FGF and canonical Wnt signaling cooperate to induce paraxial mesoderm from tailbud neuromesodermal progenitors through regulation of a two-step epithelial to mesenchymal transition

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ABSTRACT
Mesoderm induction begins during gastrulation. Recent evidence from several vertebrate species indicates that mesoderm induction continues after gastrulation in neuromesodermal progenitors (NMPs) within the posteriormost embryonic structure, the tailbud. It is unclear to what extent the molecular mechanisms of mesoderm induction are conserved between gastrula and post-gastrula stages of development. Fibroblast growth factor (FGF) signaling is required for mesoderm induction during gastrulation through positive transcriptional regulation of the T-box transcription factor brachyury. We find in zebrafish that FGF is continuously required for paraxial mesoderm (PM) induction in post-gastrula NMPs. FGF signaling represses the NMP markers brachyury (ntla) and sox2 through regulation of tbx16 and msgn1, thereby committing cells to a PM fate. FGF-mediated PM induction in NMPs functions in tight coordination with canonical Wnt signaling during the epithelial to mesenchymal transition (EMT) from NMP to mesodermal progenitor. Wnt signaling initiates EMT, whereas FGF signaling terminates this event. Our results indicate that germ layer induction in the zebrafish tailbud is not a simple continuation of gastrulation events.

KEY WORDS: EMT, FGF, Wnt, Neuromesodermal progenitor, Tailbud, Zebrafish

INTRODUCTION
The mesodermal germ layer is the origin of essential elements of the adult body such as the musculoskeletal, cardiovascular, renal and reproductive systems. Although a large bulk of the mesodermal germ layer is specified during gastrulation, accumulating evidence across multiple vertebrate species indicates that mesoderm induction continues after gastrulation in a population of neuromesodermal progenitors (NMPs) in the posteriormost embryonic structure, the tailbud (Beck, 2015; Henrique et al., 2015; Kimelman, 2016; Kimelman and Martin, 2012; Kondoh and Takemoto, 2012; Martin, 2016). All vertebrate embryos form their bodies in an anterior to posterior progression, and the tailbud NMPs are an essential source of new neural and mesodermal cells that contribute to the posteriorly elongating body axis (Beck, 2015; Henrique et al., 2015; Kimelman, 2016; Kimelman and Martin, 2012; Kondoh and Takemoto, 2012; Martin, 2016). While the molecular mechanisms of mesoderm induction during gastrulation are well studied, much less is known about how mesoderm is induced in NMPs (Kiecker et al., 2016; Kimelman, 2006; Martin, 2016). Investigating this process will provide insight into the plasticity of mesoderm induction programs and strengthen our understanding of how the vertebrate body plan is established.

The first mesoderm-inducing signal discovered was the fibroblast growth factor (FGF) pathway (Dorey and Amaya, 2010; Kiecker et al., 2016). When overexpressed, FGF signaling is sufficient to induce mesoderm in naïve epiblast cells (Kimelman et al., 1988; Kimelman and Kirschner, 1987; Slack et al., 1987). Additionally, loss of FGF signaling across many vertebrate species results in defects in gastrula stage paraxial mesoderm (PM) induction (Amaya et al., 1991; Deng et al., 1994; Griffin et al., 1995; Mitani et al., 1990; Yamaguchi et al., 1994). A conserved downstream transcriptional target of FGF signaling is the T-box transcription factor brachyury (Latinkic et al., 1997), which itself has a conserved role in mesoderm formation through canonical Wnt signaling regulation (Martin and Kimelman, 2008, 2009). Loss of early FGF signaling causes a loss of brachyury expression, leading to defects in mesoderm induction (Ciruna and Rossant, 2001; Griffin et al., 1995; Isaacs et al., 1994; Latinkic et al., 1997). FGF signaling continues to be active in the tailbud, where it plays crucial roles in maintaining the progenitors of the spinal cord (called the neural stem zone), in promoting the proper migration of cells through the tailbud and PM, and in establishing wavefront activity necessary for somitogenesis, although its role in tailbud mesoderm induction from NMPs is unknown (Akai et al., 2005; Dubrulle et al., 2001; Hubaud and Pourquie, 2014; Lawton et al., 2013; Mathis et al., 2001; Steventon et al., 2016). By contrast, canonical Wnt signaling is known to have a conserved essential role during the induction of mesoderm from NMPs (Bouldin et al., 2015; Garriock et al., 2015; Gouti et al., 2014; Henrique et al., 2015; Junberg et al., 2014; Martin and Kimelman, 2012; Tsakiridis et al., 2014; Wymeersch et al., 2016). In the absence of Wnt signaling, NMPs fail to become mesoderm and instead give rise to the spinal cord.

The formation of mesoderm during gastrulation requires an epithelial to mesenchymal transition (EMT) as cells move from the epithelial epiblast to the mesenchymal mesoderm (Acloque et al., 2009). Several mesoderm-inducing signaling pathways, including canonical Wnt, TGFβ and FGF, promote the gastrula stage mesodermal EMT (Acloque et al., 2009). The study of post-gastrula EMT in NMPs has been hampered by the lack of tailbud-specific EMT molecular markers, and has been limited to analysis of cell behaviors in the tailbud (Lawton et al., 2013; Manning and Kimelman, 2015; Steventon et al., 2016). After gastrulation, cells exhibit behavioral changes as they transition from NMP to PM. NMPs exhibit collective epithelial-like migration, whereas the mesoderm derived from NMPs exhibits rapid individual cell migration consistent with mesenchyme (Lawton et al., 2013). In zebrafish, the mesodermal EMT during both gastrulation and...
later in the tailbud occurs as a two-step process (Manning and Kimelman, 2015; Row et al., 2011). In the first step, cells initially transition from epithelium to non-directionally migrating mesenchyme, followed by a second EMT completion step, in which cells transition from non-directional to directional migration. The transcription factors Tbx16 and Msgn1 are essential for promoting the second step of the EMT, and in their absence cells become stuck in the intermediate state and fail to develop into PM (Manning and Kimelman, 2015; Row et al., 2011).

We identified new molecular markers of EMT in zebrafish and performed high-resolution imaging of tailbud cells undergoing EMT. These new tools were used in combination with reagents to temporally manipulate signaling pathways and gene activity to examine FGF regulation of tailbud mesoderm induction. We find that FGF cooperates with Wnt signaling to induce PM from NMPs during a two-step EMT event. Wnt signaling initiates the EMT, and FGF signaling terminates this event. Together, our results shed light on the molecular control of a two-step EMT, as well as highlighting previously unrecognized differences in the mechanisms of mesoderm induction between gastrula and post-gastrula stages of development.

**RESULTS**

**FGF signaling is required for PM induction from NMPs**

To determine whether FGF signaling continues to be required for mesoderm induction in the tailbud, we used a heat shock-inducible dominant-negative FGF receptor transgenic line to temporally inhibit FGF signaling (HS:dnfgfr1-gfp; hereafter abbreviated as HS:dnfgfr1) (Lee et al., 2005). Loss of FGF signaling at the 12- or 18-somite stage resulted in a significant deficit in the generation of posterior somitic mesoderm, as indicated by a loss of posterior somites (Fig. 1A-E). Posterior notochord, which is formed from separate populations of plastic progenitor cells (Row et al., 2016), is relatively unaffected after loss of FGF signaling (Fig. 1F-I). The undulating notochord in FGF loss-of-function embryos indicates expansion of notochord despite the failure of the tail to continue to extend. These results imply that FGF signaling is required for post-gastrula PM induction specifically in the posterior wall NMPs (in the posteriormost domain of the tailbud) that generate the somites, and not the midline NMPs that form notochord (Row et al., 2016).

During gastrula stage mesoderm induction, FGF signaling is required to activate and maintain brachyury expression (Amaya et al., 1993; Delaune et al., 2005; Fletcher and Harland, 2008; Griffin et al., 1995; Isaacs et al., 1994; Schulte-Merker and Smith, 1995). We confirmed that loss of FGF signaling using the HS:dnfgfr1 line during gastrulation resulted in near complete loss of T, brachyury homolog a (a; referred to here by the synonym ntlα) expression (Fig. 1J,K). Loss of FGF signaling after gastrulation at the 8-somite stage resulted in the opposite effect – an expansion of ntlα expression in the posterior tailbud (Fig. 1L,M). Tailbud NMPs are characterized by the co-expression of ntlα and sox2 (Martin and Kimelman, 2012; Olivera-Martinez et al., 2012). Similar to ntlα, sox2 expression in the tailbud was expanded after loss of FGF signaling (Fig. 1N,O). These results suggest that the role of FGF signaling during mesoderm induction in the tailbud differs mechanistically from its role during gastrulation, and that in the tailbud FGF signaling is required to repress NMP markers ntlα and sox2 to promote PM differentiation.

**Two new vimentin-related genes are expressed specifically in tailbud cells undergoing EMT**

The expansion of ntlα in the tailbud after loss of FGF signaling is reminiscent of embryos that are mutant for tbx16 (also known as spadetail). Homozygous tbx16 mutants exhibit greatly expanded ntlα expression in the tailbud (Fior et al., 2012; Yabe and Takada, 2012). During tailbud mesoderm induction from NMPs, future mesodermal cells undergo a two-step EMT (Manning and Kimelman, 2015). In the first step, cells go from an epithelial-like to a mesenchymal state without directional movement. In the second step, non-directional mesenchyme acquires directional movement and cells exit the tailbud. The second step is dependent on Tbx16 and Msgn1 function; they promote exit from the tailbud as well as repression of ntlα expression (Bouldin et al., 2015; Fior et al., 2012; Manning and Kimelman, 2015; Row et al., 2011). Based on the similarity in phenotype, we reasoned that loss of FGF signaling might specifically affect the ability to complete the second step of the EMT process.

There is currently a lack of characterized molecular EMT markers in the zebrafish tailbud. Expression of the intermediate filament vimentin is routinely used as a marker of cells undergoing EMT, but the expression pattern of a zebrafish vimentin ortholog is absent from the tailbud (Cerdà et al., 1998; Lowery et al., 2015; Ye and Weinberg, 2015). To determine whether zebrafish has other vimentin genes that are expressed in the tailbud, we searched the genome and found two additional vimentin-related genes. We named these genes (with approval from the Zebrafish Nomenclature Committee) vimentin-related 1 (vimr1 – currently annotated as CABZ01079764) and vimentin-related 2 (vimr2 – currently annotated as si.dkey-76115.1). Both genes are expressed in the ventral tailbud precisely where new mesoderm is being generated from NMPs (Fig. 2A,B; Fig. S1). An amino acid alignment of Vimr1 and Vimr2 with vimentin proteins from other species indicates that Vimr1 and Vimr2 contain all of the conserved functional vimentin domains (Fig. 2C,E). Additionally, a phylogenetic analysis of vertebrate vimentin proteins and the closely related desmin intermediate filament proteins indicates that Vimr1 and Vimr2 cluster with vimentin proteins (Fig. 2D; Fig. S2). To determine whether vimr1 and vimr2 expression is specifically localized to cells undergoing EMT, we examined their expression in tbx16 mutant embryos, in which tailbud cells are trapped in the intermediate EMT process. Both genes showed a dramatic expansion in tbx16 mutants, suggesting that they are indeed specific to tailbud mesoderm undergoing EMT (Fig. 2F-I).

**FGF signaling promotes completion of tailbud mesodermal EMT and mesoderm exit from the tailbud**

To investigate whether FGF regulates EMT in the tailbud, we conducted in situ hybridization using the vimr1 and vimr2 markers in HS:dnfgfr1 and in heat shock-inducible constitutively active fgfr1 (HS:cafgfr1) embryos. We find that inhibition of FGF signaling leads to expansion of vimr1 and vimr2 expression in the tailbud (Fig. 3A-D), whereas overactivation of FGF results in the reduction of vimentin-related gene expression (Fig. 3E-H; Fig. S3). These results suggest that FGF regulates the completion of EMT in tailbud mesodermal progenitors.

Since loss of FGF signaling in the tailbud produces a phenotype similar to loss of tbx16 and msgn1 function, and FGF regulates tbx16 expression during gastrulation, we examined whether FGF signaling activates tbx16 and msgn1 expression in the tailbud (Griffin et al., 1998). Loss of FGF signaling resulted in a reduction of both tbx16 and msgn1, particularly in the posteriormost domain where new cells are joining the PM (Fig. 3I-L’, white arrowheads). The regulation of msgn1 in the tailbud by FGF signaling has also been demonstrated previously (Fior et al., 2012). Gain of FGF function had the opposite effect, again most notably in the
Fig. 1. FGF is required for post-gastrula mesoderm induction and repression of the NMP state. (A−E) Zebrafish embryos from an HS:dnfgfr1 hemizygous outcross were heat shocked at the 12- or 18-somite stage and analyzed for myoD expression at 24 hpf. Wild-type siblings exhibit ~31 somites (A,C,E), whereas HS:dnfgfr1 embryos heat shocked at 12 somites have 16 somites and those heat shocked at 18 somites have 22 somites (B,D,E). The number of embryos showing the illustrated phenotype among the total number examined is indicated. Error bars indicate s.d. *P<0.001 using unpaired t-test. (F−I) Expression of ntla (arrowheads) indicates that there is no posterior loss of notochord after FGF inhibition at the 12- or 18-somite stage. (J,K) Embryos heat shocked at 50% epiboly (just at the start of gastrulation) and fixed 3 h after heat shock show a near complete loss of ntla expression. (L,M) Embryos heat shocked at the 8-somite stage and fixed 3 h later exhibit an expansion of ntla into lateral and anterior domains (arrowhead). (N,O) Inhibition of FGF signaling at the 8-somite stage also leads to an expansion of sox2 3 h after the heat shock. (A−D,F,G,H,I) Lateral view, anterior left; (F′,G′,H′,I′,L−O) dorsal view, anterior left; (J,K) vegetal view, dorsal top.

The expansion of vimer1 and vimer2 expression in the tailbud in tbx16 mutant embryos and after loss of FGF signaling suggests that cells lacking FGF function fail to exit the tailbud and join somites, similar to tbx16 mutant cells. To directly visualize the effect of FGF inhibition on the movement of mesodermal progenitors, we performed live quantitative imaging of wild-type, SU5402-treated wild-type, HS:tbx16, and SU5402-treated HS:tbx16 tailbuds. Embryos were labeled with a nuclear-localized photoconvertible protein (NLS-kikume) and heat shocked at the 12-somite stage, followed by green to red photoconversion of small groups of cells along the posterior wall of the tailbud (where NMPs normally reside). These embryos were time-lapse imaged by spinning disc confocal microscopy (Fig. 4A−E; all conditions can be viewed in Movies 8−17). Control wild-type progenitors are able to undergo ventral diving and rapid displacement into the maturation zone, where they mix with each other (Fig. 4Aa−d′). By contrast, FGF-inhibited progenitor cells exhibited a delayed cell movement, which resulted in fewer cells moving into the maturation zone and the PM (Fig. 4Ca−d′). Cell nuclei were tracked using Imaris software (Fig. 4Fa−e,Ga−e) and tracks were quantified. Loss of FGF signaling caused a significant decrease in mean displacement length and mean track speed compared with wild-type cells (Fig. 4I; Table S1). The forced expression of tbx16 in FGF loss-of-function cells caused a statistically significant rescue of mean displacement length and mean track speed (Fig. 4H,I; Table S1). Track straightness remained largely unaffected in all treatment groups (Fig. 4I; Table S1). These results show that FGF is required for cell movement out of the tailbud, and that expression of Tbx16 is sufficient to rescue movement in the absence of FGF signaling.

To further confirm that tbx16 and msgn1 function downstream of FGF signaling to promote EMT termination, we performed epistasis experiments. Wild-type embryos, embryos from the HS:tbx16 transgenic line, or embryos from an HS:msgn1 transgenic line were treated with SU5402 (Fig. 5A−P) (Row et al., 2016). Heat shock induction of tbx16 or msgn1 alone caused complete loss of vimer1 and vimer2 expression in the tailbud, similar to activation of FGF signaling (Fig. 5C,G,K,O). The combined loss of FGF signaling and gain of tbx16 or msgn1 expression resulted in the complete absence of vimer1 and vimer2 expression, indicating rescue of the enhanced vimer1 and vimer2 expression seen with loss of FGF signaling alone (Fig. 5D,H,L,P). These results support a model in which FGF signaling promotes EMT completion and PM induction through positive regulation of tbx16 and msgn1 transcription.

To add support to this model, we performed mosaic epistasis analysis of NMPs that have changes in FGF signaling levels, tbx16 or msgn1 levels, or both FGF signaling and tbx16 or msgn1, by transplanting cells with heat shock-inducible constructs into wild-type hosts. Cells from sphere stage donor embryos were transplanted into the ventral margin of unlabeled shield stage wild-type embryos, which is an established strategy for targeting donor cells to the NMP
Host embryos were heat shocked at the bud stage and live imaged at 30 h post fertilization (hpf) and analyzed for whether the cells contribute to the somites (Fig. 5Q-U). The vast majority of cells that join zebrafish somites become skeletal muscle, the fate of which can be easily identified by morphology and location (Fig. 5R). Approximately 70% of wild-type cells, HS:tbx6 cells, or HS:msgn1 cells transplanted into wild-type host embryos contribute to posterior somites in the form of skeletal muscle (Fig. 5V; Table S2). Transplanted cells lacking FGF signaling exhibit a significant reduction in somite contribution.

Fig. 2. Two vimentin-related genes, vimr1 (A) and vimr2 (B) in wild-type 18-somite stage embryos. Expression pattern of vimr1 (A) and vimr2 (B) in wild-type 18-somite stage embryos. Expression of both genes is limited to the notochord and tailbud cells during somitogenesis (white arrowheads indicate notochord expression, black arrowheads tailbud expression). (C) Protein alignment derived from vimentin gene sequences. Red indicates a highly conserved motif, which has been shown to have a role in vimentin assembly (Herrmann et al., 1992); blue indicates the helix termination motif and purple indicates the beta site. Zebrafish sequences include that of another vimentin gene, vimentin-like (vml). (D) Bayesian phylogenetic analysis of Vimr1 and Vimr2 protein sequences with desmin proteins serving as an outgroup. (E) Schematic of vimentin-related intermediate filament. Head and tail domains are indicated by dashed lines, whereas helix-rich regions of the rod domain are represented by filled boxes. (F-I) Expression of vimr1 and vimr2 in tbx16 (sptb104) mutants (H,I) and their wild-type control siblings (F,G). (A,B,F-I) Lateral views of the posterior tailbud domain.

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which is down to 20%. The activation of tbx16 or msgn1 in FGF loss-of-function cells results in a significant rescue of somite muscle contribution (Fig. 5V). These results suggest that an essential role of FGF signaling during PM induction from NMPs is to activate transcription of tbx16 and msgn1.

An essential role of Tbx16 and Msgn1 during NMP mesoderm specification is the transcriptional repression of the NMP markers ntlα and sox2 (Bouldin et al., 2015; Fior et al., 2012). We demonstrated that loss of FGF signaling at the 8-somite stage results in the expansion of ntlα and sox2 expression. To demonstrate that transplanted cells lacking FGF signaling also fail to repress ntlα and sox2 expression, we transplanted HS:dnfgfr1 cells into the ventral margin of wild-type host embryos, heat shocked them at the 8-somite stage, and fixed them at the 12-somite stage (Fig. 5W-AAf). In hosts containing transplanted wild-type cells, ectopic ntlα or sox2 expression was never observed (Fig. 5Xa-f,Za-f). By contrast, host embryos containing transplanted HS:dnfgfr1 cells exhibited punctate ectopic expression of ntlα and sox2 in the posterior of the embryo (Fig. 5Ya-f,AAa-f). These results imply that cells lacking FGF signaling fail to join the PM owing to their inability to repress the NMP state and to progress into a PM program.

FGF signaling cooperates with Wnt signaling for the continuous generation of new PM from the NMP population

Previous work has shown that transplanted cells lacking Wnt signaling in the NMP population fail to become mesoderm but,
Fig. 4. FGF regulates tailbud cell displacement through tbx16 regulation. (A-E) Time-lapse images of photoconverted tailbud cells of NLS-kikume mRNA-injected wild-type cells (Aa-d', Ca-d') and HS:tbx16 (Ba-d', Da-d') and HS:cafgfr1 (Ea-d', Da-d') embryos at 12-somite stage and onward, as indicated. DMSO-treated wild-type cells were able to move rapidly from the progenitor zone (Aa-d'), whereas SU5402-treated wild-type cells remained within the tailbud (Ca-d'). Activation of tbx16 rescues cell displacement and speed in the presence of SU5402 (Da-d'). Cells with activated FGF signaling also enter the maturation zone similarly to wild-type embryos (Ba-d' versus Aa-d'), but not as rapidly as tbx16-overexpressing cells (Ba-d'). White arrowheads point to cells entering the maturation zone. (F,G) Tracking of photoconverted cells as shown in trajectories (Fa-e) and displacement vector (Ga-e). (H-J) The mean displacement, mean track speed and mean track straightness of photoconverted cells. The mean displacement and the speed decrease in SU5402-treated wild-type embryos compared with vehicle-treated wild-type embryos (H versus I). tbx16 overexpression rescues the displacement and speed in SU5402-treated embryos. Track straightness did not differ significantly among the treatment groups (J). *P<0.05, unpaired two-way t-tests.
Fig. 5. FGF promotes mesoderm induction and inhibition of the NMP state via tbx16 and msgn1. (A–P) Expression of vimr1 and vimr2 was analyzed in SU5402- or DMSO-treated HS:tbx16, HS:msgn1 and wild-type sibling control embryos. Embryos were heat shocked at the 12-somite stage and analyzed at the 20-somite stage. Activation of tbx16 eliminates vimr1 and vimr2 expression in DMSO-treated (C,G) and SU5402-treated (compare D,H with B,F) embryos. Similarly, msgn1 activation inhibits vimr1/2 expression in DMSO-treated (K,O) and SU5402-treated (compare L,P with J,N) embryos. (Q–V) A transplant assay was used in epistasis experiments to determine whether tbx16 and msgn1 function downstream of FGF during termination and if these genes could rescue somite fate of FGF-inhibited tailbud cells. Wild-type donor embryos were injected with a mixture of fluorescein-dextran and heat shock-inducible HS:tbx16, HS:msgn1 or control HS:NLS-kikume plasmids. At sphere stage, the cells from these donor embryos were transplanted into the ventral margin of unlabeled wild-type shield stage host embryos, which targets them to the NMP population (Q). Embryos were heat shocked at the bud stage and examined at 30 hpf. The kikume protein was photoconverted prior to imaging and the lineage analysis was performed based on cell shapes and location of the transplanted cells. The majority of the transplanted wild-type cells contribute to somites, as do cells with tbx16 and msgn1 overexpression (R,V). The majority of the transplanted HS:dnfgfr1 cells are excluded from somites and do not form muscle (S-V) and remain in the tail region. However, upon the presence of tbx16 or msgn1, FGF-inhibited cells contribute to somites and form skeletal muscle (V). (W-AAf) A similar assay was used to determine whether transplanted cells that lack FGF function cell-autonomously maintain NMP markers sox2 and ntla (W). Host embryos containing transplanted wild-type cells and stained for sox2 (Ya-f) or ntla (AAa-f) exhibit normal sox2 and ntla expression patterns, whereas host embryos with HS:dnfgfr1 cells have ectopic sox2 (Ya-f) and ntla (AAa-f) expressing cells in the tailbud (red arrowheads). Xa-e,Ya-e,Za-e,AAa-e, lateral views, anterior bottom; Xi,Yi,Zi,AAf, dorsal views, anterior left.
Unlike cells lacking FGF signaling, these cells translocate to neural ectoderm (Martin and Kimelman, 2012). With respect to the two-step mesodermal EMT, this suggests that Wnt signaling initiates the EMT, whereas FGF signaling terminates it, allowing cells to join the PM. In the presence of Wnt but absence of FGF, cells are trapped in the intermediate EMT state and fail to join the PM. To test this model with respect to vimr1 and vimr2 expression, we used the HS:TCF:AC transgenic line to inhibit Wnt signaling at the 12-somite stage and examined vimr1 and vimr2 expression 5 h after the heat shock. We observed a dose-dependent loss of vimr1 and vimr2 expression after Wnt loss of function, where one copy of the transgene caused a reduction of vimr1 and vimr2 expression compared with wild-type embryos, and two copies of the transgene resulted in near complete loss of vimr1 and vimr2 expression (Fig. 6A-F). Whereas msgn1 expression was reduced in Wnt loss-of-function embryos, tbx16 expression was unaffected (Fig. 6K-P'). These results show that Wnt signaling induces initiation of mesodermal EMT.

We next asked whether activation of Wnt signaling is sufficient to cause an accumulation of vimr1- and vimr2-expressing cells as a consequence of too many cells initiating the EMT event. Surprisingly, we found that activation of Wnt signaling using an HS:caβ-catenin transgenic line resulted in a loss rather than gain of vimr1 and vimr2 expression (Fig. 6G-J). We examined tbx16 and msgn1 expression in these embryos and found strong expansion of both genes upon Wnt activation (Fig. 6Q-T'). This implies that elevated Wnt signaling is sufficient to promote the second EMT exit step. To determine whether Wnt is sufficient to induce the completion of the EMT event in the absence of FGF signaling, we compared vimr1 expression in embryos with activated Wnt signaling alone or with activation of Wnt and inhibition of FGF signaling using the small molecule FGF receptor inhibitor SU5402. Whereas activation of Wnt signaling led to a complete loss of vimr1 expression within 5 h after the heat shock induction, it was unable to do so in the absence of FGF signaling. After simultaneous induction of β-catenin and inhibition of FGF receptor, vimr1 expression was similar to, or slightly stronger than, that in wild-type embryos (Fig. 6U-X). Together, these results suggest that during PM induction from NMPs, Wnt signaling initiates the EMT event and FGF promotes the completion of EMT and exit into the PM.

**High-resolution imaging of the tailbud EMT**

In order to directly visualize the tailbud EMT process, we developed a new transgenic line that expresses membrane-localized mCherry and nuclear-localized kikume after heat shock induction [HS: (CAAX)mCherry-p2a-(NLS)kikume]. Cells from this stable transgenic line were transplanted into the ventral margin of unlabeled wild-type host embryos to target them to the NMP population. We observed that cells in the NMP domain of the posterior wall of the tailbud adhere to each other and to the border between the epidermis and the NMP population along the apical edge of the NMPs. In a process that appears strikingly similar to that described in a recent report of mouse epiblast cells undergoing EMT to form mesoderm during gastrulation (Ramkumar et al., 2016), individual cells were observed to undergo apical constriction, ingestion, and epithelial layer exit, while remaining tethered to the epithelial layer by a long apical extension of the membrane for a period of time before complete dissociation (Fig. 7A,B, Movies 1 and 2). This process, as in the mouse, appears stochastic. After cells ingress from the epithelial layer, they exhibit rapid membrane protrusions (including lamellipodia, filopodia and blebs), before eventually migrating out of the tailbud, as previously observed (Fig. 7G-I, Movies 4 and 5). We repeated these observations in transplanted cells lacking either Wnt signaling or FGF signaling, using the HS:TCF:AC or HS:dnfgfr1 lines, respectively. Cells lacking Wnt signaling were unable to leave the NMP epithelial layer and remained in the posterior wall of the tailbud adjacent to the epidermis (Fig. 7E,F compared with C,D, Movie 3), whereas cells lacking FGF signaling appeared to leave the NMP epithelial layer normally. Like wild-type cells, after leaving the NMP layer the cells lacking FGF signaling exhibited rapid membrane protrusions, but these did not result in directional migration out of the tailbud (Fig. 7J-L, Movies 6 and 7). These results are consistent with our quantitative cell tracking and EMT marker analysis, and imply that Wnt signaling initiates the EMT whereas FGF signaling promotes completion and exit into the mesenchymal PM.

**DISCUSSION**

**Wnt and FGF interactions ensure a steady movement of cells from the NMPs to the PM**

Our results show that during mesoderm induction within the tailbud NMP population, Wnt signaling initiates the EMT event required for mesoderm induction and that FGF signaling subsequently promotes completion of the EMT (Fig. 7M). Upon Wnt inhibition, fewer cells enter the EMT transitional state from the NMPs, whereas loss of FGF signaling prevents cells from exiting EMT, causing them to remain trapped in the vimr1/vimr2-positive transitional state (Fig. 7M). Our results help explain previous observations that loss of Wnt signaling in the tailbud primarily causes an opposite response to the loss of FGF signaling with regard to the transcription of co-regulated genes (Stulberg et al., 2012). Since one signal promotes the transitional state and the other inhibits it, it follows that they should oppositely regulate specific target genes. In particular, many of the oppositely regulated genes are involved in cell adhesion, suggesting that Wnt signaling antagonizes cell-cell adhesion whereas FGF signaling promotes it. Interestingly, the same study also showed that Wnt and FGF positively regulate the signaling of one another (Stulberg et al., 2012). Based on our results, this positive interaction ensures that a continuous flow of cells enters and then exits the transitional EMT state during the generation of PM from NMPs.

The factors that function downstream of Wnt signaling to initiate EMT in NMPs remain unknown. Canonical EMT pathways, such as Snail repression of cdh1, do not appear to be relevant in this context, as embryos with loss of snai1a function (the snai1 ortholog that is expressed in tailbud mesoderm) do not have deficits in mesoderm formation (Fior et al., 2012). Additionally, cdh1 expression is uniform throughout the tailbud, without any clear difference between NMPs and mesodermal progenitors (Thisse and Thisse, 2005). Given that Wnt signaling promotes metastasis in a variety of cancers, the tailbud will serve as an important in vivo model to decipher the molecular mechanism of Wnt-induced EMT.

**The role of FGF signaling during mesoderm induction changes between gastrula and post-gastrula stages**

Our understanding of the molecular mechanisms of mesoderm induction is based largely on data from gastrula stages of development. The discovery that mesoderm continues to be induced after gastrulation from an NMP population in the tailbud raised the question of whether there are multiple ways to induce mesoderm or, alternatively, that the mechanism is entirely conserved during gastrula and tailbud stages of development. Here we show that the role of FGF signaling changes between the two periods of mesoderm induction. As opposed to gastrulation, where FGF
Fig. 6. Wnt promotes EMT initiation and cooperates with FGF to promote EMT termination in tailbud NMPs. (A-F) vimr1 and vimr2 expression was analyzed in 20-somite stage wild-type sibling (A,B), hemizygous HS:TCF\(\Delta C\) (C,D) and homozygous HS:TCF\(\Delta C\) (E,F) embryos. Wnt inhibition leads to the loss of vimr1 and vimr2. (G-J) Expression of vimr1 and vimr2 was also analyzed in HS:ca\(\beta\)-catenin embryos (I,J) and their wild-type siblings (G,H). Wnt overactivation leads to a loss of vimr1 and vimr2 expression and a shift towards the ventral anterior portion of the tailbud (black arrow in I,J). (K-T) tbx16 and msgn1 expression was examined in control (K-L,Q-R), hemizygous HS:TCF\(\Delta C\) (M-N), homozygous HS:TCF\(\Delta C\) (O-P) and HS:ca\(\beta\)-catenin (S-T) embryos. Wnt inhibition had little effect on tbx16 expression but led to decreased expression of msgn1. Wnt overactivation led to expansion of the tbx16 and msgn1 expression domains. (Ua-Xd) Epistasis experiments were performed to examine the control of vimr1 expression by the Wnt and FGF signaling pathways. HS:ca\(\beta\)-catenin embryos were heat shocked at the 12-somite stage and treated with SU5402 or vehicle only (DMSO). These embryos were subsequently fixed 3 h, 4 h, 5 h and 6 h after heat shock induction for in situ hybridization. DMSO-treated control embryos exhibited consistent expression of vimr1 during somitogenesis (Ua-d), whereas DMSO-treated HS:ca\(\beta\)-catenin embryos had decreased expression of the EMT marker in the tailbud (Va-d). Consistent with previous data (Fig. 3), FGF inhibitor-treated embryos had increased expression of vimr1 (Wa-d). HS:ca\(\beta\)-catenin embryos in the presence of SU5402 maintained strong expression of vimr1 (Xa-d). All tailbud images are lateral views, except where indicated otherwise.
signaling promotes mesoderm induction through the positive regulation of Brachyury expression, FGF signaling serves to repress Brachyury in NMPs (Amaya et al., 1993; Ciruna and Rossant, 2001; Delaune et al., 2005; Fletcher and Harland, 2008; Griffin et al., 1995; Isaacs et al., 1994; Schulte-Merker and Smith, 1995). In NMPs, FGF induces PM through positive regulation of tbx16 and msgn1 transcription, which in turn repress the NMP markers sox2 and ntl/sox2 and permit the completion of the mesodermal EMT event, allowing exit into the PM (Fig. 7M). In the chick, temporal loss of FGF signaling causes a loss of brachyury expression in the tailbud (Olivera-Martinez et al., 2012) 24 h after signal inhibition. Our experiments showed expanded ntl/sox2 expression in the tailbud analyzed in embryos just 3 h after FGF inhibition. The result from chick embryos might reflect additional roles of FGF in the tailbud, such as the long-term maintenance of NMPs.

The variable usage of the FGF signaling pathway during gastrula and post-gastrula zebrafish mesoderm induction shows that there is considerable plasticity in the control of mesoderm induction within this species. Such variability might provide insight into the differential usage of the FGF pathway during gastrula stage mesoderm induction in the deuterostome lineage. For instance, within the deuterostomes, the echinoderm clade does not require FGF signaling for mesoderm induction during gastrulation (McCoon et al., 1996, 1998; Rottinger et al., 2008), yet all other major clades do, including vertebrates, tunicates, cephalochordates and hemichordates (Bertrand et al., 2011; Darras and Nishida, 2001; Dorey and Amaya, 2010; Green et al., 2013; Imai et al., 2002; Kim and Nishida, 2001; Kimelman, 2006; Miya and Nishida, 2003; Yasuo and Hudson, 2007). This suggests that FGF signaling was required for mesoderm induction in the deuterostome ancestor, but this requirement was subsequently lost in the echinoderm lineage. Further analysis of the molecular mechanisms of mesoderm induction between gastrula and post-gastrula stages within and between species will better inform our understanding of the evolution and utilization of mesoderm-inducing gene networks.

**Molecular control of a two-step EMT**

EMT can be defined by several morphological and molecular measures, such as changes in cell shape and migratory activity, as well as the downregulation of epithelial-specific genes and upregulation of mesenchyme-specific genes. In the zebrafish tailbud, EMT has been defined primarily by changes in cell movement and morphology (Lawton et al., 2013; Manning and Kimelman, 2015). EMT and EMT-like events during development, homeostasis and metastasis are characterized by expression of the intermediate filament protein vimentin (Lowery et al., 2015). As such, vimentin is one of the most commonly used markers of cells undergoing EMT. We identified two vimentin genes in the zebrafish genome (vimr1 and vimr2) and found that they are both expressed in the tailbud in precisely those cells that are actively undergoing EMT, between the initiation (Wnt-mediated) and termination (FGF-mediated) phases of the process. Although vimentin expression is
associated generally with the mesenchymal state, other work has demonstrated specific and strong expression of vimentin in a partial EMT state during chick epiboly (Futterman et al., 2011). Additionally, recent work indicates that a partial or intermediate EMT state is associated with more invasive and pathogenic cancer cells (Jolly et al., 2015; Nieto et al., 2016). Therefore, the vimentin expression often observed in actively metastasizing cells may reflect a partial EMT cellular condition.

EMT has traditionally been thought of as a binary single-step event, in which polarized epithelial cells transition directly to an invasive and migratory mesenchyme. Zebrafish PM formation, however, is a multistep process that includes an intermediate or partial EMT step (Manning and Kimelman, 2015; Row et al., 2011). Similarly, a growing body of experimental and theoretical evidence in several systems suggests that EMT involves multiple transitional states (Futterman et al., 2011; Grande et al., 2015; Lu et al., 2013; Mandal et al., 2016; Nieto et al., 2016; Revenu and Gilmour, 2009; Tian et al., 2013). Little is known about the molecular factors governing these intermediate states. During vertebrate mesoderm formation, both Wnts and FGFs signaling promote the eventual formation of mesenchymal PM from the epithelial epiblast (Kiecker et al., 2016; Kimelman, 2006). Here we show that although both signals promote the formation of mesenchymal mesoderm from an epithelium, they have differential effects on the transitional or partial EMT state. Wnt signaling promotes the transitional state by initiating the EMT event, whereas FGF signaling inhibits the transitional state by regulating termination of the EMT.

Conclusions

The formation of the three primary germ layers was historically thought to occur exclusively during gastrulation. The discovery that mesoderm and ectoderm continue to be generated from a basal progenitor cell pool in the tailbud after gastrulation raises questions about the relatedness of mesoderm induction during and after gastrulation. We find that FGF has a unique role in mesoderm induction in the tailbud that is different from its role during gastrula stage mesoderm induction. This supports a model in which germ layer induction in the tailbud and the development of the posterior body is not a direct continuation of gastrulation, but rather a distinct embryonic process involving a specialized multi-germ layer competent progenitor (the NMP). Additionally, we further characterized the molecular control of a two-step EMT event during tailbud mesoderm induction that involves a distinct partial EMT phase. There is growing evidence that multistep EMT, with metastable partial EMT intermediates, is a common process, and that the partial EMT state is particularly pathogenic in disease conditions (Nieto et al., 2016). The zebrafish tailbud provides an excellent model to further characterize the molecular control and cell biological properties of multistep EMTs, for which there are currently few developmental models.

MATERIALS AND METHODS

In situ hybridization and immunohistochemistry

Single-probe whole-mount in situ hybridization was performed as previously described (Griffin et al., 1995). For immunohistochemistry, Tbx16 expression was detected in fixed embryos using a Xenopus laevis VegT antibody (ZIRC) at 1:1000, followed by Alexa Fluor 488-conjugated anti-mouse secondary (Thermo Fisher Scientific, A-11001, 1:500). Double-fluorescence in situ hybridization was performed as previously described (Martin and Kimelman, 2012).

Phylogenetic analysis of vimentin-related genes

Amino acid alignments were made using MUSCLE 3.7 on the CIPRES portal (http://www.phylo.org/) and alignment errors were corrected manually (Edgar, 2004). Bayesian phylogenetic analysis was performed using MrBayes 3.2.2 with mixed-model option on the CIPRES portal (Ronquist and Huelsenbeck, 2003). Four independent runs of 1×10^6 generations each were performed with a sampling frequency of every 100 generations. A ‘consensus tree’ was generated from MrBayes from the first 9000 trees of each run (total of 36,000).

Fish lines and heat shocks

All zebrafish methods were approved by the Stony Brook University Institutional Animal Care and Use Committee. HS:dnfgfr1-GFP (Lee et al., 2005), HS:cafl-catenin (Veldman et al., 2013), HS:caflgr1 (Marques et al., 2008), HS:msgn1-p2a-ΔNLS-kikume (Row et al., 2016), HS:TCPα-GFP (Martin and Kimelman, 2012), HS:tbx16-p2a-ΔNLS-kikume (this study) and HS:CAAXmCherry-p2a-ΔNLS-kikume (this study) fish provided embryos that were heat shocked at the previously described temperatures for 30 min. Transgenic embryos were sorted from their wild-type siblings based on fluorescence or unique phenotypes. Heterozygous spb^tm1 mutant fish were used for thbx16 loss-of-function experiments (Ho and Kane, 1990).

Cell transplantation

Cell transplantation was performed as previously described with the following adjustments (Martin and Kimelman, 2010). Donor embryos were injected with 2% Rhodamine or Fluorescein-dextran at the one-cell stage. Cells from sphere stage donor embryos were transplanted into the ventral margin of unlabeled shield stage hosts using a CellTram vario (Eppendorf).

For lineage tracing, a mix of 2% Fluorescein-dextran and 25 pg Tol2 plasmid encoding NLS-kikume with or without the thbx16 or msgn1 gene was injected into wild-type or HS:dnfgfr1 donors. Transplants were conducted as above with heat shocks at bud stage and analysis at 30 hpf.

Kikume photoconversion, microscopy and image analysis

Tailbuds of NLS-kikume mRNA-injected (25 pg per embryo) embryos were photoconverted in the NMP region and imaged using a Leica DM6000B inverted microscope at 20× magnification or using a spinning disc confocal microscope (CSU-10, Yokogawa; AxioImager, Carl Zeiss) equipped with a camera (EM-CCD; Hamamatsu Photonics) with a 20× differential contrast objective. Stacks of tailbud images, spaced 5 μm apart, were taken every 5 min for 5 h beginning at the 12-somite stage. For lineage analysis, transplants were imaged at 30 hpf using both the inverted microscope with a 40× objective and the spinning disc confocal microscope with a 10× objective. Live imaging of HS:CAAXmCherry-p2a-ΔNLS-kikume transgenic cells was performed by spinning disc confocal microscopy using a 40× dipping objective lens at 5 min intervals for 8 h.

Time-lapse movies were analyzed on ImageJ and Imaris (Bitplane). The tracking of photoconverted nuclei was performed on Imaris through the spot detection scene. The generated tracks were corrected manually, and the mean track speed and displacement were calculated using Imaris.

Drug treatment

For the time-lapse experiments, NLS-kikume mRNA-injected embryos were heat shocked at the 10-somite stage, dechorionated immediately, then 30 min after the heat shock the embryos were placed in either 50 μM SU5402 (Sigma) or an equivalent volume of DMSO for 2.5 h. Subsequently, the embryos were mounted in low melting point agarose containing 50 μM drug or vehicle for microscopy imaging.

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Competing interests

The authors declare no competing or financial interests.

Author contributions

D.O.M. analyzed the data and edited the manuscript. S.C.K. and R.H.R. performed experiments and edited the manuscript. H.G. and B.L.M. performed experiments, analyzed the data and wrote the manuscript.
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Supplementary information

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