile</td>
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<td>NR</td>
<td>NR</td>
<td>8 weeks</td>
<td>36 weeks</td>
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<tr>
<td></td>
<td>Sitting Unsupported</td>
<td>9 months</td>
<td>NR</td>
<td>NR</td>
<td>10 months</td>
<td>11 months</td>
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<tr>
<td></td>
<td>Waking Unaided</td>
<td>17 months</td>
<td>NR</td>
<td>NR</td>
<td>22 months</td>
<td>2.5-3 years</td>
<td>4-5 years</td>
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<td>First Words</td>
<td>17 months</td>
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<th>Current Developmental Level</th>
<th>General</th>
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<th>Mild learning difficulties attended special school</th>
<th>Mild developmental delay</th>
<th>Global developmental delay</th>
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<tr>
<td>Language</td>
<td>Mild delay in expression and comprehension</td>
<td>Learning difficulties</td>
<td>Unable to read or write but very talkative</td>
<td>Non-verbal (Makaton)</td>
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<tr>
<th>Growth</th>
<th>Height</th>
<th>76cm (&lt;0.4&quot;)</th>
<th>167cm (9&quot;)</th>
<th>120cm (2&quot;)</th>
<th>159.4cm (25th)</th>
<th>121.2cm (9th)</th>
<th>121.6cm (2&quot;)</th>
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<tbody>
<tr>
<td>Weight</td>
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<td>69.9kg (50-75&quot;)</td>
<td>20.9kg (&lt;0.4&quot;)</td>
<td>41.1kg (0.4&quot;)</td>
<td>21.2kg (9th)</td>
<td>20.2kg (2&quot;)</td>
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<tr>
<td>OFC</td>
<td>42cm (-5sd)</td>
<td>52cm (-3sd)</td>
<td>48cm (-5sd)</td>
<td>48cm (-5sd)</td>
<td>47cm (-5sd)</td>
<td>54.3cm (75th)</td>
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<tbody>
<tr>
<td>Aggression</td>
<td>-</td>
<td></td>
<td></td>
<td></td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Poor Attention</td>
<td>+</td>
<td></td>
<td></td>
<td></td>
<td>obsessive compulsive traits</td>
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<tr>
<td>Other</td>
<td>-</td>
<td>-</td>
<td></td>
<td></td>
<td>disrupted sleep</td>
<td>-</td>
</tr>
<tr>
<td>Other</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td></td>
<td>Pain insensitivity, urinary incontinence</td>
<td>-</td>
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</table>
| Seizures (nocturnal tonic clonic), gait ataxia
| Gastrointestinal | Infantile feeding difficulties | + | NR | NR | - | + |
| Other | Dietician input | | | | | |

| Skeletal | Digits | Short tapering fingers with swelling of PIP joints, 5th finger cleinodactyly | Short tapering fingers with swelling of PIP joints, 5th finger cleinodactyly, 2/3 left-sided toe syndactyly | Short tapering fingers with swelling of PIP joints, 5th finger cleinodactyly, 2/3 left-sided toe syndactyly | 2/3 toe syndactyly and almost absent 5th toe nail | - |
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**COMPETING INTERESTS**

None to declare.

**REFERENCES**


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Pedigree of Individuals 1, 2 and 3 (III1, II1 and II2 respectively) obtained through the Wessex Clinical Genetics Service. Affected individuals are shaded in black. Individuals who underwent whole exome sequencing are labelled with a “+”. Genotypic information confirmed by Sanger sequencing is displayed where known.

196x215mm (300 x 300 DPI)
Clinical Photographs

Photographs of individuals 1 to 6, taken at ages 3, 25 years, 22 years, 18, (2 & 11), and (18 months, 7 & 10) respectively. All individuals harbour TRIO mutations. Individual 1 is the daughter of individual 2. Individuals 2 and 3 are brothers and have been previously described.[32] Individuals 4, 5 and 6 are unrelated. Common features amongst studied individuals include microcephaly, mild dysmorphic facies, tapering fingers with prominent proximal interphalangeal joints, 5th finger clinodactyly and 2/3 toe syndactyly.

254x169mm (300 x 300 DPI)
TRIO and its functional domains

(A) Genomic location of TRIO on the short arm of chromosome 5p15.2. (B) Graphical representation of the TRIO gene, comprising its 57 exons (vertical lines) spanning 366.5 Kb. Exons are numbered alongside their relative position to coding domains. (C) Schematic overview of the Trio protein and its domains alongside the four mutations identified in the 6 patients from this study. Trio displays three enzymatic domains. Each GEF module contains a catalytic domain, called Dbl Homology (DH) domain (in reference to Dbl, the first RhoGEF identified as an oncogene in mammalian cells), and a Pleckstrin-Homology (PH) domain that plays a role in GEF activation and localisation. The first GEF domain, GEFD1, activates Rac1 and RhoG. The second GEF domain, GEFD2, acts on RhoA. In addition, Trio harbours numerous accessory domains. Listed from the N-terminus to the C-terminus, these include: a CRAL-Trio/Sec14 motif; several spectrin-like repeats; two Src-Homology 3 (SH3) motifs; and an Immunoglobulin (Ig)-like domain. (D) Rac1-GTP pull down assay. HEK293T cells (transfected as indicated) were lysed and active GTP-Rac1 was affinity purified using the

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Cdc42/Rac1-interactive binding (CRIB) domain of PAK1, immobilised on Glutathione-Sepharose beads. Purified GTP-bound and total Rac1 were detected by Western blot, using an anti-Rac1 antibody. Protein expression in the cell lysates was verified by immunoblotting with an anti-GFP antibody. One representative experiment is shown. (E) Quantification of the Rac1-GTP pull down assay shown in (D). Rac1 activation mediated by wt Trio was arbitrarily set to 100%, in order to be able to compare the individual experiments. The % of Rac activation was calculated from at least six independent experiments (mean ±SEM). *p < 0.015, ***p < 0.0001. Of note, all three mutations lying in the DH1 domain strongly affect Trio-mediated Rac1 activation.

84x122mm (300 x 300 DPI)
(A) Quaternary structure of the DH domain of Trio (teal) in complex with the small GTPase substrate (yellow). Mutations within the DH seen in patients 4 and 5 are indicated in red; both mutations can be seen to occur at the protein-substrate interface. PDB IDs: DH domain – 1NTY; GTPase substrate – 1KZ7. [33,34] Figure generated using PyMOL. [35]

(B) Sequence alignment of the DH1 domain of Trio (and Kalirin) across evolution. Sequences were obtained from NCBI databases and aligned with Clustal Omega. Identical residues are labelled in red, similar residues in blue. The structural features of the protein domain (alpha-helices) are depicted schematically and labelled on top of the sequence. The position of the mutations R1428Q and P1461T are indicated in bold and boxed in red. Note that R1428Q and P1461T each affect a highly conserved residue within a very conserved region of the DH domain, in helices alpha-5 and alpha-6. Helices alpha-1, alpha-3b, alpha-5 and alpha-6 make contact with the target GTPase. Represented species are: homo sapiens (h); mus musculus (m); rattus norvegicus (r); xenopus laevis (x); danio rerio (z); drosophila melanogaster (d); caenorhabditis elegans (c).

355x266mm (96 x 96 DPI)