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Comparison of Phenotypes between Different vangl2 Mutants Demonstrates Dominant Effects of the Looptail Mutation during Hair Cell Development

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Abstract

Experiments utilizing the Looptail mutant mouse, which harbors a missense mutation in the vangl2 gene, have been essential for studies of planar polarity and linking the function of the core planar cell polarity proteins to other developmental signals. Originally described as having dominant phenotypic traits, the molecular interactions underlying the Looptail mutant phenotype are unclear because Vangl2 protein levels are significantly reduced or absent from mutant tissues. Here we introduce a vangl2 knockout mouse and directly compare the severity of the knockout and Looptail mutant phenotypes by intercrossing the two lines and assaying the planar polarity of inner ear hair cells. Overall the vangl2 knockout phenotype is milder than the phenotype of compound mutants carrying both the Looptail and vangl2 knockout alleles. In compound mutants a greater number of hair cells are affected and changes in the orientation of individual hair cells are greater when quantified. We further demonstrate in a heterologous cell system that the protein encoded by the Looptail mutation (Vangl2S464N) disrupts delivery of Vangl1 and Vangl2 proteins to the cell surface as a result of oligomer formation between Vangl1 and Vangl2S464N, or Vangl2 and Vangl2Looptail, coupled to the intracellular retention of Vangl2S464N. As a result, Vangl1 protein is missing from the apical cell surface of vestibular hair cells in Looptail mutants, but is retained at the apical cell surface of hair cells in vangl2 knockout mice. Similarly the distribution of Prickle-like2, a putative Vangl2 interacting protein, is differentially affected in the two mutant lines. In summary, we provide evidence for a direct physical interaction between Vangl1 and Vangl2 and a knockout of in vitro and in vivo approaches and propose that this interaction underlies the dominant phenotypic traits associated with the Looptail mutation.

Introduction

Planar polarity is the polarized organization of cells and cellular structures within the plane of a tissue, perpendicular to the apico-basolateral cell axis [1,2,3]. In the sensory epithelia of the vertebrate inner ear, planar polarity is evident in the organization of a stereocilia bundle and kinocilium atop the sensory receptor hair cells that mediate hearing and balance. Movements of the bundle towards the kinocilium produce excitatory electrophysiological responses in the hair cell, while movements away are inhibitory. As a result, loss of planar polarity for even a subset of auditory hair cells is sufficient to produce a measurable decrease in auditory function [4]. Individual hair cells are polarized by the asymmetric, subcellular distribution of the core Planar Cell Polarity (PCP) proteins including Frizzled (Fz), Dishevelled (Dvl), Van Gogh (Vangl), Prickle (Pk) and CELSR [3]. The polarized distribution of these proteins in vestibular hair cells of the mouse appears to be highly conserved, resembling the organization of core PCP proteins in epithelia cells of the Drosophila wing. Taken together, several recent studies indicate that Fz and Dvl proteins form a complex on one side of the hair cell that is opposite to Vangl and Pk proteins on the other [5,6,7,8]. Similar to Drosophila, vertebrate PCP proteins also coordinate planar polarity between cells so that, in the case of hair cells, the stereocilia bundles of neighboring cells are oriented in the same direction.

An early demonstration the functional significance of planar polarity and PCP signaling mechanisms in hair cells came from analysis of the vangl2 (Entrez Gene ID: 93840) mutant line Looptail (Lp) [9,10]. Lp is a missense mutation of vangl2 resulting in a Serine to Asparagine substitution at amino acid position 464, which is located in the cytoplasmic domain of the protein. In vangl2Lp/Lp mutants, hair cell stereocilia are properly formed and polarized, yet individual hair cells are frequently misoriented relative to neighboring cells in the cochlea and utricle [7,11]. A greater proportion of hair cells are misoriented in the cochlea of embryos with mutations in both vangl1 (Entrez Gene ID: 229658) and vangl2 demonstrating functional redundancy of the two homologous genes [12,13]. In addition to hair cell planar polarity
phenotypes, \textit{vangl2}^{Lp/Lp} mutants have craniorachischisis, which is a severe neural tube defect (NTD). The iconic looped tail of the \textit{Lp} line is due to a milder neural tube phenotype in heterozygous mice. Craniorachischisis is a class of NTD specifically resulting from disrupted planar polarity during convergent extension of the embryo prior to neurulation, and is a common feature of vertebrate PCP mutants. Other mouse lines that develop craniorachischisis and hair cell planar polarity defects include \textit{fz/6} double knockouts [8], \textit{CELSR} mutants \textit{spin cycle} and \textit{crash} [14], \textit{scribble} mutants [15], and \textit{pkd2} knockout mice [16]. In addition, mutations in \textit{vangl1} and \textit{vangl2} have been linked to neural tube defects in humans [17,18].

The \textit{Lp} mouse has served as an important animal model for studying vertebrate planar polarity [11] that is frequently used to query genetic interactions between PCP and other signaling pathways [19,20,21]. The original characterization of the \textit{Lp} line classified the \textit{Lp} mutation as having a partially penetrant and dominant phenotype [22]. Consistent with these conclusions, when female reproductive tract explants are cultured \textit{ex vivo}, heterozygous tissue develops pathologic characteristics similar to mutant tissue [23]. A confounding factor however, is that the severity of the phenotype can also be strain dependent suggesting the additional influence of genetic modifiers [3]. Moreover, in the time since the \textit{Lp} mutation was mapped to \textit{vangl2} [9,10], molecular assays have demonstrated reduced \textit{vangl2}^{S464N} protein stability and expression in \textit{vangl2}^{Lp/Lp} mutants [7,24,25]. This has led to a reinterpretation of \textit{Lp} as a null allele with a heterozygous phenotype resulting from haploinsufficiency. The \textit{Lp} line has implicated PCP signaling in a number of developmental events such as axon pathfinding not originally associated with planar polarity. In addition, genetic interactions between \textit{Lp} and other mutant lines suggest that other signaling pathways, including those functional in cilia, incorporate Vangl2 [20,26]. In order to accurately interpret Vangl2 function in these different contexts it is important to establish the true molecular basis and phenotypic nature of the \textit{Lp} mutation.

One explanation is that the \textit{Lp} mutation inhibits Vangl2 function by disrupting Vangl2 protein trafficking through the endoplasmic reticulum (ER). Consistent with this hypothesis, mutations in \textit{sec24b}, which encodes an ER transport protein that is required for \textit{vangl2} movement to the plasma membrane, result in a dominant lethal phenotype similar to \textit{vangl2}^{Lp/Lp} [27]. Similarly \textit{Vangl2}^{S464N} is not loaded into ER vesicles indicating that the mutated region of the \textit{Vangl2} cytoplasmic domain may be required for sorting by \textit{Sec24b}. Furthermore, a second \textit{vangl2} point mutant (\textit{mtM6}) fails to enter ER vesicles [27], and \textit{vangl2}^{Lp/D} mice have craniorachischisis similar to \textit{vangl2}^{Lp/Lp} [29]. Moreover mutant Vangl2 trafficking deficits are consistent with the reduced levels of Vangl2 protein detected in mutant tissues [25] and unstable recombinant mutant protein reported in \textit{vitro} [7]. Still it is unclear whether the heterozygous phenotype of \textit{vangl2}^{Lp/Wt} is due to haploinsufficiency or if it is a partially penetrant, dominant phenotype as described in the original characterization of the line.

We have generated a complementary mouse line in which a single exon encoding the \textit{Vangl2} transmembrane domains is disrupted by \textit{LoxP} site addition and subsequent excision by Cre recombinase. At the chromosomal level, the mutation in these \textit{vangl2} knockout mice is more severe than the \textit{Lp} and \textit{mtM6} mutations because remaining elements of \textit{vangl2} are not sufficient to encode a membrane spanning protein. Using the sensory hair cells of the inner ear, we compared the mutant phenotype of \textit{vangl2} knockout and \textit{Lp} mutant mice to establish the phenotypic nature of the \textit{Lp} mutation during hair cell development.

**Results**

To further evaluate Vangl2 function during sensory hair cell development, a \textit{vangl2} knockout (KO) mouse was generated and compared to the established \textit{Looping} (\textit{Lp}) mouse line to determine the effect of the \textit{S464N} substitution on Vangl2 function. The \textit{vangl2} gene was modified by homologous recombination in ES cells to introduce tandem \textit{LoxP} sites flanking exon 4, which encodes the four Vangl2 transmembrane domains (Fig. 1A). Accurate recombination was confirmed by Southern blot assay, and a single line was used for blastocyst injections (Fig. 1B). Following germline transmission of the targeted allele, \textit{exo 4} and the NeoR selection cassette were permanently deleted by sequentially crossing the line with transgenic mice expressing ubiquitous Cre recombinase [30] or \textit{FLPe} [31] (Fig. 1A). Since targeting \textit{exo 4} deletes the Vangl2 transmembrane domains, this knockout allele is called \textit{vangl2}^{ATM} to distinguish it from other \textit{vangl2} alleles. Western blot analyses of whole brain lysates using an antibody against the amino terminus of Vangl2 (N-13) confirms a loss of Vangl2 protein in \textit{vangl2}^{ATM/ATM} embryos (Fig. 1C). A \textit{Vangl2} doublet that is present in wild type and \textit{vangl2}^{ATM/ATM} Western blots likely reflects the different phosphorylated states of Vangl2 [32]. Although the amino terminus is not encoded by \textit{exo 4}, no smaller mutant isoforms of Vangl2 were detected in lysates from heterozygotes or knockouts. In addition mutant \textit{vangl2} cDNAs were synthesized, cloned from \textit{vangl2}^{ATM/ATM} tissues and sequenced. None of these cDNAs encoded alternative mutant protein isoforms that could escape detection by the Vangl2 N-13 antibody (data not shown). Therefore \textit{vangl2}^{ATM} is a complete null allele.

\textit{Vangl2}^{ATM} mice were backcrossed to C57Bl6 for at least 5 generations before experimental intercrosses. On this genetic background the majority of \textit{vangl2}^{ATM/ATM} mutants exhibited craniorachischisis, a severe NTD (Fig. 1D-G) that is a characteristic phenotype of \textit{Lp} mutants [22]. However, unlike \textit{vangl2}^{Lp/Lp} mice, 26% of \textit{vangl2}^{ATM/ATM} mice (6/23) present only with spina bifida, a milder NTD restricted to the posterior neural tube adjacent to the tail (Fig. 1F-G). Similarly, on the C57Bl6 background only 11% of \textit{vangl2}^{ATM/Wt} mice (11/99) had the tail loops or kinks that are characteristic of the \textit{Lp} line. Tail phenotypes were never observed in \textit{vangl2}^{ATM/Wt} mice backcrossed for a minimum of 5 generations to the FVB (0/66 heterozygotes) or strain A/J (0/15 heterozygotes) inbred lines. Finally in some \textit{vangl2}^{ATM/ATM} KO mice, incomplete or failed eyelid closure was observed that was similar in appearance to that described for other PCP mutants [3,36]. However this was highly variable with some eyelids only partially closed and some animals showing unilateral penetrance. As a result this feature was not quantified. Together these observations suggest that aspects of the mutant phenotype are milder in \textit{vangl2}^{ATM/ATM} mice than in \textit{vangl2}^{Lp/Lp} mutants.

The \textit{vangl2}^{ATM/ATM} phenotype was assayed in greater detail in the inner ear because the sensory hair cells have distinct planar polarity that is readily visualized and quantified for direct comparison with the \textit{Lp} mutant phenotype. The apical surface of a hair cell extends a bundle of stereocilia that is organized in a staircase pattern with the tallest stereocilia adjacent to single kinocilium. Planar polarity is apparent in the shared stereocilia-kinocilium polarity of neighboring cells (Fig. 2A-B). Vestibular hair cells in the utricle are further divided between two groups separated by a line of polarity reversal (LPR, Fig. 2C), an organization that is analogous to the pattern of ommatidia in the \textit{Drosophila} compound eye [33]. The LPR is located adjacent to a
specialized region called the striola, and this region can be labeled with antibodies against the transcription factor Gata3 or the calcium binding protein Oncomodulin for use as an anatomical landmark (Fig. 2D–F, Fig. S1) [34,35].

For polarity analyses the utricular maculae was divided into three analysis fields positioned about the immunolabeled striola. Field1 was located in the medial utricle, field2 encompassed the striola and was adjacent to the LPR, while field 3 was in the lateral utricle and contained hair cells of opposite orientation to fields 1 & 2 (Fig. 2C). Misoriented vestibular hair cells were identified in vangl2<sup>TMS/ATM</sup> utricles using phalloidin to mark the stereocilia and antibodies against pericentrin to label the basal body beneath the kinocilium (Fig. 2B,D–E). Affected hair cells were restricted to field2 while the organization of hair cells in fields 1 and 3 were similar to wild type controls. This contrasts with the number and distribution of misoriented vestibular hair cells in vangl2<sup>Lp/Lp</sup> mutants, where affected cells are reported throughout the utricular maculae [7].

In order to determine if this difference is due to a dominant phenotype resulting from the <i>Lp</i> mutation, the two mouse lines were intercrossed and the orientation of utricular hair cells was analyzed in vangl2<sup>TMS/Lp</sup> embryos (Fig. 2F). If the <i>Lp</i> mutation is dominant, then the vangl2<sup>TMS/Lp</sup> phenotype should be more severe than the vangl2<sup>TMS/ATM</sup> phenotype. Alternatively if <i>Lp</i> is recessive or hypomorphic then the vangl2<sup>TMS/Lp</sup> phenotype should be the same or less severe than vangl2<sup>TMS/ATM</sup>. Prior to these intercross experiments, <i>Lp</i> mice were backcrossed to C57Bl6 for a minimum of four generations. Unfortunately after five backcross generations, male vangl2<sup>Lp/WT</sup> offspring were infertile and it was not possible to produce a pure congenic line. In vangl2<sup>TMS/Lp</sup> compound mutants, both the number of misoriented cells and the extent of their disorganization were increased in comparison to vangl2<sup>TMS/ATM</sup>. This included the appearance of misoriented cells in field1 and increased disorganization throughout field2. These trends were quantified by graphing the orientation (from 0–360°) of individual hair cells from all embryos using circular histograms (Fig. 3A), and by measuring the average absolute value of bundle orientations relative to a reference drawn perpendicular to the three analysis fields (Fig. 3B). Each approach demonstrated a significant difference in bundle orientation between vangl2<sup>TMS/ATM</sup> and controls in field1, and between vangl2<sup>TMS/Lp</sup> and controls throughout the utricle (Fig. 3A,C). Moreover, in each of the three fields, a larger proportion of hair cells were misoriented in vangl2<sup>TMS/Lp</sup> than in vangl2<sup>TMS/ATM</sup> mice, although orientation was least affected in field3 for all genotypes with only moderate changes in vangl2<sup>TMS/Lp</sup>. Together these observations reveal a stronger mutant phenotype in vangl2<sup>TMS/Lp</sup> mice and demonstrate potential dominant effects of the <i>Lp</i> mutation during hair cell development.

The planar polarity of auditory hair cells was also disrupted in the cochlea of vangl2<sup>TMS/ATM</sup> KO s (Fig. 4–6). In the cochlea, a progression of hair cell differentiation and polarization occurs along the length from the base to the apex. As a result, more mature stereocilia bundles are present on hair cells positioned in regions closer to the base (analyzed at 25% of the cochlear length) than in apical regions (analyzed at 75% of the cochlear length). In
addition, morphogenesis of outer hair cells (OHCs) initiates after inner hair cells (IHCs). Consequently at E18.5, OHC3 stereocilia bundles are still transiently oriented towards the apical tip of the cochlea (see wild type OHC3, Fig. 5) [36]. OHC3 is also the most susceptible to mutations in PCP genes. Consistent with this, OHC3 is most affected in the \textit{vangl2} \textit{D\textsuperscript{TMs/D\textsuperscript{TMs}}} mice, with misoriented cells in this row along the length of the cochlea (Fig. 6). IHC orientation is also altered in \textit{vangl2} \textit{D\textsuperscript{TMs/D\textsuperscript{TMs}}} mice but primarily in the less mature apical positions (Fig. 6B–C).

The quantification of auditory hair cell polarity in \textit{vangl2} \textit{\Delta\textsuperscript{TMs/Lp}} mice provides additional evidence that the \textit{Lp} mutation is dominant. Similar to the utricle, a larger proportion of auditory hair cells are affected than in \textit{vangl2} \textit{\Delta\textsuperscript{TMs/ATM}} or controls, and within a given row of cells there is an increase in the extent of disorganization. This can be seen for IHCs labeled with phalloidin and pericentrin in the base of the cochlea (Fig. 4). This is further evident when the orientations of all cells are graphed in circular histograms (Fig. 5), and when the average absolute value of bundle orientations is measured relative to neural to abneural axis at three separate points along the length of the cochlea (Fig. 6). Overall the greatest difference between \textit{vangl2} \textit{\Delta\textsuperscript{TMs/Lp}} and \textit{vangl2} \textit{\Delta\textsuperscript{TMs/ATM}} phenotypes occurs for IHCs, and this difference can be measured at all points along the length of the cochlea. It should also be noted that a statistically significant difference in averaged bundle orientation can be detected between \textit{vangl2} \textit{\Delta\textsuperscript{TMs/Lp}}/\textit{WT} and \textit{vangl2} \textit{\Delta\textsuperscript{TMs/WT}} or wild type control littermates (Fig. 6B–C). Although this difference is only detected for OHC3 hair cells in the apical turns of the cochlea, it is consistent with a partially penetrant and dominant \textit{Lp} phenotype. In comparison no differences were seen between \textit{vangl2} \textit{\Delta\textsuperscript{TMs/WT}} and wild type hair cells.

In contrast to vestibular hair cells in the utricle, the orientation of auditory hair cells in \textit{vangl2} \textit{\Delta\textsuperscript{TMs/Lp}} mutants does not appear random. Instead a large proportion of IHCs and OHC3s appear to be reversed by 180 degrees (Fig. 5). This is similar to the reversed orientation of IHCs observed in \textit{fz3/6} DKO s [8] and may reflect the activity of residual polarity mechanisms that function in parallel to core PCP signals. In addition, and as
expected based upon previous Lp analyses [11], a portion of the vangl2 ΔTMs/ΔTMs and vangl2 ΔTMs/Lp cochleae analyzed had extra rows of outer hair cells at the 75% position. In these samples the orientation of stereocilia bundles for OHC3 was not significantly altered and was more similar to OHC2 than the outermost row of ectopic cells. Therefore for quantification purposes, all hair cells located between OHC1 and the last row of outer hair cells (lastOHCs) were grouped and analyzed together as the middle rows (midOHCs, Fig. 6). It was unclear whether the appearance of these rows was due to defects in convergent extension movements or was secondary to craniorachischisis in these mutants.

Together these experiments suggest that the presence of the Vangl2 S464N mutant protein has a greater effect on cellular polarization than the loss of wild type Vangl2. Recently it was shown that the Lp mutation disrupts Vangl2 association with Sec24b, a trafficking protein required for export from the endoplasmic reticulum [27]. This mechanism may also be the basis of craniorachischisis in LpΔPv, a second vangl2 mutant line.
with an aspartic to glutamic acid substitution at amino acid position 255 (Vangl2D255E) [29]. As a result, in each of these mutants, Vangl2 protein is retained within the endoplasmic reticulum and fails to be delivered to the plasma membrane. Two separate mutations in Sec24b also disrupt Vangl2 trafficking resulting in similar craniorachischisis phenotypes [27,28]. One explanation for the stronger phenotype that occurs in vangl2D255E mutants than vangl2D255K/K mice is that altered Vangl2S464N trafficking disrupts the distribution of other polarity molecules. A likely candidate is Vangl1 because Vangl1 expression overlaps with Vangl2, and enhanced planar polarity defects are seen in mice lacking both vangl1 and vangl2[12,37]. Remarkably Van Gogh proteins oligomerize into larger protein complexes in Drosophila [38] raising the possibility that if similar oligomeric complexes are formed in vertebrates, then Vangl2S464N or Vangl2D255E may disrupt Vangl1 or Vangl2 delivery to the plasma membrane. This hypothesis was tested using a heterologous system in which hemagluttinin (HA) tagged Vangl2 constructs were co-expressed with EGFP-tagged Vangl1 or Vangl2. Specifically these experiments utilized 3XHA-tagged Vangl2, 3XHA-Vangl2S464N and 3XHA-Vangl2D255E constructs characterized by Merte et al. [27]. Consistent with previous reports, following electroporation into MDCK cells, the control constructs 3XHA-Vangl2, EGFP-Vangl2 and EGFP-Vangl1 were delivered to the plasma membrane and were enriched at cell boundaries (Fig. 7A, B, G–H, Fig. S2). This distribution was enhanced 96 hours post-electroporation, presumably due to the maturation of intercellular junctions between MDCK cells (data not shown). However there was never an asymmetric redistribution of Vangl1 or Vangl2 fusion proteins in the cultured cells. In contrast, 3XHA-Vangl2S464N or 3XHA-Vangl2D255E constructs were found predominantly in cytoplasmic compartments (Fig. 7C, E, I, K, O, Q) similar to the distribution of the mutant proteins in COS cells [27]. Vangl2 mutant proteins were also less stable than wild type with a half life of approximately 48 hours. Therefore protein distribution studies were conducted 72 hours post-electroporation when the majority of wild-type proteins were present at cell boundaries (Fig. 7B, H, N). At this time co-expression of 3XHA-Vangl2S464N or 3XHA-Vangl2D255E significantly changed the subcellular distribution of EGFP-Vangl1 (Fig. 7A–F) and EGFP-Vangl2 (Fig. 7G–I). In the presence of mutant Vangl2, detectable EGFP-Vangl1 or EGFP-Vangl2 protein was reduced at the membrane and increased in intracellular compartments. Furthermore the distribution of
EGFP-Vangl1 (arrowheads, Fig. 7E) or EGFP-Vangl2 (arrowheads, Fig. 7K) appeared similar to mutant Vangl2 within cells expressing both constructs. This effect specifically occurred between Vangl proteins as 3XHA-Vangl2S464N and 3XHA-Vangl2D255E did not alter the distribution of E-Cadherin-GFP, another membrane spanning protein enriched at MDCK cell boundaries (Fig. 7M–R). MDCK cell electroporation with the tagged constructs also did not alter the distribution of endogenous E-cadherin (Fig. S2).

The potential for physical interactions between Vangl1 and Vangl2, and between different Vangl2 molecules were further assayed by co-immunoprecipitation of 3XHA and EGFP-tagged proteins from MDCK cells. Using this approach, immunoprecipitation of EGFP-Vangl1 or EGFP-Vangl2 with GFP antibodies pulled down 3XHA-Vangl2 when the constructs were co-expressed (Fig. 8A). Similarly EGFP-Vangl1 and EGFP Vangl2 bound and co-precipitated 3XHA-Vangl2S464N. Doublets in HA (Fig. 8B) and EGFP blots (Fig. 8C) demonstrate that the phosphorylation of tagged-Vangl2 proteins is similar to wild type (Fig. 1C and [32]). Altogether these in vitro studies utilizing MDCK cells argue that the molecular basis of dominant Lp mutations is the disrupted trafficking of multimeric Vangl1/2 complexes resulting in an overall reduction in planar polarity.

To determine if the Lp mutation disrupted Vangl1 distribution in vivo, wholemount immunolabelling was used to visualize Vangl1 protein distribution in vangl2ΔTMs/ΔTMs and vangl2ΔTMs/Lp utricles. Although Vangl1 and Vangl2 are 71% identical (NCBI pair-wise BLAST), the Vangl1 antibody appears specific for Vangl1 because there are no differences in Western blot analyses between protein lysates collected from WT and vangl2ΔTMs/ΔTMs embryos (Fig. 5).

**Figure 5. Circular histograms quantifying the orientation of all auditory hair cells.** The orientation of individual auditory hair cells was measured at a position corresponding to 50% of the cochlear length based upon phalloidin and pericentrin immunolabelling. Hair cells from each row (IHC, OHC1, OHC2, OHC3) were analyzed separately, and each column of histograms corresponds to the separate genotypes listed beneath. The number of cells in each bin is graphed along the x-axis and the total number of cells for each histogram is listed. For these histograms 90° is pointed away from the spiral ganglion and 180° is pointed towards the apex of the cochlea. The average orientation of each group of cells is marked by a bold black line.

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Figure 6. Quantification of averaged stereocilia bundle orientation for auditory hair cells. (A–C) The averaged mean deviation of stereocilia bundle orientation was determined by measuring the absolute value of the angle formed by the bundle axis and a reference line drawn perpendicular to the 4 rows of hair cells. (A) In this schematic red indicates the position of the kinocilium and green is the cell periphery. The averaged deviation was graphed separately for positions located at (A) 25%, (B) 50%, and (C) 75% the length of the cochlea as measured from the base to the apex. For some mutant samples, additional rows of outer hair cells were present at the 75% position. To facilitate comparisons between genotypes, all hair cells located between OHC1 and the last row of hair cells (lastOHCs) are combined and graphed as MidOHCs (middle rows of OHCs). Error bars indicated standard deviation. Statistical significance was calculated by Student’s t-test with unequal variance. (*P < 0.05, **P < 0.001, ***P < 10^-5).

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Despite this, the antibody cannot distinguish EGFP-Vangl1 and EGFP-Vangl2 by Western blot when the EGFP-tagged proteins are over-expressed in MDCK cells. Still there is a 10-fold greater affinity of the antibody for EGFP-Vangl1 than EGFP-Vangl2 (Fig. S3B). Vangl1 immunolabeling of the mouse utricle is enriched at the apical surface of vestibular hair cells, and labeling is frequently asymmetric at boundaries (Fig. 9A, arrowheads). Vangl1 immunolabeling is maintained at the apical cell surface in vangl2−/−/− utricles; however Vangl1 distribution frequently appears more uniform and often surrounds mutant hair cells (Fig. 9B, arrows). For these experiments the position of the striola region was determined by Oncomodulin immunolabeling in a second channel (data not shown) and is indicated by brackets (Fig. 9 A–F). In dramatic contrast, the apical localization of Vangl1 protein fails to occur throughout all regions of the vangl2−/−/− mutant utricle (Fig. 9C). Instead fluorescent puncta are visible which may reflect the redistribution of Vangl1 within intracellular organelles. These in vivo results are consistent with those in vitro, and support the hypothesis that disrupted trafficking of Lp mutant Vangl2S464N protein inhibits delivery of Vangl1 to the cell surface.

Figure 7. Mutant Vangl2 protein alters the distribution wild type Vangl1 and Vangl2. (A–F) The effect of mutant Vangl2 proteins on the distribution of Vangl1 was determined by co-expressing EGFP-Vangl1 in MDCK cells together with 3XHA Vangl2 (A–B), 3XHA Vangl2D255E (C–D) or 3XHA Vangl2S464N (E–F). Recombinant protein distribution was visualized after 72 hours in culture using antibodies against GFP (green) or HA (red). (G–L) Similarly the effect of mutant Vangl2 proteins on the distribution of wild type Vangl2 was determined by co-expression of EGFP-Vangl2 with 3XA Vangl2 (G–H), 3XHA Vangl2D255E (I–J) or 3XHA Vangl2S464N (K–L). (M–R) Mutant Vangl2 proteins do not disrupt the membrane localization of E-Cadherin-GFP. (E,K,Q) Representative cells only expressing EGFP-Vangl1, EGFP-Vangl2 or E-Cadherin-GFP are marked by arrows and representative cells co-expressing 3XHA Vangl2S464N and EGFP-constructs are marked by arrowheads. (B,D,F,J,L,N,P,R). The subcellular distribution of EGFP in co-transfected cells was scored as membrane associated (blue), cytoplasmic (light gray), or both membranous and cytoplasmic (gray) and graphed. Quantification was completed for cells obtained from one round of electroporations and the total numbers of co-transfected cells analyzed for each condition are indicated beneath the pie chart. These findings were consistent with additional electroporations experiments in which cells were imaged but not quantified.

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Figure 8. Co-Immunoprecipitation assays show oligomeric complex formation consisting of EGFP-Vangl1 and 3XHA-Vangl2, or EGFP-Vangl2 and 3XHA-Vangl2. (A) Immunoprecipitation (IP) of EGFP-Vangl1 or EGFP-Vangl2 using an antibody against GFP pulls down 3XHA-tagged Vangl2 when co-expressed in MDCK cells demonstrating the formation of an oligomeric complex. Similarly, EGFP-Vangl1 or EGFP-Vangl2 IPs also pull down mutant 3XHA-Vangl2S464N protein showing that the Looptail mutation does not disrupt oligomerization. (B,C) Western blots of MDCK cell lysates alone were used to confirm expression of HA-tagged (B) and EGFP-tagged constructs (C), and equilibrate the amount of cell lysates used for immunoprecipitation. Phosphorylated 3XHA-Vangl2 runs in a slower migrating band (arrow, B) and phosphorylated EGFP-Vangl2 generates a doublet (arrowhead, C) in denaturing SDS-PAGE gels of immunoprecipitates or cell lysates. Phosphorylation of 3XHA-Vangl2S464N mutant protein is decreased under all conditions.

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To establish whether altered Vangl2 trafficking, or the resulting changes in planar polarity, affected the behavior of other PCP proteins, the distribution of Prickle 2 (Pk2, Entrez Gene ID: 243548) was assayed in vangl2^{Dm/Tm} mice and vangl2^{Lp/Lp} utricles. In Drosophila, Prickle binds to Van Gogh and the two proteins are localized in hair cells and support cells throughout the vestibular epithelia (Fig. 9D, arrowheads, and [5]). In vertebrates, Pk2 is also asymmetrically localized to the proximal side of wing epidermal cells [39] where Prickle promotes the intracellular amplification of cellular polarity [40]. In the mouse, Pk2 is also asymmetrically localized at many cell boundaries (arrowheads). (B) Apical localization of Vangl1 is maintained in the vangl2^{Dm/Tm} utricle although asymmetric localization is lost, and individual hair cells are frequently surrounded by Vangl1 protein (arrows). (C) Vangl1 protein is significantly reduced from apical cell boundaries in vangl2^{Lp/Lp} utricles. (D) Pk2 is enriched at hair cell:support cell boundaries throughout the wild type utricle (examples marked by arrowheads). (E) In vangl2^{Dm/Tm} tissue, the distribution of Pk2 changes in a region specific manner. In the bracketed striola region, Pk2 protein frequently surrounds individual hair cells (arrows). In lateral regions apical protein localization is lost, while Pk2 is maintained in a normal pattern in the medial utricle (arrowheads). (F) Similar to changes in Vangl1 distribution, the presence of Pk2 at apical cell boundaries is lost throughout the vangl2^{Lp/Lp} utricle. Brackets indicate the approximate positions of the striola region based upon Oncomodulin labeling in a separate channel. Scale bar is 25 μm.

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Discussion

By generating a novel vangl2 knockout line and intercrossing those mice with Lp mutants, we have demonstrated the dominant nature of the Lp mutant phenotype during inner ear development. This was completed through a detailed quantification and comparison of the planar polarity phenotypes of hair cells in vangl2^{Dm/Tm} and vangl2^{Lp/Lp} mice. In addition we propose a mechanism for the dominant effect of the Lp mutation in which disrupted trafficking of Vangl2^{S464N} alters the distribution of Vangl1, Vangl2 and Pk2. Together these findings will guide interpretation of studies employing the Looptail line, particularly when Looptail mice are used for molecular dissections of the PCP signaling pathway.

At a molecular level, the decreased protein stability and cell-surface presentation of Vangl2^{S464N} is due to disrupted trafficking of the mutant protein and its retention in the ER [27]. We have demonstrated that co-expression of Vangl2^{S464N} with Vangl1 in a heterologous system also prevents Vangl1 delivery to the cell...
surface. Since vangl1 and vangl2 regulate planar polarity in many tissues including the inner ear [12,13], it stands to reason that the combined loss of Vangl1 and Vangl2 would increase hair cell orientation defects. Consistent with this hypothesis, planar polarity defects are less in those vangl2ATM/ATM; vangl1-/- vestibular hair cells that maintain apical localization of Vangl1 than in vangl2ATM/ATM hair cells where apical Vangl1 is lost. We also demonstrate that Vangl2 forms oligomers with Vangl1 and Vangl2 in heterologous cells. This is similar to findings from Drosophila where Van Gogh oligomerizes in vivo [30]. Many integral membrane proteins are folded and assembled into oligomeric structures in the ER and inappropriate assembly or transport out of the ER results in protein degradation by “quality control” systems [31,42]. Therefore our results, together with these previous findings, suggest that the Vangl2S464N protein encoded by the Lp mutation exerts dominant effect on planar polarity by inhibiting the membrane trafficking and localization of Vangl1 and Vangl2, likely leading to their degradation.

This mechanism is sufficient to explain the milder neural tube phenotype that occurs in vangl2D23/WT heterozygotes if the presence of Vangl2S464N reduces but does not eliminate all Vangl1/2 protein from the cell surface. By comparison the uterine epithelium of the female reproductive tract (FRT) is more sensitive to the Lp mutation than the neural tube. In a recent study where embryonic FRT tissues were cultured in vitro, similar developmental deficits were observed explants from vangl2Lp/WT and vangl2D23/WT embryos, further demonstrating the dominant effect of Lp [23]. Consistent with this study, we also found a mild planar polarity phenotype in the cochlea of vangl2D23/WT heterozygotes that was restricted to OHC3 and was only present in the less developed apical turns (Fig. 6B–C). In contrast OHC3 is not affected in vangl2ATM/WT cochlea. Although the molecular basis of Lp sensitivity was not established in the FRT, tissue specific responses to the Lp mutation in heterozygotes are likely determined by the complement of PCP proteins expressed in the tissue and their capacity to compensate for the presence of Vangl2S464N.

The severity of the Lp mutant phenotype is also influenced by genetic modifiers and can vary between different labs [3], presumably due to differences in husbandry practices and strain background. We have attempted to control this variable using two parallel approaches. First, the vangl2ATM and Lp lines were maintained through successive heterozygote backcrosses with wild type C57Bl6 mice. This approach is limited however, because vangl2D23/WT males are infertile after five backcross generations. In contrast, vangl2ATM/WT mice can be backcrossed with C57Bl6 for at least nine generations without significant decreases in breeding potential. Second, by analyzing vangl2ATM/mL compound mutants rather than vangl2D23/mL, we sought to make heterozygous any genetic modifiers that may be unique to our colony of Looptail mice. Therefore the phenotypic differences between vangl2ATM/mL and vangl2D23/mL mutants are unlikely to be due to genetic modifiers. Overall these phenotypic comparisons combined with in vitro and in vivo protein localization studies demonstrate the dominant nature of the Lp mutation and provide a molecular basis for this effect.

The impact of the dominant nature of the Lp mutation on genetic interactions between this allele and other mutations should not be overlooked. However our results do not imply that conclusions drawn from previous intercrosses with Lp are false. In contrast, these findings demonstrate that crosses with Lp may represent a more sensitive assay of genetic interactions with the PCP signaling pathway than analogous crosses that could be generated using vangl2ATM. Still it is important to distinguish between mutations that are merely permissive and only increase the penetrance of the vangl2ATM/WT phenotype versus mutations that may have an additive effect when combined with vangl2ATM/ATM, because the former genes may only be indirectly involved in planar polarity. Two additional vangl2 mutations should also prove useful for genetic analyses. One is the Lp-m2Jus mutation that has similar molecular and phenotypic characteristics as the Lp mutation [27,29]. The second is Lp-m2Jns which has a recessive phenotype with partially penetrant and hypomorphic characteristics in homozygotes such as looped tails and spina bifida [43]. Moreover the orientation of auditory hair cells is undisturbed in Lp-m2Jns mutants. Together the growing collection of vangl2 mutant mouse lines could be employed as an allelic series for distinguishing subtler aspects of planar polarity during tissue development.

**Materials and Methods**

**Ethics Statement**

Mice were maintained at Harvard Medical School or The Johns Hopkins University School of Medicine under the corresponding IACUC-approved guidelines. The Johns Hopkins University School of Medicine Institutional Animal Care and Use Committee specifically approved this study under animal use protocols MO08M408 and MO11M394.

**vangl2 gene targeting**

A gene targeting vector was assembled from mouse genomic DNA purified from the TC1 mouse ES cell line (P. Leder, Harvard Medical School). The vector contained a 4.2 kb 5' arm that was modified by inserting LoxP and Hind3 sequences into a unique Xmn1 restriction site located in the intron upstream of vangl2 exon 4. A second LoxP sequence and NeoR cassette flanked by FRT sequences was introduced into a unique BstB1 RE site located in the intron downstream of exon 4. The remainder of the vector consisted of a 5.1 kb 3' homologous arm and DTA negative selection cassette. Mouse genomic DNA sequences used as homologous arms were amplified by PCR using the Roche Expand Long Template PCR System (Roche) and coding sequence exons located within the homologous arms were sequenced to check for PCR induced mutations. Following electroporation into the TC1 ES cell line and positive selection with G418, homologous recombination was validated in surviving clones by PCR and Southern blot (Fig. 1). A single ES cell line was injected into C57Bl6 blastocysts by the Brigham and Women's Hospital Transgenic Core Facility (Boston, MA). Following germline transmission, founders were crossed with transgenic mice ubiquitously expressing FlpE recombinase (ACTB-FlpE) to remove the NeoR gene. The resulting allele (vangl2D23f) was not viable when homozgyosed because the positions of the remaining LoxP sites disrupted vangl2 expression. As a result, vangl2D23f was crossed to transgenic mice ubiquitously expressing Cre recombinase (ACTB-Cre) to permanently delete exon 4 in the germ line and produce the vangl2ATM knockout line.

**Mouse husbandry and genotyping**

For general colony maintenance, vangl2ATM/WT mice were crossed to mice from the C57Bl6 inbred line. For backcrossing, vangl2ATM/WT female mice were bred to male mice from the C57Bl6, FVB or A/J inbred lines for a minimum of 5 generations prior to phenotypic analysis of heterozygotes or experimental intercross. The Lp mouse line was maintained by breeding with...
B6129S3F1/J hybrid mice and heterozygotes were identified based upon the presence of looped or kinked tails. Prior to experimental intercross with vangl2<sup>ATm</sup>, the Lp mice were backcrossed to C57Bl6 for 4 generations. Additional backcrosses were not possible as Bx−5 male mice were infertile and female mice had a high frequency of imperforate vagina that is common to this line. Mice from strains A/J, B6129S3F1/J, ACTB-<sup>C</sup>Cre and the Lp mutant line were purchased from The Jackson Laboratory (Bar Harbor, ME), C57Bl6 and FVB mice were purchased from Charles River Laboratories (Wilmington, MA) and the ACTB-<sup>F</sup>LPs were obtained from S. Dymecki (Harvard Medical School).

**Antibodies and Immunolabeling**

Immunofluorescent labeling of auditory and vestibular hair cells was completed using E18.5 inner ear slices fixed for 2 hours in a solution of 4% paraformaldehyde prepared in Sorenson’s phosphate buffer (pH7.4). Utricles and cochleae were subsequently removed, dissected to expose the surface of the sensory epithelia, permeabilized and blocked using blocking solution (5% donkey serum, 1% BSA, PBS) supplemented with Triton X-100 to 0.5%. Primary antibodies and phallloidin Alexa488 (Invitrogen A12379) were included in blocking solution supplemented with Tween-20 to 0.1%, and incubated with the tissue overnight at 4°C. Tissue was washed thoroughly with PBS-T (PBS, 0.05% TWEEN-20) followed by incubation with species-specific, Alexa Fluor (Invitrogen) or DyLight (Jackson ImmunoResearch) conjugated secondary antibodies. Tissue was subsequently washed with PBS-T, mounted using Fluoro-Gel (Electron Microscopy Sciences), and imaged using a Zeiss LSM510 confocal microscope. Image frames were limited to 1.5 microns in the Y-dimension and a stack of images 3–6 microns containing the stereocilia and apical surface of the hair cells was collected. A single image was generated by Z-projection using maximum or averaged pixel intensities. For preparations in which the striola region was marked using Gata3 antibodies, a second stack positioned deeper in the tissue was necessary to identify hair cell planar polarity. All samples were analyzed for quantitative immunolabeling by confocal microscopy at two positions spanning the Gata3- or Oncomodulin-positive striola and images were combined by confocal microscopy at three positions corresponding to 25%, 50% and 75% of the length of the cochlea measured from the base. The orientation of individual hair cells was measured using the ImageJ (NIH) angle measurement tool. The short arm of each hair cell was drawn parallel to three adjacent hair cells within the same row. This yields a measurement range of 0 to 180 degrees in which a perfectly aligned hair cell has a raw measurement of 90 degrees. For those cells determined to have reversed bundles (i.e. kinocilium pointed toward the spiral ganglia) the orientation was calculated with the formula x = (360−y) where x is orientation and y is the measured angle. This calculation and additional analyses were completed using Microsoft Excel. These absolute measurements of auditory hair cell orientation were assembled as a circular histograms using Oriana circular graphing software (Kovach Computing Services). Planar polarity phenotypes were further quantified by averaging the mean absolute deviation of hair cell polarities from an arbitrary reference (defined as 0°) for each animal as illustrated in Fig. 6B. These analyses were completed for each genotype at the three cochlear positions. Statistical significance was calculated by a two-tailed Student’s t-test with unequal variance.

For vestibular hair cell analyses the utricular maculae was imaged by confocal microscopy at two positions spanning the Gata3-positive or Oncomodulin-positive striola and images were combined based upon regions of overlap. As outlined in Fig. 2, stereocilia bundle polarity was measured in three 100 µm×50 µm analysis fields. Using Canvas11 illustration software (Dencha), analysis fields were positioned with field2 centered on the striola. Field1 was positioned in the medial utricle and field3 was in the lateral utricle, with each separated from field2 by 50 µm and 20 µm gaps respectively. The orientation of individual hair cells within each analysis field was marked using the Canvas11 line tool and ROIs were exported to ImageJ for orientation measurements. This yields a measurement range of 0–180’s for cells oriented towards the lateral utricle (i.e. WT cells in field2). For those cells determined to be oriented towards the medial region (i.e. WT cells in field3) bundle orientation was calculated with the formula x = (180+y) where x is orientation and y is the measured angle. Vestibular hair cell orientation was assembled as a circular histogram using Oriana circular graphing software. Planar polarity phenotypes were further quantified by averaging the mean absolute deviation of hair cell polarities from an arbitrary reference (defined as 0°) for each animal as illustrated in Fig. 3B. Statistical significance was calculated by a two-tailed Student’s t-test with unequal variance.

**See Table S1 for sample sizes at each position, tissue and genotype. Because there was some variability of severity of NTDs in vangl2<sup>ATm/ATm</sup> KO mice, only KO’s with craniorachischisis were included in the measurement of hair cell planar polarity. All vangl2<sup>ATm</sup> and vangl2<sup>ATm/−</sup> mutants collected had craniorachischisis. Hair cells in which the bundle polarity or pericentrin labeling could not be visualized were not included in the auditory or vestibular analyses.**

MDCK and HEK293 cell culture, electroporation and immunolabeling

MDCK cells (SIGMA S8412093) were grown in EMEM supplemented with 2 mM L-Glutamine, 1× non-essential amino acids, 10% FBS and 1× Penn/Strep. HEK293 cells (American Type Culture Collection ATCC-CRL-1573) were grown in DMEM, 10% FBS and 1× Penn/Strep. MDCK cells were transfected via electroporation, by combining 1×10<sup>7</sup> cells with 30 µg plasmid DNA (60 µg total for co-electroporations) in a 2 mm gap electroporation cuvette, followed by electroporation at 260 V with 950 uF capacitance and 25 Ohm resistance using a BTX ECM630 electroporation box. MDCK cells were plated into single wells of a Lab-Tek II 8-well Chamber Slides (Thermo Scientific) and incubated 72 hours to allow adherence junctions to form at cell boundaries before the distribution of EGFP-tagged
proteins was assayed by immunofluorescent labeling. HEK293 cells were transfected using Lipofectamine reagent as per the manufacturer's recommendation, cultured for 24–48 hours and harvested for Western blot analysis. For these experiments a plasmid expressing EGFP-Vangl1 was generated by PCR amplification from mouse cDNA and cloned into the pEGFP-C1 vector (Invitrogen) to generate an amino-terminus EGFP fusion, EGFP-Vangl2 [7], 3XHA-tagged Vangl2 constructs [27], and E-Cadherin-GFP have been described elsewhere [44]. The E-Cadherin-GFP construct was distributed by Addgene (Addgene plasmid 29009).

For labeling, MDCK cells were fixed with 4% paraformaldehyde prepared in PBS, permeabilized and blocked as described previously. Cells were immunolabeled with anti-HA and anti-GFP antibodies diluted in 1% BSA/PBS followed by Alexa Fluor conjugated secondary antibodies, and then examined by fluorescent microscopy using a Nikon E600 compound microscope. For protein localization assays only cells expressing both HA-tagged and EGFP-tagged constructs were evaluated, and the distribution of EGFP-tagged proteins were scored as membrane associated, cytoplasmic or present in both locations.

Western blot and Co-immunoprecipitation

Protein lysates were prepared from tissues, MDCK or HEK293 cells using a lysis buffer consisting of 25 mM Tris pH 7.4, 1% Triton X-100, 50 mM NaCl and 1 × protease inhibitor cocktail (SIGMA P8340) and quantified by UV absorption at 280 nm using a NanoDrop. Following SDs-PAGE electrophoresis proteins were transferred to nitrocellulose filters and blotted with standard Western blot techniques using anti-GFP or anti-HA antibodies followed by chemiluminescent detection using BioRad Immun-Star HRP substrate. Immunoprecipitations were completed using Nynal protein G beads (Invitrogen) bound to rabbit anti-GFP or mouse anti-HA antibodies and combined with protein lysates from electroporated MDCK cells. Prior to immunoprecipitation, levels of recombinant protein expression were determined by Western blot analysis and equivalent amounts of recombinant protein were used from each electroporation condition. Target antigens were absorbed at 4°C, and washed using the manufacturers recommended protocols and solutions, then eluted from the beads using Laemmli 2 × Gel-loading Buffer with DTT prior to denaturing SDS-PAGE and conventional Western blot analysis.

Supporting Information

Figure S1 Gata3 and Oncomodulin immunolabeling marks the position of the striola in developing mouse utricle. (A) The transcription factor Gata3 (red) is expressed by multiple cells types located in the striola region of the developing utricle and Gata3 immunolabeling can be used to visualize this region. (B) The calcium binding protein Oncomodulin (red) is expressed exclusively by type1 hair cells located in the striola, and Oncomodulin immunolabeling can also be used to visualize this region. (A–B) Phalloidin (green) was used to assay stereocilia bundle orientation (arrows) and map the position of the line of polarity reversal (LPR, dashed lines). In mouse, the LPR is located along the lateral border of the striola. (TIF)

References


