Insight into DEG/ENaC Channel Gating from Genetics and Structure

The founding members of the superfamily of DEG/ENaC ion channel proteins are C. elegans proteins that form mechanosensitive channels in touch and pain receptors. For more than a decade, the research community has used mutagenesis to identify motifs that regulate gating. This review integrates insight derived from unbiased in vivo mutagenesis screens with recent crystal structures to develop new models for activation of mechanically gated DEGs.

The Physiology of DEG/ENaC Channels

DEG/ENaCs are nonvoltage-gated, sodium-selective, amiloride-sensitive channels with diverse cellular functions (reviewed in Ref. 42). Four major functional subclasses are shown in FIGURE 1. Three DEG/ENaC proteins are confirmed, pore-forming subunits of mechanosensitive ion channels critical for touch and pain sensation: MEC-4, MEC-10, and DEG-1 (25, 52). They belong to the DEG subfamily that also includes UNC-8 and UNC-105, which are linked to mechanosensation in neurons and muscle (reviewed in Ref. 26). These DEG channels open in response to both the delivery and removal of mechanical stimulation and close during the stimulus pulse (FIGURE 1).

Such phasic response dynamics are a shared feature of five classes of mechanoreceptor neurons in C. elegans (26), have been reported in mammalian somatosensory neurons probed in vitro (54), and were first described in the 1950s in the vibration sensors of mammals (Pacinian corpuscles) (3, 29). This consensus suggests that many mechanoreceptor neurons detect both the application and withdrawal of mechanical stimulation.

Classical genetic approaches including unbiased chemical screens have uncovered >50 missense mutations in the DEG/ENaC proteins that mediate C. elegans touch sensation (12, 20, 24, 27, 31–33, 51, 57, 66, 72). Such mutations disrupt behavioral responses to mechanical stimuli either because of a loss of DEG channel function or because of neuronal cell death caused by inappropriate activation of DEG channels. The latter phenotype results from gain-of-function mutations, including those affecting the so-called d (for degeneration) position in DEG-1 and MEC-4 (12, 20). In this review, insight inferred from analysis of these mutations will be combined with data from other members of the superfamily in building hypotheses about the closed, open, and desensitized states of DEG channels.

Trimeric DEG/ENaC Channel Structures

All DEG/ENaC proteins share a common topology consisting of two transmembrane helices (TM1, TM2), a large ectodomain, and intracellular NH2- and COOH-terminal domains (FIGURE 2A). Sequence conservation suggests abundant structural similarities and allows for integration of experimental data across the various family members (FIGURE 3). For example, replacing the native, small-volume residue found at the d position at the top of TM2 with larger-volume residues increases open probability in most, if not all, DEG/ENaC channels tested.
The two structures of the proton-activated chicken (c) ASIC1a likely capture the channel in a desensitized state (28, 35). Their ectodomains are identical and are compared with that of a hand (FIGURE 2A): a wrist joins the seven-stranded β-sheet palm and disulfide-rich α-helical thumb to the TM domain, whereas an α-helical knuckle and finger help the palm and thumb grasp a five-stranded β-ball (35). The two structures differ in their resolution and the orientation of their TM helices. The 1.9-Å resolution 2007 structure is derived from a nonfunctional channel with kinked TM helices (35), and the 3.0-Å resolution 2009 structure (FIGURE 2, B AND C) is of a functional cASIC1a channel with symmetrically oriented helices (28). The higher-resolution structure (35) will be used for analysis of the ectodomain, and the subsequent lower-resolution structure of a functional channel (28) will be used for analysis of the TM domain.

A Dynamic Rule of Thumb

The thumb is made up of two α-helices and several structured loops (35) (FIGURE 2). Five highly conserved disulfide bridges stabilize its architecture and likely lock it into a rigid rod that hinges where it connects to the base of the palm. The proximity of the thumb’s hinge to the top of the TM domain led to the proposal that this region is important for transferring gating motions from the ectodomain to the TM domain (35). Experimentation supports this view (47, 64). Genetic screens identified several mutations in the thumb that disrupt touch sensation in C. elegans; many cluster at the tip, but none localize to the hinge (FIGURE 2, B AND C). Thus, although experiments with ASICs (47) and ENaCs (64) suggest that residues in the hinge are crucial for gating, genetic screens have not recovered mutations in this region in DEGs. Instead, key regions highlighted by mutation cluster on the face of α5 that is adjacent to the finger and on the surface of the α4–α5 linker that is in contact with the β-ball (FIGURE 2B).

Among the mutations that map onto the thumb domain, only one is a gain-of-function mutation presumed to induce channel hyperactivation. This residue, UNC-8 A586T, is predicted to be at the tip of α5 (66) (FIGURES 2B AND 3). Gessmann et al. (27) proposed that the increase in steric bulk or the presence of a novel hydrogen-bonding partner might account for the change in function induced by this mutation. Mutations at the tip of α5 in cASIC1a also affect channel gating: cASIC1a P338A displays decreased proton sensitivity, a change attributed to disruptions of a favorable hydrophobic interaction between the thumb and the finger (70). A screen for suppression of hyperactivation caused by the MEC-4 d mutation (57) identified a mutation one turn down α5, MEC-4 R619L (FIGURE 2B AND 3), that suppresses degeneration. This finding suggests that this residue plays an important role in the open state. Neighboring this residue is a histidine linked to zinc potentiation of rat (r) ASIC2a-containing channels (6). The next two turns down α5 contain aspartates critical to proton sensitivity in cASIC1a, D346 and D350 (35, 70) (FIGURE 3). These two aspartates are likely involved in proton-dependent carboxyl-carboxylate interactions with residues in the finger (35).

Three touch-disrupting mutations (MEC-4 G598E, D599N, and R601C) (32) are found in the structured loop between α4 and α5 that packs against the β-ball (35) (FIGURES 2B AND 3). This interface likely regulates the open state of the channel since these three mutations also suppress degeneration caused by a hyperactivating mutation at the d position (32). When the residue aligned with MEC-4 R601 in cASIC1a (H328) (FIGURE 3) is mutated to alanine, proton sensitivity is decreased (70). Yang et al. (70) argued that this effect was caused by a decrease in a favorable hydrophobic interaction. A mutation at the bottom of α4 in UNC-8 (E552K) that disrupts locomotion (27) further supports the importance of the thumb-β-ball interface since this mutation is found at the other major contact point between these two domains (FIGURES 2B

![A Dynamic Rule of Thumb](http://physiologyonline.physiology.org/)

**FIGURE 1.** DEG/ENaC channels can be activated by both mechanical and chemical stimuli

A: DEGs are gated by mechanical loads at both the onset and offset of stimulus. B: ENaCs are constitutively active and can be modulated by shear stress. C: ASICs are gated by protons. D: FaNaCs are gated by the FMRFamide-like peptides.
AND 3). Thus channel gating may involve important interactions not only between the thumb and finger but also between the thumb and β-ball.

The two last thumb mutations to discuss may affect the disulfide bridges knitting the thumb together. The first is at a conserved proline (MEC-4 P643L) (57) adjacent to a disulfide bridge connecting the structured loops at the base of the thumb (FIGURES 2B AND 3). This mutation suppresses degeneration caused by mutation of the d position. Perhaps it reorients the disulfide bridge, preventing the thumb from adopting its open-state conformation. The second (MEC-4 C595Y) (32) is predicted to eliminate the disulfide bridge connecting α4 with α5 (FIGURES 2B AND 3). However, the equivalent cysteine is not required for rENaC constitutive activity (23). Perhaps the rigid association between α4 and α5 provided by this particular disulfide bridge is critical for the gating movements of the thumb during mechanical activation but not for the constitutive activity of ENaCs.

**Finger Tuning Channel Function**

The finger is the region of lowest sequence conservation and highest variability between DEG/ENaC subclasses. Thus this region may underlie much of the functional specificity between proteins within the superfamily. In the cASIC1a crystal structure (35), the finger is made up of three α-helices and several well structured loops. The structures of DEG and ENaC fingers likely differ considerably since large cysteine-rich insertions are found in the mechanosensitive DEG protein fingers, whereas smaller insertions are found in the fingers of the constitutively active ENaCs (FIGURE 3). The DEG insertions include a short stretch of residues called the extracellular regulatory domain (ERD), which can mutate to cause channel hyperactivation (24, 66). [The mutations found through genetic screens were DEG-1 A393T and UNC-8 G387E (24, 66) (FIGURE 3).] Touch-disrupting mutations are spread throughout the finger of the MEC-4 protein (G230E, A321T, P395L, E397K, A420V, and E445K) (32) (FIGURE 3), underscoring the importance of the entire domain on protein function.

The finger is involved in a wide range of functions in ASICs. The finger’s association with the thumb (35), role in zinc potentiation (6), and importance for proton sensitivity (35) were mentioned above. Residues in the thumb of ASICs regulate the proton dependence of activation and steady-state inactivation (5), the level of channel

**FIGURE 2. Structure and sequence conservation link DEG/ENaC proteins**

A: topographical map of a single DEG/ENaC subunit (inspired by Ref. 37). The TM helices (red), palm (yellow), β-ball (orange), knuckle (blue), thumb (green), and finger (purple) are colored as in Ref. 35. The NH₂ and COOH termini, wrist, DEG-specific finger insertions (dotted), and ERD (thick dotted) are also identified. B: ribbon diagram of one subunit of the cASIC1a channel is color coded according to domain (see A). Residues shown in space-filling representation indicate positions that can mutate to disrupt function. Residues in red can mutate to cause channel hyperactivation, and those in blue disrupt touch sensation. C: ribbon diagram of a trimeric cASIC1a channel showing the interaction between adjacent subunits. One subunit is color coded by domain; the other two are black (rear) or gray (right). B and C were prepared using VMD and PDB 3HGC.
expression (70), and binding of the ASIC1a inhibiting toxin psalmotoxin-1 (55).

The finger is important for FaNaC and ENaC activation as well. Residues in the finger of FaNaCs that align with \(/H9251\) in cASIC1a determine the EC50 of FMRFamide (16). In ENaCs, the finger has been functionally linked to both shear stress sensitivity (63) and proteolytic regulation (10, 34, 36). ENaC-\(/H9251\) and \(-/H9253\) subunits are proteolytically cleaved at two sites in the finger domain, resulting in the removal of dozens of residues and an increase in open probability (10, 34). If the deleted ENaC peptides are applied to the mouse (m) ENaC-\(/H9251\) channel, they inhibit activity through an interaction with both the finger and the tip of the thumb (36). Residues implicated in this interaction include mENaC-\(/H9251\) E470 and D473, which align near the hyperactivating UNC-8 A586T thumb mutation (66) discussed above (36) (FIGURE 3). Kashlan et al. (36) proposed that the intact finger inhibits the thumb through a physical interaction between the two and that proteolysis relieves this intramolecular inhibition. ASIC1 can also be proteolytically cleaved at a site in the finger in vitro, but in this case cleavage results in decreased channel function (14, 69).

The Importance of the Palm

The core of the ectodomain is comprised of a network of \(-/H9252\) sheets that come together to form an internal solvent-filled central cavity in the ASIC1a crystal structure (35). Mutagenesis screens identified an acidic residue in UNC-105 (E677) located on \(/H9252\) that can mutate to cause channel hyperactivation.
and is predicted to extend into this central cavity (51) (FIGURES 2B AND 3). The corresponding residue in rASIC3 is accessible to small molecule derivatives of 2-guanidine-4-methylquinazoline (GMQ) in the closed state (71), and binding of GMQ leads to channel activation. Furthermore, this residue likely packs against a glutamate in β1 that is also accessible to derivitizing reagents when the channel is closed but not once it is desensitized (18, 71). Mutation of this latter residue to alanine speeds desensitization but has no effect on activation (18). [In cASIC1α, the homologous residues are E417 and E80 (FIGURE 3).] The inaccessibility of the derivitizing reagents during desensitization agrees with the isolated central cavity seen in the cASIC1α structure (35), whereas the accessibility in the closed state argues for a means of entry to this central cavity in other channel states. An inter-subunit widening of the lower portion of the palm could allow reagents into the central cavity through lateral fenestrations. A widening could also account for the hyperactivating phenotype of UNC-105 E667K since the larger cavity volume might minimize clash caused by the mutant lysine. This model parallels what is expected of the P2X channel family.

The inaccessibility of the derivitizing reagents during desensitization rates swaps their rates of desensitization (15, 48, 50). This region carries another mutation that suppresses necrosis caused by mutation of the d position: MEC-4 T701I (57) (FIGURES 2B AND 3). Although it is close to UNC-105 E667, MEC-4 T701 does not extend into the central cavity. Instead, it projects into the extracellular space in the cASIC1α structure (35). Data in ASICs suggest that the inter-subunit interactions seen in this region of the cASIC1α crystal structure (35) are important for channel function (6, 18). Perhaps mutation of MEC-4 T701 disrupts similar inter-subunit interactions that occur in the open state, explaining its suppression of hyperactivation phenotype.

The upper portion of the palm contains five mutations that disrupt touch sensitivity, MEC-4 G533S, G539E, S542F, and UNC-8 T664I (32, 66) (FIGURES 2B AND 3). The first three MEC-4 mutations and one other, MEC-4 P655L, suppress degeneration caused by the MEC-4 d mutation (32, 57). Therefore, these residues are likely important for the channel’s open state. The cASIC1α residues that correspond to MEC-4 G533, S542, and P655 pack in a ring where the β-sheets come together at the top of the central cavity. When analyzing their MEC-4 homology model, Gessmann et al. (27) proposed that these mutations introduce deformations and break hydrogen bonds important for this region’s β-sheet structure. The palm is littered with conserved glycines marking tight turns and β-sheets. Two of the residues identified by mutation, MEC-4 G533 and G539, initiate the β-ball’s β8-and the palm’s β9-sheets, respectively (FIGURE 2C). MEC-4 S542F affects a conserved residue in β9 (FIGURE 2C) that projects toward β8 in the β-ball. Thus distortions in this region could disrupt intra- and inter-subunit interfaces important for channel gating.

In the cASIC1α structure (35), the residues corresponding to MEC-4 G539 and UNC-8 T664 cluster at the tip of the palm, just below the knuckle. Also aligning in this cluster is a human (h) ENaC-α residue linked to cystic fibrosis and increased ENaC activity (56) (corresponding to mENaC-α W520 in FIGURE 3). Perhaps these residues properly orient the knuckle with respect to the rest of the channel.

The Pore-Lining GxxxD Motif

Any discussion of the mutations identified through genetic screens in the TM domain must begin with the degeneration-causing mutations that gave the DEG family its name. These mutations, DEG-1 A1707V (12) and MEC-4 A11001V (20), affect a residue at the top of TM2 called the d position (FIGURES 2B AND 3). The d position is occupied by glycine, alanine, or serine in most DEG/ENaC proteins, and introducing larger residues results in channel hyperactivity regardless of the channel’s normal mode of activation. In some ENaCs (61, 65) and ASICs (67), nearby residues behave similarly when modified with derivitizing reagents. Single-channel in vitro recording of MEC-4 channels mutated at the d position determined that increasing side-chain volume at this site stabilizes the open state of the channel (9). The d position is buried in the pore occlusion in the desensitized cASIC1α structure (28); it packs between the side-chain of the d + 1 aspartate and the d + 3 and d + 4 glycines. Derivitizing reagents modified the d position of hASIC2 in open but not closed states (2), whereas no change in current was seen in a similar test performed on ENaCs (65). However, in the closed state of a non-desensitizing ASIC mutant, the d position...
Beyond the Glycines in the Pore

Six other mutations have been identified in TM2. MEC-10 L679R (33) affects a conserved leucine at $d + 6$ (FIGURES 2B AND 3), disrupts touch sensation, and decreases sodium selectivity in vivo (4). This $d + 6$ site also regulates lateral sheer stress sensitivity of ENaCs (1). Two additional touch-disrupting mutations follow the GxS motif and affect conserved residues (FIGURES 2B AND 3): MEC-4 T729I and E732K (31). The corresponding residues in mENaC-α are needed for normal sodium selectivity of the mENaC-αβγ channel in vitro (60, 62). Three nonconserved residues also affect touch sensation by suppressing degeneration caused by mutation of the $d$ position: MEC-4 C723Y falls just before GxS motif at $d + 10$, whereas MEC-4 L728F and L738E follow the GxS motif (57). Their proximity to the GxS sequence (FIGURE 3) suggests that they may be important for refining the selectivity filter, although this idea awaits experimental confirmation.

The Intracellular Domain

A cluster of touch-disrupting mutations, including MEC-4 T91I, MEC-4 S92F, and the homologous MEC-10 S105F, UNC-8 H114Y, and MEC-4 G95E (32, 33, 66), highlights the importance of NH$_2$-terminal domain (FIGURE 3). This domain contains an invariant HG sequence that can mutate to cause not only touch insensitivity in C. elegans but also pseudohypoaldosteronism type I in humans (13). Both MEC-4 S92F and MEC-10 S105F decrease sodium selectivity in vivo, and MEC-10 S105F requires slightly more force than wild type for channel activation (4). The impact of these intracellular mutations on selectivity implies that they may shape the pore.

A Proposed Gating Model

Having covered DEG channel structure and function from top to bottom, what does this analysis suggest about channel gating? We propose a model in which activation involves a shift in the relative orientation of the thumb, finger, and palm (FIGURE 4, A AND B). These motions coincide with conformational changes in the lower palm domains, perhaps an inter-subunit widening similar to the structural changes predicted for the P2X receptors (30) (FIGURES 4, A AND B). A widening and rotation of the TM helices releases the pore occlusion, freeing the $d$ position and potentially forcing the formation of a constriction further down the pore-lining TM2 (FIGURE 4, A AND B). The extent of this rotation and expansion may be constrained by interactions...
between adjacent subunits, as inferred from the introduction of inter-subunit disulfide bonds (67). The palm rearranges upon desensitization, reforming the occlusion seen in the closed state (FIGURE 4, B AND C).

It is straightforward to imagine how binding of protons to the acidic pocket in ASICs (35) or peptides to the finger in FaNaCs (17) could trigger the movements hypothesized for channel opening. Yet, how does a mechanical strain initiate the gating pathway? Current models for mechanical gating of DEG channels involve either tethering of the ectodomain of the channel to the extracellular matrix (FIGURE 4A, spring on the left side) or sensitivity of the channel to the lipid bilayer (FIGURE 4A, spring on the right side) (11). In these models, mechanical strain on the matrix or on the membrane would then translate into channel opening. Potential extracellular matrix tethers for MEC-4-dependent MeT channels include MEC-1 and MEC-9, Kunitz-domain containing proteins required for touch sensitivity (21, 22). These proteins are attractive candidates since a Kunitz domain-containing snake toxin was recently found to activate rASIC1 (8). These tethers could activate DEGs in a top-down fashion, similar to the direction of motion expected for the gating of ASICs by protons and this snake toxin.

Alternatively, if strain in the membrane gates the channel, then the gating pathway could begin in the TM domain and culminate in the reorientation of the ectodomain (FIGURE 4B). The hyperactivation that results from mutation of the $d$ position sets the precedent that gating can occur in this direction. Perhaps mechanical strain results in a thinning or curving of the membrane and destabilizes the occlusion around the $d$ position, which drives the constriction downward and initiates the conformational changes that occur in the ectodomain. In this hypothetical model, the grasp of the finger on the thumb could tune how much mechanical strain on the membrane is needed to open the channel. Consistent with the idea that changes in the lipid bilayer can initiate channel activation, MscL and MscS are known to be gated by membrane tension and to be sensitive to the shape and thickness of the lipid bilayer (53, 68). In these bacterial channels, changes in membrane curvature induce a rotation and tilt of the TM helices along the plane of the membrane that widens and opens the pore (53, 68). If correct, this model implies that specific properties of the native membrane are needed for DEG channel mechanical gating since these channels are impervious to membrane stretch when expressed in heterologous cells.

Conclusions

The present collection of DEG channel data supports a model in which the TM domain and the ectodomain work in concert to regulate DEG channel gating. How the initial mechanical stimulus is applied to the channel and what conformational changes occur during the gating of the channel are still open questions. Further work is needed to test
the gating models presented here and to determine exactly how mechanosensitive DEG/ENaC channels operate. Ultimately, a thorough understanding of how these channels function should provide much needed insight into the molecular details of touch sensation and guide future studies on the molecular and physiological origins of touch sensation in animals.

While this review was in press, new ASIC1a structures were published that provide insight into the psalmotoxin-1 binding site and the conformation of putative open channels (5a, 18a). Consistent with the ideas presented here, Bacoinguis and Gouaux (5a) note that the lower palm and pore domains are wider in the open structure than they are in the desensitized structure.

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