ORIGINAL ARTICLE

The kinetochore protein, *CENPF*, is mutated in human ciliopathy and microcephaly phenotypes

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ABSTRACT

**Background** Mutations in microtubule-regulating genes are associated with disorders of neuronal migration and microcephaly. Regulation of centriole length has been shown to underlie the pathogenesis of certain ciliopathy phenotypes. Using a next-generation sequencing approach, we identified mutations in a novel centriolar disease gene in a kindred with an embryonic lethal ciliopathy phenotype and in a patient with primary microcephaly.

**Methods and results** Whole exome sequencing data from a non-consanguineous Caucasian kindred exhibiting mid-gestation lethality and ciliopathic malformations revealed two novel non-synonymous variants in *CENPF*, a microtubule-regulating gene. All four affected fetuses showed segregation for two mutated alleles [IVS5-2A>C, c.1744G>T, p.R582X and c.9380G>A, p.R2898X] by whole exome sequencing. We found that CENP-F colocalised with Ninein at the subdistal appendages of the mother centriole in mouse inner medullary collecting duct cells. Intraflagellar transport protein-88 (IFT-88) colocalised with CENP-F along the ciliary axonemes of renal epithelial cells in age-matched control human fetuses but did not in truncated cilia of mutant CENPF kidneys. Pairwise co-immunoprecipitation assays of mitotic and serum-starved HEK293 cells confirmed that IFT88 precipitates with endogenous CENP-F. 

**Conclusions** Our data identify *CENPF* as a new centriolar disease gene implicated in severe human ciliopathy and microcephaly related phenotypes. CENP-F has a novel putative function in ciliogenesis and cortical neurogenesis.

INTRODUCTION

Centrioles are microtubule (MT)-derived structures that play an essential role in centrosome and cilia formation.1 Mutations in centrosomal and MT-regulating genes have been described in cancer, disorders of neuronal migration2,3 and microcephaly (MCPH) including Majewski osteodysplastic primordial dwarfism type II.4,5 Disrupted processes include abnormalities of centriole duplication, centrosome maturation and spindle pole formation6 with defective asymmetric divisions of neuronal progenitors and failure of cortical neurogenesis.7,8 Following mitosis, the distal appendages of the mother centriole become the transition fibres of the ciliary basal body.9 Transition fibres promote ciliogenesis by recruiting intraflagellar transport (IFT) proteins which traffic tubulin subunits and other proteins to the ciliary tip.10 Mutations in genes regulating centriole length have recently been described in ciliopathies characterised by heterotaxia, retinal degeneration, skeletal dysplasia, renal disease and cerebral anomalies including microcephaly.11–13 These findings support emerging evidence that certain centriolar protein complexes have dual roles in spindle orientation and ciliogenesis.8,14

In the current study, we identify *CENPF*, the MT-regulating gene, as a new centriolar disease gene implicated in severe human ciliopathy and MCPH-related phenotypes. Our data suggests a novel putative function for CENP-F in ciliogenesis as well as cortical neurogenesis.

**Methods**

In order to determine the genetic basis of a novel congenital malformation disorder and MCPH, we employed a next-generation sequencing approach using whole exome sequencing combined with genome-wide linkage analysis.

**Research subjects**

Approval for research involving human subjects was obtained from the Institute of Child Health research ethics board, University College London, and the Scottish multicentre research ethics committee.

**Linkage analysis**

For genome-wide SNP mapping, the GeneChip Human Mapping 500 k Array from Affymetrix was used. Genotypes from DNA of the three affected
and two unaffected children in the index kindred in addition to
the parents were generated. Genotypes were examined with the
use of a multipoint parametric linkage analysis, and haplotype
reconstruction performed with GENEHUNTER V2.1 through
stepwise use of a sliding window with sets of 110 SNPs and the
program, ALLEGRO, in order to identify regions of homozgy-
osity as described using a disease allele frequency of 0.0001
and Caucasian marker allele frequencies.

Exome capture
Targeted capture was performed on genomic DNA from one
affected and one unaffected sibling of the index kindred with the
EZ Exome Library (Roche Nimblegen, V1) and sequenced on a
single lane of a Solexa/Illumina Genome Analyser II. Reads
were aligned to the human reference genome (GRCh37 release, down-
loaded from the ENSEMBL database). Three different software
programs were used for sequence evaluation: Maq, BWA and
Novoalign. The coverage along the genome was calculated using
BEDtools (GenomeCoverageBed function), without omitting zero
values. Variant calling was undertaken using UnifiedGenotyper.16
The final output was then converted to variant call format. On
average, we obtained about 43 million single short reads per lane
with 91.8% of reads correctly mapped to the genome. The median
sequencing depth per coding nucleotide was 23, with 90% of the
targeted exons covered at least once. Variants from all samples were
annotated and prioritised to identify pathogenic mutations as previ-
ously described.16 Variants annotated in dbSNP132 and the 1000
Genomes project or in our in-house databases with an allele fre-
quency above 0.5% were removed. An autosomal recessive inherit-
ance model was applied for gene identification in both kindreds,
with known ciliopathy and MCPH genes manually analysed using
the Integrative Genomics Viewer (http://www.broadinstitute.org/
igv/). Candidate pathogenic variants were validated and assessed
for familial segregation by Sanger sequencing.

Sanger sequencing
Mutations were analysed by Sanger sequencing. CENPF primer
pairs are described in online supplementary table S1.

Immunofluorescence microscopy
NIH 3T3 fibroblasts, mouse inner medullary collecting duct
(mIMCD3) and retinal pigmentary epithelial (RPE) cells were
seeded onto glass coverslips and grown in Dulbeccos modified
eagle medium (DMEM) with 10% fetal bovine serum (FBS) and
penicillin/streptomycin, until they reached 70% confluence.
Cells were fixed in 4% PFA/phosphate buffered saline overnight at 4°C. WISH for
southpaw (GeneTools) were designed against the 25 bps upstream of tran-
scription start codon of cdfp and against the splice junction of the
intron 3–exon 4 boundary (see online supplementary table S2). For controls, a standard control MO (5’-CCT CTT ACC TCA
GTT ACA ATT TAT A 3’) was injected into wild-type embryos.
Specificity of splice MO was confirmed by RT-PCR (see online supplemen-
tary figure S1). RNA was extracted from 25 mor-
phants and 25 controls at 48 hpf using the TRIzol (Invitrogen)
method. First-strand cDNA was synthesised using random hex-
amers (Sigma-Alrich) and Omniscript transcriptase (QIAGEN),
according to the manufacturer’s instructions. Fertilised eggs were injected with MO (2 ng/embryo) at the 1-cell to 2-cell
stage and allowed to develop at 28.5°C to the desired stages.
For rescue experiments, full-length human CENPF plasmids
were injected with MO (2 ng/embryo) at the 1-cell to 2-cell
stage and allowed to develop at 28.5°C to the desired stages.
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stage and allowed to develop at 28.5°C to the desired stages.
RESULTS
Mutations in human CENPF cause a novel congenital malformation syndrome and MCPH

We identified a non-consanguineous Caucasian kindred with four affected fetuses exhibiting mid-gestation lethality and dysmorphic craniofacial features (figure 1A, B; table 1). Autopsy findings revealed ciliopathy features, such as cerebellar vermis hypoplasia, corpus callosum agenesis, cleft palate, diencephalic atresia and bilateral renal hypoplasia.

A search of several validated dysmorphology databases including the London Dysmorphology Database failed to show phenotypical identity with any known syndrome. Genome-wide SNP analysis using high-density SNP arrays (Affymetrix 500 k Marshfield V2) was undertaken on all except one family member (CIL 1.1). Linkage analysis using GENEHUNTER V2 lr5 (multipoint) revealed 10 regions with a maximum positive HLOD of 1.32. Linked intervals were identified on chromosome 1 (2 intervals), 2, 6, 7, 8, 13, 19 and 20. One of the intervals on chromosome 1 and the interval on Chromosome 19 were the largest and contained the most homozygous markers covering a total of 839 genes (see online supplementary figure S2).21 Using Identity by Descent Finder, significant regions of homozygosity were not present, consistent with declared non-consanguinity. Given that the linked regions were large, spanning up to 15 Mb on 19p13.3, whole exome capture and consecutive massive parallel deep sequencing of one affected and one unaffected offspring was employed as a strategy to identify the underlying genetic etiology of this novel phenotype. Variants were prioritised for analysis on the basis of novel coding non-synonymous SNPs, splice variants, truncating variants and InDels (see online supplementary table S3). A further variant filtering strategy based on an autosomal recessive mode of inheritance, as suggested by the pedigree, identified two novel homozygous and 40 novel compound heterozygous mutations in 20 genes that were unique to the affected offspring. Only one of the 22 candidate genes was present in a linked interval located on chromosome 1. Two novel non-synonymous variants in the CENPF gene (NM_016343.3), involving a heterozygous IVS5-2A>C nucleotide change, which was predicted to abolish the consensus splice-acceptor site from exon 6, and a second heterozygous c.1744G>T nucleotide change in exon 12 were identified (figure 2A, B). Sanger sequencing of both variants confirmed segregation with affected offspring and revealed that each parent carried a single variant (see online supplementary figure S3A). The variant was detected neither in the 200 ethnically-matched control alleles nor in the 200 control in-house exomes. The protein-truncating non sense variant, c.1744G>T, p.E582*, was predicted to be disease-causing in the Mutation Taster programme (score 6.0). The expected damaging effect provides strong support for its likely pathogenic effect. The mutation c.1744G>T, p.E582* was shared between two kinds. Western blot analysis of protein lysates from CENPF mutant MCPH fibroblasts revealed a much greater reduction in CENPF protein levels compared with wild-type controls (see online supplementary figure S5). The presence of residual protein could be explained by incomplete nonsense-mediated decay. Truncation of the residual protein as a result of the p.R2898* mutation is possible but the estimated difference in molecular weight of 23.7 kDa (estimated by loss of 216 amino acids) was difficult to resolve by SDS-PAGE gel electrophoresis owing to the high molecular weight of CENPF (see online supplementary figure S9).

Mutational screening did not identify mutations in CENPF in 12 consanguineous patients with Meckel Grüber syndrome (MKS) who had compatible clinical features, potential autozygous regions and did not have a mutation in known MKS genes and in three patients with isolated nephronphthisis (NPHP) who showed homozygosity by descent at the CENPF locus out of a cohort of 150 families with NPHP or Joubert syndrome (JBTS). We also conducted mutational screening of 96 unrelated patients with Bardet Biedl syndrome (BBS) who were not preselected based on known BBS mutations. We did not detect recessive CENPF mutations in any of the MKS, NPHP, JBTS or BBS families, and because of the small sample size, we were unable to conclude that the heterozygous mutations in CENPF detected in BBS pedigrees act as phenotypical modifiers as has been described for other ciliopathy disease genes (see online supplementary table S5).
CENP-F is localised to the subdistal appendages of the mother centriole

The findings of mid-gestation fetal lethality together with abnormal craniofacial, cerebellar, palate, foregut and renal development, and the known role of Hedgehog signalling in organogenesis, suggested that these features may represent a ciliopathy disorder. Immunofluorescence microscopy of ciliated NIH 3T3 fibroblasts revealed a basal body localisation for CENP-F (figure 3A). Furthermore, CENP-F colocalised with Ninein at the subdistal appendages of the mother centriole of

**Table 1** Clinical characteristics of index kindred with novel ciliopathy phenotype

<table>
<thead>
<tr>
<th>Pedigree ID</th>
<th>Cerebral</th>
<th>Craniofacial</th>
<th>Gastrointestinal</th>
<th>Genitourinary</th>
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<tr>
<td>I.1*</td>
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<td>Cleft palate</td>
<td>Duodenal atresia</td>
<td>Bilateral renal hypoplasia</td>
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<td>XY</td>
<td>Cerebellar hypoplasia</td>
<td>Micrognathia</td>
<td>Rounded head</td>
<td>Low-set ears</td>
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<td>TOP 21 weeks</td>
<td>Agenesis of corpus callosum</td>
<td>High nasal bridge</td>
<td>Duodenal atresia</td>
<td>Bilateral renal hypoplasia</td>
</tr>
<tr>
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<td>Prominent nose</td>
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<td></td>
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<tr>
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<td>Normal</td>
<td>Short columella</td>
<td>Low-set ears</td>
<td></td>
</tr>
<tr>
<td>IUD 17 weeks</td>
<td>Normal</td>
<td>Wide mouth</td>
<td>Duodenal atresia</td>
<td>Bilateral renal hypoplasia</td>
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<td>I.3</td>
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<td>Normal</td>
<td>Normal</td>
<td>Normal</td>
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<td>Agenesis of corpus callosum</td>
<td>Malrotation</td>
<td>Accessory spleens</td>
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<td>Hypertelorism</td>
<td>Multiple SI atresia</td>
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*Affected.
SI, small intestine.
mIMCD3 cells (figure 3B). Transmission electron microscopy following immunogold labelling of CENP-F in serum-starved human RPE cells confirmed a centriolar localisation for CENP-F at the subdistal appendages and the distal end of the mother centriole (figure 3C).

Zebrafish cenpf knockdown results in ciliopathy phenotypes
To understand the functional relevance of CENP-F in relation to its localisation at the basal body, we performed knockdown experiments using both translation-blocking and splice-blocking antisense MO against zebrafish cenpf which shares 60%
Figure 4R2 (A) Zebrafish cenpf morphants display increased body axis curvature at 24 h postfertilisation (hpf) compared with control embryos (black arrow). Cenpf knockdown in cardiac myosin light chain (cmlc2)-gfp transgenic zebrafish causes laterality heart defects at 48 hpf. Hydrocephalus (arrow) is evident at 72 hpf in cenpf morphants compared with control embryos. At 96 hpf, pronephric cysts (arrow) are evident in cenpf morphants compared with control embryos. (B) Quantitative graph showing increased occurrence of axis curvature defects, laterality malformations, hydrocephalus and pronephric cysts in cenpf morphants (blue bars) compared with control embryos (red bars) and compared with cenpf morphants injected with human CENPF RNA (black bars). Bars represent an average of three experiments. Error bars denote SE of the mean (SEM). Std-MO (n=266) % ventral axis curvature at 24 hpf vs cenpf-MO (n=173) 12.7±1.5 vs 88.7±1.4, *p<0.001; cenpf-MO (n=173) vs cenpf-MO with human CENPF RNA (n=256) 88.7±1.4 vs 38.7±2.0, *p<0.001; Std-MO (n=223) % laterality defects at 48 hpf vs cenpf-MO (n=152) 4.0±0.6 vs 81.7±2.8, *p<0.001; cenpf-MO (n=152) vs cenpf-MO with human CENPF RNA (n=229) 81.7±2.8 vs 28±2.6, ****p<0.0001; Std-MO (n=204) % hydrocephalus at 72 hpf vs cenpf-MO (n=93) 1±0.6 vs 68.3±1.7, *p<0.001; cenpf-MO (n=93) vs cenpf-MO with human CENPF RNA (n=197) 68.3±1.7 vs 40.3±1.7, *p<0.001; Std-MO (n=158) % pronephric cysts at 120 hpf vs cenpf-MO (n=76) 1.2±0.9 vs 96±0.6, ****p<0.0001; cenpf-MO (n=76) vs cenpf-MO with human CENPF RNA (n=122) 96±0.6 vs 37.3±1.9, *p<0.001. (C) Representative images of southpaw mRNA expression in the lateral plate mesoderm at 18-somites (ss) of control (a) and cenpf morphant embryos (b-d). (a) left-sided expression in control embryos (arrow, top left panel). (b) right-sided expression (arrow), (c) bilateral expression and (d) absent expression in stage-matched cenpf morphant embryos (arrows). Scale bar 50 μm. (D) Representative micrographs following immunofluorescent labelling of Kupffer’s vesicle (KV) cilia with anti-α-acetylated tubulin antibody at 8 ss. Short KV cilia are noted in cenpf morphants (white arrows) (E) Quantitative graph showing a quantitative difference in KV cilia length (μm) in cenpf morphants (n=136 cilia; n=5 embryos) vs controls (SD MO) (n=228 cilia; n=4 embryos); 4.2±0.4 vs 2.6±0.1 **p<0.0001. (F) Quantitative graph showing that KV cilia number were significantly less in cenpf morphants (n=5 embryos) vs controls (SD MO) (n=5 embryos); 56.4±1.9 vs 38.6±1.7 **p<0.001. (G) Long cilia are observed in the lumina of collecting ducts of control fetuses (white arrow) while short cilia are evident on renal epithelial cells of CENPF mutant fetal kidneys (white arrow). Sections are counterstained with 4’,6-diamidino-2-phenylindole. Scale bar 10 μm. MO, morpholino oligonucleotides.
Ciliary function.28

Morphological analysis of surviving zebrafish embryos at 24 hpf, revealed axis curvature defects and at 48 hpf, cenpf morphants exhibited abnormal heart looping compared with controls (figure 4A). At 72 hpf, hydrocephalus was observed in cenpf morphants, and at 120 hpf, all surviving cenpf morphants exhibited pronephric cysts (figure 4A). Conjection of cenpf MO with human wild-type CENPF RNA rescued significantly the axis curvature defects (p<0.001) and pronephric cysts in cenpf morphants (p<0.001; figure 4B, online supplementary figure S5). The occurrence of these morphological findings support a role for CENPF in zebrafish ciliary function.28

Cilia-driven fluid flow within zebrafish Kupffer’s vesicle (KV), or across the mouse ventral node, has been shown to underlie a conserved symmetry-breaking event that establishes a left–right (LR) pattern.29 To corroborate our findings of early lethality and abnormal heart looping in embryos surviving to 48 hpf, we next determined whether LR patterning defects are evident in cenpf morphants. At mid-somite stages, normal LR patterning can be defined by southpaw mRNA expression in the left lateral plate mesoderm.28 In cenpf morphants, right-sided (top right panel), bilateral (bottom left panel) and absent (bottom right panel) expression of southpaw mRNA was observed compared with left-sided expression in control embryos (figure 4C and also see online supplementary figure S7). To determine whether the laterality defects are caused by defects in KV cilia, we next analysed cilia formation in 8-somite-stage (ss) control and cenpf morphants. Following labelling of KV ciliary axonesmes with anti-α-acetylated tubulin antibody in stage-matched embryos at 8-somites (figure 4D), analysis of cenpf morphants revealed that the length of KV cilia were shorter compared with controls (p<0.0001; figure 4E) and the number of KV cilia was significantly less in cenpf morphants compared with controls (p<0.001; figure 4F).

Following our observations that cenpf morphants show defective KV ciliogenesis, we next determined whether defective ciliogenesis was a feature of mutant CENPF renal epithelia. Immunofluorescence labelling of ciliary axonesmes with anti-α-acetylated tubulin antibody in kidney sections of autopsy tissue from age-matched control fetuses were longer compared with those in renal epithelia of fetuses carrying the identified CENPF mutations (figure 4G). While renal epithelial cilia were noted to be present on some but not all cells, morphologically, the cilia that were present were stumpy with a terminally distended appearance (figure 4G).

CENPF-F colocalises with IFT88 along the ciliary axoneme and precipitates with endogenous IFT88 and other IFT-B components

Previous work has demonstrated that during mitosis, CENPF-F localises to the spindle poles in a process that relies on cytoplasmic dynein-1.12–14 Similar findings for IFT88 have recently been reported,19 suggesting that ciliary proteins may have specific roles in mitosis.19–21 Consequently, we tested the hypothesis that CENPF-F might interact with IFT88. To test this, we showed that CENPF-F co-localised with IFT88 and KIF3B at the centrosome of asynchronous NIH 3T3 fibroblasts (figure 5A, B) and along the ciliary axonesmes of ATDC5 cells (chondrocytes) (figure 5A). Furthermore, in human autopsy samples, IFT88 colocalised with ciliary axonesmes of renal epithelial cells of control fetuses (figure 5D). However, IFT88 did not localise to ciliary axonesmes and centrioles in mutant CENPF kidneys (figure 5E). These data prompted us to test a possible functional relationship between CENPF-F and IFT88. Pairwise co-immunoprecipitation assays of mitotic and serum-starved HEKT293 cells confirmed that IFT88 precipitates with endogenous CENPF-F (figure 5F). In unsynchronised HeLa cells, endogenous CENPF-F co-fractionated with other IFT-B components such as IFT52 and IFT20 in addition to motors, such as cytoplasmic dynein-1 and KIF3A (figure 5G). Therefore, this data suggest that CENPF-F interacts with proteins involved in cilia formation and function.

Together with our findings that CENPF mutations result in a microcephalic phenotype and recent evidence for a role for IFT88 and Pericentrin in mitotic spindle orientation,8 19 we hypothesised that CENPF-F may also interact with proteins implicated in the cortical polarity pathway which could account for defective cortical neurogenesis. This hypothesis was supported by co-immunoprecipitation assays suggesting an interaction between CENPF-F and the NuMA/p150 Glued dynactin/Par 3 protein complex, proteins implicated in asymmetric cell division22 (see online supplementary figure S8).

DISCUSSION

Mutations in CENPF link the kinetochore complex to human ciliopathy and MCPh phenotypes

Our discovery of a novel severe human ciliopathy-related phenotype attributed to mutations in a kinetochore protein, supports recent evidence for a dual role for ciliary proteins in spindle orientation and ciliogenesis.19 CENPF-F was first characterised in cancer cell lines as a component of the outer kinetochore and as a binding partner of the retinoblastoma (Rb) protein.31–35 CENPF-F is dynamically expressed throughout the cell cycle. It binds to the nuclear envelope at the transition between G2 and M phase of the cell cycle. In early prophase until anaphase onset, it is found at the kinetochore where it stabilises the attachment of MTs to the centromere. In early anaphase, CENPF-F is found at the spindle mid-zone, while in late anaphase, it migrates with cytoplasmic dynein-1 and recruits the spindle checkpoint regulatory complex to the spindle poles.22 In early G0, it undergoes proteasome degradation.36 Depletion of CENPF-F in vitro results in mitotic delay, with failure of kinetochore assembly and misalignment of chromosomes in a subset of mitotic cells.37 38 Studies in murine embryonic stem cells and in avian myocyte lines suggest primary roles for this protein complex in differentiation, but the exact mechanism is unknown.39 Several studies have highlighted an additional role for CENPF-F in the regulation of cell shape and vesicle transport.40–42 Given the overlap of features in fetuses with CENPF mutations with human ciliopathy phenotypes, we hypothesised that CENPF-F may play a role in cilia formation and function. The finding that CENPF-F colocalises with IFT88 along the ciliary axoneme, and the existence of CENPF-IFT88 protein complexes is further supported by the co-migration of CENPF-F with other IFT-B components. Furthermore, the absence of IFT88-stained ciliary axonesmes and mislocalisation of IFT88 within renal tubular epithelia of CENPF-mutant kidneys proposes a putative role for CENPF-F-dependent IFT88-ciliary targeting.

We attribute, for the first time, that mutations in the CENPF gene play a causal role in human congenital malformation syndromes. All four affected fetuses of the index kindred had compound heterozygous mutations in CENPF. Further supporting the pathogenicity of these mutations was the finding that one of these mutations also occurred in the context of MCPh in a
Figure 5  (A) Colocalisation of CENP-F at the centrosome with intraflagellar transport-88 (IFT88) (B) Representative micrographs of asynchronous 3T3 fibroblasts following dual immunofluorescent labelling of 3T3 cells with KIF3B and C-terminus CENP-F antibody. CENP-F localises to the centrioles with KIF3B (arrows). Scale bar 5 μm. Inset: high-power view of CENP-F localisation between two KIF3B foci. (C) Co-localisation of CENP-F alone with ciliary axonemes labelled with IFT88 antibody. (D) IFT88 localises to long cilia within the lumina of renal collecting ducts of 22-week-old control human fetuses (arrows). Inset shows colocalisation of IFT88 with GT335-positive ciliary axonemes in xy and xz plane of confocal projection. Scale bar, 15 μm. (E) IFT88 does not localise with GT335-positive ciliary axonemes, if present, of CENPF mutant fetal kidneys (arrows). GT335-positive cilia are shorter than cilia in control kidneys. Scale bar 10 μm. Inset shows that IFT88 and GT335 do not colocalise in the xy and xz plane of confocal projection. Scale bar 10 μm. (F) Representative images of co-immunoprecipitation experiments carried out on protein lysates from mitotic HEKT293 cells containing endogenous CENP-F. Immunoblots show that IFT88, KIF3B and CENP-F co-immunoprecipitate with endogenous CENP-F, while an immunoglobulin G (IgG) isotype control does not co-immunoprecipitate with CENP-F. IN=input; 10% of total input is indicated. (b) Reciprocal co-immunoprecipitation experiments carried out on protein lysates from serum-starved HEKT293 cells containing endogenous IFT88. Immunoblots show that CENP-F co-immunoprecipitates with endogenous IFT88, while an IgG isotype control does not co-immunoprecipitate with IFT88. IN=input; 10% of total input is indicated. (G) Asynchronous HeLa cell lysate was fractionated over a superose-6 gel filtration column. Eluted fractions were probed with antibodies against CENP-F, IFT complex B members: IFT88, IFT52 and IFT20, and motors: cytoplasmic dynein 1 intermediate chain (Dyn IC 74.1) and Kif3a. CENP-F co-eluted with the IFT proteins and motors, suggesting that it exists as a complex with these proteins. Arrows indicate peak elution fractions for calibration proteins: thyroglobulin (669 KDa; fraction 23), β-amylase (200 KDa, fraction 28) and bovine serum albumin (BSA) (67 KDa, fraction 31). V, void volume.
second unrelated kindred. Phenotypical disparity is not a unique finding to mutations in the CENPF gene. Divergent phenotypes have been previously described in several disorders associated with mutations in genes encoding centrosomal proteins. For example, for mutations in the CEP290 gene, 90 mutations have been reported exclusively in only one phenotype, while 14 others have segregated with two diseases, and eight have been associated with three or more phenotypes. In most cases, these phenotypes are partially overlapping, although few mutations were observed to lead to strongly divergent disorders, such as Leber’s Congenital Amaurosis (LCA) and MKS. It is interesting that mutations causing JBTS tend to cluster in the second half of the CEP290 gene, whereas mutations segregating with LCA, Senior Loken Syndrome and MKS are homogeneously distributed throughout the gene. Of note, domains within the CEP290 protein share significant similarity with CENP-F, with several putative coiled-coil domains, a region with homology to structural maintenance of chromosomes segregation ATPases, a bipartite nuclear localisation signal and six RepA/Rep+ protein kinase inductive domain motifs and an ATF4-binding domain.

In the current study, we sought to explain the divergent phenotypes by an analysis for potential modifier alleles in genes known to be associated with ciliopathy phenotypes, but did not find any variants which were predicted to change the amino acid sequence. A plausible explanation could be perhaps that the more severe phenotype in the embryonic lethal disorder was associated with a lack of a protein product necessary for ciliary function. Because residual CENP-F protein was observed in the fibroblasts of our MCPH patient, a dosage-dependent mechanism could be proposed in which complete loss of function of both CENPF alleles would lead to an embryonic lethal ciliopathy phenotype, whereas residual CENP-F activity would be sufficient for normal ciliary targeting of IFT88 and, perhaps, a less severe phenotype.

Genes involved in centrosome maturation and spindle-pole formation have been implicated in MCPH phenotypes. As CENP-F migrates with cytoplasmic dynein-1 and recruits the spindle checkpoint regulatory complex to the spindle poles in late anaphase, the findings of CENPF mutations in a MCPH phenotype is therefore not unexpected. MCPH phenotypes have been ascribed to defective asymmetric divisions of neuronal progenitors and failure of correct neural cell fate specification. Our data supports a role for CENPF in asymmetric cell divisions through its putative interactions with p150-dynactin, NuMA and Par3, proteins which have been implicated in this pathway. Future investigations using conditional Cenpf-deleted transgenic mice will be needed to dissect the role of CENP-F in cortical neurogenesis.

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Authors AMW, MW and PLB designed the study with substantial contributions from FL and ES for bioinformatics analysis. CB, EC, AB helped with pilot exome pipeline analysis. SC-S, RA and GO helped with immunofluorescence studies. GO and PC sequenced MCPH family for CENPF variants. AC provided technical expertise with co-immunoprecipitation assays and genetic analysis. HS and CD identified the study families. HS and RK helped with linkage analysis. DMB and PMW shared critical reagents. AB and SD helped with microscopy, biochemical assays, cell rescue experiments and intellectual contributions to the manuscript. ED and NK sequenced BBS cohorts, CAI and KS sequenced MKS cohorts and FH and EO sequenced NPHP cohorts for CENPF mutations. PC and AI provided sequencing and western blot data on MCPH patient. AMW designed the study, performed exome capture, analysis, mutation segregation, microscopy, biochemical assays, cell, zebrafish and fetal kidney experiments and wrote the manuscript.

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Erratum: The kinetochore protein, *CENPF*, is mutated in human ciliopathy and microcephaly phenotypes


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