

# A Feasible Role of Neuropilin Signaling in Pharyngeal Pouch Formation in Zebrafish

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## Conflict of interests

The authors declare no potential conflict of interest.

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## Authors' contributions

The article is prepared by a single author.

## Ethics approval

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## Abstract

Pharyngeal pouches are an important epithelial structure controlling facial skeletal development in vertebrates. A series of pouches arise sequentially in the pharyngeal endoderm through collective cell migration followed by rearrangement of pouch-forming cells. While crucial transcription factors and signaling molecules have been identified in pouch formation, a role for Neuropilins (Nrps) in pouch development has not yet been analyzed in any vertebrates. Nrps are cell surface receptors essential for angiogenesis and axon guidance. In all vertebrates, the two Nrp family members, Nrp1 and Nrp2, are conserved in the genome, with two paralogs for Nrp1 (Nrp1a and Nrp1b) and Nrp2 (Nrp2a and Nrp2b) being identified in zebrafish. Here, I report a potential requirement of Nrp signaling in pouch development in zebrafish. *nrp1a* and *nrp2b* were expressed in the developing pouches, with *sema3d*, a ligand for Nrps, being expressed in the pouches. Knocking down Nrps signaling in the pharyngeal endoderm led to severe defects in pouches and facial cartilages. In addition, blocking Mitogen-activated protein kinase (MAPK) activities, a downstream effector of Nrp signaling, in the pharyngeal endoderm caused similar defects in pouches and facial skeleton to those by knocking down Nrps signaling. My results suggest that Nrp signaling acts for pouch formation through MAPK.

**Keywords:** Neuropilin, Pharyngeal pouch, Facial cartilages, Craniofacial development, Zebrafish

## INTRODUCTION

The pharyngeal pouches are a transient epithelial structure essential for craniofacial development in vertebrates. They arise in the pharyngeal endoderm as a series of branches, which segment the pharyngeal arches and provide survival signals, such as sonic Hedgehog, to the cranial neural crest cells (cNCCs) in the arches. The segmented cNCCs then differentiate into the facial skeletal elements, including facial cartilages (Mork & Crump, 2015). The pouches, per se, further differentiate into endocrine glands in the head and neck, including the thymus and parathyroid (Grevelléc & Tucker, 2010). Consistent with essential roles for the pouches in craniofacial development, defects in pouches led to severe loss or malformation of facial cartilages as well as hypoplasia of the thymus and parathyroid in mice and zebrafish (Piotrowski & Nusslein-Volhard, 2000; Dickmeis et al., 2001;

Kikuchi et al., 2001; Grevellec & Tucker, 2010). In humans, abnormal pouches are an etiology of DiGeorge syndrome, a congenital craniofacial disability (Driscoll et al., 1992; Piotrowski & Nusslein-Volhard, 2000; Lindsay et al., 2001; Tran et al., 2011). Given the importance of pouches in craniofacial development, the genetic and cellular mechanisms controlling pouch formation are less understood in vertebrates. Genetically, *Tbx1*, *Pax1*, and *Foxi1* transcription factors and *Fgf*, *Wnt*, *Ephrin*, and *VEGF-C* signaling molecules are essential for pouch formation (Lindsay et al., 2001; Nissen et al., 2003; Piotrowski et al., 2003; Crump et al., 2004; Ober et al., 2004; Tran et al., 2011; Choe & Crump, 2014; Okada et al., 2016; Jin et al., 2018; Liu et al., 2020). In zebrafish, *Tbx1* initiates pouch formation by promoting a collective migration of pouch-forming cells through *Wnt11r* and *Fgf8a* (Choe et al., 2013; Choe & Crump, 2014). Migrating pouch-forming cells are then rearranged into a bi-layered structure by *Wnt4* and *Ephrin B2* and *B3* ligands to mature pouches, with *wnt4a* expression being regulated by *Foxi1* in zebrafish (Choe et al., 2013; Choe & Crump, 2015; Jin et al., 2018). In medaka and zebrafish, *Pax1* regulates the expression of *tbx1* and *fgf3* in the pharyngeal endoderm to control pouch formation (Okada et al., 2016; Liu et al., 2020). Besides these transcription factors and signaling molecules, barely anything has been identified in pouch formation in vertebrates. Here, I tested the potential role of Neuropilins (Nrps) in developing pouches in zebrafish.

The Nrps are a family of cell surface receptors with many critical biological functions in the cardiovascular and neuronal systems (Guo & Vander Kooi, 2015). In vertebrates, two Nrp family members, *Nrp1* and *Nrp2*, are conserved and transduce *VEGF* and *Semaphorin* signals in the cardiovascular and neuronal systems (Guo & Vander Kooi, 2015). In angiogenesis, Nrps form a ligand/receptor complex, including *VEGF* and *VEGFR* (Guo & Vander Kooi, 2015). *Nrp1* interacts with *VEGF-A* and *VEGFR2* in mice and controls endothelial cell migration (Soker et al., 1998). In particular, it functions in endothelial tip cells as a downstream effector of a Notch signaling pathway (Fantin et al., 2013). The knockout of the *Nrp1* gene in mice consistently led to embryonic lethality due to severe defects in endothelial cell migration (Jones et al., 2008). In zebrafish, knockdown of *nrp1* has shown similar defects in angiogenesis (Lee et al., 2002). *Nrp2* acts with *VEGF-C* and *VEGFR2/3* in mice and is important for lymph angiogenesis (Yuan et al., 2002; Kärpänen et al., 2006). *Nrp2* functions in lymphatic tip cells and modulates tip cell extension at the cellular level (Caunt et al., 2008; Xu et al., 2010). Although a functional validation has remained, zebrafish *Nrp2* also has been implicated in lymph angiogenesis as it is expressed in lymphatic vessels during embryogenesis (Yaniv et al., 2006). To transduce Nrp signals in endothelial cells, Mitogen-activated protein kinase (MAPK) has been implicated as a critical downstream effector of *Nrp1* and *Nrp2* (Wey et al., 2005; Bechara et al., 2008; Fung et al., 2016). Although the roles of *Nrp1* and *Nrp2* are distinct, it has been implicated that they can compensate for each other in angiogenesis as the double knockout mouse displayed more severe defects in angiogenesis (Takashima et al., 2002). Besides *VEGFs*, Nrps are receptors for *Semaphorin3* (*Sema3*) ligands. They act with the *Plexin* receptor to bind *Sema3* and control axon guidance in the neuronal system (Parker et al., 2012). *Sema3* ligands have been demonstrated as endogenous inhibitors of angiogenesis and lymphogenesis through Nrps (Mumblat et al., 2015; Nakayama et al., 2015; Yang et al., 2015). Indeed, Nrps integrate competitive *VEGF* and *Sema3* signals to control endothelial cell migration (Serini et al., 2003; Tamagnone & Mazzone, 2011).

At the cellular level, the directed collective migration of endodermal cells initiates pouch formation, which is similar to the collective migration of endothelial cells in angiogenesis (Costa et al., 2016). Although *VEGFRs* have not been identified yet, the *Vegf-C* ligand is required for pouch formation in zebrafish (Ober et al., 2004). Furthermore, I found that Nrps and a *Sema3* ligand were expressed in the pharyngeal endoderm during pouch formation in zebrafish. Based on

this observation, I tested the potential role of Nrp signaling in pouch morphogenesis. Blocking the Nrp signal, specifically in the pharyngeal endoderm during pouch formation, led to severe defects in pouches and facial cartilages whose formation depended on appropriate pouch development. Knockdown of MAPK activities in the endoderm demonstrated defects in pouches and facial skeletons. This preliminary functional analysis suggests that Nrps are able to function in the pharyngeal endoderm to form pouches through MAPK.

## MATERIALS AND METHODS

### 1. Zebrafish lines

Zebrafish were handled according to the Animal Protection Act (2017) in Korea. All zebrafish work was approved by Gyeongsang National University Institutional Animal Care and Use Committee. Published lines include *Tg(-3.4her5:EGFP)* (Tallafuss & Bally-Cuif, 2003) and *Tg(nkx2.3:Gal4VP16)* (Choe et al., 2013). *Tg(UAS:DN-Nrp1a)*, *Tg(UAS:Sema3d)*, and *Tg(UAS:DN-MAPK3)* transgenic constructs were generated using the Gateway (Invitrogen, Carlsbad, CA, USA) Tol2kit (Kwan et al., 2007). For pME-DN-Nrp1a, a dominant-negative form of Nrp1a that is missing its cytoplasmic domain was produced by PCR using primers DN-Nrp1a-B1F2 and DN-Nrp1a-B2R from multi-stage zebrafish cDNA (Renzi et al., 1999). For pME-Sema3d, the coding sequence of *sema3d* was amplified using primers Sema3d-B1F2 and Sema3d-B2R from multi-stage zebrafish cDNA. For pME-DN-MAPK3, a dominant-negative form of MAPK3 was produced by fusion PCR with primers designed to produce a lysine to arginine substitution at lysine 85 (Izumi et al., 2001). 30 ng of transgenic constructs and 35 ng of DNA construct bearing Tol2 transposase gene were injected into one-cell stage wild-type Tübingen embryos. Three independent transgenic lines for *Tg(UAS:DN-Nrp1a:pA)*, two for *Tg(UAS:Sema3d:pA)*, and three *Tg(UAS:DN-MAPK3:pA)* were established based on  $\alpha$ -crystallin: Cerulean eye fluorescence. *Tg(UAS:DN-Nrp1a:pA)<sup>GNU125</sup>*, *Tg(UAS:Sema3d:pA)<sup>GNU141</sup>*, and *Tg(UAS:DN-MAPK3:pA)<sup>GNU152</sup>* were used for this study. Primers are listed in Table 1.

**Table 1. List of primers used to create transgenic lines**

Primer	Sequences (5' to 3')
DN-Nrp1a_F	ATG CAT TGT GGA TTA GTG
DN-Nrp1a_MR	ACT CAT GGC GAT GAT AGT TGT AGG CAC TTC CAT TTC
DN-Nrp1a_MF	GAA ATG GAA GTG CCT ACA ACT ATC ATC GCC ATG AGT
DN-Nrp1a_R	TCA CGC TTC CGA GTA CGA
DN-Nrp1a_B1F2	<u>GGGGACAAGTTTGTACAAAAAAGCAGGCT</u> ATG CAT TGT GGA TTA GTG TTG
DN-Nrp1a_B2R	<u>GGGGACCACTTTGTACAAGAAAGCTGGGT</u> TCA CGC TTC CGA GTA CGA
Sema3d_B1F2	<u>GGGGACAAGTTTGTACAAAAAAGCAGGCT</u> ATG AAG ACT GCA GGG GAG
Sema3d_B2R	<u>GGGGACCACTTTGTACAAGAAAGCTGGGT</u> CTA GTG GTG GCG TCG GTT TCT
DN-MAPK3_F	ATG GCG GAA TCG GGC AGT
DN-MAPK3_MR	CAA ATG GAC TTA TCT TCT TAA TGG CCA CTC GGA TCT
DN-MAPK3_MF	AGA TCC GAG TGG CCA TTA AGA AGA TAA GTC CAT TTG
DN-MAPK3_F	TCA GGA GCC CTG GTA ATT
DN-MAPK3_B1F2	<u>GGGGACAAGTTTGTACAAAAAAGCAGGCT</u> ATG GCG GAA TCG GGC AGT
DN-MAPK3_B2R	<u>GGGGACCACTTTGTACAAGAAAGCTGGGT</u> TCA GGA GCC CTG GTA ATT

\*Att sites are underlined.

MAPK, mitogen-activated protein kinase.

## 2. Staining

Immunohistochemistry for Zn8 (Zebrafish International Resource Center, 1:400), fluorescent in situ hybridization in conjunction with GFP immunohistochemistry (Torrey Pines Biolabs, Secaucus, NJ, USA; 1:1,000), and Alcian blue staining were carried out as described previously (Crump et al., 2004; Zuniga et al., 2011). Partial cDNA fragments of *nrp1a*, *nrp2b*, and *sema3d* were amplified from mixed-stage zebrafish cDNA. The PCR fragments were cloned into the pGEM®-T easy vector (Promega, Madison, WI, USA) and were confirmed by DNA sequencing. Digoxigenin (DIG)-labeled antisense riboprobes were transcribed with T7/SP6 RNA polymerase (Roche Life Sciences, Basel, Switzerland) from linearized plasmids. Primers used for riboprobes are listed in Table 2.

## 3. Imaging

An Olympus FLUOVIEW FV3000 confocal microscope using FV31S-SW software (Olympus, Tokyo, Japan) captured fluorescent images for immunohistochemistry and in situ hybridization. Approximately 100  $\mu\text{m}$  Z-stacks at 3.5- $\mu\text{m}$  intervals were taken with an Olympus UPLXAPO 20X objective lens, then were projected into a single image. An Olympus BX50 upright microscope using mosaic V2.1 software (Tucsen Photonics, Fuzhou, China) imaged flat-mounted facial cartilages dissected manually from Alcian Blue staining larvae. Any adjustments were applied to all panels using Adobe Photoshop (Adobe Systems, San Jose, CA, USA).

## 4. Statistics

Pouches and ceratobranchial (Cb) cartilages were scored to quantify defects in pouches and Cb cartilages. The normal pouch was scored as 1, abnormal and hypoplastic as 0.5, and missing as 0. Similarly, normal Cb was scored as 1, hypoplastic or fused Cb as 0.5, and missing Cb as 0. The multiple comparison test of Tukey–Kramer was employed to quantify defects.

# RESULTS

## 1. Zebrafish *nrp1a*, *nrp2b*, and *sema3d* are expressed in pharyngeal endoderm forming pharyngeal pouches

There are four *nrp* genes, *nrp1a*, *nrp1b*, *nrp2a*, and *nrp2b*, in zebrafish. Previously, it has been reported that all four *nrp* genes are expressed in the brain at 24 to 72 hours-post-fertilization (hpf), with *nrp1a* and *nrp2b* being expressed specifically in mandibular cartilages at 36 to 72 hpf (Bovenkamp et al., 2004). However, the expression of *nrp* genes in the pharyngeal regions of the embryonic head has yet to be analyzed. To investigate a potential role of Nrp signaling in craniofacial development, I first examined the expression of *nrp* genes in the pharyngeal endoderm at 26 hpf, in which a series of pouches arises (Choe et al., 2013). To do so, I carried out in situ hybridization for *nrp* genes in wild-type embryos harboring *Tg(her5:GFP)* transgene, a reporter of the pharyngeal endoderm and pouches (Tallafuss & Bally-Cuif, 2003). When the posterior

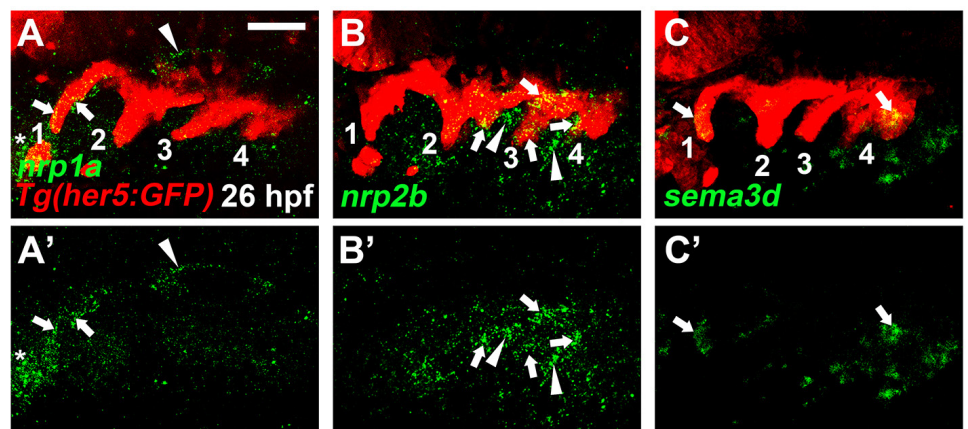
**Table 2.** List of primers used to create in situ probes

Gene	Forward primer (5' to 3')	Reverse primer (5' to 3')
<i>nrp1a</i>	CAG TCA CAA CCG TAT GCA	CGA AGG ATC ATT TGC CCA
<i>nrp1b</i>	TAT CTA CCC TGA GCG TGG	TCC GTC TCC ATC TCA TCC
<i>nrp2a</i>	GAG CTC CAG GGAATG TTG	GTT GTG TTG GTT TGC TCG
<i>nrp2b</i>	AGAACT TTA CGG CTG TCA	TGG TGG TAG ATT CTG GCA
<i>sema3d</i>	TTG GGC ACA GAT ATG GGA	CAC GCT CGT CTG GTT TAA

pouches formed at 26 hpf, *nrp1a* was expressed in the first pouch, with its expression not seen in other pouches (arrows in Fig. 1A). In addition, its expression was seen in the brain (arrowhead in Fig. 1A) and heart (asterisk in Fig. 1A). Transcripts for *nrp2b* were observed in the posterior pouches, including the second to fourth pouches at 26 hpf, whereas they were not seen in the first pouch (arrows in Fig. 1B). Besides, *nrp2b* was also expressed in the adjacent mesoderm to the pouches (arrowheads in Fig. 1B). Apparently, *nrp1b* and *nrp2a* were not expressed in the pharyngeal regions at 26 hpf. Next, I analyzed the expression of *sema3* genes, ligands for Nrp receptors, in the endoderm during pouch formation. Among *sema3* genes, I found that *sema3d* was expressed in the matured pouches as well as in the pharyngeal endoderm forming the fifth pouch at 26 hpf (arrows in Fig. 1C). Expression of *nrp1a*, *nrp2b*, and *sema3d* in the pharyngeal pouches at 26 hpf suggests that they could work together to form pouches during craniofacial development.

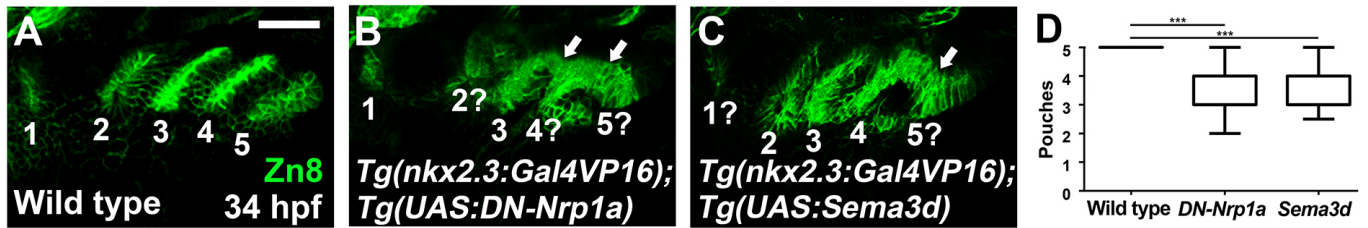
## 2. Nrp signaling is required in the pharyngeal endoderm to develop pharyngeal pouches

I utilized a dominant-negative approach to access the function of Nrp signaling in pouch formation. To do so, I generated *Tg(UAS:DN-Nrp1a)* lines harboring a dominant-negative mutant allele of *nrp1a*. Utilizing the pharyngeal endoderm driver *Tg(nkx2.3:Gal4VP16)* lines that are able to express target genes in pouch-forming endoderm, including the third and fourth pouches (Choe et al., 2013), I overexpressed DN-Nrp1a specifically in the endoderm during pouch formation. Overexpression of the DN-Nrp1a in the endoderm was expected for the endodermal cells to prevent them from receiving signals mediated by Nrps, including Nrp1a. In wild types, five pouches were visualized by Zn8 immunostaining at 34 hpf (Fig. 2A and D). However, compound animals bearing *Tg(nkx2.3:Gal4VP16)* and *Tg(UAS:DN-Nrp1a)* transgenes displayed abnormal pouches at 34 hpf (Fig. 2B). Although the first pouch was normal, the remaining pouches were hypoplastic, misshaped, or missing (Fig. 2B and D). In addition, pouches 3–5 were not separated from each other (arrows in Fig. 2B). This result suggests that Nrp signals are required in pharyngeal endoderm for pouch formation. I further verified the role of Nrp signals in pouch development by analyzing Cb cartilages whose formation relied on normal pouch development (Crump et al., 2004). Five pairs of Cbs formed symmetrically in wild types at 4 dpf (dots in Fig. 3A and D). In the compound

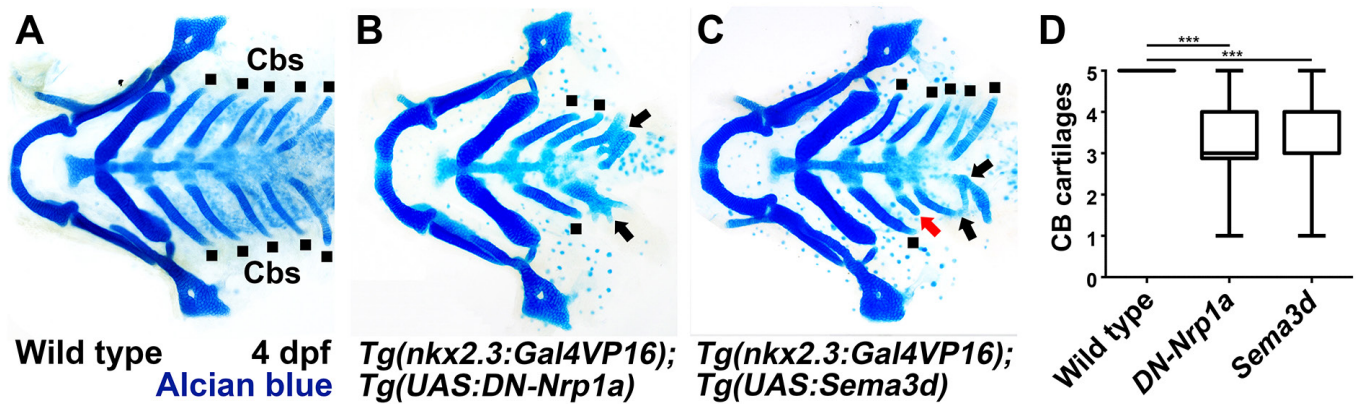


**Fig. 1. Expression of *nrp1a*, *nrp2b*, and *sema3d* at 26 hpf.** (A–C) Fluorescent in situ hybridization (green) in conjunction with the GFP immunohistochemistry (red) in wild-type *Tg(her5:GFP)* animals. (A) Arrows indicate *nrp1a* expression in the *her5*-positive first (1) pouch. *nrp1a* expression in other pouches is not seen. Expression of *nrp1a* in the brain and heart is marked with an arrowhead and asterisk, respectively. (B) *nrp2b* expression in the *her5*-positive second (2) to fourth (4) pouches is marked with arrows, with its expression in the adjacent mesoderm being indicated with arrowheads. (C) *sema3d* expression in the *her5*-positive first pouch (1) and developing fourth pouch (4) is marked with arrows. (A'–C') Green channel only. Pouches are numbered. Scale bars: 40  $\mu$ m. Anterior is to the left.





**Fig. 2. Requirement of Nrp-Sema3 signaling in pharyngeal endoderm for pouch formation.** (A–C) Zn8 immunohistochemistry (green) visualizes pouches at 34 hpf. (A) Zn8 staining labels five pouches in wild types. (B) In compound animals bearing *Tg(nkx2.3:Gal4VP16)* and *Tg(UAS:DN-Nrp1a)* transgenes, pouches 2, 4, and 5 are malformed, with the first (1) and third (3) pouches being fairly normal. Arrows indicate pouches 3–5 that are not separated completely. (C) Overexpression of Sema3d in *nkx2.3*-positive endoderm formed abnormal first (1) and fifth (5) pouches, with the fifth one not completely separated from the fourth one (arrow). Scale bars: 40  $\mu$ m. Anterior is to the left. (D) Quantification of pouch defects. Number of pouches examined for each genotype: wild type (37), *Tg(nkx2.3:Gal4VP16); Tg(UAS:DN-Nrp1a)* (45), *Tg(nkx2.3:Gal4VP16); Tg(UAS:Sema3d)* (41). Data represent on a boxplot. \*\*\*  $p < 0.001$ .



**Fig. 3. Requirement of Nrp-Sema3 signaling in developing ceratobranchial cartilages (Cbs).** (A) Dots indicate five pairs of Cbs in wild types at 4 dpf. (B) Arrows mark Cbs fused to each other, with dots marking normal Cbs in compound animals bearing *Tg(nkx2.3:Gal4VP16)* and *Tg(UAS:DN-Nrp1a)* transgenes. (C) Overexpression of Sema3d in *nkx2.3*-positive endoderm displays hypoplastic (red arrow) and fused (arrows) Cbs. Normal Cbs are marked with dots. Anterior is to the left. (D) Quantification of Cb defects. Number of Cbs examined for each genotype: wild type (31), *Tg(nkx2.3:Gal4VP16); Tg(UAS:DN-Nrp1a)* (39), *Tg(nkx2.3:Gal4VP16); Tg(UAS:Sema3d)* (36). Data represent on a boxplot. \*\*\*  $p < 0.001$ .

animals, however, Cbs were missing or fused, confirming defects in pouches (arrows in Fig. 3B and D). Taken together with the expression of *nrp1a* and *nrp2b* in the endoderm and pouches during pouch formation, my functional analysis suggests a critical role of Nrp signals in developing pouches and facial cartilages.

### 3. Sema3d is able to control pouch formation

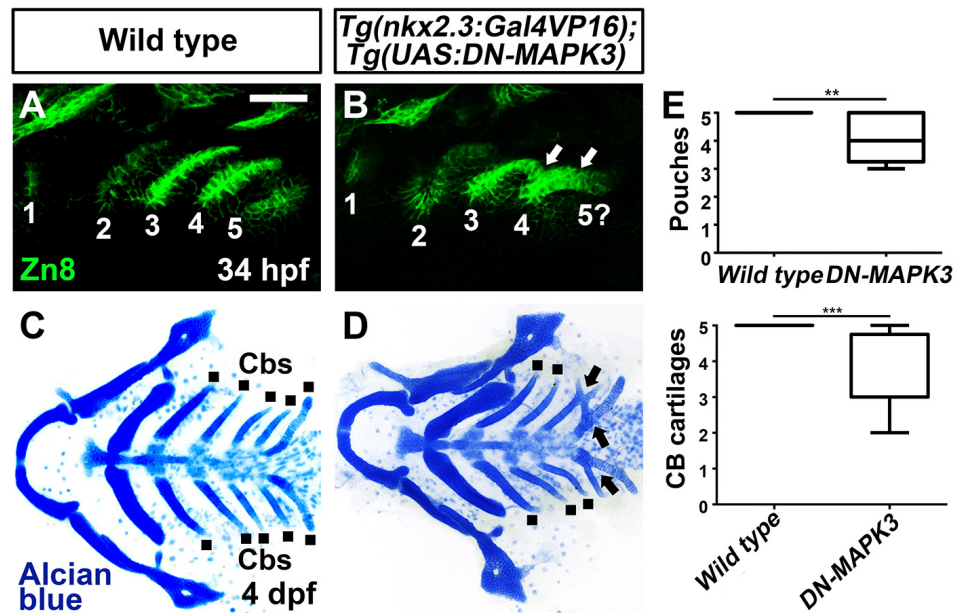
As I observed *sema3d* expression in developing pouches at 26 hpf, I also tested the potential role of Sema3d in pouch formation. To do so, I expressed *sema3d* ectopically in the pharyngeal endoderm during pouch formation by the UAS/Gal4 system. In compound transgenic animals harboring *Tg(nkx2.3:Gal4VP16)* and *Tg(UAS:Sema3d)* transgenes, pouches were missing or malformed compared to wild types (Fig. 2A, C, and D). For example, the first pouch was barely seen, and the fifth one was not completely separated from the fourth one (Fig. 2C). Consistent with defects in pouches, Cb cartilages were also fused to other Cbs or malformed in the compound animals (Fig. 3C and D). This result shows that the endodermal cells are able to respond to ectopically expressed *sema3d* during pouch formation, implying a potential role of Sema3d in pouch formation.

#### 4. Development of pouches requires mitogen-activated protein kinase (MAPK) activities in the endoderm

In the cellular contexts, activation of Nrp receptors promotes MAPK signaling, with Sema3 family ligands being required for MAPK activation (Wey et al., 2005; Bechara et al., 2008; Fung et al., 2016; Hai et al., 2022). Since I observed a potential requirement of the Nrp-Sema3d signal in pouch formation, I next examined whether MAPK was necessary in the endoderm for pouch development. To knock down MAPK activities in the endoderm during pouch formation, I overexpressed a dominant-negative form of MAPK3, specifically in the endoderm with the UAS/Gal4 system. Compared to wild types, compound *Tg(nkx2.3:Gal4VP16)* and *Tg(UAS:DN-MAPK3)* transgenic animals showed defects in pouches, including missing pouch and incompletely separated pouches (Fig. 4A, B, and E), and in Cbs such as fusion among Cbs (Fig. 4C–E). Interestingly, these defects were similar to those seen in transgenic animals knocking down Nrp signals in pharyngeal endoderm (Fig. 2B), implying a genetic interaction between Nrp and MAPK signals in the endoderm for pouch formation.

## DISCUSSION

In this study, I examined a potential requirement of the Sema3d-Nrp-MAPK signal in pouch formation in zebrafish. Expression of *nrp1a*, *nrp2b*, and *sema3d* in pharyngeal endoderm, including pouches, suggests they could be necessary for pouch formation. Indeed, knockdown of Nrp signals or ectopic expression of Sema3d, specifically in the endoderm during pouch formation, resulted in defects in pouches and facial cartilages whose formation was dependent upon normal



**Fig. 4.** Development of pharyngeal pouches and facial cartilages in compound animals harboring *Tg(nkx2.3:Gal4VP16)* and *Tg(UAS:DN-MAPK3)* transgenes. (A, B) Zn8 staining labels to visualize pouches. Compared to wild types, overexpression of DN-MAPK3 in *nkx2.3*-positive endoderm shows a missing fifth pouch (5?), with incompletely segmented pouches (arrows in B). (C, D) Ventral of dissected facial cartilages. While the wild type displays the bilateral set of five Cb cartilages (dots), overexpression of DN-MAPK3 in *nkx2.3*-positive endoderm shows fused Cbs (arrows). Scale bar: 40  $\mu$ m. Anterior is to the left. (E) Quantification of pouch and Cb defects. Number of pouches and Cb examined for each genotype: wild type (34, 37), *Tg(nkx2.3:Gal4VP16)*; *Tg(UAS:MAPK3)* (39, 32). Data represent on a boxplot. \*\*\*  $p < 0.001$ . Cb, ceratobranchial cartilage; MAPK, mitogen-activated protein kinase.

pouch formation. Furthermore, preventing MAPK activities in the endoderm showed similar defects in pouches and facial cartilages to those knocking down Nrp signals. Thus, it is feasible that the *Sema3d-Nrp-MAPK* signal is a critical signaling pathway controlling pouch formation in zebrafish. However, my transgenic analysis of the signal is unable to determine the role of the *Sema3d-Nrp-MAPK* signal in pouch formation for the following reasons. First, the dominant negative approach could knock down activities of Nrp family proteins simultaneously, but it cannot identify *nrp* genes necessary for pouch formation. Thus, to determine the role of Nrp signals in pouch formation, a loss-of-function (LOF) analysis of *nrp1a* and *nrp2b* genes using LOF mutants is required. Second, similar to the first reason, the *Sema3d-Nrp* signal cannot be determined in pouch formation without LOF analysis of *sema3d*. In particular, instead of *Sema3d*, *Vegf-C* that has been implicated in pouch formation could function in pouch formation through Nrps, as *Vegf* can transduce signals through heterodimer for VEGFR and Nrp (Soker et al., 1998; Ober et al., 2004; Guo & Vander Kooi, 2015). However, VEGFRs required for pouch formation have yet to be identified in zebrafish. Third, although MAPKs are essential downstream effectors to transduce Nrp signals, they are involved in transducing several signals from crucial growth factors, including EGF, TGF, and VEGF, in various cellular contexts (Zhang & Liu, 2002). Thus, analyzing genetic or molecular interactions between Nrps and MAPKs in pouch formation is necessary for determining the role of the *Nrp-MAPK* signal in pouch formation. Although it is still preliminary to identify a new signal to control pouch formation, my study suggests a possible role of the *Sema3d-Nrp-MAPK* signal in pouch formation. Currently, I am developing genetic and molecular tools to test the *Sema3d-Nrp-MAPK* signal in pouch formation at the genetic and molecular levels.

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