Original research

**ARF1-related disorder: phenotypic and molecular spectrum**

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**ABSTRACT**

**Purpose** ARF1 was previously implicated in periventricular nodular heterotopia (PVNH) in only five individuals and systematic clinical characterisation was not available. The aim of this study is to provide a comprehensive description of the phenotypic and genotypic spectrum of ARF1-related neurodevelopmental disorder.

**Methods** We collected detailed phenotypes of an international cohort of individuals (n=17) with ARF1 variants assembled through the GeneMatcher platform. Missense variants were structurally modelled, and the impact of several were functionally validated.

**Results** De novo variants (10 missense, 1 frameshift, 1 splice altering resulting in 9 residues insertion) in ARF1 were identified among 17 unrelated individuals. Detailed phenotypes included intellectual disability (ID), microcephaly, seizures and PVNH. No specific facial characteristics were consistent across all cases, however microtretognathia was common. Various hearing and visual defects were recurrent, and interestingly, some inflammatory features were reported. MRI of the brain frequently showed abnormalities consistent with a neuronal migration disorder.

**Conclusion** We confirm the role of ARF1 in an autosomal dominant syndrome with a phenotypic spectrum including severe ID, microcephaly, seizures and PVNH due to impaired neuronal migration.

**INTRODUCTION**

Periventricular nodular heterotopia (PVNH) is a neuronal migration disorder consisting of ectopic neuronal nodules along the lateral ventricles.
ADP-ribosylation factor proteins (ARF1/3/4/6) are anchored to the membrane via N-terminal myristoylation. At the membrane, ARF1 acts as a molecular switch thanks to a transition between two structural conformations: inactive when bound to guanosine diphosphate (GDP), and active when bound to guanosine triphosphate (GTP). ARF1 activation is induced by Guanine Exchange Factors, such as ARFGEF2, which remove the GDP, triggering the GDP to GTP exchange. This causes a conformational change allowing ARF1 to bind different targets, notably through a shift of the loop from Leu39 to Ile49. ARF1GTP promotes trans-Golgi network through the recruitment of clathrin adaptor proteins and the fission step of the vesicle formation. As the vesicle is budding, ARF1 dimerisation is required to continue the coat-and the fission step of the vesicle formation. As the vesicle is budded, ARF1 dimerisation is required to continue the coat-and the fission step of the vesicle formation.

### MATERIALS AND METHODS

Previously unreported individuals harbouring de novo pathogenic or likely pathogenic variants in ARF1 were recruited using GeneMatcher. In addition, two previously reported individuals have been included: the R99H individual in Gana et al and the R99H individual in Ge et al who was incorrectly described with PVNH.

Phenotypic and genotypic information was obtained using a standardised questionnaire to evaluate clinical, electroencephalography (EEG) and brain MRI (bMRI) findings as well as genetic variant information. Variants were identified using trio exome sequencing (ES) or genome sequencing (GS) as trio, duo or singleton analyses (table 1). When photos were available, a specific informed consent was obtained from the parents. When available, the bMRI findings were re-evaluated by a single neuroradiologist.

Variants were interpreted using the American College of Medical Genetics and Genomics/Association for Molecular Pathology guidelines. The effects of missense variants were predicted by several in silico tools (table 1, online supplemental figure 1), and mapped to the missense tolerance landscape from MetaDome.

### RESULTS

The pathogenicity of five missense variants was further supported by in vitro functional pulldown assays. We functionally analysed ARF1 activation for four of the patient variants (p Thr481Leu, p.Phe511Leu, p.Arg99His, p.Lys127Glu) as previously reported by p.Y35H. For reproducibility, p.Y35H was also included. Each of the five variants was introduced by site-directed mutagenesis into the ARF1 myc-tagged cDNA (plasmid pCMV6-ARF1-myc, transcript NM_0011530408, GenScript, Piscataway, New Jersey, USA), and verified by sequencing prior to transfection (DNA Sequencing and Genotyping Core, CCHMC). Plasmids with reference and mutant sequences were transfected into HEK293T cells in 10 cm² plates, using the Lipofectamine 3000 Transfection Kit (Invitrogen, Thermo Fisher, Waltham, Massachusetts, USA). HEK293T cells were cultured in Dulbecco's Modified Eagle's Medium with 10% fetal bovine serum, 2 mM L-glutamine, Penicillin-Streptomycin per manufacturer's recommendations. To assess activated ARF1, GST-GGA3 pulldown was performed on cell lysates prior to western blot analysis, using the Active ARF1 Pull-Down and Detection Kit (Thermo Fisher, Waltham, Massachusetts, USA), per manufacturer’s instructions. Processing of samples was performed at 4°C and followed by incubation with GST-GGA3-PBD for 1 hour. For western immunoblotting, anti-ARF1 rabbit monoclonal IgG as primary antibody was diluted at 1:2000 in Intercept buffer prior to incubation at −4°C for 24 hours under agitation. The blot was then incubated with IRDye 800CW Goat antibiotin antibody at 1:15 000 dilution for 1 hour at room temperature under agitation. Western blot analysis results were imaged using Odyssey Sa Iffred scanner (LI-COR, Bad Homburg, Germany), equipped with Imaging Studio (Analysis Software V4.0). Results were quantified using Empiria Studio V1.3 software. The experiment was performed three times.

Whole blood was collected on PAXgen tube and total RNA was extracted from patient’s lymphoblastoid cell lines using PAXgene Blood RNA kit (Qiagen). cDNA was generated from 1 μg RNA with the addition of random hexamers and oligo dT primers using the SuperScript II Reverse Transcriptase (ThermoFisher Scientific). Impact on transcription of the c.384+1G>T substitution was then characterised by PCR Sanger sequencing on cDNA according to standard procedures, using primers localised in exons 3 and 5 of ARF1 gene, (F=ACCGTGGAGTACAAGAGACATCGC, R=ACTCTTGTGGTCCGGAGCTGAT).

Structural consequence of missense variants were predicted using SwissModel11 (V4.1.0), DynaMut212 and visualised with Mol*. 

### Clinical findings

The 17 individuals (9 females, 8 males) heterozygous for de novo ARF1 variants ranged in age from 16 months to 14 years (online supplemental table 1). The recurrent substitution c.296G>A; p.(Arg99His) was found in four unrelated individuals, resulting in a total of five different de novo occurrences, including the
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Figure 1  Clinical overview of 21 individuals with ARF1 variants (17 individuals from this study, 3 individuals previously reported from Ge et al,2 and one from Gana et al.7 Tolerance landscape from MetaDome.10 Plain lines point to the missense location, dashed lines point to non-missense altered residues (either to the premature terminating codon or to the nine residues insertion).

individual from Ge et al3 (figure 1, for the detailed clinical description of the cohort, see online supplemental table 1).

All individuals with available information presented with varying degrees of ID, ranging from mild to severe. Individuals #2, #7 and #9 (aged 18, 16 and 24 months, respectively) had motor delay along with speech delay, but have not been formally diagnosed with ID.

Microcephaly below 3 SD was noted in 10 individuals (50%; 10/20), seizures of various types were reported in 8 (50%; 8/16) and PVNH in 3 (20%, 3/15). No correlation was found between seizure history and PVNH. bMRI frequently showed abnormalities: small cerebellum (3/20) and neuronal migration defects including PVNH, cortical dysplasia, polymicrogyria (45%; 9/20) and corpus callosum abnormalities (50%; 10/20) (see online supplemental figure 5).

Facial characteristics (figure 1) included micrognathia or retrognathia (26%; 5/19), low-set ears (16%; 3/19), dental malposition (10%; 2/19) and short philtrum (10%; 2/19). Of note, individual #4 had obstructive sleep apnoea secondary to her microretrognathia that benefited from mandibular distraction. Visual or hearing impairments were common (58%; 11/19), including bilateral profound sensorineural hearing loss, cortical vision impairment, strabismus, astigmatism and hyperopia.

Additional findings included sleep disturbance (32%; 6/19), cardiac defects (16%; 3/19) and hypospadias (2/6 male individuals).

Interestingly, some idiopathic cutaneous or hepatic manifestations were reported, including hand hyperkeratotic skin (individual #3, individuals from Gana et al), pernio-like rashes involving the hands, feet, upper helices of the ears (individual #9), idiopathic and persistent elevation of liver enzymes (individuals #8 and #9). For individual #9, a liver biopsy was performed at age 1, showing sparse patchy lobular necroinflammatory lesions, no sign of portal inflammation, no haemochromatosis and negative staining for glycogen storage disease.

Molecular analysis

Thirteen different de novo variants in ARF1 (NM_001658.4; ENST00000272702.10) were identified in 17 individuals: 10 missense variants, 1 splice variant and 1 frameshift variant. (Nota bene: the missense p.(Phe51Leu) was caused by two different variants, c.153C>A and c.151T>C.) All variants were absent from gnomAD14 (V.2.1.1; V.3.1.2) or deCAF15 and the 10 missense variants were predicted to be deleterious by multiple in silico tools (see ‘Discussion’ section and online supplemental figure 1A). The frameshift variant p.(Asp72Thrfs*17) is predicted to elicit nonsense-mediated decay according to the 50 nucleotides rule,16 and is identified by the Loss-Of-Function Transcript Effect Estimator (V1.0.314) to result in a loss of function with high confidence.
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The splice variant c.384+1G>T is predicted by SpliceAI17 to create an in-frame donor site, resulting in the inclusion of nine residues near the GTP-binding site (online supplemental figure 1B).

No other pathogenic or likely pathogenic variant was reported in any of the cases.

Structural analysis

The locations of the 10 missense variants in ARF1 are mostly clustered near the GDP-binding domain (figure 1 and figure 2).

The Arg19 residue is located at a key position of the GDP-GTP switch. In the inactive conformation (GDP-bound),...
Arg19 sidechain points towards an adjacent helix of ARF1 (via Tyr81), however when ARF1 binds GTP, the sidechain of Arg19 is uncovered by the switch, and binds to ARF1 target (adaptor protein AP-1 complex, gamma-1 subunit, Glu41).

Tyr35 is required for the dimerisation of ARF1 and the Tyr35Ala has been previously shown to prevent in vitro scission.10

Thr48 is directly bound to the third phosphate group of GTP. It has been demonstrated to be crucial for the exchange of GDP for GTP during the activation of ARF1.18

Lys127 is part of the conserved NKXD motif, which binds to the guanine ring of GDP (online supplemental figure 2).19 In ARF1, Lys127 closely interacts with Asp93. Asp93 stabilises the Lys127 sidechain position through a hydrogen bond (online supplemental figure 2).

The Phe51 residue is located in a switching region of ARF1, which penetrates the hydrophobic groove of guanine exchanging factor. Phe51 is thought to serve as an hydrophobic grip to be ‘pinched off’ by the GEF in order to open the switch region, enabling the GEF to dislodge the GDP from its site (online supplemental figure 3).20

The recurrent Arg99His variant is predicted to significantly destabilise the region (−1.55 kcal/mol, DynaMut2), with the disruption of one hydrogen-bond stabilising the GDP binding domain (via Asp26, online supplemental figure 2).12

Pro131 is not located in an established interacting region of ARF1 and is not in direct contact with GDP.

**Functional assay**

The following variants (p.Tyr33His, pThr48Ile, p.Phe51Leu, p.Arg99His, p.Lys127Glu, accounting for 11 known individuals) were evaluated by the functional pulldown assay all caused a significant decrease in ARF1 activity (figure 2, p<0.05).

**DISCUSSION**

PVNH has been associated with X linked dominant, autosomal recessive and autosomal dominant syndromes.21-23

The phenotypic spectrum of ARF1-related disorder includes ID, microcephaly, PVNH and seizures associated with impaired neuronal migration.

ARF1 is a small GTPase which regulates vesicle trafficking and plays a role in cell adhesion molecule turnover.2223 Furthermore, ARF1 is implicated in mitochondrial trafficking of endoplasmic reticulum proteins, as well as mitochondrial cholesterol trafficking and fatty acid uptake into the mitochondria.27 ARF1 acts as a molecular switch by alternating between GDP-bound (inactive) and GTP-bound (active) conformations. This activation is performed at the membrane via GDP/GTP exchange by brefeldin A-inhibited guanine nucleotide exchange factor 2 (BIG2, encoded by ARFGEF2). ARF1GTP then can initiate vesicle formation through recruitment of various effectors to the membrane including coat proteins and coat protein adaptors.28 Inhibition of ARF1 has been shown to disrupt neuronal migration, cell-cell adhesion and dendritic Golgi polarisation.2629

It is still unclear whether the pathogenicity of ARF1 variants results from a dominant effect or from ARF1 haploinsufficiency.

Based on gnomAD data, ARF1 is strongly constrained against missense variants.1314 GeVIR score, a missense intolerance metric,15 ranks ARF1 as the 34th most intolerant gene; GeVIR %: ARF1=17.56 (34/19 361), which is consistent with the missense observed/expected upper bound fraction (MOEUF) from gnomAD; MOEUF: ARF1=0.208 (31/19 704).

Up to now, the intolerance of ARF1 for truncating variants has been uncertain. ARF1 loss-of-function observed/expected upper bound fraction (LOEUF) metric=0.402 (3595/19 198) is in favour of intolerance, but with limited statistical significance due to the short coding sequence of ARF1. Moreover, a few heterozygous loss-of-function variants have been identified in control individuals: two males (aged >45 years and >60 years) carrying a 25 nucleotides deletion resulting in frameshift (rs1010202646) in gnomAD V2.1.1 (non-neuro), and eight individuals carrying multigenic deletions encompassing ARF1 (nsv523935; nsv516409). For additional information, see online supplemental note 1.

Based on clinical data, the pathogenicity mechanism of ARF1 variants remains unsolved. First, as suggested by ARFGEF2 biallelic loss-of-function mutations222131-33 and the clinical overlap of the two syndromes (ID, microcephaly, PVNH, seizures, growth retardation), the defect in neuronal migration is presumed to be caused by reducing the BIG2-ARF1 pathway activity, rather than a gain of function. Furthermore, the two individuals described with truncating variants (one frameshift variant in our cohort and one nonsense variant from Gana et al’) favour a loss-of-function mechanism through haploinsufficiency, rather than a toxic gain of function. However, this is discordant with the existence of several control individuals with putative loss-of-function variants in ARF1 (rs1010202646; nsv523935; nsv516409). Interestingly, in vitro and in vivo functional assays on ARF1 mutants have shown dominant negative effects. For example, ARF1T31N, a constitutively inactive mutant, has been reported to act as dominant negative when overexpressed.26 The functional assay of Arf1Y35H reduced activation previously reported could not discriminate between a toxic gain of function or a loss of function16 (see online supplemental note 2). Still, to further delineate the exact pathogenicity mechanism, future studies with additional patients will be needed.

The recurrence of the chr1(GRC38):g.228097627G>A p.(Arg99His) de novo transition in five individuals suggests a highly mutable position, consistent with the CpG nucleotide context (see online supplemental figure 4).

We compared the ability of six in silico prediction tools to discriminate pathogenic missense from benign missense variants. Since MISTIC34 showed the best performance (online supplemental figure 1), we recommend its use to apply the prediction criteria (PP3 for variants with MISTIC scores >0.90) during the interpretation of future variants in ARF1.

Clinical findings confirm the phenotypic spectrum of a neuronal migration disorder, with severe ID, microcephaly and seizures. Unexpectedly, PVNH appeared to be inconsistent (30%), and seizures were poorly correlated with the presence of PVNH, or any other brain malformation. Seizure types were not consistent either: generalised tonic-clonic epilepsy was present in only one individual (#13). bMRI frequently showed abnormalities related to neuronal migration disorders (microcephaly, corpus callosum hypoplasia, polymicrogyria and PVNH), and occasional small cerebellum, which is uncommon in PVNH. Facial characteristics revealed some more common features, like microretrogнатhia, but were not universal, even between subjects with the same variant. Visual or hearing defects were frequent.

No major correlation between genotype and phenotype was found. Although of the four verbal individuals (#4, #5, #6, #13), three had alterations of residue Thr48 or Phe51, located in a conserved conformational switch domain.28 This could suggest an association between alterations of this switch-1 region (residues Gly40 to Phe51) and a milder cognitive phenotype, compared with the other alterations.

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**Developmental defects**

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**Supplemental note 1.**

**Supplemental note 2.**
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Except for the Pro131 residue, all missense variants were located on patently important residues for ARF1 function. We report two different likely pathogenic missense variants on Pro131: one replacing the hydrophobic proline with a positively charged arginine (Pro131Arg), and the other replacing it with another hydrophobic residue (Pro131Leu). This last hydrophobic to hydrophobic change could suggest a proline-specific role of Pro131 in ARF1 function. To our knowledge, Pro131 does not interact with other ARF1 partner. However, proline residues are known to rigidify the peptidic backbone. Pro131 does not interact with other ARF1 partner. However, proline residues are known to rigidify the peptidic backbone. Pro131: one replacing the hydrophobic proline with a positively charged arginine (Pro131Arg), and the other replacing it with another hydrophobic residue (Pro131Leu). This last hydrophobic to hydrophobic change could suggest a proline-specific role of Pro131 in ARF1 function. To our knowledge, Pro131 does not interact with other ARF1 partner. However, proline residues are known to rigidify the peptidic backbone. Pro131 connects the GDP binding loop to the rest of the C-terminal chain. Notably, the precise position and orientation of Asp129 and Lys127 are likely to be crucial for GDP binding. It is possible that Pro131 exerts a favourable constraint to the backbone of this loop, and helps the favourable positioning of GDP binding residues.

Cutaneous and hepatic manifestations among several individuals are rare and still not significant. However, this could suggest some more systemic roles for ARF1, beyond its implications in cortical neurons development. More patients need to be described to investigate this hypothesis.

Interestingly, C9orf72, a gene implicated in neuronal degeneration, has recently been reported to act as an effectors of ARF1. While none of the subjects in this series had evidence of neurodegeneration, the large number of young subjects makes this an important feature to evaluate in the future, as the natural history of this entity becomes better known.

In summary, we confirm the role of ARF1 as an autosomal dominant ID gene associated with neuronal migration defects. The phenotypic spectrum is characterised by ID, microcephaly, seizures and PVNH.

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