Human and Mouse Mutations in WDR35 Cause Short-Rib Polydactyly Syndromes Due to Abnormal Ciliogenesis

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Defects in cilia formation and function result in a range of human skeletal and visceral abnormalities. Mutations in several genes have been identified to cause a proportion of these disorders, some of which display genetic (locus) heterogeneity. Mouse models are valuable for dissecting the function of these genes, as well as for more detailed analysis of the underlying developmental defects. The short-rib polydactyly (SRP) group of disorders are among the most severe human phenotypes caused by cilia dysfunction. We mapped the disease locus from two siblings affected by a severe form of SRP to 2p24, where we identified an in-frame homozygous deletion of exon 5 in WDR35. We subsequently found compound heterozygous missense and nonsense mutations in WDR35 in an independent second case with a similar, severe SRP phenotype. In a mouse mutation screen for developmental phenotypes, we identified a mutation in Wdr35 as the cause of midgestation lethality, with abnormalities characteristic of defects in the Hedgehog signaling pathway. We show that endogenous WDR35 localizes to cilia and centrosomes throughout the developing embryo and that human and mouse fibroblasts lacking the protein fail to produce cilia. Through structural modeling, we show that WDR35 has strong homology to the COPI coatamers involved in vesicular trafficking and that human SRP mutations affect key structural elements in WDR35. Our report expands, and sheds new light on, the pathogenesis of the SRP spectrum of ciliopathies.

There are a number of recessive disorders characterized by skeletal dysplasia and multiorgan anomalies,1 some of which have been shown to be caused by mutations in the development, structure, or function of primary cilia (ciliopathies).2 Short-rib polydactylies (SRPs) are a prime example, being a heterogeneous group of disorders characterized by skeletal defects, short ribs and limbs, and polydactyly. Visceral features can include polycystic kidneys, laterality defects, and cardiovascular and brain abnormalities. SRPs have been classified into four types, (Saldino-Noonan syndrome, type I [MIM 263530]; Majewski syndrome, type II [MIM 263520]; Verma-Naumoff syndrome, type III [MIM 263510]; Beemer-Langer syndrome, type IV [MIM 269860]), which display clinical and molecular overlap. Although locus heterogeneity has been demonstrated in SRP (see below), the relative contribution of both allelic heterogeneity and genetic background modification remains unclear. This question extends to other disorders that share similar overlapping clinical features. Asphyxiating thoracic dystrophy (ATD, Jeune syndrome [MIM 208500]) has skeletal features similar to those of SRP, and patients usually die in infancy, although some survive and later may develop liver and kidney disease and retinal degeneration.3 Ellis van Creveld syndrome (EVC, chondroectodermal dysplasia [MIM 22550]) is most similar histologically to SRP III but often presents postnatally, with distinct radiological and clinical features such as congenital heart disease, supernumerary digits, and ectodermal dysplasia.1 In addition, patients with cranioectodermal dysplasia (CED, Sensenbrenner syndrome [MIM 218830]) display craniofacial and skeletal abnormalities, hair and tooth defects, and variable liver, kidney, brain, and retinal anomalies.4

Primary cilia are complex organelles protruding from the surface of nondividing cells. Their formation is organized by the basal body; a modified centriole structure from which the microtubule-based axoneme extends. The assembly and maintenance of cilia requires the dynamic bidirectional movement of the multiprotein complexes along the axoneme from cell body to cilia tip.5 This process, termed intraflagellar transport (IFT), involves a conserved core machinery organized into trains composed of either IFT-B (anterograde) or IFT-A (retrograde) components and is driven by kinesin or dynein molecular motors, respectively.6–8 In addition to the transport of structural units, IFT is also essential for the localization and function of key developmental signaling components, such as the Gli transcription factors, which transduce Hedgehog (Hh) signaling.9 The loss of Hh regulation may be a hallmark of some clinical features observed in ciliopathies.

In cases in which mutated genes have been identified in skeletal dysplasias, it is not known whether a correlation exists between severity of disease and the particular...
Figure 1. WDR35 Is Mutated in Atypical Short-Rib Polydactyly Syndrome in Humans and in the yeti Mutant Mouse
(A and B) Characteristic postaxial polydactyly, extreme micromelia, and short ribs (A) as presented in postmortem survey of 13 week conceptus (SRP-3-1) (B).
(C) Genomic PCR spanning exons 4, 5, or 6 of WDR35 from DNA of parents (SRP-1-1, SRP-1-2) or affected concepti (SRP-1-4, SRP-1-6). Deletion of a 2847 bp genomic fragment (2:20177392-20180238, assembly GRCh37) results in the loss of exon 5 in homozygous individuals. Reaction products for the control (C1) and no template (-ve) are shown.
protein or ciliary process affected. Homozygous and compound-heterozygous mutations in the retrograde dynein motor DYNC2H1 (MIM 603297) have recently been identified in cases of both SRP type III and ATD/Jeune syndrome,\textsuperscript{10,11} and IFT80 (MIM 611177), which encodes a component of the anterograde IFT-B complex, is mutated in some other cases of ATD.\textsuperscript{12} In contrast, mutations recently identified in the less severe CED/Sensenbrenner syndrome affect components of the IFT-A retrograde complex IFT122 (MIM 606045)\textsuperscript{13} or WDR35 (MIM 613602).\textsuperscript{14} Most recently, mutations in Never-in-mitosis Kinase 1 (NEK1 [MIM 604588]), a gene involved in initiating ciliogenesis,\textsuperscript{15–17} were identified in several SRP type II cases, including a potential example of digenic diallelic inheritance with DYNC2H1.\textsuperscript{18} Mouse mutations have been found in many of these genes\textsuperscript{17,19–22} and will be valuable models for understanding ciliopathic phenotype-genotype correlations.

We previously identified a New Zealand family of Maori descent with two consecutive pregnancies complicated by an unclassifiable SRP syndrome that was most similar to SRP type III but was novel in that it was associated with acromesomelic hypomineralisation and campomelia.\textsuperscript{23} These affected siblings exhibited several additional hallmarks of ciliopathic disease, including polysisndactyly, laterality defects, and cystic kidneys. After institutional ethics approval and informed consent, human samples were collected for molecular analysis. Using genome-wide SNP genotyping and CNV analysis, we mapped the disease locus to a 5.5 Mb region of chromosome 2p24 (Figure S1A available online) and identified a homozygous deletion of three SNPs within WDR35 (NM_001006657.1) (Figure S1B). This deletion was heterozygous in both parents and the unaffected sibling but was homozygous in the two affected siblings. Direct sequencing of the parents and affected siblings over this region identified a 2847 bp deletion spanning exon 5 of WDR35 (Figure 1C). PCR analysis of cDNA from patient cell lines confirmed the loss of the 129 bp exon 5 from the WDR35 mRNA (Figure 1D). WDR35 encodes two isoforms that share seven closely spaced WD40 repeats at the amino terminus and a tetratricopeptide repeat-like motif at the carboxyl terminus (Figure 1E). WD40 repeats are involved in intra-cellular trafficking, cargo recognition, and binding,\textsuperscript{24,25} and the WDR35\textsuperscript{25} mutation results in the in-frame deletion of one of these repeats (Figure 1E). WDR35 is orthologous with Ift121, which fractionates with complex A IFT particles in C. reinhardtii\textsuperscript{25} and mammals.\textsuperscript{26} Mutations in the C. elegans ortholog (ifta-1) display classic truncated retrograde cilia phenotypes with accumulations of IFT machinery and transport profiles consistent with phenotypes observed when other complex A subunits are mutated.\textsuperscript{27} We also performed candidate-gene sequencing of WDR35 in two cases with a clinical diagnosis of Jeune syndrome and four additional cases with severe SRP phenotypes (two unclassifiable SRPs, one Beemer-Langer [type IV] SRP, and one Majewski [type II] SRP). Heteroallelic mutations in WDR35 were identified in one fetus (Figure S1C) with an SRP phenotype associated with extreme micromelia, postaxial polydactyly, and facial abnormalities (Figures 1A and 1B). A de novo nonsense mutation (c.1633C>T [p.Arg545X]) was identified on the paternal allele, and a missense mutation affecting a highly conserved tryptophan residue (c.781T>C [p.Trp261Arg]) (Figure 4A) was shown to be maternally inherited.

Independently, we isolated the mutant mouse line yeti in a recessive ENU mutagenesis screen for genes affecting embryonic development. Mutant embryos die before late day 12.5 postcoitum (12.5 dpc) and exhibit a range of severe defects. They display cardiovascular defects including generalized edema, hemorrhages, and a randomized and mislooped heart tube. Delayed and randomized embryo turning is also observed, and polysyndactyly is seen in rare, surviving, later-stage embryos (Figures 11 and 1J). Additionally, yeti mutants display failure of the somite derivatives, including the putative ribs, to migrate and properly differentiate (Figure 1K), hydroplastic lungs with tracheal-esophageal fistula, and diaphragmatic hernia. We mapped the yeti locus to a 3.5 Mb interval between rs6278243 and rs29154438 on chromosome 12 and undertook genomic sequencing of candidate genes. A single G>A mutation was identified in the splice acceptor site of exon 22 of Wdr35 (Figure 1E; chr12:9026683, ENSMUST00000085745, NCBIM37). RT-PCR analysis of cDNA from yeti mutant litters using primers in the adjacent exons confirmed aberrant splicing of the Wdr35 mRNA in heterozygous and homozygous yeti embryos (Figure 1L). Sequencing of these mutant splice variants revealed framenhifts in all yeti transcripts. In situ hybridization with 5’ and 3’ UTR Wdr35 riboprobes

(D) RT-PCR amplification of WDR35 spanning exons 4–6 from affected concepti (SRP-1-4, SRP-1-6) and control fibroblasts (C1, C2).

(E) Schematic of the predicted domain organization of two coding human WDR35 transcripts, with or without exon 11 (violet). The location of the WDR35 mutations in SRP-1 (blue; homosympathetic SRP45) and SRP-3 (p.Trp261Arg and p.Arg545X) -affected concepti are shown. The splice acceptor mutation at the intron 21-exon 22 junction in yeti mice is indicated (*).

(F–K) Gross embryonic phenotypes of wild-type (F–H) compared to yeti mutant littermates (I–K). Embryonic day 12.5 (E12.5) forelimb (F, I) and hindlimb (G, J) defects in yeti mouse mutants include impaired outgrowth along the proximal-distal axis and polysyndactyly. (H, K) E11.5 transverse hematopoietin- and eosin-stained sections of the Wdr35\textsuperscript{yeti} thoracic cavity show failure of the somite derivatives, such as the sclerotome (sc) derivatives (ri, ribs; ve, vertebra), to migrate out from the midline in mutants and tracheoesophageal fistula with hypoplastic lungs (asterisk).

(L) RT-PCR amplification of a Wdr35 fragment covering exons 21–24 shows the presence of aberrantly spliced of transcripts in the yeti mutant (white arrowheads) compared to wild-type (black arrowhead).

(M) Whole-mount in situ hybridization of Wdr35 in E10.5 wild-type and yeti littermates shows nonsense-mediated decay of mRNA in mutant embryos.
Figure 2. 

Wdr35 Localizes to Cilia and Is Required for Ciliogenesis

(A and B) NIH-3T3 (A) or IMCD3 (B) cells were microporated with full-length mouse Wdr35::GFP and serum starved for 36 hr before costaining with antibodies directed against γ-tubulin (A) or acetylated α-tubulin (red; B). Nuclei are stained with DAPI (blue). Magnification of regions of interest are shown in single-channel images indicating colocalization.
in mutant embryos revealed that mutant transcripts are subject to nonsense-mediated decay (Figure 1M). Noncomplementation of the *yeti* allele with an embryonic-stem-cell-derived “targeted trap” null *tm2a* allele of *Wdr35* proves that the *yeti* mutant phenotype is due to this point mutation in *Wdr35* (Figure S2). The phenotypic parallels, in particular polydactyly and failure of migration and differentiation of somite derivatives leading to absent or shortened ribs, strongly suggest that the human mutations in *WDR35*, like the mouse mutations, result in a complete loss of function.

Little is functionally known about mammalian *WDR35* aside from its biochemical association with other IFT-A components, so we characterized the cellular and in vivo localization of *WDR35*. Initially, we generated a full-length mouse *Wdr35* protein tagged with GFP and expressed it in cultured cells. Significant staining was observed in the periciliary region in mouse NIH 3T3 cells, shown by partial colocalization with γ-tubulin (Figure 2A). In IMCD3 cells, which have more prominent cilia, *Wdr35-GFP* was also detected along the cilia axonemes, where it colocalized with acetylated α-tubulin (Figure 2B). To examine endogenous *WDR35* localization, we generated two independent antibodies directed against different, unique epitopes. Immunofluorescence studies in IMCD3 cells confirmed that *Wdr35* accumulated at and around centrosomes and basal bodies of serum-starved cells, with fainter punctate staining along the cilia axoneme (Figures 2C and 2D). Immunofluorescence analysis of wild-type mouse sections labeled both primary and specialized cilia, as well as centrosomes, throughout the embryo. The intensity of staining was enriched in highly ciliated tissues, including the developing lung and nervous system (Figures 2E and 2F, Figure S4). Importantly, this *WDR35* localization was lost in *yeti* mutant sections, as shown in the limb bud mesenchyme at 11.5 dpc (Figures 2G and 2H). Likewise, *WDR35*545 SRP fibroblasts had only remnant expression of endogenous *WDR35*545 (Figures 2I and 2J). Collectively, these data suggest that both *WDR35*545 and *yeti* are loss-of-function alleles of *WDR35*. Given *WDR35*’s subcellular localization and the gross ciliopathic phenotype of these mammalian mutants, our data suggest that *WDR35* is an essential component of the cilia.

To independently verify that *WDR35* is required for ciliogenesis, we used a siRNA strategy to knock down expression of *Wdr35* in NIH 3T3 cells and quantified the number of cells with cilia. Reduction of *Wdr35* mRNA levels by 85% resulted in a 50% reduction in the number of ciliated cells compared to the scrambled siRNA control (Figures 2K and 2L).

To better characterize the cellular function of WDR35 in primary cilia, we analyzed primary fibroblasts from human (Figures 3A–3D) and mouse (Figures 3E–3K) controls and *WDR35* mutants. Cilia axonemes were clearly detectable by acetylated α-tubulin staining, a marker of stabilized microtubules, in human (Figures 3A and 3B) and mouse (Figures 3E and 3F) control cells. However, these structures were completely absent in both human (Figures 3C and 3D) and mouse (Figures 3G and 3H) mutant cells. Instead, extended perinuclear microtubule arrays were prominent via acetylated α-tubulin staining in both human and mouse mutant cells (Figure 3C compared to Figure 3A and Figure 3G compared to Figure 3E). Because loss of retrograde IFT transport results in accumulation of anterograde IFT components in mutant cilia, we examined the localization of complex B protein IFT88 (MIM 600595) in *WDR35* mutant fibroblasts. Consistent with a functional role in retrograde IFT trains, some cilia-like structures remained in these mutant cells, as shown by restricted IFT88 accumulations around the γ-tubulin-positive basal bodies (Figures 3D and 3H).

Clinical distinction between syndromes in the skeletal dysplasia spectrum could result from underlying differences in the degrees of disruption to cilia structure and/or function, as a result of different mutations in the same gene. Mutations in *WDR35* were recently identified in a subset of patients with Sensenbrenner syndrome/CED. Therefore, we undertook homology modeling of *WDR35* mutations on the predicted protein structure to gain additional insight into the molecular genetics underlying the clinical phenotypes (Figure 4). All of the *WDR35* missense mutations identified to date in both Sensenbrenner and SRP (Figure 4A) affect highly conserved WDR35 residues, suggesting that they are all
likely to be pathogenic. However, homology modeling reveals striking differences in the functional consequences of the WDR35 mutations in SRP versus Sensenbrenner syndrome cases. A similar configuration of N-terminal WD40 repeats and C-terminal tetratricopeptide repeat (TPR)-like motifs observed in WDR35 (Figure 1E) is found in other IFT complex A and B proteins.24 The WD40/WD40-like repeats are involved in intracellular trafficking, cargo recognition, and binding.24,25 A similar protein structure is also shared with the coat complexes COPI, COPII, and clathrin, which are involved in vesicle trafficking, and was recently shown that in coat proteins, the N-terminal WD40-like β-propeller is essential for vesicular cage formation.29 Taking advantage of the high secondary-structure homology of WDR35 to the structure of yeast β-COP29, we used structure-prediction algorithms and homology to model the structure of WDR35 (Figure S6). WDR35 is predicted to fold into two seven-bladed β-propellers, each with an offset WD40-like repeat, followed by an extended TPR-containing α-solenoid domain (Figures 4B and 4C). This model highlights the consequences of the human SRP mutations: the WDR35D5 mutation results in an in-frame deletion of the third blade in the N-terminal seven-bladed propeller, whereas the SRP-3-1 missense mutation (p.Trp261Arg) changes one of seven highly conserved tryptophan residues at the inner face of the same propeller (Figures 4C and 4D). That both SRP deletion and missense mutations impact the N-terminal β-propeller, which has been implicated in higher-order organization of COPI complexes, suggests that these mutations interrupt key interaction motifs required for IFT-A train assembly or stability, resulting in abrogated retrograde transport. This hypothesis is consistent with the severe ciliogenesis phenotype observed in our SRP human and mouse WDR35 mutants. In contrast, missense mutations identified in the milder Sensenbrenner/CED cases14 are found in more C-terminal domains of WDR35, suggesting that interactions with specific cargo or other IFT components may be affected, resulting in impairment, but not complete inhibition, of retrograde transport.

WDR35 has been recently implicated in Sensenbrenner syndrome/CED and now, through our work, in a clinically distinct syndrome of severe SRP. Our results show that SRP and CED are allelic, demonstrating not only that the SRPs show locus heterogeneity but that clinically distinct ciliopathies with severe and moderate presentation can result from allelic heterogeneity in the same gene. Given the parallels with the null mouse mutants, our current study suggests that the more severe human disease, SRP, is the result of complete loss of function of WDR35, resulting in profound ciliogenesis defects. Furthermore, molecular modeling has shown that SRP mutations affect key structural elements in the N-terminal β-propeller domain, which by homology with the COPI, COPII, and clathrin proteins is involved in higher complex organization of transport modules. Given the broad developmental expression of WDR35 and the multisystem defects observed in both human and mouse mutants, future tissue-specific mutation studies of Wdr35 in mice will be needed to determine which are the primary defects underlying the pleiotropic loss of function of WDR35, resulting in profound ciliogenesis defects. Furthermore, molecular modeling has shown that SRP mutations affect key structural elements in the N-terminal β-propeller domain, which by homology with the COPI, COPII, and clathrin proteins is involved in higher complex organization of transport modules. Given the broad developmental expression of WDR35 and the multisystem defects observed in both human and mouse mutants, future tissue-specific mutation studies of Wdr35 in mice will be needed to determine which are the primary defects underlying the pleiotropic loss of WDR35. Mutant studies in lower-order model organisms, such as Chlamydomonas and C. elegans, have been very powerful for identifying cilia phenotypes. However, the complexities of mammalian cilia’s structure and function, in particular with respect to its role in developmental signaling, emphasize the

![Figure 3. Wdr35 Is Required for Mammalian Ciliogenesis](image-url)
importance of mouse molecular genetics. The use of mouse models for investigating the role of the IFT machinery and specific cargo will provide further insight into the pathogenesis of ciliopathies and the reasons underlying the variability in clinical presentation.

Supplemental Data

Supplemental data include six figures and two tables and can be found with this article online at http://www.cell.com/AJHG.

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Web Resources

The URLs for data presented herein are as follows:
Mouse Genome Informatics, http://www.informatics.jax.org/

References


