The ETS domain transcriptional repressor Anterior open inhibits MAP kinase and Wingless signaling to couple tracheal cell fate with branch identity

Sara Caviglia* and Stefan Luschnig*

SUMMARY
Cells at the tips of budding branches in the Drosophila tracheal system generate two morphologically different types of seamless tubes. Terminal cells (TCs) form branched luminalized extensions that mediate gas exchange at target tissues, whereas fusion cells (FCs) form ring-like connections between adjacent tracheal metameres. Each tracheal branch contains a specific set of TCs, FCs, or both, but the mechanisms that select between the two tip cell types in a branch-specific fashion are not clear. Here, we show that the ETS domain transcriptional repressor anterior open (aop) is dispensable for directed tracheal cell migration, but plays a key role in tracheal tip cell fate specification. Whereas aop globally inhibits TC and FC specification, MAPK signaling overcomes this inhibition by triggering degradation of Aop in tip cells. Loss of aop function causes excessive FC and TC specification, indicating that without Aop-mediated inhibition, all tracheal cells are competent to adopt a specialized fate. We demonstrate that Aop plays a dual role by inhibiting both MAPK and Wingless signaling, which induce TC and FC fate, respectively. In addition, the branch-specific choice between the two seamless tube types depends on the tracheal branch identity gene spalt major, which is sufficient to inhibit TC specification. Thus, a single repressor, Aop, integrates two different signals to couple tip cell fate selection with branch identity. The switch from a branching towards an anastomosing tip cell type may have evolved with the acquisition of a main tube that connects separate tracheal primordia to generate a tubular network.

KEY WORDS: Drosophila melanogaster, anterior open, Yan, TEL1, ETS domain, MAPK, Wingless, spalt, Tracheal system, Epithelial tube morphogenesis, Angiogenesis, Tip cell specification

INTRODUCTION
Tip cells are specialized endothelial cells that lead the migration of sprouting vessels and mediate Anastomosis formation during vascular development in vertebrates (Geudens and Gerhardt, 2011; Herwig et al., 2011). Signaling through Vascular endothelial growth factor receptor (VEGFR), a receptor tyrosine kinase (RTK), is involved in selecting tip cells and in guiding their directed migration. However, the mechanisms that select between different tip cell behaviors (migration versus Anastomosis formation) are not clear. In the Drosophila tracheal system, 20 groups of epidermal cells generate a tubular network through a sequence of branching and tube fusion events (Ghabrial et al., 2003; Uv et al., 2003; Affolter and Caussinus, 2008; Maruyama and Andrew, 2012). Tracheal cells invaginate from the epidermis and subsequently migrate in a stereotyped pattern guided by the local expression of the Fibroblast growth factor (FGF) homolog Branchless (Bnl) (Sutherland et al., 1996). Bnl activates the FGF receptor (FGFR) Breathless (Btl) on tracheal tip cells, which lead the concerted migration towards the Bnl source. Reminiscent of the role of VEGFR signaling in angiogenesis, Bnl promotes and guides cell motility, but also stimulates differentiation of tracheal tip cells through activating Ras-MAPK signaling (Samakovlis et al., 1996b; Samakovlis et al., 1996a). Whereas the branch stalk cells form tubes with extracellular lumina sealed by cell-cell junctions, tip cells generate two different types of seamless tubes with intracellular lumina. Terminal cells (TCs), which express the Drosophila Serum response factor homolog (DSRF; Bs – FlyBase) (Guillemin et al., 1996; Montagne et al., 1996) under the control of Ras-MAPK signaling, develop branched and luminalized cytoplasmic extensions that mediate gas exchange at the target tissues. The second type of seamless tubes, generated by fusion cells (FCs), mediates the connection of adjacent tracheal metameres. A single FC expressing the Zn-finger protein Escargot (Esg) (Samakovlis et al., 1996b; Tanaka-Matakatsu et al., 1996) and the bHLH protein Dysfusion (Dys) (Jiang and Crews, 2003) is specified at the tip of each branch that will connect with a cognate branch from a neighboring or contralateral tracheal metamere. FC specification involves FGF signaling and branch-specific Wingless (Wg) and TGFβ signals, which promote the FC fate (Steneberg et al., 1999; Chihara and Hayashi, 2000; Llimargas, 2000). Conversely, Delta/Notch-dependent lateral inhibition prevents neighboring cells from assuming FC fate, thus ensuring that a single FC is specified at each branch tip (Ikeya and Hayashi, 1999; Llimargas, 1999). Although high-level MAPK activation in tip cells promotes both FC and TC specification, the choice between the two tip cell fates is regulated in a branch-specific fashion. The tips of most tracheal branches contain a single FC and at least one TC. However, the main longitudinal dorsal trunk (DT) tube contains only FCs, whereas the visceral branches (VB), which originate from the same region as the DT, contain only TCs. Although the correct choice between the two different seamless tube types is essential for the formation of a functional respiratory network, how tip cell fate choice is coordinated with branch identity remains unclear. It has been shown that DT identity and FC specification in the DT depend on Wg signaling (Chihara and Hayashi, 2000; Llimargas, 2000), but how
Wg and MAPK signals are integrated within tip cells to control FC specification is not known.

We show here that the ETS domain transcriptional repressor Anterior open (Aop; also known as Yan) (Lai and Rubin, 1992; Tei et al., 1992) plays a key role in the region-specific selection of tip cell fate in the tracheal system. Aop blocks signaling downstream of different RTKs by competing with the ETS domain transcriptional activator Pointed (Pnt) for binding to shared cis-regulatory elements (Rebay, 2002). Phosphorylation by MAPK activates Pnt and inactivates Aop, thus resulting in target gene activation (Brunner et al., 1994). Interestingly, Aop was recently found to repress not only RTK signaling, but also Wg signaling in the developing Drosophila eye, possibly through interacting with Armadillo (Arm) (Olson et al., 2011). We show that Aop acts in a dual fashion by inhibiting both MAPK-dependent TC specification and Wg-dependent FC specification in tracheal non-tip cells. In the absence of aop function, every tracheal cell is able to adopt a specialized (TC or FC) fate. We show that the choice between the two fates is determined not only by the nature of the inducers (Wg or Bnl), but it is constrained by factors that define tracheal branch identity: expression of the selector gene spalt major (salm) biases the competence of tracheal tip cells towards FC fate. Thus, a single transcriptional repressor, Aop, integrates two different signals to couple tip cell fate selection with tracheal branch identity.

MATERIALS AND METHODS
Drosophila strains
The aopO199 mutation was isolated in an ethyl methanesulfonate mutagenesis screen (Förster et al., 2010). Unless otherwise mentioned, Drosophila stocks were obtained from the Bloomington Stock Center: Df(2L)BSC688, 69B-Gal4, UAS-mCherry-NLS, UAS-GFP (FlyBase), UAS-Vern-mRFP (Förster et al., 2010), btl-Gal4 (Shiga et al., 1996), esg-LacZ^{2-2} (Samakovlis et al., 1996b), aop^{1}, salm^{1} (Nusslein-Volhard et al., 1984), pnt^{600} (Brunner et al., 1994), sty^{262} (Kramar et al., 1999), UAS-aop, UAS-Aop^{6CT} (Rebay and Rubin, 1995), UAS-ds, dsc1.7::nsbGFP (Jiang et al., 2010), E-Cad-mTomato (Huang et al., 2009), UAS-bnl (Sutherland et al., 1996), UAS-Bdt (Lee et al., 1996), UAS-iTop (Queenan et al., 1997), UAS-arm^{88} (Pai et al., 1997), UAS-dnTCF (UAS-dTFCAN-HA) (van de Wetering et al., 1997), UAS-Asin-GFP (Cliffe et al., 2003) and UAS-salm (Kühnlein and Schuh, 1996).

Sequencing of aop alleles
Homozygous aopO199 and aop^{1} embryos were selected by the absence of the CyO Dfd-YFP balancer chromosome (Le et al., 2006). Genomic DNA was extracted from 15 embryos. The aop locus was amplified by PCR with oligonucleotides SC1 (5'- GTTTTCCGGTTTGCATGCAT and SC2 (5'-CTGACCGGGAATTCTTGA) PCR products were sequenced by both strands.

Immunostainings
Embryos were fixed in 4% formaldehyde for 20 minutes and devitellinized by shaking in methanol/heptane. Primary antibodies (mouse anti-GFP, rabbit anti-GFP, rabbit anti-mCherry) were used as previously described (Förster et al., 2010). Other antibodies used were mouse anti-Aop 8B12H9 (1:10); (Rebay and Rubin, 1995), mouse anti-Arm N27A1 (1:7, DSHB), rabbit anti-β-Galactosidase (1:1000; Cappel), mouse anti-Delta extracellular domain C594.9D (1:100; DSHB), mouse anti-DSRF (1:300; Samakovlis et al., 1996b), rabbit anti-Dys (1:500; Jiang and Crews, 2003), mouse anti-GFP (1:500; Roche), rat anti-ΔHA 3F10 (1:300; Roche), rabbit anti-Salm (1:40; Kühnlein and Schuh, 1996) and guinea pig anti-Δuf (1:1000; Zhang and Ward, 2009). Goat secondary antibodies were conjugated with AlexaFluor 488, 559 (Molecular Probes) or Cy5 (Jackson ImmunoResearch). Chitin was detected using SNAP-tagged chitin-binding domain from chitinase A1 of Bacillus circulans (plasmid provided by Yinhua Zhang, New England Biolabs) (Watanabe et al., 1994), which was expressed as a His-tagged protein in E. coli, purified using Nickel-NTA sepharose and labeled with SNAP-Surface AlexaFluor 425, 488, 546 or 647 (New England Biolabs).

Imaging and quantifications
Specimens were imaged using an Olympus FV1000 confocal microscope. For live imaging, staged embryos were dechorionated, glued on a coverslip and immersed in Voltalef 105 oil. Z-stacks (0.5-1.5 µm step size) were projected using Imaris (v7.3.1, Bitplane) or Fiji (GPL v2). The Imaris oblique slicer tool was used to create virtual projections (1-3 µm thick) oriented in z (Fig. 1C, D; Fig. 2E, F) or xy (Fig. 4L, M). For FC and TC quantification, Dys- or DSRF-positive nuclei in the DT (Tr1-10), DB (Tr1-10), LT (LT1, LT1-LT, Tr10) and GB (Tr1-10) were counted using the spot tool in Imaris. At least seven embryos per genotype were analyzed. To calculate average TC and FC numbers per branch tip, the total number of TCs or FCs found in each branch type was divided by the number of branch tips that were scored in a given embryo. P values were calculated using two-tailed, unpaired Student’s t-test. Salm protein levels were measured in aopO199 and btl-Gal4; UAS-Aop^{6CT} embryos, which were co-stained with wild-type control embryos in the same reaction. Nuclei of tracheal cells in DT metameres Tr8-9 were segmented using the Imaris spot tool. Mean intensities from a total of at least 200 nuclei from at least seven embryos per genotype were averaged. Average values from wild-type controls for each genotype were set to 100% to calculate fold change values. Standard deviations were calculated from the mean of normalized values. P values were calculated using two-tailed, unpaired Student’s t-test.

RESULTS
O199 mutants show cellular inclusions within the tracheal lumen
We isolated a new class of embryonic lethal mutants showing abnormally shaped tracheal tubes. In one such mutant, O199, the tracheal branching pattern was normal, but the lumen of the DT showed apparent ‘holes’ where luminal material was excluded (Fig. 1A, B). These structures were variable in size and occurred mainly within metameres 5-9 near to DT fusion joints (data not shown). The exclusion of luminal material was due to cellular bridges traversing the DT lumen (Fig. 1C, D). Time-lapse imaging revealed the origin of these structures (Fig. 1E; supplementary material Movie 1). After completion of DT fusion, the lumen began to bend towards one side, leading to a local indentation. Shortly afterwards, two fine luminal extensions invaded the indentation from both sides and subsequently joined, giving rise to a secondary lumen separated from the original lumen by a cellular bridge.

O199 is a loss-of-function mutation in the ETS domain transcriptional repressor anterior open
We mapped the O199 mutation to the aop locus (Lai and Rubin, 1992; Tei et al., 1992). Tracheal defects of aopO199 homozygotes were similar to those of aopO199/Df(2L)BSC688 hemizygous embryos (supplementary material Fig. S1), indicating that O199 is an amorphic aop allele. O199 failed to complement the aop^{1} mutation (Nusslein-Volhard et al., 1984; Rogge et al., 1995) and aop^{1} embryos showed tracheal defects resembling those of O199 mutants (data not shown). Sequence analysis revealed that aop^{1} carries a premature stop codon resulting in a predicted truncated protein lacking the ETS DNA-binding domain (Fig. 1G, H). O199 carries a 203 bp deletion in the first coding exon, resulting in a frame shift and a predicted protein that is truncated after the Pointed (PNT) domain. Aop protein was not detectable in aopO199 embryos (supplementary material Fig. S2). Tracheal-specific expression of an aop cDNA (Rebay and Rubin, 1995) completely rescued the tracheal defects of aopO199 mutants (supplementary material Fig. S1). We conclude that aopO199 is an aop loss-of-function allele and that aop function is required in tracheal cells for the normal shape of the DT lumen.
Luminal bifurcations in aop mutants are due to extra tracheal fusion events

We hypothesized that the formation of secondary lumina in the DT of aop mutants could result from extra tracheal fusion events. Wild-type embryos contain a single Dys-positive FC per branch tip (Fig. 2A). By contrast, aopO199 mutants showed extra (2.8 ± 0.3 per tip) Dys-positive cells in the DT (Fig. 2B). Like wild-type FCs, every Dys::nls-GFP-positive cell in aopO199 mutants showed elevated levels of E-Cadherin-mTomato (E-Cad-mTomato) at adherens junctions (AJs; Fig. 2C-F) (Tanaka-Matakatsu et al., 1996). At least four FCs were located adjacent to the luminal bifurcations in aopO199 mutants. Tube cross-sections of such sites revealed two adjacent triple-ring-shaped AJs, characteristic of FC toroids, flanking the separated part of the lumen (Fig. 2E,F). Thus, DT cells in aopO199 become mis-specified as FCs. These supernumerary FCs undergo morphological transformations that are characteristic of wild-type FCs and they accomplish extra fusion events, which result in the formation of luminal bifurcations.

MAPK signaling promotes specification of tracheal fusion cells and terminal cells in a complementary pattern

Interestingly, supernumerary FCs in aop mutants were limited to the DT, whereas in all other branches numbers and positions of FCs were normal (Fig. 2G,I,K). However, aop mutants showed many extra TCs, as detected by DSRF expression in dorsal branches (DB), VB, lateral trunk (LT) and ganglionic branches (GB), but not in the DT (Fig. 2H,J,L). These supernumerary TCs gave rise to additional terminal ramifications, reminiscent of mutations in sprouty (sty), a negative regulator of MAPK signaling (Hacohen et al., 1998). Notably, sty mutants showed supernumerary FCs and TCs in the same complementary pattern as in aop mutants (supplementary material Fig. S1). These results suggest that negative regulation of MAPK signaling through aop and sty prevents ectopic specification of FCs and TCs, respectively, in distinct, non-overlapping regions of the tracheal system.

aop function is dispensable for tracheal cell migration and branching morphogenesis

Interestingly, despite the dramatic effect on FC and TC specification, the tracheal branching pattern was unaffected in aop mutants (Fig. 1B), suggesting that aop is dispensable for directed tracheal cell migration. We therefore monitored the appearance of FCs and TCs in aop mutants (Fig. 3A-F). Supernumerary Dy-expressing cells were first detectable in the DT during tracheal branch outgrowth at stage 13, slightly after Dys expression appeared in the regular FCs at DT fusion points (Fig. 3B). The number of extra FCs increased during later stages, possibly reflecting the
depletion of maternal aop gene products (Fig. 3C). Extra DSRF-positive TCs were detectable in the DB, LT, and GB during the extension of these branches in stage 14 (Fig. 3D-G). Together, these findings suggest that directed cell migration can proceed normally in the presence of multiple ectopic tip cell-like cells distributed throughout the tracheal primordium.

**aop prevents tracheal cells from assuming fusion or terminal cell fate**

To understand how Aop blocks FC and TC differentiation, we examined Aop protein distribution during tracheal development. Although Aop is expressed throughout the tracheal system, Aop protein levels change dynamically with peak levels at stage 14 (supplementary material Fig. S2) (Lai and Rubin, 1992). At this stage, Aop is detectable in all Dys-positive cells in aop<sup>2199</sup> mutants (D,F, arrows). (C’,E’) Cross-sections taken at the levels of the broken lines reveal a single ring-shaped adherens junction at the wild-type fusion joint (C’), whereas two separate rings are visible in the aop<sup>2199</sup> mutant (E’), indicating that two fusion events took place. DT lumen is outlined by a dotted line in C,E. (G-J) Wild-type (G,H) and aop<sup>2199</sup> (I,J) embryos stained with FC- (Dys, cyan) and TC- (DSRF, red) specific markers. aop<sup>2199</sup> embryos show supernumerary FCs in the DT, but not in other branches. Conversely, supernumerary TCs are present in dorsal branches (DB), lateral trunks (LT) and ganglionic branches (GB), but not in the DT. (K,L) Quantification of FC and TC number in wild-type and aop<sup>2199</sup> embryos. Branch types are indicated below the bars. Numbers inside bars indicate numbers of branch tips scored. Error bars represent s.d. ***P<0.001. Scale bars: 10 μm in A-F; 50 μm in G-J.

Fig. 2. **aop mutations lead to ectopic specification of fusion cells and terminal cells in a complementary pattern.** (A) Wild-type embryos contain two FCs labeled by nuclear Dysfusion (Dys, green) staining at each DT fusion joint. (B) aop<sup>2199</sup> embryos contain extra Dys-positive cells distributed throughout DT metameres. Luminal chitin is labeled in magenta. (C-F) Living stage 15 wild-type (C-D) and aop<sup>2199</sup> (E-F) embryos expressing Dys::nlsGFP (cyan) and E-Cad::mTomato (signal intensities displayed as a heat map). E-Cad levels are elevated in all Dys-positive cells in aop<sup>2199</sup> mutants (D,F, arrows). (C’,E’) Cross-sections taken at the levels of the broken lines reveal a single ring-shaped adherens junction at the wild-type fusion joint (C’), whereas two separate rings are visible in the aop<sup>2199</sup> mutant (E’), indicating that two fusion events took place. DT lumen is outlined by a dotted line in C,E. (G-J) Wild-type (G,H) and aop<sup>2199</sup> (I,J) embryos stained with FC- (Dys, cyan) and TC- (DSRF, red) specific markers. aop<sup>2199</sup> embryos show supernumerary FCs in the DT, but not in other branches. Conversely, supernumerary TCs are present in dorsal branches (DB), lateral trunks (LT) and ganglionic branches (GB), but not in the DT. (K,L) Quantification of FC and TC number in wild-type and aop<sup>2199</sup> embryos. Branch types are indicated below the bars. Numbers inside bars indicate numbers of branch tips scored. Error bars represent s.d. ***P<0.001. Scale bars: 10 μm in A-F; 50 μm in G-J.

EGFR and Btl/FGFR have distinct capacities in inducing fusion cells and terminal cells

To uncover the nature of these signals, we examined factors that subdivide the tracheal primordium into distinct regions. Epidermal growth factor receptor (EGFR) and Wg signaling act in the central region, which will give rise to the DT (Wappner et al., 1997; Chihara and Hayashi, 2000; Llimargas, 2000). Conversely, Btl is initially expressed in all tracheal cells, but subsequently declines in the central region (Ohshiro et al., 2002). Given the distinct spatiotemporal patterns of Btl/FGFR and EGFR in the tracheae, we asked whether the two receptors differ in their capacity to induce FC and TC differentiation, respectively. To test this idea, we expressed in all tracheal cells constitutively active forms of either Btl (λBtl) (Lee et al.,
reporter gene was markedly increased in specific genes, including sufficient to induce FCs in the DT by activating transcription of FC-trunk by antagonizing Wingless signaling. Aop blocks fusion cell induction in the dorsal trunk by antagonizing Wingless signaling. Besides RTK signaling, Wingless (Wg) signaling is necessary and sufficient to induce FCs in the DT by activating transcription of FC-specific genes, including esg and Delta (Chihara and Hayashi, 2000; Llimargas, 2000). To test whether aop might interfere with Wg signaling, we analyzed the expression of Wg target genes in aop mutant embryos (Fig. 4A-H; supplementary material Fig. S4). Notably, levels of Delta protein in the DT were increased in aop mutants compared with wild-type controls, and was absent from AopAC expressing tracheal cells (supplementary material Fig. S4). Furthermore, levels of Salm protein, the expression of which in tracheal cells depends on Wg signaling (Llimargas, 2000), were increased by 20% in the DT of aop mutants (Fig. 4E,F) and decreased by 30% in embryos expressing AopAC (Fig. 4G,H). Finally, we analyzed the distribution of the Wg signaling effector Arm in aop mutants. Although Arm levels at AJs were similar in aop and wild-type embryos (data not shown), aop mutants showed conspicuous accumulations of Arm in the cytoplasm and in intracellular punctae (supplementary material Fig. S4). Together, these findings suggest that aop negatively impacts on Wg signaling and consequently Wg target gene expression in tracheal cells. Consistent with this idea, Aop was recently shown to antagonize Wg signaling during Drosophila eye development (Olson et al., 2011). To corroborate that Aop also antagonizes Wg signaling in tracheal cells, we expressed in all tracheal cells a constitutively active form of Arm (ArmS10), which led to the specification of supernumerary FCs in the DT, transverse connective branch, VB and LT (Fig. 4I) (Chihara and Hayashi, 2000; Llimargas, 2000), while TC specification remained largely normal (Fig. 4J). Interestingly, in all ArmS10-induced FCs Aop was undetectable, suggesting that absence of Aop is necessary for FC induction through Wg signaling (Fig. 4K-M). To test whether FC mis-specification in aop mutants is due to deregulated Wg signaling, we blocked Wg-induced transcriptional activation by expressing a dominant-negative form of TCF (dTCFΔN) (van de Wetering et al., 1997) in tracheal cells. dTCFΔN expression led to a partial loss of FCs in the DT and to DT fusion defects (Fig. 4N,O) (Llimargas, 2000). Strikingly, in aopΔ199
mutants, dTCFΔN suppressed FC specification to nearly the same level as it did in a wild-type background (Fig. 4P-R). Importantly, however, dTCFΔN expression did not affect DT tube morphology, suggesting that DT identity was largely unimpaired by the partially reduced Wg signal in this situation (Fig. 4N,P). These results show that FC mis-specification upon loss of aop requires TCF function, consistent with the idea that aop antagonizes Wg signaling at the level of Arm (Olson et al., 2011). Interestingly, although tracheal expression of Delta and Dys was lost in AopACT-expressing embryos (Fig. 4C), their expression was maintained in pnt mutants (Fig. 4D), suggesting that Aop regulates Wg target gene expression through a mechanism that is independent of pnt function. As Wg
signaling in the tracheae is confined to the DT region (Llimargas, 2000), aop-dependent inhibition of Wg signaling explains why supernumerary FCs in aop mutants are restricted to the DT. In addition, Aop blocks MAPK signaling in non-tip cells of the other tracheal branches and thereby prevents these cells from adopting TC fate. Thus, aop plays a dual role in controlling FC and TC specification by inhibiting Wg and MAPK signaling (Fig. 4S).

The choice between fusion and terminal cell fate is constrained by the selector gene salm

Our results show that most or all tracheal cells are competent to adopt a specialized fate if the Aop inhibitory block is absent. However, the chosen fate (FC or TC) depends on the position of the cell in the tracheal system. Region-specific cell fate choice results in part from the distinct distribution of signals (Wg, Bnl) that act on cells in different regions of the tracheal primordium. We hypothesized that branch-specific selector genes could constrain the competence of tracheal cells to adopt a given fate in response to the inductive signals. Consistent with this scenario, global misexpression of bnl causes most tracheal cells to acquire TC fate (Sutherland et al., 1996; Gervais and Casanova, 2011), whereas DT cells are mainly mis-specified as FCs (supplementary material Fig. S3). Importantly, global Bnl misexpression causes degradation of Aop (Ohshiro et al., 2002) and MAPK phosphorylation (Gervais and Casanova, 2011) in all tracheal cells, suggesting that all tracheal cells are equally competent to receive the Bnl signal, but that the downstream responses are branch specific. One branch identity gene with key roles in subdividing the tracheal primordium is the selector gene salm (Kühnlein and Schuh, 1996). Tracheal salm expression becomes restricted to the DT, where it is sustained by Wg signaling and determines DT identity (Fig. 4E) (Kühnlein and Schuh, 1996; Llimargas, 2000; Franch-Marro and Casanova, 2002). In salm mutants, cells of the DT region migrate dorsoventrally instead of anteroposteriorly and assume VB identity (Fig. 5A,B; chitin staining showing branch architecture) (Franch-Marro and Casanova, 2002). Conversely, pan-tracheal salm misexpression transforms most branches into multicellular DT-like tubes (Fig. 5E,F) (Ribeiro et al., 2004). To determine whether salm influences the choice between the two tip cell fates, we analyzed FC and TC induction in salm mutants and in salm misexpressing embryos. In both situations, only tip cells differentiated into FCs or TCs, but the choice between the two fates reflected the transformed identity of each branch. In salm mutants, where dorsal tracheal cells were transformed into ventral identity, the tips of the transformed branches contained TCs and FCs, as in the lateral trunk of wild-type embryos (Fig. 5A,B) (Franch-Marro and Casanova, 2002). Conversely, upon salm misexpression, VB cells were transformed into DT identity and the tip cells assumed FC fate (Fig. 5E,F, arrows). We also noticed that in this situation overall TC number was dramatically reduced. The altered tip cell fate choice becomes more evident when the aop-mediated differentiation block is released: in aop salm double mutants, FC specification was not changed compared with salm1 mutants (Fig. 5C,D). Interestingly, however, the transformed DT cells now became TCs, the default fate of the VB tip cells, instead of FCs. Conversely, misexpression of salm in aop199 mutants led to supernumerary FC formation throughout the tracheae, whereas TC formation was largely suppressed (Fig. 5G,H). Thus, salm is necessary and sufficient to constrain the competence of tracheal cells towards FC fate.

As Wg signaling is required to maintain tracheal salm expression, it is formally possible that Wg acts solely via salm to control FC induction. In this scenario, ectopic salm expression should obviate the requirement for Wg in FC induction. To test this idea, we blocked Wg signaling by overexpressing Axin-GFP in tracheal cells, and then asked whether co-overexpression of salm is sufficient to rescue FC specification in the absence of Wg signaling (Fig. 6A–C). As expected, Axin-GFP expression nearly completely abolished FC induction and DT formation (Fig. 6A) (Chihara and Hayashi, 2000). Co-expression of ArmS10 restored both FC induction and DT formation (Fig. 6B). By contrast, co-overexpression of salm with Axin-GFP failed to restore FC formation, although salm overexpression was sufficient to transform the remaining tracheal branches towards DT identity, as indicated by their characteristic lumen morphology (Fig. 6C). Consistent with these results, Delta expression was upregulated more strongly by constitutively activating Wg signaling (through ArmS10 expression; Fig. 6G-I) than by overexpressing salm (Fig. 6J-L) when compared with wild-type embryos (Fig. 6D-F). Furthermore, salm expression was previously shown to restore DT identity, but not DT fusion defects in arm mutants (Llimargas, 2000). These results indicate that salm expression is not sufficient for FC induction and suggest that other Wg targets besides salm are required to induce FCs in the DT. Thus, expression of the selector gene salm is not only necessary to specify branch identity but also to constrain the choice between alternative tip cell types in response to MAPK signaling.
DISCUSSION

In this work we have investigated how the choice between the two types of specialized tip cells in the tracheal system is controlled. We show that the transcriptional repressor Aop plays a key role in linking tracheal tip cell fate selection with branch identity. First, we describe a novel tube morphogenesis phenotype in aop mutants, which is due to the massive mis-specification of regular epithelial cells into specialized tracheal tip cells. We show that aop is specifically required for controlling tracheal cell fate, whereas aop, like pnt (Samakovlis et al., 1996a; Ribeiro et al., 2002), is dispensable for primary tracheal branching, thus uncoupling roles of RTK signaling in cell fate specification and cell motility. Our finding that tracheal branching morphogenesis proceeds normally in the presence of excess tip cell-like cells suggests that collective cell migration is surprisingly robust and that mis-specified cells apparently do not impede the guided migration of the tracheal primordium. Second, we demonstrate that in the absence of inhibitors of MAPK signaling (aop and sty), all tracheal cells are competent to assume either TC or FC fate. The transcriptional repressor Aop globally blocks both TC and FC differentiation, but high-levels of MAPK signaling in tip cells relieve Aop-mediated inhibition, thus permitting differentiation. Third, our results suggest that in the DT region Aop limits FC induction through a distinct mechanism by antagonizing Wg signaling in addition to MAPK signaling. Conversely, in the other branches, Aop limits TC differentiation by blocking MAPK-dependent activation of Pnt (Hacohen et al., 1998). Fourth, we show that the region-specific choice between the two cell fates in the DT is determined by Wg signaling and by the selector gene salm. Based on these results, we propose a model in which a single repressor, Aop, integrates MAPK and Wg signaling to couple tip cell fate selection with branch identity (Fig. 6M). High levels of Bnl signaling triggers Aop degradation.

Fig. 6. Salm expression is not sufficient to trigger fusion cell specification. (A-C) Expression of Axin-GFP in tracheal cells abolishes DT formation (A; remaining FCs are indicated by arrows). ArmS10 expression in this background restores DT formation and FC specification (B). By contrast, salm expression fails to restore FC specification and DT fusion, although it is sufficient to transform tracheal branches towards DT identity, as indicated by the large diameter of chitin-labeled tracheal lumen (C). FCs are indicated by arrows in C. In A, UAS-Axin-GFP is co-expressed with UAS-mCherry-NLS (not shown) to maintain copy number of UAS sites equal between genotypes in A-C. (D-L) Immunostaining of Salm and Delta in stage 14 wild-type (D-F), ArmS10-expressing (G-I) and salm-overexpressing (J-L) embryos. Expression of ArmS10 in tracheal cells leads to a moderate increase of tracheal Salm (H, red in G) levels, whereas tracheal Delta levels (I, cyan in G) are more strongly increased. Embryos overexpressing salm show higher Salm levels (K, red in J) in tracheal cells compared with wild-type and ArmS10-expressing embryos, but only slightly increased Delta levels (L, cyan in J) compared with wild-type control embryos. Non-tracheal expression of Salm in oenocytes (OE) and of Delta in the Hindgut (HG) is indicated. Salm levels in oenocytes (OE) remain similar between genotypes. (M) Model of tip cell specification. The combination of inductive signals (Bnl, Wg) and branch identity gene (salm, knirps) expression determines tip cell fate in a branch-specific manner. Aop antagonizes both MAPK and Wg signaling, and restricts differentiation to branch tips, where MAPK signaling triggers Aop degradation. Scale bars: 50 μm in A-C; 10 μm in D-L.
Aop degradation in tracheal tip cells. We propose that in the DT, unlike in other tracheal cells, MAPK-induced degradation of Aop releases inhibition of Wg signaling. This is consistent with recent work showing an inhibitory effect of Aop on Wg signaling, possibly through direct interaction of Aop and Arm (Olson et al., 2011), or through Aop-mediated transcriptional repression of Wg pathway components (Webber et al., 2012). Our work extends the evidence for this unexpected intersection between two major conserved signaling pathways, suggesting that this function of Aop is likely to be more widespread than previously appreciated. Our findings also provide an explanation for the puzzling observation that, in pnt mutants, TCs are lost, while FCs become ectopically specified (Samakovlis et al., 1996a). As pnt is required for expression of the feedback inhibitor sty (Hacohen et al., 1998), loss of pnt is expected to lead to MAPK pathway activation and consequently to increased Aop degradation. This would release Aop-mediated repression of Wg signaling, resulting in extra FCs, whereas TCs are absent because of the lack of pnt-dependent induction. This suggests that excessive FC specification in the DT of aop and sty mutants is mainly due to deregulated Wg signaling, rather than to de-repression of pnt-dependent MAPK target genes. Consistent with this notion, we showed that pnt is not required for Delta and Dys expression in tracheal cells, although constitutively active AopACT represses their expression.

Our results further show that salm function constrains the fate that is chosen by cells when released from the Aop inhibitory block. MAPK signaling triggers Aop degradation in all tip cells, but only in the absence of salm does this signal lead to TC induction. In salm-expressing cells, degradation of Aop releases Wg signaling, resulting in FC specification. Thus, salm biases the choice between two morphologically different types of seamless tubes. This is reminiscent of the role of salm in switching between different cell types in the peripheral nervous system and in muscles (Elstob et al., 2001; Rusten et al., 2001; Schönauer et al., 2011). We show that salm expression is sufficient to repress TC formation. Our genetic results, consistent with biochemical data showing that Salm acts as a transcriptional repressor (Sánchez et al., 2011), suggest that salm promotes FC fate by repressing genes involved in TC development. However, salm is not sufficient to overcome the requirement for Wg signaling in FC induction, indicating that Wg does not act solely via salm to induce FC fate. Indeed, FC induction requires genes whose expression is independent of salm (esg, dys) (Chihara and Hayashi, 2000; Jiang et al., 2010). In addition, we propose that a feedback loop between Wg signaling and salm expression maintains levels of Wg signaling in the DT sufficiently high to induce FC fate (Fig. 6M). Taken together, these results suggest that the default specialized tip cell fate, and possibly an ancestral tracheal cell state, is TC fate. Although FCs and TCs differ in their morphology, they share a unique topology as seamless unicellular tubes (Uv et al., 2003). FCs and TCs might therefore represent variations of a prototypical seamless tube cell type. Salm might modify cellular morphology by repressing TC genes, including DSRF, which mediates cell elongation and shape change (Gervais and Casanova, 2011). Intriguingly, Wg-dependent salm expression in the DT of dipterans correlates with a shift towards FC as the specialized fate adopted by the tip cells of this branch (X. Franch-Marro, personal communication). We showed that salm expression inhibits TC fate, while promoting the formation of a multicellular main tracheal tube by inhibiting cell intercalation (Ribeiro et al., 2004). It is therefore tempting to speculate that the salm-dependent switch from a branching towards an anastomosing tip cell type in the DT may have evolved with the acquisition in higher insects of a main tube that connects separate tracheal primordia to generate a tubular network. It will be of great interest to identify the relevant target genes that mediate the effect of Salm on tube morphology and tip cell fate.

The mechanisms of tip cell selection during angiogenesis in vertebrates are beginning to be understood at the molecular level (Ellertsdóttir et al., 2010; Geudens and Gerhardt, 2011; Herbert and Stainier, 2011). However, the signals that control the formation of vascular anastomoses by a particular set of tip cells are not known. Intriguingly, the development of secondary lumina in aop mutants is reminiscent of transluminal pillar formation during intussusceptive angiogenesis, which is thought to subdivide an existing vessel without sprouting (Burri et al., 2004). Although the cellular basis for this process is not understood, it is conceivable that specialized endothelial cells are involved in transluminal pillar formation. Our work provides a paradigm for deciphering how two major signaling pathways crosstalk and are integrated to control cell fate in a developing tubular organ. It will be interesting to see whether similar principles govern tip cell fate choice during tube morphogenesis in vertebrates and invertebrates.

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