An exclusively mesodermal origin of fin mesenchyme demonstrates that zebrafish trunk neural crest does not generate ectomesenchyme

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SUMMARY
The neural crest is a multipotent stem cell population that arises from the dorsal aspect of the neural tube and generates both non-ectomesenchymal (melanocytes, peripheral neurons and glia) and ectomesenchymal (skeletogenic, odontogenic, cartilaginous and connective tissue) derivatives. In amniotes, only cranial neural crest generates both classes, with trunk neural crest restricted to non-ectomesenchyme. By contrast, it has been suggested that amniotes might generate derivatives of both classes at all axial levels, with trunk neural crest generating fin osteoblasts, scale mineral-forming cells and connective tissue cells; however, this has not been fully tested. The cause and evolutionary significance of this cranial/trunk dichotomy, and its absence in anamniotes, are debated. Recent experiments have disputed the contribution of fish trunk neural crest to fin osteoblasts and scale mineral-forming cells. This prompted us to test the contribution of amniote trunk neural crest to fin connective tissue cells. Using genetics-based lineage tracing in zebrafish, we find that these fin mesenchyme cells derive entirely from the mesoderm and that neural crest makes no contribution. Furthermore, contrary to previous suggestions, larval fin mesenchyme cells do not generate the skeletogenic cells of the adult fin, but persist to form fibroblasts associated with adult fin rays. Our data demonstrate that zebrafish trunk neural crest does not generate ectomesenchymal derivatives and challenge long-held ideas about trunk neural crest fate. These findings have important implications for the ontogeny and evolution of the neural crest.

KEY WORDS: Fin mesenchyme, Dermomyotome, Ectomesenchyme, Fibroblast, Neural crest

INTRODUCTION
The neural crest is a multipotent embryonic stem cell population formed during neurulation from which numerous cell types derive, including pigment cells and neurons and glia of the peripheral nervous system (Le Douarin and Kalcheim, 1999). Pioneering histological (Landacre, 1921; Platt, 1893), xenotransplantation (Raven, 1932), quail-chick chimera (Le Lièvre and Le Douarin, 1975), cell labelling (Chibon, 1967; Horstadius and Sellman, 1946; Johnston, 1966) and cell extirpation (Stone, 1926; Stone, 1929) experiments have provided considerable evidence that, in addition to melanocytes and cells of the peripheral nervous system, anterior dorsal neural folds form cranial ectomesenchyme during neurulation. From this population arise skeletogenic, odontogenic and connective tissues of the craniofacial skeleton (reviewed by Le Douarin and Kalcheim, 1999). Despite the long history of neural crest research and the wealth of resulting information, many aspects of neural crest biology remain obscure or contentious. In particular, the precise lineage restriction of neural crest and the extent of its potency are debated.

In amniotes, the cranial neural folds are a major source of cartilage, skeletal and connective tissues of the head, whereas there appears to be no contribution of trunk neural crest to these tissues types of the body. How this dichotomy between trunk and cranial neural crest contributions arose during evolution is unclear. Hypotheses include a trunk environment not permissive for ectomesenchyme (McGonnell and Graham, 2002) and a topologically distinct (and cranial specific) source of ectomesenchyme within the neural ectoderm (Breau et al., 2008; Weston et al., 2004). In fish and amphibia, however, there have been a number of studies proposing that larval fin mesenchyme cells derive from trunk ectomesenchymal neural crest (reviewed by Hall and Hörstadius, 1988; Le Douarin, 1982; Le Douarin and Kalcheim, 1999). This was first suggested in the 1930s based on xenotransplantation and cell staining experiments (Detwiler, 1937; Holtfreter, 1935; Raven, 1936; Raven, 1932). This cell type was assumed to contribute to the connective tissue of the fins and thus to represent an ectomesenchyme derivative. In line with this, we recently described a role for larval fin mesenchyme cells in maturation of fin extracellular matrix (ECM) (Asharani et al., 2012).

The topic was largely neglected for decades until the advent of fluorescent vital dyes permitted cell fate analyses. Fluorescent labelling of Xenopus and zebrafish neural tissue supported a contribution of neural crest to larval fin mesenchyme (Collazo et al., 1993; Krotoski et al., 1988; Smith et al., 1994). However, in many of these experiments it was noted that tissue labelling was not always precise, and definitive characterisation of the derivative cells was not possible. Indeed, further vital dye labelling experiments identified an additional mesodermal contribution to fin mesenchyme cells of both the ventral (Tucker and Slack, 2004) and dorsal (Garriock and Krieg, 2007) larval fins, which has been confirmed by transplantation experiments in axolotls (Sobkow et al., 2006). Crucially, the relative contribution of the neural crest and mesoderm to fin mesenchyme cells has never been determined.

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Accepted 29 April 2013
In addition to larval fin mesenchyme cells, trunk neural crest of teleosts had also been assumed to generate other ectomesenchymal derivatives, namely components of the adult post-cranial exoskeleton, which include the bony fin rays (lepidotrichia) and scales (Sire and Akimenko, 2004; Smith et al., 1994; Smith and Hall, 1990). Such assumptions were based on the fact that some intersegmental skeletal elements were believed to comprise odontogenic tissues and/or dermal bone. In mammals, these tissue types were long assumed to be generated exclusively from the cranial ectomesenchymal neural crest. For example, in evolutionary terms, the first mineralised tissue to arise in vertebrates is considered to be the mineralised body armour and teeth of stem gnathostomes [specifically conodont teeth; although conodont classification as stem gnathostomes and even vertebrates is contested (Donoghue et al., 2000; Turner et al., 2010)]. The fact that mineralised body armour was formed from dentine, a tissue unique to neural crest, led to speculation that the post-cranial odontogenic skeletal elements of early vertebrates were generated from trunk neural crest (Sire et al., 2009). The identification of a latent skelet/odontogenic potential of chick and mouse trunk neural crest cells, as revealed upon culturing in appropriate artificial conditions, was supportive of this scenario, as was the identification of trunk ectomesenchyme in extant fish and amphibia (Abzhanov et al., 2003; Lumsden, 1988; McConnell and Graham, 2002). Evidence for the existence of trunk ectomesenchyme thus has important implications for understanding the evolution of skeletogenesis. However, more recent identification of an additional mesodermal contribution to the dermal bones of the cranial vault (reviewed by Gross and Hanken, 2008) suggested that dermal bones of the fins might not necessarily derive exclusively from neural crest. We have recently provided the first test of a neural crest origin of post-cranial dermal bone and scales in fish, and found that fin osteoblasts and scale mineral-forming cells, previously considered to be a trunk ectomesenchymal neural crest derivative, are in fact generated by paraxial mesoderm, with no discernible contribution from neural crest (Lee et al., 2013) (see also Mongera and Nüsslein-Volhard, 2013; Shimada et al., 2013). This surprising result led us to question the extent to which trunk neural crest generates larval fin mesenchyme, the only other described ectomesenchymal neural crest derivative of the trunk.

Through marker analysis, genetic ablation, transgenic labelling and time-lapse approaches we demonstrate that, as with fin osteoblasts, the mesenchyme of both the dorsal and ventral larval fins derives almost exclusively from the dermomyotome compartment of the paraxial mesoderm, whereas neural crest does not contribute. Further, we show that larval fin mesenchyme cells are retained into the adult fin where they become fin fibroblasts. Our data demonstrate that the trunk neural crest of zebrasfish does not contribute any ectomesenchymal derivatives and suggest that amniotic trunk neural crest possesses the same diversity of fates as the trunk neural crest of amniotes.

### MATERIALS AND METHODS

#### Fish husbandry and lines

Fish were maintained in the IMCB zebrafish facility and embryos were generated by natural breeding or transgenesis marker where required. For transverse sections, embryo steaks were cut after in situ hybridisation or immunostaining using scalpels. Alternatively, cryosectioning was performed on embryos or adult fins using a Leica CM1900 cryostat, and the 16 μm sections then fluorescently immunostained. Confocal images and time-lapse movies were taken on an inverted Zeiss LSM700 or an upright Olympus BX61 Fluoview microscope, and high-magnification brightfield or Nomarski images were taken on a Zeiss AxioImager M2. For low-magnification brightfield images a Leica MZ16F stereoscope was used. For time-lapse recordings of caudal fin development, anaesthetised embryos were mounted in 1% low melting point agarose and imaged by confocal microscopy. A selected region of interest was converted using 60-80 pulses of 405 nm wavelength UV laser illumination. Embryos were then re-imaged immediately before being rescued from the agarose, and then re-examined 1 day later at 48 hpf.

#### Tamaroff treatment

To induce Cre activity at specific time points in CreER2 transgenic embryos, 4-hydroxytamoxifen (Sigma) was dissolved in ethanol and added to dechorionated embryos in embryo medium at a final concentration of 5 μM as described (Mosimann et al., 2011). After exposure, the embryo medium was replaced and embryos were allowed to develop and then assessed for mCherry expression.

#### PCR, transgene construct cloning, BAC recombineering and RNA synthesis

PCR amplification was performed using PrimeStar (Takara Bio) on a DNA Engine thermocycler (BioRad). A 2.1 kb promoter region of ntlα was amplified by PCR from genomic DNA and cloned into the pSE-MCS vector (Kwan et al., 2007) by restriction digestion and ligation to generate pSE-2.ntlα. The 7.2 kb sox10 promoter (Dutton et al., 2008) and the 1.7 kb tbx6 promoter (Szeto and Kimelman, 2002) were transferred from standard vectors to pSE-MCS by restriction digestion and ligation. All transgene constructs were generated using multisite Gateway cloning methodology through the zebrasfish Tol2kit (Kwan et al., 2007). Middle entry vectors containing Lyn-tdTomo, Gal4VP16, Cre and CreER2 were used in LR Clonase II Plus (Invitrogen) based recombination reactions. Reactions were conducted with Tol2-containing destination vectors, with or without the cmlc2:eGFP transgenesis marker where required.

The hnc2.CreER2 BAC was generated by recombining a CreER2 cassette flanked by 60 bp arms homologous to the region around the translation start of the hnc2 gene. Recombination was performed using
RedET methodology (GeneBridges). A second recombination was performed targeting a Tol2-containing cassette (Suster et al., 2009) to the BAC vector, thus allowing improved efficiency of transgenesis.

Tol2 RNA was synthesised from SmaI-linearised plasmid template and transcription performed with T3 RNA polymerase (Ambion).

**Embryo injection and transgenesis**

Plasmid DNA was prepared using the HiSpeed Plasmid Midi Kit (Qiagen) and BAC DNA using NucleoBond BAC 100 (Machery-Nagel). Embryos were injected with 30 ng/μl plasmid DNA and 30 ng/μl Tol2 RNA diluted in Phenol Red and Danieau’s buffer using a PLI-100 microinjector (Harvard Apparatus).

**RESULTS**

**Substantial mesodermal contribution to larval fin mesenchyme**

We have recently identified that in situ probes detecting bmp1a (Asharani et al., 2012), hemicentin 2 (hmcn2) (Carney et al., 2010) and fibulin 1 (fbln1) (Feitosa et al., 2012) mark fin mesenchyme cells from 48 hpf onwards (Fig. 1G,J,M). In addition, these cells are labelled by the enhancer trap lines ET37 and ET5 (Parinov et al., 2004), which also express eGFP in the apical ridge of the fins (Fig. 1A,D). Preceding this fin mesenchyme expression, all these markers shared a somitic expression domain, rather than neural crest expression, although ET5 was somewhat broader (Fig. 1B,C,E,F,H,I,K,L,N,O). This was surprising given the previous reports of at least a partial neural crest contribution to fin mesenchyme, and led us to investigate the source of these cells.

Expression domains can be dynamic, and it is possible that the somitic expression is not temporally contiguous with fin mesenchyme expression. To test this, we used time-lapse microscopy of the ET37 line to visualise the source of fin mesenchyme cells and noted that expression of eGFP was not biphasic, but continuous from the somitic expression through to fin mesenchyme cells (supplementary material Movies 1 and 2). We were able to track individual cells emigrating from both the ventral (Fig. 2A; supplementary material Movie 1) and dorsal (Fig. 2B; supplementary material Movie 2) somites into the fins where they became fin mesenchyme cells. To confirm that we were not tracking ectopically labelled neural crest cells, we generated a transgenic line expressing Kaede fluorescence at 48 hpf in the ventral fin, and this line showed that Kaede-positive cells were seen as epithelial cells within somitic regions (Fig. 2C, left panel), a location and morphology consistent with neural crest cells. Time-lapse analysis of this line in the ET37 background confirmed that the eGFP-positive fin mesenchyme cells were derived from these ntlα-expressing epithelial mesodermal cells (Fig. 2C; supplementary material Movie 3).

To determine whether the contribution of the mesoderm was more extensive, we generated two lines expressing Gal4 in paraxial mesoderm using either the ntlα promoter or the tbx6 promoter (Szeto and Kimelman, 2004), and crossed them to the uas:kaede transgenic line (Hatta et al., 2006). In both lines, we noted strong paraxial mesodermal Kaede fluorescence at 24 hpf (Fig. 3A,D; data not shown), with the tbx6 promoter exhibiting a slightly more restricted expression pattern. Kaede protein was then photoconverted by UV laser at 24 hpf in either broad ventral or dorsal regions of the tail mesoderm (Fig. 3B,B’E,E’). Imaging these embryos the following day revealed extensive labelling of mesodermal derivatives within the converted region, including muscle fibres as well as a large number of mesenchyme cells in the adjacent fin (Fig. 3C,C’,F,F’). This is consistent with our time-lapse data in demonstrating that fin mesenchyme derives from directly adjacent somitic domains.

**Neural crest does not generate fin mesenchyme**

Our data demonstrate that in zebrafish at least a significant proportion of both the dorsal and ventral fin mesenchyme cells are derived from the mesoderm. Recent literature has suggested that in amphibia the fin mesenchyme cells have a dual origin, deriving from both mesoderm and neural crest (Garriock and Krieg, 2007; Sobkow et al., 2006; Tucker and Slack, 2004). We quantified the extent of neural crest labelling, we counted the number of Kaede-positive melanophores at 30 hpf, and noted that...
at least 93% (507/545 in five embryos) of melanophores examined were Kaede positive. We observed a limited number of Kaede-positive cells in the posterior fin (Fig. 4B,B′); however, crossing these double transgenics onto the ET37 background and immunostaining for eGFP and Kaede demonstrated that Kaede-positive neural crest cells never co-expressed eGFP (0/12 embryos analysed; Fig. 4C–C′), and thus cells of the fins that were derived from sox10-expressing neural crest do not appear to be fin mesenchyme cells. Indeed, upon imaging these cells under transmitted or incident light, we noted that in most cases the Kaede-positive cells displayed clear characteristics of pigment cells, either black melanophores (supplementary material Fig. S2A–B′), blue/yellowish xanthophores (supplementary material Fig. S2B–C′) or iridescent iridophores (supplementary material Fig. S2C–C′). Occasionally Kaede-positive cells were seen in the fin that had no discernible pigmentation yet had a morphology inconsistent with fin mesenchyme and were never eGFP positive in the ET37 line. The identity of these cells is unknown but they might represent immature pigment cells. We conclude that, although neural crest cells do invade the zebrafish fin, they mostly generate pigment cells and do not appear to contribute to fin mesenchyme.

As an independent confirmation of our Kaede result, we generated a transgenic line expressing Cre recombinase under the sox10 promoter and crossed this to the ubi:switch reporter line (Mosimann et al., 2011), thus permanently labelling sox10-expressing cells with mCherry. The neural crest is labelled robustly and broadly at all axial levels (Lee et al., 2013). Imaging these embryos at 72 hpf demonstrated again that, whereas neural crest derivatives were mCherry positive, there were no mCherry-positive fin mesenchyme cells (supplementary material Fig. S3A–A′).

We complemented these cell labelling data with an analysis of zebrafish embryos in which the neural crest had been genetically ablated. Zebrafish embryos doubly deficient for both tfap2a (mont blanc, motm610) and foxd3 (mother superior, mosm188) (mob;mos embryos) have been shown to lack neural crest induction and are devoid of almost all neural crest derivatives (Wang et al., 2011) (Fig. 4D,E). If there is a neural crest contribution to fin mesenchyme, we might expect a reduction in the number of fin mesenchyme cells in mob;mos embryos. These embryos fully retained their medial fins, within which statistically indistinguishable numbers of fin mesenchyme cells were observed in both the wild-type and mos;mob embryos (Fig. 4F–H). It remains possible that loss of neural crest-derived fin mesenchyme could be obscured in this experiment through compensation from the mesoderm. However, in light of the genetic labelling experiments described above, we interpret the lack of any measurable fin mesenchyme reduction upon neural crest ablation as indicating no, or extremely limited, neural crest contribution.

**Paraxial mesoderm is the source of all fin mesenchyme**

We have provided evidence that both dorsal and ventral fin mesenchyme derives, at least partially, from paraxial mesoderm and not from neural crest. We next sought to determine whether the mesodermal contribution could account for all fin mesenchyme cells. We noted during our analysis of the tbx6;gal4; uas:kaede and the ntlα:gal4; uas:kaede embryos there was strong perdurance of Kaede protein to 48 hpf within fin mesenchyme and that in both lines the majority of fin mesenchyme cells were Kaede positive (Fig. 5A; data not shown). Neither migratory neural crest nor its derivatives were labelled by Kaede at 24 hpf (supplementary material Fig. S4A–A′) or 48 hpf (data not shown). Crossing the ntlα:gal4; uas:kaede line to ET37 demonstrated that all fin mesenchyme cells labelled by eGFP are also Kaede positive (Fig. 5B–B′). This co-expression could be due to de novo expression from the ntlα promoter within the fin mesenchyme cells at 48 hpf or represent perdurance from earlier promoter activity within the mesoderm. The former is unlikely as in situ hybridisation fails to detect ntlα transcripts in fin mesenchyme cells at 48 hpf (data not shown) and our time-lapse analysis of the ntlα:lyn-tdTomato transgenics (Fig. 1C; supplementary material Movie 3) revealed rapid and permanent loss of tdTomato fluorescence in fin mesenchyme cells after immigration into the fin. To demonstrate
that the expression in the fin mesenchyme represents perdurance from earlier mesodermal expression, we photoconverted the Kaede in the tail of 
\textit{ntlα:gal4, uas:kaede} transgenics at 24 hpf (supplementary material Fig. S5A-B'). Twenty-four hours later we observed almost complete expression of converted Kaede in the fin mesenchyme (supplementary material Fig. S5C,C'), demonstrating that the expression of Kaede in fin mesenchyme derives from the earlier somitic expression.

In addition, we used the Cre-Lox system as an independent lineage labelling method to confirm this result. \textit{tbx6:Cre; ubi:switch} double-transgenic embryos showed induction of mCherry within the \textit{tbx6} expression domain and, later, broad mCherry expression within the fin mesenchyme (supplementary material Fig. S3B,B'), indicating that the expression of Kaede in fin mesenchyme derives from the earlier somitic expression.

### Fin mesenchyme is a dermomyotome derivative

To delineate the somitic compartment from which fin mesenchyme is derived, we labelled the myotome using the \textit{α}-actin transgenic line \textit{Tg(actc1b:Gal4i269)} (Maurya et al., 2011) and the sclerotome with a transgenic line, \textit{Tg(Ola-Twist:Gal4)}, in which the medaka \textit{Twist} promoter (Inohaya et al., 2007) drives Gal4. Crossing both of these to the \textit{uas:kaede} line allowed us to trace derivatives of the myotome and sclerotome. Despite observing cells in the expected locations at 24 hpf and 48 hpf (supplementary material Fig. S4B-B'; data not shown), we did not observe Kaede fluorescence in the fin mesenchyme in either case (Fig. 5C-D'). Lack of myotome or sclerotome contribution to fin mesenchyme indicated they were likely to be derived from the dermomyotome compartment. Indeed, when we analysed the \textit{TgBAC(pax3a:eGFP)} transgenic line (Seger et al., 2011), which reproduces the expression of Pax3 in the dermomyotome (see also supplementary material Fig. S4C-C'), we noted expression of eGFP in almost all fin mesenchyme cells at 48 hpf (Fig. 5E,E'). To confirm that this is not \textit{de novo} expression in the fin mesenchyme and represents perdurance of eGFP from the dermomyotome at 24 hpf, we performed time-lapse microscopy and observed eGFP-positive fin mesenchyme cells emerging from the somites and invading the fin (two dermomyotome cells are tracked in Fig. 5F; supplementary material Movie 4). Additionally, the neural crest is strongly labelled in this line. Although neural crest cells also invaded the fins they were clearly discernible from fin mesenchyme cells based on their size, eGFP intensity and migratory behaviour.

We conclude that fin mesenchyme cells are dermomyotome derivatives and that, coupled with their morphology, expression of ECM molecules and modifying enzymes as well as a described role in ECM remodelling, they can be considered fibroblasts.

### Fin mesenchyme cells persist in the fins into adulthood as fibroblasts

We have recently shown that lepidotrichial skeletogenic cells invade the adult fin between 2 and 3 weeks of age, and do not arise from cells present in the larval fin fold at 5 dpf (Lee et al., 2013). If fin mesenchyme cells do not generate the osteoblasts of the fin...
rays, we questioned whether they contribute to any of the cells of the adult fin or are lost during juvenile stages of development. To address this, we conducted time point analysis of tbx6:CreERt2; ubi:switch transgenics. Embryos were treated with 4-hydroxytamoxifen from 8 hpf to 48 hpf to label cells of the paraxial mesoderm. As with the tbx6:Cre; ubi:switch double transgenics, we observed fin mesenchyme cells in the fins of a number of individuals at 5 dpf (Fig. 6A). We followed these cells over subsequent days and noted that they remained within the fin until at least 21 dpf, when chains of cells were also observed (Fig. 6B).

To assess whether they persist into adult stages, we permanently and specifically labelled them by generating an hmcn2:CreERt2 transgene through BAC homologous recombination (see Materials and methods). This construct was injected into the ubi:switch transgenic line and subsequently treated with 4-hydroxytamoxifen at 80-116 hpf. Three days later at 7 dpf, scattered mCherry-positive fin mesenchyme cells could be seen within the fin (Fig. 6C). At 3 months of age, these embryos showed extensive labelling of fibroblast-like cells both within the fin rays and in the inter-ray region, but no labelling of osteoblasts (as detected with zns-5 antibody) (Fig. 6D,E). Thus, we confirmed that fin mesenchyme cells do not later generate osteoblasts of the fin rays but persist into the adult fin ray as fibroblasts.

**DISCUSSION**

The emergence of neural crest was a pivotal moment in the evolution of vertebrates and has been proposed to have occurred at the anterior of a hypothetical protochordate during the generation of a ‘new head’ (Gans and Northcutt, 1983). Here, neural crest was proposed to take on many roles of the trunk mesoderm, generating head connective and skeletal tissues (ectomesenchyme). There has been considerable conjecture as to whether trunk neural crest also evolved to generate such ectomesenchymal derivatives. Evidence of a neural crest contribution to fin connective tissue in amphibia has been invoked as evidence in support of this. Indeed, we have demonstrated that fin mesenchyme does resemble and function as fibroblastic connective tissue cells. However, through transgenic cell lineage tracing and mutant analysis, we have shown that zebrafish fin mesenchyme is not a derivative of trunk neural crest but is entirely derived from paraxial mesoderm, specifically the dermomyotome. This, in combination with our previous result that mineralising cells of the adult fin rays and scales are not an ectomesenchymal
neural crest derivative (Lee et al., 2013), suggests that the trunk neural crest of zebrafish does not have ectomesenchymal fates, and thus resembles mammalian trunk neural crest in its repertoire of derivatives. This challenges long-held ideas about trunk neural crest lineages in anamniotes.

It should be noted that previous work has led to the belief that trunk neural crest in amphibia partially contributes (along with mesoderm) to fin mesenchyme. A single cell type originating from two distinct germ layers in a simple tissue such as the fin fold seems unusual, although a mixed origin is observed in more complex anatomical structures such as the calvaria (Gross and Hanken, 2008). While it is possible that the trunk neural crest of amphibia is unique in this regard and has acquired ectomesenchyme fates during evolution (or, conversely, mammals and teleosts have independently lost this lineage from trunk neural crest), in light of our data it would be worthwhile re-examining the fates of amphibian trunk neural crest more precisely. Our analysis indeed demonstrated the extremely close proximity of neural crest and dermomyotome during early development as well as a neural crest contribution of pigment cells to the fin. This challenges long-held ideas about trunk neural crest lineages in anamniotes.

One implication of our findings concerns the existence and properties of neural crest cells in vivo. An extensive body of evidence has shown that pigment cells, peripheral neurons and glia share a common precursor with ectomesenchymal derivatives within cranial neural folds (Baroffio et al., 1991; Blentic et al., 2008; Chan and Tam, 1988; Essex et al., 1993; Osumi-Yamashita et al., 1994; Pohl and Knöchel, 2001). More recent experiments in the mouse mapped the cranial neural fold territory with greater spatial and temporal resolution, and led to the controversial proposal of a distinct origin (the metablast) for ectomesenchyme (Breau et al., 2008; Weston et al., 2004). Although this contentious notion is less well accepted, such a topological partitioning of ectomesenchyme and non-ectomesenchyme birth sites would be incompatible with the model of a homogeneous multipotent neural crest territory. In agreement with this segregation model was the observation that neural crest cells are fate restricted in the zebrafish head and trunk prior to delamination (Raible and Eisen, 1994; Schilling and Kimmel, 1994). Although our investigations do not address the question of the existence of a metablast directly, they do argue...
against the existence of a neural crest stem cell in the trunk of fish that generates both neuronal/pigment and ectomesenchyme, which had previously been invoked as evidence for neural crest multipotency. It must be stressed that we have only interrogated the fates of trunk neural crest, which must be seen as distinct from questions of potency. Indeed, it has been reported that trunk neural crest cells are, under certain experimental conditions, able to generate bone, cartilage and dentine (Abzhanov et al., 2003; Smith et al., 1994). Our data cast doubt on this hypothesis and on the generation of ectomesenchymal derivatives of trunk neural crest and found in all cases that they are mesoderm derived. Thus, the trunk neural crest of zebrafish is restricted, as is that of amniotes, to non-ectomesenchymal derivatives. The ability of trunk neural crest to generate ectomesenchyme was considered to be a feature of early vertebrates and central to the formation of the first mineralised skeleton of the vertebrate subphylum, the dermal armour of stem gnathostomes. The zebrafish fin mesenchyme and post-cranial exoskeleton were assumed to represent a relic of this early trunk neural crest ectomesenchyme (Smith et al., 1994). Our data cast doubt on this possibility that the first mineralised skeleton of vertebrates was in fact of mesodermal origin.

Acknowledgements

We thank the V. Korzh lab. for supplying the ET37 and E5 transgenic lines; the P. W. Ingham lab. for providing the Tg(actc1b:Gal4)i269 and TgBAC(pax3a:EGFP)i150 lines; the S. L. Amacher lab. for providing the tbx6 promoter; the L. I. Zon lab. for the ubi:switch line; and the Zebrafish International Resource Center (University of Oregon, Eugene, OR 97403-5274, USA) for the zns-5 antibody.

Funding

This work was supported by the Biomedical Research Council of A*STAR (Agency for Science, Technology and Research), Singapore; the Zebrafish Initiative of the Vanderbilt University Academic Venture Capital Fund; and the National Institutes of Health National Institute of Dental and Craniofacial Research [grant R01 DE018477 to E.W.K.]. Deposited in PMC for release after 12 months.

Competing interests statement

The authors declare no competing financial interests.

Author contributions

R.T.H.L. and T.J.C. designed and performed experiments and wrote the paper. E.W.K. and J.P.T. provided reagents and edited the manuscript.

Supplementary material

Supplementary material available online at http://dev.biologists.org/lookup/suppl/doi:10.1242/dev.093534/-/DC1


