

# Assembly of hair bundles, an amazing problem for cell biology

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**ABSTRACT** The hair bundle—the sensory organelle of inner-ear hair cells of vertebrates—explains the ability of a cell to assemble complex, elegant structures. Proper construction of the bundle is required for proper mechanotransduction in response to external forces and to transmit information about sound and movement. Bundles contain tightly controlled numbers of actin-filled stereocilia, which are arranged in defined rows of precise heights. Indeed, many deafness mutations that disable hair-cell cytoskeletal proteins also disrupt bundles. Bundle assembly is a tractable problem in molecular and cellular systems biology; the sequence of structural changes in stereocilia is known, and a modest number of proteins may be involved.

## Monitoring Editor

William Bement  
University of Wisconsin

Received: May 11, 2015

Revised: May 28, 2015

Accepted: Jun 2, 2015

## INTRODUCTION

The remarkable structure of the vertebrate hair bundle derives from an equally remarkable assembly process. Actin-rich stereocilia form, lengthen, and widen in a precisely determined order (Tilney *et al.*, 1992), giving the bundle its asymmetric, staircase appearance (Figure 1). The importance of bundle assembly and structure is highlighted by the number of deafness-causing mutations, a subset of which are in genes that encode actin or actin-associated proteins (for examples, see Table 1). Assembly of the bundle involves multiple overlapping and interacting cellular processes, such as stereocilia lengthening and widening, each of which is responsible for one or more features of the final structure.

Tom Pollard has written eloquently on the reductionist-synthetic strategy to characterize complex biological mechanisms (Pollard, 2013). His first step is to frame a good problem—and I believe that hair-bundle assembly fits the bill. Like other subcellular processes, including cytokinesis or cell migration, bundle development is relatively circumscribed mechanistically and may require a modest number of proteins, perhaps 100 or fewer. As a reasonably simple systems-biology problem, it is both amenable to study with present technology and suitable as a model for more complex problems. I

suggest that now is the time to use systems and cell biology to study how the bundle is built and that this problem is ideal for young cell biologists looking for a career-defining problem to solve.

## DESCRIPTION OF HAIR-BUNDLE ASSEMBLY

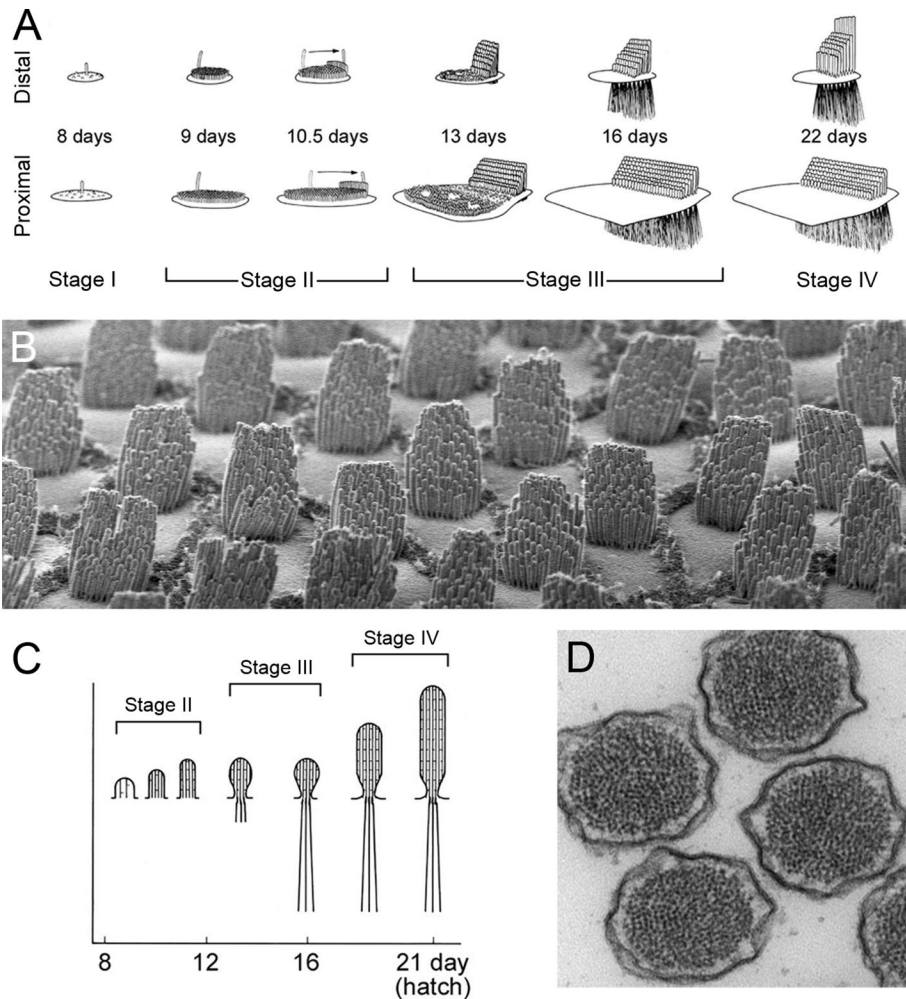
First, I present what is known about molecular mechanisms of bundle assembly. Part of Pollard's first step is to define the problem of interest in enough detail that it can be interrogated using a molecular approach. Lew Tilney's landmark studies of hair-bundle development from the 1980s, using electron microscopy, remain the most comprehensive description of bundle assembly. Focusing on the chick cochlea, he and his colleagues identified four distinct stages of bundle growth (Figure 1A). In stage I, before embryonic day 8 (E8), a hair cell's progenitor undergoes its terminal division, and the hair cell begins to differentiate. In stage II (E8–E13), the kinocilium moves to one side of the bundle, stereocilia adjacent to the kinocilium elongate, tip links appear, and cross-linking of actin filaments increases. By the end of stage II, the bundle has a robust staircase separation of stereocilia length. In stage III (E13–E16), stereocilia lengthening stops, but the stereocilia begin to widen, from ~100 to as many as 900 filaments per stereocilium. During this time, the anchoring structure for the stereocilia—the cuticular plate—begins to form and the stereocilia bases taper, presumably essential for proper bundle flexibility. Finally, lengthening resumes in stage IV (E16–postnatal day 3, P3), stopping only when stereocilia reach their mature lengths. The cochlea encodes sounds of different frequencies using different hair cells; high frequencies are encoded at the proximal (basal) end, and low frequencies are encoded at the distal (apical end). Indeed, the number and length of stereocilia vary systematically from proximal to distal ends. Nevertheless,

DOI:10.1091/mbc.E14-04-0940

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**FIGURE 1:** Development of the hair bundle. (A) Progression of hair-bundle morphology in chick cochlea. (B) Chick cochlea hair bundles at hatch. Hair cells imaged are at an intermediate position between the apical and basal extremes. Note the cell-to-cell reproducibility of the numbers of stereocilia, their orientation, and their lengths. Hair bundles are ~10  $\mu\text{m}$  tall. (C) Progression of stereocilia actin paracrystal development in chick cochlea. (D) Actin paracrystals in mouse vestibular stereocilia. Note the stereocilium-to-stereocilium reproducibility of the size and organization of the actin cores. Stereocilia are ~200 nm in diameter. A and C are reproduced from Tilney *et al.* (1992) with permission.

adjacent cells control bundle assembly very reproducibly (Figure 1B). The general principles of Tilney's scheme for chick-bundle morphogenesis, especially the temporal and spatial segregation of stages of bundle development, are believed to apply to all hair-cell organs.

### COMPONENTS OF THE HAIR BUNDLE

Pollard's second step in characterization of molecular mechanisms is to develop a parts list. The auditory neuroscience field has been engaged in this problem for the last several decades, using both genetics and biochemistry to determine which proteins are present in hair bundles and which are functionally important. "Deafness genes," which, when mutated, lead to deafness, are good candidates for key molecules, particularly if their protein products are present in bundles (Petit and Richardson, 2009; Dror and Avraham, 2009). Several dozen already identified proteins fit this category, and geneticists continue to slowly add more. Examples of key deafness genes that are expressed in hair bundles are listed in Table 1; locations for many of the proteins are shown in Figure 2. Because

the genetic strategy could easily miss many key proteins, including those whose activity can be compensated for by functional paralogues or those with pleiotropic effects, other approaches are needed to identify all functionally important proteins of the bundle.

Protein biochemistry offers a complementary approach. Development of methods for purification of hair bundles (Shepherd *et al.*, 1989; Gillespie and Hudspeth, 1991) provided enough starting material to specifically examine which proteins are present in bundles. Although initial experiments used one-by-one examination of proteins by immunoblotting, development of modern mass spectrometry methods now allow parallel examination of thousands of proteins. Mass spectrometry analysis of purified bundles has identified hundreds of bundle-specific proteins from vestibular and auditory organs of the chick (Shin *et al.*, 2013; Avenarius *et al.*, 2014). Present challenges include determining which of these proteins are most important for bundle assembly and the features of bundle development in which they participate.

### SPECIFICATION OF STEREOCILIA NUMBER AND POSITION

A close look at hair-bundle assembly with the parts list in mind allows us to associate some proteins with stages of morphogenesis. At early points during hair-cell differentiation, short stereocilia cover the apical surface of the cell; these cilia can nonetheless be distinguished from the shorter microvilli on adjacent supporting cells. The position of the kinocilium—an axonemal cilium (with 9 + 2 microtubule doublets)—may then specify bundle polarity. Stereocilia adjacent to the kinocilium first elongate, followed by succeeding rows (Tilney *et al.*, 1992; Kindt

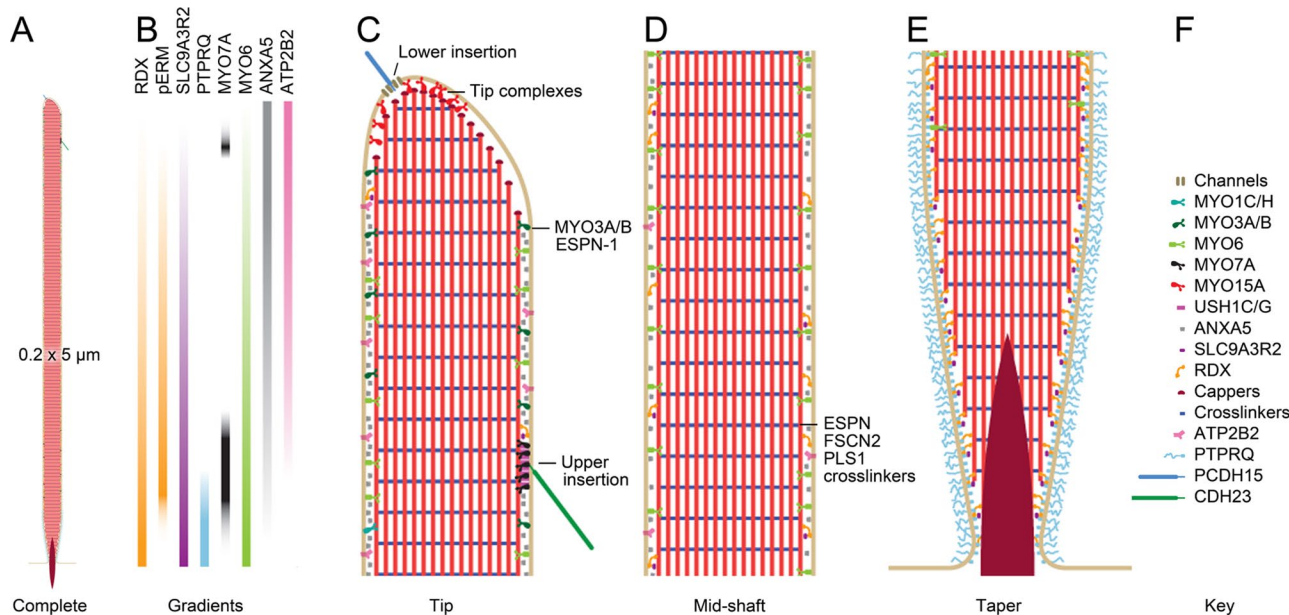
*et al.*, 2012). These results show the essential role of the kinocilium (or the basal body) in establishing subcellular planar polarity (Deans, 2013).

The number and placement of stereocilia can vary systematically along one or more tissue axes. How different cells specify stereocilia number is unknown, but an intriguing suggestion is that they arise as Turing patterns from simple reaction-diffusion mechanisms (Jacobsohn and Hudspeth, 2014). Stabilization of stereocilia by a Turing mechanism could complement developmental stimulation of stereocilia elongation; together these mechanisms would allow for growth of the rows followed by pruning of unstabilized stereocilia. Candidates for components for control of Turing patterns or stereocilia stabilization include RAC1 and its downstream effector p21-activated kinase (Grimsley-Myers *et al.*, 2009, 2012), both of which are detected in stereocilia (Shin *et al.*, 2013). Upstream control of those mechanisms may be exerted by Sonic hedgehog (SHH); eptopic SHH reduces the numbers of stereocilia in basal hair cells, which typically have many stereocilia (Son *et al.*, 2015).

Gene symbol	Gene name	Deafness mutant	Hair-bundle phenotype	Protein location
ACTB	Actin beta	Actb knockout	Progressive degeneration of hair bundles	Stereocilia shafts
ACTG1	Actin gamma 1	DFNA20/26, Actg1 knockout	Progressive degeneration of hair bundles	Stereocilia shafts
ANXA5	Annexin V	Anxa5 knockout	None	Shafts
ATP2B2	ATPase, Ca <sup>2+</sup> transporting, plasma membrane 2	Atp2b2 knockout	Progressive degeneration of hair bundles	Shafts (excluded from taper); concentration toward tips
CAPZ	Capping protein (A1, A2, and B genes)	n/a	Unknown	Stereocilia tips
CDH23	Cadherin 23	USH1D, DFNB12	Disorganized hair bundles	Tip links; transient lateral links; kinocilial links
DFNB31	Whirlin	USH2D, DFNB31	Short stereocilia	Tips; ankle links
EPS8	Epidermal growth factor receptor pathway substrate 8	Eps8 knockout	Short stereocilia	Stereocilia tips
EPS8L2	EPS8-like 2	Eps8l2 knockout	Progressive degeneration of hair bundles	Stereocilia tips
ESPN	Espin	DFNB36	Short and thin stereocilia; degeneration in the cochlea	Short ESPN splice forms throughout stereocilia shafts; long isoform (ESPN-1) at tips
FSCN2	Fascin 2	Fscn2 <sup>R109H</sup>	Progressive degeneration of hair bundles	Stereocilia shafts
MYO1C	Myosin IC	Myo1c <sup>Y61G</sup>	Slowed adaptation	Toward stereocilia tips
MYO1H	Myosin IH	n/a	Unknown	Toward stereocilia tips
MYO3A	Myosin IIIA	DFNB30	Progressive hearing loss	Thimble-like pattern at tips
MYO3B	Myosin IIIB	n/a	Unknown	Thimble-like pattern at tips
MYO6	Myosin VI	DFNA22, DFNB37	Fusion and elongation of stereocilia; apical membrane uplifting	Shafts and taper region
MYO7A	Myosin VIIA	USH1B, DFNA11, DFNB2	Disorganized hair bundles	Tip links; transient lateral links; kinocilial links
MYO15A	Myosin XV A	DFNB3	Short stereocilia	Stereocilia tips
PCDH15	Protocadherin 15	USH1F, DFNB23	Disorganized hair bundles	Tip links; transient lateral links; kinocilial links
PLS1	Plastin 1	Pls1 knockout	Progressive degeneration of hair bundles	Stereocilia shafts
PTPRQ	Protein tyrosine phosphatase receptor Q	DFNB84	Fusion and elongation of stereocilia	Ankle region, stereociliary shafts
RDX	Radixin	DFNB24, Rdx knockout	Progressive degeneration of hair bundles	Concentrated near base of stereocilia; activated RDX only found above the taper region
USH1C	Harmonin	USH1C, DFNB18	Disorganized hair bundles	Tip link upper insertion; tips in early development
USH1G	Sans	USH1G	Disorganized hair bundles	Tip link upper insertion; tips in early development

Most of these were initially flagged as being important because mutations in their genes caused deafness.

TABLE 1: **Selected key proteins for hair bundles.**



**FIGURE 2:** Model chick vestibular stereocilium. Scale model of stereocilium showing selected molecules; these molecules are drawn in at the approximate density for each as determined by mass spectrometry experiments (Shin *et al.*, 2013). (A) Complete stereocilium at low magnification showing dimensions. (B) Selected molecular gradients in the stereocilia. See Shin *et al.* (2013) for details. (C) High-magnification view of the tip region of the stereocilium. The two insertions of the tip link are highlighted; the lower insertion includes transduction channels, and the upper insertion has USH1C, USH1G, and MYO7A. In addition, the MYO15A tip complex is indicated; DFNB31, EPS8, and perhaps EPS8L2 are part of this complex. MYO3A and MYO3B are found, along with their cargo ESPN-1, in the tip region as well. (D) The stereocilia shaft is made of parallel actin filaments cross-linked by a variety of proteins, most prominently ESPN, FSCN2, and PLS1. Major components of the shaft include the calcium pump ATP2B2, the membrane-associated ANXA5, the actin-to-membrane connector radixin (RDX), and SLC9A3R2, a ligand for RDX. RDX with the activating phosphorylation is found above the taper region. (E) The taper region. Most actin filaments terminate at the membrane, but a few project through into the soma as the rootlet (density). The lipid phosphatase PTPRQ is concentrated in the taper region, as is unactivated RDX. (F) Key to molecules included in the diagram.

## DIFFERENT MOLECULES FOR TWO STAGES OF STEREOCILIA LENGTHENING

Actin elongation in stereocilia does not appear to depend on the usual suspects, such as the Arp2/3 complex, formins, or the Ena/vasodilator-stimulated phosphoprotein (VASP) family. Although the Arp2/3 complex is present in hair bundles (Shin *et al.*, 2013), this complex forms only branched actin networks. Formins and Ena/VASP proteins do generate parallel bundles of actin (Campellone and Welch, 2010), but neither is found at significant levels in chick (Shin *et al.*, 2013) or mouse (unpublished data) bundles. Other less-well-characterized elongation-promoting proteins, such as Spire and cordon bleu (Campellone and Welch, 2010), are also absent from bundles. This is not to say that none of these proteins is involved in the very earliest stages of development of the stereocilia, when they are growing as microvilli; nevertheless, subsequent lengthening must be promoted by different proteins.

Myosin molecules instead play critical roles in promoting and regulating stereocilia length, presumably by controlling the levels of actin itself or actin-regulating molecules. Key myosin isozymes involved in stereocilia length regulation include myosins IIIA, IIIB, VIIA, and XVA; indeed, length regulation in stereocilia may employ multiple redundant systems, offering substantial robustness.

Myosin XVA (MYO15A) certainly participates in stereocilia length regulation. As part of a complex with DFNB31 (whirlin), EPS8, and perhaps EPS8L2, MYO15A is essential for growth of cochlear stereocilia past  $\sim 0.5 \mu\text{m}$  (Manor *et al.*, 2011); similarly, vestibular

stereocilia of mice lacking MYO15A are only a few micrometers long (Belyantseva *et al.*, 2005). In both auditory and vestibular hair bundles, adjacent stereocilia in a single rank do show increasing lengths, but the staircase spacing is only 100–200 nm (Stepanyan and Frolenkov, 2009). These observations suggest that MYO15A is required for Tilney's first step of stereocilia elongation, that which occurs beyond the initial development of a short staircase.

The cross-linking protein espin (ESPN) is necessary for the second stage of stereocilia lengthening (Sekerova *et al.*, 2011); lengthening stops prematurely in mice homozygous for the *jerker* mutation, which disables *Espn* (Sekerova *et al.*, 2011). The longest splice form of ESPN, called ESPN-1, may exert its effects after transport to stereocilia tips by myosin IIIA or IIIB (MYO3A or MYO3B; Salles *et al.*, 2009; Merritt *et al.*, 2012). Short forms of ESPN elongate microvilli in cultured cells, however, suggesting that control of stereocilia length might involve multiple ESPN splice forms (Loomis *et al.*, 2003).

## STEREOCILIA WIDENING

In the chick cochlea, widening of stereocilia from  $\sim 50$  to  $>400$  filaments occurs as a distinct step, sandwiched in time between the first and last lengthening phases (Figure 1, C and D; Tilney *et al.*, 1980). By contrast, in the mammal, widening occurs concurrently with the second lengthening phase (Kaltenbach *et al.*, 1994; Sekerova *et al.*, 2011). As with second-phase lengthening, widening during this period is dependent on ESPN; moreover, the tapered stereocilia



seen in *jerker* heterozygotes, with half the normal ESPN levels, suggest that widening occurs from the base of the stereocilium to the tip (Sekerikova *et al.*, 2011). This observation and the relationship between the myosin III paralogues and the ESPN-1 splice form suggests that widening may occur as myosin III motors transport ESPN-1 toward stereocilia tips, with ESPN-1 catalyzing barbed-end growth of new filaments that are nucleated at stereocilia taper regions.

## CONTROL OF STEREOCILIA LENGTH BY MECHANOTRANSDUCTION

The remarkable precision of stereocilia length in adjacent rows begs for local feedback control within the hair bundle; it would seem impossible for the cell to control lengths so reproducibly from the cytoplasm. Phenotypes of mutant hair bundles for which mechanotransduction is known to be disrupted—for example, in *Cdh23* and *Ush1g* mice—suggest that when mechanotransduction is disrupted, length regulation is altered (Caberlotto *et al.*, 2011).

Possible mechanisms for transduction control of stereocilia length are few. Tip links—the extracellular filaments that gate the transduction channels—are tensioned by myosin motors at the tip-link upper insertion point (LeMasurier and Gillespie, 2005). The upward force on tip links apparently puckers the membrane of a shorter stereocilium enough to allow actin polymerization (Kachar *et al.*, 2000), producing a zone of actin turnover at tips (Zhang *et al.*, 2012; Drummond *et al.*, 2015; Narayanan *et al.*, 2015). Thus tip-link force may elongate stereocilia, at least over a short distance.

There must also be a mechanism that opposes the upward tip-link force, or stereocilia would elongate until the upper insertion point reached the stereocilia tip. Myosin motors that control tip-link tension—probably MYO1C or MYO7A—should be sensitive to Ca<sup>2+</sup>; perhaps Ca<sup>2+</sup> that enters at a stereocilium tip and diffuses down to the upper insertion point of the next tip link could be responsible, providing a constant brake to upward movement of the myosin motors (Gillespie and Müller, 2009). This mechanism could account for differences in spacing of the staircase step, as the reach of Ca<sup>2+</sup> will depend not only Ca<sup>2+</sup> entry, but also on concentrations of mobile Ca<sup>2+</sup> buffers, which can vary substantially from cell to cell (Hackney *et al.*, 2005). Of course, because the tallest stereocilia do not have active transduction channels (Beurg *et al.*, 2009), for this model to be correct, there would need to be an alternative route for Ca<sup>2+</sup> entry at their tips.

As an alternative model, the force could come from the active turnover of actin filaments at the tips of shorter stereocilia, those associated with the base of a tip link (Zhang *et al.*, 2012; Drummond *et al.*, 2015; Narayanan *et al.*, 2015). Active disassembly of actin there could lead to increased tension in the membrane that would pull the tip link downward, which could counter the upward force of the myosin motors. These two models could be tested by manipulating Ca<sup>2+</sup> or actin-depolymerizing molecules in the stereocilium and examining effects on stereocilia length.

## A CALL TO ARMS

Although individual steps of hair-bundle assembly are beginning to be understood, the problem begs for a systematic approach, given the large number of overlapping and partially redundant molecular mechanisms. Modern technology allows for experiments that could only be dreamt of even a few years ago. As a systems-biology problem, assembly of the bundle seems highly tractable. What additional information is needed? Will this information require new approaches?

Pollard argues that three large areas of research—biochemical, cellular, and structural—are needed for complete characterization of

a biological problem of interest. One need is for description of the order of expression and appearance in stereocilia of key hair-bundle proteins. Single-cell transcriptomics experiments now allow for a temporal ordering of expression of genes in a cellular process (Durruthy-Durruthy *et al.*, 2014) and can be used to understand bundle development. Complementary experiments showing developmental progression of protein expression are needed. The lack of coordination of hair-cell development in vestibular organs (Goodyear *et al.*, 1999; Burns *et al.*, 2012) suggests that these protein expression experiments will require single-cell mass spectrometry. Although some efforts have been made in this direction (Wu and Singh, 2012), detection of rare proteins in single hair cells will require increasing the sensitivity of mass spectrometry by at least 100-fold. Given the spectacular advances in instrumentation in the last two decades, this goal seems achievable.

We also need to know the activities, protein–protein interactions, and activity-modifying posttranslational modifications of all proteins important for bundle assembly (Pollard, 2013). Activities of many proteins are known or can be inferred from better-characterized paralogues. Because we expect that only a few hundred proteins are needed for bundle assembly, examining, for example, a 100 × 100 matrix of interactions would be straightforward with a variety of techniques, including yeast two-hybrid assays (Bruckner *et al.*, 2009) and direct protein–protein binding assays (Syafrizayanti *et al.*, 2014), as well as with methods for testing the relevance of those interactions *in vivo*. Systematic characterization of all of these parameters is essential.

Finally, computational biologists need to develop mathematical models that describe hair-bundle assembly. The models need to be of sufficient complexity that meaningful hypothesis-testing experiments can be inferred from them (Pollard, 2013). The advent of CRISPR technology means that these testing experiments can be conducted relatively quickly (Hsu *et al.*, 2014; Incontro *et al.*, 2014).

All of these steps will require the creativity of new investigators approaching the problem of hair-bundle assembly from fresh perspectives. We are on the cusp of the truly exciting experiments: with a description of assembly at the structural level, a parts list that is likely near completion, and systematic experiments imminent, we should be able to soon determine how the hair cell controls stereocilia length, diameter, and spacing to make a functional bundle.

## ACKNOWLEDGMENTS

Work in my lab is supported by National Institutes of Health Grants R01 DC002368, R01 DC011034, and P30 DC005983. I thank Lori Vaskalis for the original scale stereocilium drawing.

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