How morphogenetic signals are prepared for intercellular dispersal and signaling is fundamental to the understanding of tissue morphogenesis. We discovered an intracellular mechanism that prepares *Drosophila melanogaster* FGF Branchless (Bnl) for cytoneme-mediated intercellular dispersal during the development of the larval Air-Sac-Primordium (ASP). Wing-disc cells express Bnl as a proprotein that is cleaved by Furin1 in the Golgi. Truncated Bnl sorts asymmetrically to the basal surface, where it is received by cytonemes that extend from the recipient ASP cells. Uncleavable mutant Bnl has signaling activity but is mistargeted to the apical side, reducing its bioavailability. Since Bnl signaling levels feedback control cytoneme production in the ASP, the reduced availability of mutant Bnl on the source basal surface decreases ASP cytoneme numbers, leading to a reduced range of signal/signaling gradient and impaired ASP growth. Thus, enzymatic cleavage ensures polarized intracellular sorting and availability of Bnl to its signaling site, thereby determining its tissue-specific intercellular dispersal and signaling range.

**Introduction**

Intercellular communication mediated by signaling proteins is essential for coordinating cellular functions during tissue morphogenesis. Owing to decades of research, the core pathways of developmental signaling and their roles and modes of action in diverse morphogenetic contexts are well characterized. We now know that a small set of conserved paracrine signals is universally required for most developing tissues and organs. These signals are produced in a restricted group of cells and disperse away from the source to convey inductive information through their gradient distribution (Christian, 2012; Akiyama and Gibson, 2015). It is evident that to elicit a coordinated response, cells in a receptive tissue field interpret at least three different parameters of the gradient: the signal concentration, the timing, and the direction from where they receive the signal (Briscoe and Small, 2015; Kornberg, 2016). Therefore, understanding how different cellular and molecular mechanisms in signal-producing cells prepare and release the signals at the correct time and location and at an appropriate level is fundamental to understanding tissue morphogenesis. It is also critical to know how these processes in source cells spatiotemporally coordinate and integrate with cellular mechanisms in the recipient cells to precisely shape signal gradients and tissue patterns.

To address these questions, we focused on interorgan communication of a canonical FGF family protein, Bnl, that regulates branching morphogenesis of tracheal airway epithelial tubes in *Drosophila melanogaster* (Sutherland et al., 1996). Migration and morphogenesis of each developing tracheal branch in embryo and larvae is guided by a dynamically changing Bnl source (Sutherland et al., 1996; Jarecki et al., 1999; Sato and Kornberg, 2002; Ochoa-Espinosa and Affolter, 2012; Du et al., 2017). For instance, in third instar larva, Bnl produced by a restricted group of columnar epithelial cells in the wing imaginal disc activates its receptor Breathless (Btl) in tracheoblast cells in the transverse connective (TC), a disc-associated tracheal branch (Sato and Kornberg, 2002). Bnl signaling induces migration and remodeling of the tracheoblasts to form a new tubular branch, the Air-Sac-Primordium (ASP), an adult air-sac precursor and vertebrate lung analogue (Fig. 1A). Such dynamic and local branch-specific signaling suggests a mechanism for precise spatiotemporal regulation of Bnl release and dispersal in coordination with the signaling response.

A critical role of regulated Bnl release can also be predicted from the way cells exchange Bnl to sculpt recipient branch-specific gradient shapes (Du et al., 2018a). Bnl is produced in the wing disc cells, but it forms a long-range concentration gradient only within the recipient ASP. Bnl gradient formation depends on signaling through actin-based signaling filopodia named cytonemes (Ramírez-Weber and Kornberg, 1999; Sato...
and Kornberg, 2002; Roy et al., 2011, 2014; Du et al., 2018a). ASP cells extend Btl-containing cytonemes to contact the basal surface of the wing disc source and directly receive Bnl (Fig. 1B). Bnl reception through a graded number of cytonemes that are formed along the distal-proximal (D-P) axis of the ASP epithelium sculpts the Bnl gradient within the ASP. In the distal ASP cells, high to medium levels of Bnl reception through cytonemes induces an ETS transcription factor Pointed-P1 (PntP1), which elicits positive feedback on Btl synthesis and cytoneme production (Du et al., 2018a). Cut and PntP1, expressed from the opposite poles of the ASP, reciprocally antagonize each other’s expression. Consequently, zones of high to low numbers of cytonemes are formed that can sculpt the Bnl gradient in coordination with recipient ASP growth. Initiation of this self-regulatory and tissue-specific gradient might require limited signal release from the source, probably only at cytoneme contact sites.

The intracellular mechanisms in the source cells that prepare Bnl for cytoneme-mediated exchange and branch-specific signaling are uncharacterized. In this study, while analyzing various functional forms of GFP-tagged Bnl, we uncovered a

Figure 1. Separate GFP fusion sites in Bnl result in different distribution patterns. (A) Drawing depicting the organization of the ASP and bnl-expressing wing disc cells from third instar larva. DB, dorsal branch; TC, transverse connective. (B) Drawing of a sagittal view showing the tubular ASP epithelium, upper-lower Z-axis, ASP cytonemes that contact the disc bnl-source (green nuclei), and the spatial domains of pntP1 and cut induced by high to low Bnl levels (green; Du et al., 2018a). (C) Schematic map of the Bnl protein backbone showing its conserved FGF domain, signal peptide (SP), and four different GFP insertion sites. (D–H) Representative images of maximum-intensity projection of lower (wing disc source) and upper (ASP) Z-sections of third instar larval wing-discs expressing CD8-GFP, Bnl:GFP1, Bnl:GFP2, Bnl:GFP3, or Bnl:GFP4 under bnl-Gal4 as indicated. Red, αDlg staining marking cell outlines. (I–K) Representative ASP images showing MAPK signaling (αdpERK, red) zones when Bnl:GFPendo was expressed under native cis-regulatory elements (I), and when bnl-Gal4 over-expressed Bnl:GFP3 (J) or Bnl:GFP1 (K). In D–K, white dashed line, ASP; white arrow, disc bnl-source; dashed arrow, Bnl:GFP puncta in the ASP; arrowhead, ASP without Bnl:GFP1 puncta. Scale bars: 30 µm.
posttranslational endoproteolytic modification of Bnl. We show that Bnl cleavage determines its polarized intracellular trafficking to the basal surface of the source cells from whence ASP cytonemes can receive the signal. This process limits Bnl availability to the ASP cytonemes and determines the range of Bnl gradient dispersal and tissue morphogenesis. Given the conservation of fundamental developmental signaling mechanisms, our demonstration of how a signal is endowed with information for its target-specific intercellular distribution has fundamental implications for understanding tissue morphogenesis.

Results

Bnl:GFP chimeras with different tag sites show different dispersion patterns

To identify various functional forms of GFP-tagged Bnl proteins, we generated four different Bnl:GFP variants and examined their signaling activities (Fig. 1, A–C; Materials and methods; and Tables S1 and S2). The Bnl protein is 770 amino acids long, with an N-terminal 31-residue signal peptide and a conserved FGF domain spanning from amino acids 243 to 379 (Fig. 1 C). Each of the four variants contained a GFP tag at a single internal site: at the 87th (Bnl:GFP₂), 206th (Bnl:GFP₃), 432nd (Bnl:GFP₄), and 701st (Bnl:GFP₅) amino acid residue. Transgenic Drosophila lines harboring these constructs were crossed to bnl-Gal4 flies and analyzed for activity in third instar larvae. In 3D confocal stacks of wing discs, the lower Z sections revealed the Bnl-expressing cells in the wing disc columnar epithelium, and the upper Z sections (close to the objective) showed the associated ASP fluorescent puncta (Fig. 1, B, D, and D'; and Video 1).

When the Bnl:GFP variants were expressed under bnl-Gal4 control, all of the variants were detected in the disc Bnl source as bright fluorescent puncta (Fig. 1, E–H). Overexpression of all four Bnl:GFP variants led to ASP overgrowth (Fig. 1, E–H’), which phenocopied a Bnl overexpression condition (Sato and Kornberg, 2002). Thus, all of the Bnl:GFP variants could signal nonautonomously. Unlike a membrane-tethered CD8:GFP protein, the fluorescent puncta comprising Bnl:GFP₂, Bnl:GFP₃, and Bnl:GFP₆ were detected in the recipient ASP, suggesting that the signals moved from the source to the ASP (Fig. 1, D–H'; and Video 2). Surprisingly, although Bnl:GFP₁ puncta were visible in the source cells and its overexpression induced ASP overgrowth, the fluorescent puncta were absent from the recipient ASP (Fig. 1, E–E'; Fig. S1, A–B'; and Video 3). Generally, as shown with an ASP derived from a genome-edited bnl:GFP₆ gene (Fig. 11), in contrast, overexpression of Bnl:GFP₃ or Bnl:GFP₅ in the source activated MAPK signaling in all of the ASP cells (Fig. 1, J and K). Thus, Bnl:GFP₁, like Bnl:GFP₃, is an active signal, but GFP fluorescence was undetectable in the recipient ASP.

Bnl is cleaved before its transport to the recipient ASP

One possibility for Bnl:GFP₁ being functional yet undetectable in the ASP could be that the protein was cleaved downstream of tagging site 1 before the interorgan transport of its untagged C-terminal fragment (Fig. 1 C). To test this possibility, we generated a double-tagged Bnl chimera with HA inserted at site 1 and GFP inserted at site 3 (Fig. 2 A). We performed Western blot analyses on total protein lysates of cultured S2 cells that were transfected with the bnl:GFP₃, bnl:GFP₅, or bnl:HA:GFP₃ constructs. An aGFP antibody recognized a common 150-kD band, which likely represented the full-length protein (Fig. 2 B). Although the molecular weight of full-length Bnl:GFP₁ was predicted to be ~113 kD, a larger band size could be due to posttranslational modifications. Similar observations were reported earlier for two Drosophila FGFs, Pyramus and Thisbe (Tulin and Stathopoulos, 2010). Bnl:HA:GFP₅ and Bnl:GFP₆ had similar band profiles, but Bnl:GFP₁ and Bnl:GFP₅ had multiple variant-specific bands (Fig. 2 B). The detection of unique smaller bands (~37 and 60 kD) for N-terminally tagged Bnl:GFP₁ and unique larger bands (~100 kD) for C-terminally tagged Bnl:GFP₃ or Bnl:HA:GFP₃ was consistent with a cleavage near tagging site 1. An aHA antibody recognized a weak ~20-kD band (Fig. S2, A and B) from lysates containing Bnl:HA:GFP₅, and Bnl:HA (HA-tag at position 1), but not from Bnl:HA (HA-tag at site 3). Therefore, the ~20-kD band represented the N-terminal cleaved product. These biochemical analyses suggested a cleavage in the Bnl backbone, but it was difficult to estimate the actual molecular size of the cleaved bands. Furthermore, the intracellular and intercellular fates of the cleaved products cannot be directly visualized in tissues using biochemical assays.

Therefore, we used a fluorescence microscopy–based assay to simultaneously visualize both the HA- and GFP-tagged parts of Bnl in cells. Immunostaining with a HA in S2 cells harboring uncleaved Bnl:HA:GFP₃ molecules was expected to show both HA and GFP localizing together. In contrast, a cleavage in the molecules would separate the HA tag from GFP₃. Indeed, in transfected S2 cells, Bnl:HA:GFP₃ was present in two distinct spatially separated forms (Fig. 2, C–F). An internal perinuclear zone showed colocalized GFP and HA signal, suggesting that the zone contained uncleaved Bnl. In addition, there were a number of exclusively GFP-positive puncta that localized more toward the periphery of the S2 cells. Cells that were cultured and allowed to adhere to a coverslip contained peripheral lamellipodial and filopodial projections at the adherent surface. These peripheral lamellipodial/filopodial projections contained only a truncated Bnl:GFP portion (Fig. 2, D–F; and Videos 4 and 5). Spatial separation of the C-terminal GFP-tagged portion from the rest of the Bnl:HA:GFP₃ molecule suggested Bnl cleavage.

To further test the peripheral distribution of the truncated C-terminal fragment, we generated two different constructs: bnl:HA:GFP₄ and bnl:GFP₃HA₂, where the HA and GFP tags were interchanged between sites 1 and 4 (Materials and methods). Although the tag positions were changed in these constructs, irrespective of the tags and tagging sites the cleaved N- and C-terminal Bnl fragments showed consistent subcellular localization patterns (Fig. S2, C and D). These results showed that Bnl is cleaved and a truncated C-terminal portion is trafficked toward the cell periphery, possibly for release. To test interorgan dispersion of cleaved/uncleaved forms of Bnl, we generated transgenic Drosophila lines harboring the bnl:HA:GFP₃ construct. When bnl-Gal4 overexpressed Bnl:HA:GFP₃
in the wing disc source, the N-terminal HA-tagged portion of Bnl remained in the signal-producing cells, and a truncated GFP-tagged C-terminal portion of Bnl (Bnl:GFP3) localized only in the recipient ASP cells (Fig. 2, G–I; and Fig. S2, E–G). These results strongly suggested that Bnl is cleaved in the source and only a truncated Bnl derivative is received by the ASP.

**Bnl is cleaved at a single endoproteolytic site in the Golgi network**

Evolutionarily conserved serine proteases, namely the proprotein convertases (PCs) that include Furins, cleave many growth factors and hormones that are synthesized in the form of proligands (Thomas, 2002). With an artificial neural network-based in silico PC site prediction tool (Duckert et al., 2004), we identified three putative PC sites (PCS1–3) in the Bnl backbone. Among them, PCS1 was Furin-specific with a core R–X–[R/K]–R domain (Fig. 3, A–A`). Coincidentally, the four selected tagging sites in the Bnl backbone were perfectly structured for testing the putative cleavage sites (Fig. 3 A). To test for cleavage at PCS3 (Fig. 3 A), we generated a chimeric Bnl:GFP3HA4 construct in which the GFP and HA tags were inserted at sites 3 and 4, respectively. Immunostaining with an aHA antibody on S2 cells transfected with bnl:GFP3HA4 showed colocalization of GFP3 and HA4 (Fig. 3 B). Based on this cell biological assay, PCS3 is an unlikely cleavage site. However, we did not investigate the possibility of potential PCS3 cleaved products remaining closely associated during their intracellular trafficking. In contrast, a cleavage at either PCS1 or PCS2 could explain the observed differential distribution of the N and C portions of Bnl:HA1GFP3 (Fig. 2, C–H).

To test PCS1 and PCS2, we replaced their arginine (R) residues with glycine (G) and generated bnl:HA1GFP3-M1 (henceforth referred as M1), a construct with mutations in PCS1 ((R/G)161TE^SI(R/G)166), and bnl:HA1GFP3-M2 (henceforth referred as M2) with mutations in PCS2 ((R/G)233NE(R/G)236; Fig. 3 A). R-to-G substitutions in PC sites were shown to successfully block PC cleavage (Künnapuu et al., 2009). In transfected S2 cells, the putative cleavage sites (Fig. 3 A). To test for cleavage at PCS3 (Fig. 3 A), we generated a chimeric Bnl:GFP3HA4 construct in which the GFP and HA tags were inserted at sites 3 and 4, respectively. Immunostaining with an aHA antibody on S2 cells transfected with bnl:GFP3HA4 showed colocalization of GFP3 and HA4 (Fig. 3 B). Based on this cell biological assay, PCS3 is an unlikely cleavage site. However, we did not investigate the possibility of potential PCS3 cleaved products remaining closely associated during their intracellular trafficking. In contrast, a cleavage at either PCS1 or PCS2 could explain the observed differential distribution of the N and C portions of Bnl:HA1GFP3 (Fig. 2, C–H).

To test PCS1 and PCS2, we replaced their arginine (R) residues with glycine (G) and generated bnl:HA1GFP3-M1 (henceforth referred as M1), a construct with mutations in PCS1 ((R/G)161TE^SI(R/G)166), and bnl:HA1GFP3-M2 (henceforth referred as M2) with mutations in PCS2 ((R/G)233NE(R/G)236; Fig. 3 A). R-to-G substitutions in PC sites were shown to successfully block PC cleavage (Künnapuu et al., 2009). In transfected S2 cells,
PCS1 mutation rendered the M1 molecules uncleavable, as HA and GFP colocalized in the intracellular compartments (Fig. 3, C–E; and Video 6). However, M2 molecules were cleaved like WT proteins (Fig. 3 F). To compare the cleavage efficiency among the Bnl mutants, we estimated the fraction (index of correlation $I_{corr}$) of colocalized pixels of HA and GFP channels from 3D...
images (Jaskolski et al., 2005). The average Icorr value was significantly higher for M1 and M1M2 than either the control Bnl:HA1GFP3 or M2 cells, suggesting that the PCS1 mutation inhibited cleavage (Fig. 3 H). We also generated transgenic flies harboring the M1, M2, or M1M2 constructs and analyzed their distribution in the disc and ASP. When the M1 and M1M2 mutants were expressed in the wing disc source, the recipient ASPs received the colocalized HA-GFP puncta comprising the uncleaved full-length molecules (Fig. 3, I–I’ and L–M; and Video 7). In contrast, only the GFP-tagged C-terminal part of M2 was distributed within the ASP (Fig. 3, J and K). Collectively, these results suggest that Bnl:HA1GFP3 molecules are cleaved at PCS1 before their delivery from the disc source to the ASP.

Bnl cleavage could be intracellular or, alternatively, could occur on the surface of the source cell plasma membrane where the signal is delivered to the recipient ASP cytoines (Fig. 1 B). To test this possibility, we employed a detergent-free αGFP-based immunostaining protocol (henceforth referred to as αGFPex), which was previously used to detect surface-exposed Bnl:GFP (Du et al., 2018a). The αGFPex assay detected only Bnl:GFP3 on the expressing source cell surface, but not Bnl:GFP1 (Fig. 4, A and B). Thus, Bnl cleavage is intracellular, and only the truncated C-terminal Bnl portion is displayed on the basal surface of the source cells. To determine the subcellular location of Bnl cleavage, we performed standard immunostaining with αGM130 antibody, a cis-Golgi probe, on discs expressing Bnl:GFP3, Bnl:HA1GFP3, or Bnl:HA1GFP3–M1. In the wing disc source, 100% of either Bnl:GFP3, or uncleaved Bnl:HA1GFP3 puncta were localized in the GM130-marked cis-Golgi (Fig. 4, C–D’), whereas the truncated Bnl:GFP3 derivative (GFP-only puncta) localized in many small uncharacterized intracellular vesicles, some of which were enriched with Syntaxatin6, a target-SNAP receptor for intra/trans-Golgi sorting (Charng et al., 2014; Fig. 4, D, D’, F, and F’). On the other hand, uncleaved M1 puncta were seen in all of the vesicular compartments, indicating their routing through the secretory pathway (Fig. 4, E, E’, G, and G’). Similar intracellular distribution profiles of the cleaved and uncleaved portions of Bnl were observed in cultured S2 cells (Fig. 4, H–J’). Collectively, these results showed that Bnl is cleaved during its trafficking through the Golgi network.

**Bnl is cleaved by Furin1 in the wing disc bnl source**

Intracellular Bnl cleavage at PCS1, which is a Furin-specific site, indicated that Bnl is likely cleaved by a Furin. To identify the specific protease, we performed RNAi-mediated knockdown of two Drosophila furin genes, Dfurin1 (fur1) and Dfurin2 (fur2), in cell culture assay. We did not investigate the role of amontillado (amon), a mammalian PC2 orthologue, since it is expressed only in neurons and neuroendocrine cells (Roebroek et al., 1992, 1993; Künnapuu et al., 2009). In S2 cells, RNAi treatment of fur1, fur2, or both significantly reduced Bnl:HA1GFP3 cleavage in comparison to a nonspecific control RNAi (Fig. 5, A–E). Thus, Bnl cleavage is Fur1 and Fur2 dependent. However, in vivo, only fur1 knockdown in the wing disc Bnl source resulted in a stunted ASP development, which phenocopied the bnl knockdown condition (Fig. 5, F–I; Fig. S3, A–D; and Table S3). Measurement of the allometric ratio of the recipient ASP length along its major D–P axis to the width of the wing disc confirmed that the growth abnormality was ASP specific and was not due to a systemic developmental delay (Fig. 5, J and K). Lack of a fur2 knockdown phenotype in the ASP is likely due to the absence of fur2 expression in the bnl source, as expression analyses of fur1 and fur2 showed only fur1 expression in the bnl source (Fig. S3, E–K). Thus, although both Fur1 and Fur2 could cleave Bnl in S2 cells, their substrate specificity might depend on their tissue-specific expression.

The RNAi analyses provided correlative evidence of Furin’s role in Bnl cleavage. For direct evidence, we ex vivo cultured larval wing discs expressing Bnl:HA1GFP3 in the bnl source in either the presence or absence of Furin inhibitors. In spite of the prolonged (up to 16 h) ex vivo culture conditions, Bnl:HA1GFP3 was cleaved in the absence of inhibitors, and the truncated Bnl:GFP3 moved to the growing ASPs (Fig. 6, A–C’). In the presence of inhibitors (Fig. 6, D–F’), Bnl cleavage in the disc source was blocked, and the amount of uncleaved puncta received by the ASP gradually increased with the increase in incubation time (Fig. 6 G). The time-dependent inhibition of Bnl cleavage by Furin inhibitors confirmed Furin-dependent Bnl cleavage. Importantly, these results, together with the M1 mutant analyses (Fig. 2 I), showed that when Bnl cleavage is blocked the uncleaved signals can still move from the disc to the ASP. These results indicated that cleavage might not be essential for molecular activation of the Bnl protein and led us to examine the physiological roles of Bnl cleavage.

**Uncleaved Bnl can signal and is dispersed by cytoines, but only within a narrow range**

To examine M1 distribution and activity at its physiological levels of expression, we modified a previously reported bnl:GFPendo allele into bnl:HA1GFPendo (henceforth referred as wtendo) and corresponding bnl:HA1GFP3–M1endo mutant alleles (henceforth referred as m1endo) by using genome editing (Materials and methods; Fig. 7 A). Consistent with earlier observations for bnl:GFPendo (Du et al., 2018a), wtendo flies were homozygous viable and had normal tissue morphology (Table S4). Although bnl is an essential gene, m1endo mutant flies were homozygous viable, indicating that the PCS1 mutation was nonlethal. As expected, the endogenous Bnl:HA1GFP3endo (wendo) molecules were cleaved and ASPs received only the truncated Bnl:GFP3 portion (henceforth referred as t-WTendo; Figs. 7 B and S4 A). The m1endo ASPs also received uncleaved Bnl:HA1GFP3–M1endo (m1endo) puncta containing both HA and GFP (Figs. 7 C and S4 B). Furthermore, ex vivo cultured wendo wing discs grown in the presence of Furin inhibitors had uncleaved Bnl:HA1GFP3endo puncta in the ASP (Fig. 7, D and E). Thus, in the absence of cleavage, uncleaved Bnl could move to the ASP and sustain tracheal growth.

When we genetically combined either wendo or m1endo with a btl:cherryendo allele, which expressed endo-tagged Btl-Cherry (Du et al., 2018a), both t-WTendo and M1endo puncta colocalized with the receptors in the ASPs (Fig. 7, F–G’). As reported earlier (Du et al., 2018a), the distal ASP tip, which is closest to the disc bnl source, had a high concentration of the receptor-colocalized t-WTendo or M1endo puncta. With increasing distance from the
source, their concentration gradually decreased. Bnl is known to be transported by cytonemes to form a receptor-associated gradient (Du et al., 2018a). To examine cytoneme-mediated transport, we live imaged CD8:Cherry-marked ASPs in the homozygous wtendo or m1endo larvae (>30 discs/genotype). In both conditions, ASPs extended long (>15-µm) polarized cytonemes toward the source cells and received GFP-tagged fluorescent puncta comprising either t-WTendo or M1endo (Fig. 7, H–I; and Fig. S4, C and D). Surface αGFPex immunostaining showed that both M1endo and t-WTendo colocalized with Btl:Cherryendo on the recipient cytoneme surfaces before their endocytosis (Fig. 7, J and J ′); therefore, the pattern of tissue-specific dispersion of M1endo was comparable to that of t-WTendo.

However, thorough scrutiny revealed that the m1endo allele produced hypermorphic phenotypes due to a reduced signaling range. The distal tip area of m1endo ASPs had significantly fewer long (>15-µm) signal-receiving cytonemes than the wtendo ASPs (Fig. 7 K). All of the cells (~6–7 cells in Z-projected images) within a 60-µm periphery surrounding the tip of wtendo ASPs extended long signaling cytonemes. In contrast, only one to two distal tip cells in the comparable region of the m1endo ASPs extended M1endo-receiving cytonemes. A restricted zone of M1endo-receiving cytonemes is reflected in the narrow gradient range and attenuated m1endo ASP growth (Fig. 8, A–E). While t-WTendo formed a long-range gradient along the ~10–12-cell-long ASP D-P axis, M1endo formed a narrow, steeper gradient along the ~5–6-cell-long D-P axis (Fig. 8, D and E). Accordingly, the m1endo ASPs had a reduced zone of nuclear dpERK in comparison to the wtendo ASPs (Fig. 8, G–I). Thus, M1endo had a narrow distribution and signaling range compared with t-WTendo (Fig. 8, G–I; and Fig. S4, G and H). Nevertheless, normalization of either the signal concentration or the signaling zone with recipient ASP length showed comparable scaling of the t-WTendo and M1endo gradients and signaling zones in relation to the recipient ASP size (Fig. 8, F and I). Previously, our work suggested that the Bnl gradient adopts recipient ASP-specific shapes due to two counteracting Bnl signaling feedbacks on cytonemes (Du et al., 2018a). Thus, scaling of the M1endo gradient to the recipient-specific shape indicated normal M1endo signaling, but within a limited range.

Ectopic expression in the salivary gland, a nontracheated organ that does not normally express bnl (Jarecki et al., 1999),
also showed a limited spatial distribution and signaling of M1. Since Bnl expression is known to induce tracheal invasion toward source cells, active Bnl expression in the salivary gland was expected to induce easily scorable tracheal invasion. We took advantage of a nonspecific expression of bnl-Gal4 (Du et al., 2017) in the salivary gland to express the Bnl mutants. Except for a CD8:GFP control, equivalent levels of expression of Bnl:HA1GFP3 (WT), M1, M2, or M1M2 all induced tracheal invasion into the salivary gland, confirming their nonautonomous signaling irrespective of cleavage (Fig. 8, J–N; and Fig. S5 A). Thus, M1 is an active signal. However, the salivary glands expressing WT and M2 had a significantly higher number of terminal branches ramifying throughout the gland surface. In contrast, glands expressing M1 or M1M2 showed poor terminal branching frequencies and surface coverage (Fig. 8, K–Q). Thus, M1 induced a spatially restricted response on the source cell surface. Since Bnl distribution pattern on a producing cell surface determines the spatial coverage of terminal branching on it (Peterson and Krasnow, 2015), attenuated terminal branching on the M1-expressing salivary glands suggested a reduced availability of M1 on the exposed basal cell surface of the salivary gland.

Bnl cleavage ensures its trafficking to the basal cell surface
To examine this possibility, we performed the surface αGFPex assay on salivary glands expressing the M1 or WT constructs. As expected, a significantly lower fraction of total M1 molecules were externalized on the basal surface of the salivary gland cells in comparison to WT (Fig. 9, A–D). Strikingly, while the WT protein covered the entire basal surface of the giant-sized salivary gland cells, most of the externalized M1 molecules were restricted to the cell junctions (Fig. 9, B and B’). Such abnormality in spatial distribution might suggest mispolarized M1

Figure 5. Knockdown of furin expression affects Bnl cleavage. (A–D’) Images of αHA-immunostained (red) S2 cells cotransfected with act-Gal4, UAS-bnl:HA1GFP3, and the synthesized RNAi as indicated. Control-i, nonspecific dsRNA; XYZ (A–D) and XZY (A’–D’) views; arrow, truncated Bnl:GFP3 derivative; arrowhead, uncleaved Bnl:HA1GFP3. (E) Graph comparing Bnl:HA1GFP3 cleavage under various furin knockdown conditions in S2 cells. Icorr, index of HA and GFP colocalization, with lower values indicating cleavage and color separation; n = 13 (control), 11 (fur1-i), 12 (fur2-i), and 14 (fur1-i, fur2-i); P values (ANOVA followed by Tukey HSD): fur1-i versus fur1-i, fur2-i, P = 0.347; all other groups, P < 0.001. (F–I) αDlg-immunostained (white) wing disc and ASP (white dashed line) from larvae where bnl-Gal4 expressed furin RNAi as indicated. Control, bnl-Gal4 > w--; (J and J’) Drawing depicting the scheme (J) of allometric measurement of ASP length (L) relative to the corresponding wing disc (WD); graph (J’) comparing the length (L) ratio of ASP to wing-disc (WD) under conditions indicated. n = 48 (control), 95 (fur1-i), 86 (fur2-i), 102 (fur1-i, fur2-i); P values (ANOVA followed by Tukey HSD): all groups versus fur1-i, P < 0.001; all groups versus fur1-i, fur2-i, P < 0.001. Scale bars: 10 µm (A–D); 30 µm (F–I).
trafficking, reducing its availability at the basal surface. Indeed, confocal sections through the salivary glands showed that most M1 signals were selectively enriched at the apical luminal sides of the cells that were inaccessible to the external trachea (Fig. 9, E–H). Notably, although salivary gland cells do not express Bnl, they contain the Bnl cleavage machinery. Bnl:HA\(_1\)GFP\(_3\) (WT) driven by bnl-Gal4 was cleaved leading to clear spatial separation of the HA- and GFP-tagged fragments (Fig. S5, B and B'). Therefore, these results suggested that Bnl cleavage promotes efficient polarized trafficking to the basal signaling surface from whence tracheal cells can receive the signal.

To confirm polarized Bnl sorting in the wing disc source, we acquired XZY sections of the disc-ASP tissue complex along the ASP D-P axis (Fig. 9, I–M). In the CD8:Cherry-marked disc bnl source, overexpressed M1 molecules preferentially populated the apical luminal and lateral sides of the columnar epithelial cells. In contrast, the truncated WT molecules had relatively higher density toward the basal side of the source cells (Fig. 9, J–L). In αHA-immunostained discs that expressed the Bnl:HA\(_1\)GFP\(_3\) construct under bnl-Gal4, the truncated Bnl:GFP\(_3\) signal was clearly polarized toward the basal surface of the columnar epithelial cells facing the overlying ASP (Fig. 9 M). A surface αGFP\(_{\text{exo}}\) assay confirmed a higher percentage of basal externalization of Bnl:GFP\(_3\) compared with M1 (Fig. S5 C). Similarly, when examining the genome-edited w\(_{\text{endo}}\) and m\(_{\text{endo}}\) larvae, we found that the basal surface of the disc source and recipient ASP

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**Figure 6. Furin-dependent Bnl cleavage in the wing disc.** (A–F) The αHA-stained (red) wing disc that expressed Bnl:HA\(_1\)GFP\(_3\) under bnl-Gal4 and were ex vivo cultured for 0 (pretreat) to 16 h in the absence and 1–5 h in the presence of Furin inhibitors as indicated. Arrow, truncated Bnl:GFP\(_3\) derivative; arrowhead, uncleaved Bnl:HA\(_1\)GFP\(_3\); blue, phalloidin-Alexa Fluor 647 marking cell outlines; merged (A–D) and either split green, red (A’–C’) or only red (D’–F’) channels are shown. (G) Graphs comparing average levels of colocalized HA and GFP in the ASP grown in presence and absence of Furin inhibitors; samples were harvested at different time points from the continuous culture. n = 11 (0 h), 11 (1 h), 10 (2.5 h), 9 (5 h control), 12 (5 h test), 5 (16 h); P values (ANOVA followed by Tukey HSD): P = 0.0001 for 5 h versus either 0 h, 1 h, or 2.5 h of Furin inhibition. Scale bars: 30 µm.
had significantly higher t-WTendo density in comparison to M1endo (Fig. 9, N–P). Thus, Bnl cleavage in the source cells directs efficient polarized sorting of the signal to the basal signaling surface, thereby affecting intercellular signaling range and tissue morphogenesis.

Discussion

This study showed that the FGF family protein Bnl is synthesized as a proprotein and then endoproteolytically cleaved at a single site by Furin1 in the Golgi network. The cleavage ensures efficient polarized intracellular sorting of a truncated C-terminal fragment containing the FGF domain to the signaling site, where the signal is received by the ASP cytonemes for intercellular dispersal and signaling.

Limited proteolysis is one of the versatile posttranslational mechanisms that activates most, if not all, developmental signals (LeMosy, 2006). Signals including Hedgehog (Hh); Dispatched; EGF; Trunk; the TGF-β/BMP family proteins Decapentaplegic (Dpp), Screw, and Glass bottom boat (Gbb); two Drosophila FGFs, Pyr and Ths; and human FGF7 were all shown to be cleaved (Lee et al., 1994; Schweitzer et al., 1995; Porter et al., 1996; Künnapuu et al., 2009, 2014; Wharton and Serpe, 2013; Constam, 2014; Johnson et al., 2015; Anderson and Wharton, 2017; Stewart et al., 2018). Although most signal cleavage is considered to activate the signal and affect the range of signaling response (Künnapuu et al., 2009, 2014; Wharton and Serpe, 2013), full-length uncleaved signals were also found to activate receptors and were shown to be secreted when expressed in cultured cells (Künnapuu et al., 2009; Sopory et al., 2010; Tokhunts et al., 2010; Tulin and Stathopoulos, 2010; Constam, 2014). Therefore, why are signals synthesized as proproteins and subsequently cleaved for their activity or dispersion?

We showed that Bnl cleavage acts as a catalytic switch that ensures its efficient polarized sorting to the basal signaling surface from where it can be taken up by the recipient cytonemes (Fig. 10). The uncleavable mutant Bnl can activate receptors but is presented on the basal surface at low levels (Fig. 9, A–M). The reduced basal presentation of uncleavable Bnl is due to its mistargeting to a far apical domain of the source cells.
which the trachea cannot access. Therefore, we predict that a pro-Bnl cleavage activates a delivery barcode for efficient target-specific intercellular dispersal. Conceptually, the cleavage ensures a signaling polarity that is relayed from within the source cells to the recipient ASP through cytonemes. Such signal bar-coding for determining intercellular destination might be conserved for all signals. Consistent with this view, a similar cleavage-dependent polarized sorting mechanism was reported for Hh in Drosophila retinal photoreceptor neurons (Huang and Kunes, 1996; Chu et al., 2006; Daniele et al., 2017). A complex choreography of apical and basal localization followed by the basal cytoneme-dependent dispersion of Hh was also described in Drosophila wing imaginal disc cells (Kornberg, 2011; Guerrero and Kornberg, 2014).

Interestingly, the efficiency of intracellular and intercellular Bnl trafficking depends on the enzymatic activity of Fur1 (Fig. 5 G and Fig. S3, A–D). Although Bnl expression is spatially restricted in tissues, the molecular machinery that cleaves Bnl

Figure 8. Bnl cleavage determines the range of gradient distribution and signaling. (A–C) Images of αDlg immunostained (white) ASPs (white outline) and wing discs from homozygous wtendo (n = 52) and m1endo (n = 64) larvae (A and B), a graphical comparison (C) of their ASP length relative to the wing disc size. (D and E) Average intensity profiles of t-WTendo (D, n = 3) and M1endo (E, n = 5) along the ASP D-P axis; lower panels, examples of signal distribution along the ASP D-P axis. Red line, exponential fit trend line; Cmax, maximum average intensity; C1/2, 1/2 Cmax; slope for the trend line between Cmax and C1/2. (F) Average intensity profiles of t-WTendo (n = 9) and M1endo (n = 12) normalized with recipient ASP length (D-P axes; Materials and methods). (G–I) Images of dP-Erk-stained (red) ASPs from homozygous weendo (n = 16) and M2endo (n = 20) larvae (G and H) and graphical comparison (I) of their nuclear dP-Erk-positive zones along the D-P axis; lower chart: average ratio (± SD) of number of dP-Erk-positive cells along the D-P axis to the total number of cells in the D-P axis. (J–N) Larval salivary glands expressing CD8:GFP, Blnt::HA, GFP3 (18), M1 (11), M2 (20), and M1M2 (18) under bnl-Gal4 as indicated. Red arrow, central branch point. (O) A quantitative assessment of the frequency of terminal branching on salivary gland determined by Sholl analysis under the conditions indicated. Scale bars: 30 µm (A, B, G, and H); 100 µm (J–N).
exists even in salivary glands that do not normally express Bnl. This might reflect the broad range of Furl expression, as reported in several studies (Roebroek et al., 1992, 1993; Künnapuu et al., 2009; Nichols and Weinmaster, 2010; Johnson et al., 2015). Alternatively, different types of cells might express different furin/PC genes that can act redundantly. Furins are known to be regulated enzymes that autoactivate in a Ca2+-dependent manner during their intracellular trafficking (Thomas, 2002). How and when the Furin activation pathway might intersect with the pro-Bnl sorting itinerary is unknown. We also do not know why a truncated Bnl is targeted only to the basal cell surface. Recently, the trans-Golgi cargo receptor AP-1γ, a component of the Clathrin AP-1 complex, was shown to be necessary for Bnl trafficking to the basolateral membranes of bnl-expressing flight muscle cells (Peterson and Krasnow, 2015). It is possible that Bnl cleavage unmasks the cargo-receptor binding site. The current

Figure 9. Cleavage ensures polarized Bnl sorting to the basal cell surface for signaling. (A–C) High-magnification (40×) images of the exposed basal surfaces (arrowhead) of salivary glands expressing WT or M1 under bnl-Gal4 from an area schematically shown in C. Red, surface αGFP immunostaining; arrow, cell junction. (D) Graph comparing fractions (red surface stain/total GFP) of overexpressed WT (n = 12) and M1 (n = 10) that got externalized on the salivary gland surface. (E–H) Images of sagittal sections of salivary glands expressing WT and M1 under bnl-Gal4. Arrow, apical lumen. (I) Drawings depicting the ASP D-P axis (dashed line; upper panel) and an XZY section along the D-P axis (lower panel) showing the tubular ASP and disc epithelia as shown in J–M. (J and K) Sagittal sections of αDlg immunostained (blue, sub-apical marker) wing disc and ASP when the disc bnl source coexpressed CD8:Cherry with either the WT or M1 construct under bnl-Gal4. Arrow, basal side; arrowhead, apical side. (L) Graph comparing apical and basal percentage of WT and M1 relative to the total amount in the disc source. n = 24 (WT) and 32 (M1). (M) Maximum projections of mid- and para-sagittal sections within ~3 μm of mid-Y of an αDlg (blue) and αHA (red) stained wing-disc/ASP, where bnl-Gal4 expressed Bnl:HA1GFP3. Arrow, truncated Bnl:GFP, white dashed line, ASP and wing disc; arrowhead, apical lumen of wing disc. (N–P) Comparison (graph in P) of levels of t-WTendo (n = 17) and M1endo (n = 33) on the surface of the disc source and ASP (dashed line). Red and arrowhead, detergent-free αGFP-staining; arrow, intracellular puncta; white staining, phalloidin-Alexa Fluor 647. Scale bars: 50 μm (E–H); 20 μm (all other panels).
knowledge of intracellular Bnl/FGF targeting is rudimentary and needs to be elucidated in the future.

Our findings revealed that although Bnl cleavage is intracellular, it plays an important role in determining the range of cytoneme-mediated intercellular Bnl dispersal. Insights on how this intracellular event might influence the range of cytoneme-dependent dispersal came from our earlier study (Du et al., 2018a). As illustrated in Fig. 10, high to low levels of Bnl signaling activate two counteracting feedback loops operating from the opposite poles of the ASP, which help to establish the zones of corresponding high to low number of Bnl-receiving cytonemes along the ASP epithelium. The consequence is a systemic self-regulatory process, where the number of Bnl-receiving cytonemes produced by ASP cells is determined by the amount of Bnl received by the cells through cytonemes, giving rise to the recipient ASP-specific Bnl gradient shapes. Therefore, the intracellular cleavage and polarized sorting pathway that modulate Bnl availability on the basal surface of source cells can determine the spatial range of cytoneme formation, signal dispersion, and signaling. These results suggest an intricate coordination of the intracellular events in the source and recipient cells with the intercellular cytoneme-mediated dispersal, which together can precisely shape signal gradients and tissue patterns.

Materials and methods

Drosophila strains and genetic crosses

All crosses were incubated at 25°C. The following strains were used in this study: UAS-bnlRNAi (34572), fur1-LacZ (10341), UAS-fur1RNAi (25837), UAS-fur2RNAi (42481), UAS-fur1RNAi (41914), UAS-fur2RNAi (51743), UAS-fur1RNAi (42577), UAS-fur1 (63077) (from Bloomington Stock Center); UASattB-Bnl:GFP1, UASattB-Bnl:GFP2, UASattB-Bnl:GFP3, UASattB-Bnl:GFP4, UASattB-Bnl:HA1, UASattB-Bnl:HA2, UASattB-Bnl:HA3, UASattB-Bnl:HA4, UASattB-Bnl:HA1GFP3, UASattB-Bnl:HA1GFP3-M1, UASattB-Bnl:HA1GFP3-M1M2, UASattB-Bnl:HA1GFP3-M1M2, btl:cherryendo (from Fenelon lab); UAS-Bnl:GFP (gifts from Kornberg lab); fur2-Gal4 (NP 4074) (from Kyoto DGGR); UAS-CD8:GFP, UAS-CD8:Cherry, btl-Gal4, bnl-Gal4 (Roy et al., 2014); bnl:gfpendo, bnl:gfpendo, btl:cherryendo (Du et al., 2018a); and UAS-Bnl:GFP, UAS-Bnl:HA1, UAS-Bnl:GFP2, UAS-Bnl:GFP3, UAS-Bnl:HA1, UAS-Bnl:GFP4, UAS-Bnl:HA1GFP3, UAS-Bnl:HA1GFP3-M1, UAS-Bnl:HA1GFP3-M2, UAS-Bnl:HA1GFP3-M1M2, UAS-Bnl:HA1GFP3-M1M2, btl:cherry, btl:cherryendo (this study).

Generation of transgenic Drosophila lines

UAS-bnl:GFP and UAS-bnl:HA variants

Each of the four Bnl:GFP variants contained an HA-tag upstream to a GFP tag at a single internal site. Bnl:GFP contained both HA and GFP tags in tandem inserted between amino acids RSSLVPSAVS and E88RSVNQPT. Bnl:GFP contained the tags inserted between amino acids SNLDRNERST and E88RSVNQPT. Bnl:GFP contained the tags inserted between amino acids KAPPHCSSNT and S433GSSSSS. Bnl:GFP contained the tags between amino acids MSSGEEQDQDN and D702QDEQSGDFGE. Previously, transgenic Drosophila lines harboring the Bnl:GFP construct at various attP loci in the second and fourth chromosomes did not show any detectable Bnl:GFP expression when driven by bnl-Gal4. Therefore, we subcloned the Bnl:GFP constructs into the pUAST vector from the original pUAST-attB constructs and resorted to the random P-element-based transgenesis to avoid any positional effects on Bnl:GFP expression. A summary of characterization of different transgenic lines is presented in Table S2.

UAS-bnl:HA1GFP3

UAS-bnl:HA1GFP3 contained an HA-tag at site 1 (between 87 and 88 amino acid residues of the original protein) and a superfolder
GFP (Pédelacq et al., 2006) at site 3 (between 432 and 433 residues of the original protein). The construct was generated by overlap extension PCR of three fragments using primers (Table S1): the N-terminal HA-tagged part, the C-terminal Bnl coding region (amplified from the pUAST-attB-Bnl:HA1), and the middle sfGFP region from a sfGFP-containing construct (Addgene). The final 3,060-bp PCR product was cloned into the pCR-Blunt II TOPO vector. The fully sequence-verified insert was subcloned into the pUAST vector at the BglII and XbaI sites. UAS-bnl:HA1GFP3 was used for analysis in S2 cells and for P-element-mediated germline transformation and transgenesis.

**UAS-bnl:HA1GFP3 mutants**
The M1 and M2 variants of Bnl:HA1GFP3 contained the following cleavage site mutations: M1, (R/G)TE(R/G)SI(R/G); M2, (R/G)NE(R/G). These mutant constructs were created using overlap extension PCR with the Bnl:HA1GFP3 construct as a template. The primers used are shown in Table S1. The final assembled PCR product was cloned into the pCR-Blunt II TOPO vector. The sequence-verified constructs were subcloned into the BglIII and XbaI sites of the pUAST vector for either analysis in S2 cell culture or for P-element-mediated germline transformation and transgenesis.

**UAS-bnl:HA1GFP4 and UAS-bnl:GFP1HA4**
UAS-bnl:HA1GFP4 was cloned using overlap extension PCR to insert a GFP tag at site 4 of Bnl:HA1. Similarly, UAS-bnl:GFP1HA4 was cloned using overlap extension PCR to insert a GFP at site 1 of Bnl:HA4. The primers used are listed in Table S1. These constructs were verified and used in S2 cell culture analyses. P-element based transgenesis was performed as described earlier (Du et al., 2017). Various transgenic lines generated are described in Table S2.

**CRISPR/Cas9-based genome editing**
The bnl:HA1GFP3endo and bnl:HA1GFP3-MIendo mutant alleles were generated by in-frame insertion of an HA tag using the first coding exon of a previously characterized bnl: sfGFP3endo allele (Du et al., 2018a) using CRISPR/Cas9-based genome editing following previously described protocols (Du et al., 2017, 2018b). The bnl: HA1GFP3-MI mutant allele includes the HA1 tag as well as mutations of three arginines (R) to glycines (G) at FCS1 that starts 82 amino acids upstream of the conserved GFP domain. For targeting Cas9-based double-stranded break near tag site 1, a guide RNA (BnHAiGRNA, 5′-CTAGTTCACCTACTGCGCTGG-3′; underlined bases represent the PAM site) with zero off targets in the fly genome was cloned by ligating two annealed complementary oligonucleotides into the pCFD3 vector (Table S1).

The replacement donors, pDonor-bnl:HA1GFP3 and pDonor-bnl:HA1GFP3-MI, were designed and generated following Du et al. (2017). These constructs contained either HA1 or the HA1-MI mutations flanked by ~1-kb long 5′ and 3′ arms that are homologous to the genomic sequence flanking tag site 1. Both 5′ and 3′ homology arms were PCR-amplified from genomic DNA from the nos-Cas9; bnl:GFP3endo parent fly, sequence verified, and assembled together into the pUC19 vector using Gibson Assembly (primers in Table S1). To prevent retargeting of the gRNA/Cas9 to the edited genome, a synonymous mutation was introduced into the replacement cassette near the PAM sequence via the primers used for amplification (Table S1). The constructs were fully sequenced before germline injection.

The gRNA-expressing vector and the respective replacement donor vector were coinjected into the germline cells of nos-Cas9; bnl: sfGFP3endo embryos. For each genome-editing experiment, a stepwise crossing strategy (Du et al., 2018b) was followed to obtain G0–F2 progeny and establish individual fly lines for screening. The desired “ends-out” homologous directed repair (HDR) was screened for by a three-step PCR-based strategy (see primers in Table S1), followed by sequencing and analyses of tissue-specific expression patterns of the tagged genes under a confocal microscope. The efficiency of genome editing–based generation of the two different genotypes and their phenotypes were summarized in Table S4. During generation of bnl:HA1GFP3-MIendo several lines were obtained that had only the HA1 insertion without the M1 mutation. We predicted that the HDR had taken place somewhere between the HA1 tag site and M1 mutation sites (219 bases apart). These lines were fully sequence verified and found to have normal tissue expression. Therefore, these lines were considered as bnl:HA1GFP3-M1 lines (see Table S4). For subsequent analyses, we used a w1endo and an m1endo line derived from the same genome-editing experiment. The w1endo F4–14 line and m1endo F4–9 line used in this study were fully sequence verified and established after outcrossing as previously described (Du et al., 2018a).

**Synthesis of double-stranded RNA (dsRNA) for gene knockdown in S2 cells**

dsRNA was synthesized by PCR from genomic DNA isolated from S2 cells following a previously described protocol (Künnapuu et al., 2009). The following PCR primers were used to synthesize the T7 transcription template carrying the T7 promoter sequence at their 5′ ends: fur1: forward, 5′-TAATAC GACTCCTATAGGGACGCAAAGATCCTCTGTGGCA-3′; reverse, 5′-TAATACGACTCCTATAGGGACATGTCTCCGGGAAACTGC-3′; fur2: forward, 5′-TAATACGACTCCTATAGGGACGCTAGAGG CAAATCGGGA-3′; reverse, 5′-TAATACGACTCCTATAGGGACGCTAGAGG CAAATCGGGA-3′; reverse, 5′-TAATACGACTCCTATAGGGACGCTAGAGG CAAATCGGGA-3′.

dsRNA against fur1 or fur2 were synthesized using the MEGAscript RNAi Kit (Thermo Fisher Scientific).
were ∼90% confluent, the medium was removed and 6 ml of fresh M3 medium was added to the flask. Cells were gently resuspended by pipetting and added to a 12-well plate with 1 ml of cells per well. After 2 h, once the cells had adhered to the bottom of the well, the M3 media was replaced with 1 ml serum-free M3 medium, and the cells were transfected with 1 µg of each DNA using Lipofectamine 2000 following the manufacturer’s protocol. After 16 h, the serum-free medium was replaced with 1 ml M3 medium containing serum. For experiments with furin RNAi, 5 µg of dsRNA was used for transfection. Under all conditions, transient expression was examined 2–3 d after transfection.

**Ex vivo organ culture and Furin inhibitor assay**

Ex vivo culturing of wing discs was performed in WM1 medium as described in Du et al. (2017). The discs were removed from a single pool of culture after 0, 5, and 16 h of incubation at 25°C, followed by fixation and αHA immunostaining of the tissues. For the Furin inhibitor assay, late third instar larval tissues were ex vivo cultured in 2 ml of WM1 medium in the presence or absence of a cocktail of Furin inhibitor I and II (50 µM final concentration each; Calbiochem; 344930 and 344931) following recommended concentrations in Johnson et al. (2015). The live tissues were incubated for 1, 2.5, or 5 h. Following incubation, the carcasses were transferred to a centrifuge tube, rinsed three times with 1× PBS, and fixed in 4% PFA before αHA immunostaining.

**Protein analyses**

S2 cells were harvested 3 d posttransfection, and the cell pellets were washed several times in 1× PBS. The pellet was re-suspended in 70 µl RIPA cell lysis buffer (Sigma-Aldrich) in the presence of a cocktail of protease inhibitors (Roche) and kept for 15 min at 4°C. An equal volume of lysed cells was combined with 2× Sample Buffer, heated at 95°C for 5 min, and loaded onto a 10% SDS-PAGE minigel. The gel was run at 50 V for 10 min for stacking and then at 200 V until the desired amount of separation occurred. Proteins were transferred from the gel to a PVDF membrane using Transblot Turbo (Bio-Rad). A standard protocol was followed to perform Western blot analyses using a standard and detergent-free immunostaining protocol was as previously described (Du et al., 2018a). The following antibodies were used in this study: α-Discs large (1:100; DSHB); α-HA (1:1,000); α-dpERK (1:100; Cell Signaling); α-GFP (1:3,000 extracellular; Abcam); and α-PH3 (1:2,000; Cell Signaling). Alexa Fluor–conjugated secondary antibodies (1:1,000; Molecular Probes) were used for immunofluorescence detection. Phalloidin–conjugated Alexa Fluor 647 was often used for marking cell outlines.

**Immunostaining**

Standard and detergent-free immunostaining protocols were as previously described (Du et al., 2017). The following antibodies were used in this study: α-Discs large (1:100; DSHB); α-HA (1:1,000); α-dpERK (1:100; Cell Signaling); α-GFP (1:3,000 extracellular; Abcam); and α-PH3 (1:2,000; Cell Signaling). Alexa Fluor–conjugated secondary antibodies (1:1,000; Molecular Probes) were used for immunofluorescence detection. Phalloidin–conjugated Alexa Fluor 647 was often used for marking cell outlines.

**Microscopic imaging**

For live imaging, wing imaginal discs and their associated trachea were prepared following Roy et al. (2014). Images were obtained as previously described (Du et al., 2018a) using a Leica SP5X with HyD detector or an CSUXI Yokogawa spinning disc confocal equipped with an Andor iXon897 EMCCD camera. The images were processed and analyzed with Fiji. Maximum-intensity projections of sections were shown for most images. All images were obtained using 40× objective in the microscopes, except for Fig. 8 (J–N), which used a 20× objective. All XZY images were obtained using the Leica SP5X with a 40× objective for S2 cells and 20× objective for wing discs.

**Analysis of ASP size**

ASP length was measured from the TC along their longest (major) D–P axis to the ASP tip. The disc size was determined by measuring from the TC, along the ASP major axis to the edge of the disc. A ratio of the ASP:disc size was used to compare different genotypes and conditions (Figs. 5 J’ and 8 C).

**Sholl analysis for terminal branching**

Salivary glands were gently dissected out from fixed larval tissues overexpressing different cleaved and uncleaved variants of Bnl and imaged under transmitted light to visualize tracheal invasion. In WT overexpressing tissue, the terminal tracheal branches ramified radically from a preexisting central branch point. Due to its morphological resemblance with neuronal dendritic arbors, we employed Sholl analysis (Binley et al., 2014) using Fiji to measure the frequency of terminal branching. The analysis created 20 concentric circles in increments of 5-µm radius from the point of origin up to 100 µm and counted the number of times any tracheal branch crossed these circles. These values were averaged across several samples and compared between the different Bnl variants expressed in the salivary gland.

**Quantitative analyses of fluorescence intensities**

For Bnl levels, all fluorescent intensity measurements were background corrected. 3D image stacks representing only either the wing disc sections or the ASP were transformed into 2D by maximum-intensity projections. The density of fluorescence intensity was measured from a selected region of interest (ROI) of the 2D images, outlining the either Bnl source cells or the recipient ASP (Figs. 2 I, 6 G, and 5 S C). For the recipient ASP, the ROI encompassed the distal tip of the ASP (a region with ∼3–4-cell diameter that received the maximum Bnl from the source). Likewise, the density of the surface-localized Bnl:GFP variants, probed by αGFP immunostaining (Fig. 9 F), was measured from selected ROIs on the maximum-intensity projections of the relevant optical sections encompassing either the ASP or wing disc source. For Fig. 9 D, the ROIs represented each salivary gland cell including the cell junctions, and the density of the red and green channel intensities were measured from the maximum-intensity projections of optical sections within the 5-µm Z-stack from the most basal surface. The ratio of surface GFP (red) to total GFP (green) was expected to be less than one. However, some average ratios were slightly greater than one, probably due to the immunofluorescent signal amplification of the surface-exposed proteins obtained through αGFP immunostaining. Second, as reported earlier (Du et al., 2018a), the surface exposed GFP was rapidly quenched, reducing its levels of...
detection on the cell surface. For Fig. 9 (J–L), ROIs representing the basal or apical part of the source cells were selected from maximum-intensity projections of the XZY sections. GFP intensities measured from the ROIs were normalized to the total intensity from the total source cell area.

For colocalization analyses in S2 cells (Figs. 3 H and S E), maximum-intensity projections of approximately four to five stacks around the center of the cell were produced. An I_corr value was obtained using the Colocalization Colormap plugin of Fiji to determine the degree of colocalization of two selected channels (HA immunostain and GFP).

Gradients of intensities of Bnl:GFP variants in the ASP (Fig. 8, D–F) were obtained along the ASP D-P axes as reported earlier (Du et al., 2018a). For Fig. 8 F, gradients were measured from homozygous wtendo (n = 9) or m1endo (n = 12) ASPs. Each position (x) within an ASP was normalized by length of the ASP (L) to obtain x/L, the x-axis of the plot. Similarly, GFP Intensity was normalized by dividing each intensity value in a single sample by the highest intensity value from that sample for the y-axis. Normalized intensity values from each sample were taken at 0.05 x/L increments from 0 to 1 (i.e., 21 data points from each sample). The normalized intensity values from each group (WT or M1) were averaged together and plotted along the x/L axis.

Cytoneme analysis
ASP cytoneme number was quantitated microscopically as previously described (Roy et al., 2011, 2014). In brief, cytonemes >15 µm in length that extended from a 60-µm total perimeter region (30 µm from the tip of the ASP in both directions) were counted.

Statistical analyses
Statistical significance was determined with two-tailed t tests or a one-way ANOVA followed by Tukey’s honestly significant different (HSD) tests. All P values in the legends were obtained using a t test, unless otherwise stated.

Online supplemental material
Fig. S1 shows additional images comparing Bnl:GFP1 and Bnl:GFP2 expression and dispersion. Fig. S2 shows additional biochemical and cell-biological evidence of Bnl cleavage. Fig. S3 shows ASP phenotypes due to bnl and fur knockdown in the disc bnl source and expression analyses of fur genes. Fig. S4 shows additional examples of localization and activity of WT and M1 wtendo and M1mendo in the ASP. Fig. S5 shows cleavage of Bnl:HA3GFP in the salivary gland, a quantitative analysis performed to identify lines of Bnl:HA3GFP variants that expressed at equivalent levels, and a graph comparing the percentage of WT and M1 proteins on the surface of the wing disc cells that overexpressed the proteins. Video 1 shows the organization of the ASP and wing disc bnl-source. Video 2 shows the Bnl:GFP3 distribution in a 3D ASP section. Video 3 shows the lack of Bnl:GFP3 in ASP 3D images. Videos 4 and 5 show the spatial distribution of cleaved Bnl portions in XYZ and XZY S2 cell sections. Video 6 shows the spatial distribution of the uncleaved M1 mutant Bnl in a S2 cell. Video 7 shows the spatial distribution of the uncleaved M1 mutant Bnl in the wing disc-ASP. Table S1 lists primers used in this study. Table S2 lists transgenic Drosophila lines created for this study and their analyses. Table S3 lists phenotypic analyses of fur expression knockdown by various RNAi lines. Table S4 shows the efficiency of generation of bnl:HA3sfGFP3 and bnl:HA3sfGFP3-M1 mutant Drosophila lines using CRISPR/Cas9.

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