Zebrafish Otolith Biomineralization Requires Polyketide Synthase

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Abstract: Deflecting biomineralized crystals attached to vestibular hair cells are necessary for maintaining balance. Zebrafish (Danio rerio) are useful organisms to study these biomineralized crystals called otoliths, as many required genes are homologous to human otoconial development. We sought to identify and characterize the causative gene in a trio of homozygous recessive mutants, no content (nco) and corkscrew (csr), and vanished (vns), which fail to develop otoliths during early ear development. We show that nco, csr, and vns have potentially deleterious mutations in polyketide synthase (pks1), a multi-modular protein that has been previously implicated in biomineralization events in chordates and echinoderms. We found that Otoconin-90 (Oc90) expression within the otocyst is diffuse in nco and csr; therefore, it is not sufficient for otolith biomineralization in zebrafish. Similarly, normal localization of Otogelin, a protein required for otolith tethering in the otolithic membrane, is not sufficient for Oc90 attachment. Furthermore, eNOS signaling and Endothelin-1 signaling were the most up- and down-regulated pathways during otolith agenesis in nco, respectively. Our results demonstrate distinct processes for otolith nucleation and biomineralization in vertebrates and will be a starting point for models that are independent of Oc90-mediated seeding. This study will serve as a basis for investigating the role of eNOS signaling and Endothelin-1 signaling during otolith formation.

Keywords: inner ear, otolith, biomineralization, calcium carbonate, polyketide synthase, zebrafish, endothelin-1, eNOS
Article

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Abstract: Deflecting biomineralized crystals attached to vestibular hair cells are necessary for maintaining balance. Zebrafish (Danio rerio) are useful organisms to study these biomineralized crystals called otoliths, as many required genes are homologous to human otoconial development. We sought to identify and characterize the causative gene in a trio of homozygous recessive mutants, no content (nco) and corkscrew (csr), and vanished (vns), which fail to develop otoliths during early ear development. We show that nco, csr, and vns have potentially deleterious mutations in polyketide synthase (pks1), a multi-modular protein that has been previously implicated in biomineralization events in chordates and echinoderms. We found that Otoconin-90 (Oc90) expression within the otocyst is diffuse in nco and csr; therefore, it is not sufficient for otolith biomineralization in zebrafish. Similarly, normal localization of Otoxelin, a protein required for otolith tethering in the otolithic membrane, is not sufficient for Oc90 attachment. Furthermore, eNOS signaling and Endothelin-1 signaling were the most up- and down-regulated pathways during otolith agenesis in nco, respectively. Our results demonstrate distinct processes for otolith nucleation and biomineralization in vertebrates and will be a starting point for models that are independent of Oc90-mediated seeding. This study will serve as a basis for investigating the role of eNOS signaling and Endothelin-1 signaling during otolith formation.

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1. Introduction

Otoconia and otoliths act as a mass load that increase the sensitivity of mechanosensory hair cells to the effects of gravity and linear acceleration in mammals and fish, respectively. While the morphology of otoconia (“ear particles”) and otoliths (“ear stones”) differ, the initial formation of bio-crystals rely on many homologous proteins [1].

Zebrafish otoliths are primarily composed of calcium carbonate (CaCO3), in the form of aragonite, which accounts for ~99% of the total otolithic mass with the remainder consisting of proteins called otoconins [2, 3]. Further analysis of teleost otoliths has identified more than 380 protein components [4]. Based on the level of protein expression or changes in the rate of otolith growth, the polymorph of calcium carbonate crystals can change [1, 5]. For example, knockdown of Starmaker results in otoliths made of calcite rather than aragonite [6]. There are three pairs of otoliths in zebrafish, which include the sagittae, lapilli, and asterisci. While the lapillus and sagitta nucleate early in zebrafish development, the asteriscus does not form until 11-12 days in development [7]. The center of the otoliths contains a proteinaceous core that acts as a site for otolith nucleation and biomineralization. This matrix lays the foundation for further otolith growth, which is mediated by
daily deposition of additional otoconins and calcium carbonate molecules [2]. Otolith nucleation
occurs when the otolith precursor particles (OPPs) bind to the tips of the immotile kinocilia of tether
cells within the otic vesicle [8, 9]. Subsequent studies have demonstrated that the critical period of
otolith seeding and nucleation starts at 18-18.5 hpf (hours post fertilization) and ceases by 24 hpf [1,
8, 10-12].

In mammalian inner ear development, Otoconin-90 (Oc90; the major protein component of
otoconia) is necessary for otoconial seed and nucleation [13-15]. Oc90 can bind Otolin-1 (Otol1) to
establish a protein-rich matrix that serves as a scaffold for subsequent deposition of calcium
carbonate [16, 17]. Additionally, in vitro studies have suggested that Oc90 and Otol1 act
synergistically to modulate otoconial crystal morphology [17]. While Oc90 is not the major protein
component in zebrafish otoliths, it plays an important role in otolith seeding and early development
as oc90-morphants do not develop otoliths [1, 18]. While additional gene mutations have been
identified that lead to otolith agenesis in zebrafish [19-24], the genes responsible for several zebrafish
otolith mutants have been undetermined.

In this study, we sought to identify and characterize the causative gene in a trio of zebrafish
mutants, no content (nco) corkscrew (csr), and vanished (vns), which fail to develop otoliths during early
inner ear development. We provide genetic evidence that the causative gene is polyketide synthase
(pks1; currently wcfc01d11), a candidate gene that was previously identified as a key factor of
bimineralization in Japanese medaka (Oryzias latipes) and sea urchin (Hemicentrotus pulcherrimus)
[25]. Furthermore, we offer potential signaling pathways for pks1 function during inner ear
development in the zebrafish.

2. Materials and Methods

Husbandry and maintenance

All zebrafish were maintained in a temperature-controlled (28.5°C) and light-controlled (14h
on/10h off) room per standardized conditions. nco strain (ji149) was generated by an ENU screen on
the AB background and obtained from ZIRC (Eugene, OR, USA)[26]. csr was a spontaneous mutant
generated in a bre-KO2/ntl-GFP line (AB background). vns was a spontaneous mutant generated in a
AB/TL background. All protocols were approved by Creighton University and the University of
Michigan Animal Care and Use Committees.

Whole genome and RNA-sequencing

Mutant nco embryos and wild-type (WT) clutchmates were phenotyped and collected during the
critical period of otolith nucleation and seeding (24 hours post fertilization, hpf) and the whole
embryo lysates (n=50) were submitted for RNA sequencing. Analysis was completed using MMAPPKR
(Mutation Mapping Analysis Pipeline for Pooled RNA-seq) as previously described [24]. Whole
genome sequencing of csr phenotypically-mutant embryos (n=150) was performed and analyzed
using MegaMapper as previously described [27]. Common SNPs were removed by the Single
Nucleotide Polymorphism Database (dbSNPs). Reference sequences for both experiments were
mapped to Zv9. All sequencing was conducted at the University of Nebraska Medical Center
Genomics Core Facility. Accession numbers for nco RNA-seq and csr genome sequencing will be
provided during review.
mRNA and plasmid DNA rescue

WT mRNA and pks1\textsuperscript{L905P} were synthesized using mMessage Machine from a clone provided by Dr. Hiroyuki Takeda (University of Tokyo), cleaned on an RNeasy column, and subsequently injected into single-cell csr and nco embryos. Naked plasmid of the medaka pks1 clone was injected into vns embryos. Overall penetrance of otolith formation was determined in all three mutants. Site-directed mutagenesis (Agilent) was used to generate the mutant clone containing the causative m mutation in csr (pks1\textsuperscript{L905P} in Japanese medaka; pks1\textsuperscript{A911P} in zebrafish). Primers used for site-directed mutagenesis were:

- pks1\_L905P\_Forward: 5’-GATATGGCGTGATGTCCGGTGACAGGTTGAAGATC-3’
- pks1\_L905P\_Reverse: 5’-ATCTTCAACCTGTCACCGGACATCACGCCATATC-3’

Pathway analysis

Pathway analysis of nco was performed using Ingenuity Pathway Analysis (QIAGEN Inc., https://www.qiagenbioinformatics.com/products/ingenuity-pathway-analysis [28]). The Ensembl Gene IDs were assigned to each gene and uploaded to IPA. Cut-off for gene expression analysis was set at 0.75 RPKM. The calculated z-score indicates a pathway with genes exhibiting increased mRNA levels (positive) or decreased mRNA levels (negative). No change in mRNA levels results in a z-score of zero.

Genotyping

csr, nco, and vns samples were PCR-amplified and submitted for Sanger sequencing using the following primers:

- nco\_Forward: 5’-GGGAGGATGCTTGTTGTTGG-3’
- nco\_Reverse: 5’-GTGGCCCAGAATAGGATCCA-3’
- csr\_Forward: 5’-AAGACGGGGACATGACTCAG-3’
- csr\_Reverse: 5’-TTCAACAAACAGTGCTCCGG-3’
- vns\_Forward: 5’-GCCATCATTGGGAATTGGATG-3’
- vns\_Reverse: 5’-GCTGGATCCATCCCCATGAGC-3’

RT-PCR

All RNA was extracted from Danio rerio wild-type embryos (A/B strain). After collecting embryos at the separate time-points, the samples were homogenised in lysis buffer from the Quick-RNA MiniPrep kit (Zymo Research-R1054) and RNA was extracted following protocol provided by the manufacturer. The RNA samples were then DNase treated using TURBO\textsuperscript{TM} DNase (ThermoFisher, AM2238) as per manufacturer instructions, in order to remove any genomic contamination that may be present in the RNA. cDNA synthesis was achieved using the GoScript\textsuperscript{TM} Reverse Transcription System (Promega, A5001) and followed the protocol provided by the manufacturer.

- actb1\_Forward: 5’-CTTCCAGCCTTCTTCTC-3’
- actb1\_Reverse: 5’-CCACCGATCCAGAGGTA-3’
- pks1\_Forward: 5’-GAATTTTTCTGCGAGTAGAACAAG-3’
- pks1\_Reverse: 5’-TCTGCGATGCAGGGCATCAG-3’
RT-PCR on the cDNA samples was carried out using the GoTaq® G2 Flexi DNA Polymerase (Promega, M7805) and PCR was done following the protocol provided by the manufacturer, using the primers stated above. The RT-PCR samples were then run on a 2% agarose gel.

**Immunofluorescence**

csr and nco embryos were collected during key stages in early inner ear development, fixed with hydrogel and washed in CHAPS-based (1% by weight) CLARITY-clearing solution [29]. Embryos were decalcified with EDTA (120 mM in 0.1% PBS-Triton) before blocking (0.1% PBS-Triton with 3.33% sheep serum and 3.33% BSA), incubating in primary and secondary antibodies diluted in blocking buffer (0.1% PBS-Triton with 3.33% sheep serum and 3.33% BSA), mounting in 50% Glycerol-PBS solution, and imaging by confocal microscopy (Leica TCS SP8). Affinity-purified rabbit polyclonal antibodies were generated to Otogelin (CGNRVDGPSASKG; 1:1000) or Oc90 (CNTQSDTVDRKPTQSKPQ; 1:1000) by conventional methods (GenScript, USA) and directly labelled before immunofluorescence. Other antibodies used were Keratan Sulfate (MZ15; 1:2000; DSHB), Hair Cell Specific-1 (HCS-1; 1:500; DSHB), and acetylated-tubulin (1:500; Sigma T6793). Phalloidin (ThermoFisher A12379) was used at a concentration of 1:500.

**Mitotracker staining**

Mitotracker Red (ThermoFisher #M22425) was resuspended in DMSO (0.25 mM) and diluted to 200 nM in E3 embryo medium. nco and csr embryos were then incubated in the dark for 20 minutes before removing Mitotracker solution and replacing with fresh E3 embryo medium. Samples were allowed to stabilize in the dark for 30 minutes before imaging at 21 hpf. Embryos were then phenotyped at 27 hpf.

**Exogenous salt solutions**

To test the effects of exogenous ions on otolith formation, embryos were kept in E3 Medium until early gastrulation (~10 hpf). Embryos were washed, dechorionated, and transferred to 1X Basic Solution (58 mM NaCl, 0.4 mM MgSO₄, and 5 mM HEPES) supplemented with 0.7 mM potassium chloride, 0.6 mM calcium nitrate or 0.6 mM calcium chloride. Embryos were then transferred to fresh 1X Basic Solution with respective supplement for the remaining development. Embryos were scored by the presence or absence of otoliths at 27 hpf and genotyped using High Resolution Melt analysis.

**Statistical analyses**

Statistical significance was calculated using Fisher’s Exact Test, G-test for Independence, and Chi-Squared Distribution.

**3. Results**

3.1 csr and nco are genetically-linked

The most apparent phenotype of the homozygous recessive csr, nco, and vns mutants is that they fail to form otoliths (lapillus and sagitta) or any observable complex calcium deposits within the inner ear (Fig. 1A-D; Table S1). Furthermore, the mutant larvae are homozygous lethal by 7 days post fertilization (dpf) as the swim bladder fails to inflate (Fig. 1A’-D’) and they are unable to feed. As a result, we do not know whether asteriscus formation is affected. While it is still unknown why the
swim bladder fails to inflate when otoliths are absent, it is a common phenotype in other mutants with otolith agenesis [18-24]. Due to this commonality within csr and nco, we sought to determine if these phenotypes would complement each other. The results of the complementation test showed that some offspring failed to develop otoliths (29.25%; n=106; Table S1), supporting that nco and csr likely are allelic.

3.2 Exogenous ions influence otolith nuclease in csr embryos; not nco or vns embryos

As an aquatic species, the environment of zebrafish can be easily controlled and adapted to assess its impact on embryonic development. Previously, small molecules have been used to block otolith development by inhibiting otolith nuclease [10]. We hypothesized that there was an error in ion homeostasis that could be affected by exogenous solutions. In water treatments supplemented with calcium chloride (n=51), we found a significant decrease in csr penetrance in homozygous embryos ($\chi^2{=}19.27, df{=}6; p{=}0.0037$) compared to treatments supplemented with potassium chloride (n=46) or calcium nitrate (n=54). Additionally, we observed no significant change in nco mutant phenotype penetrance for water treatments supplemented with potassium chloride (17.76%; n=107), calcium chloride (16.67%; n=120) or calcium nitrate (16.9%; n=112) (G-test; $p{=}0.975$). Similarly, the penetrance of otolith formation in vns was not affected by exogenous salts (data not shown).

Building on the hypothesis that there was an error in ion homeostasis, Mitotracker was used to mark mitochondria-rich cells (i.e. presumptive ionocytes) in csr and nco embryos. While nco embryos appear normal, we observed that csr embryos show a lack of Mitotracker localization at 21 hpf (Fig. S1). Altogether, this suggests the nature of the nco and csr mutation, while likely allelic, are inherently different.

3.3 Potentially deleterious mutations identified in polyketide synthase for csr, nco, and vns

To positionally clone the gene responsible for nco and csr, we used complementary approaches for each strain. MMAPPR analysis of nco-derived RNA sequencing (Fig. 2A) [24] and MegaMapper analysis of csr-derived whole genome sequencing (Fig. 2B) [27] both identified a genomic region with high homology surrounding the pks1 locus. While several other genes were in that region, a previous study on otolith biomineralization in Japanese medaka made pks1 the likely gene candidate [25]. Potentially deleterious mutations were identified in pks1 for csr (A911P) and nco (L681*), which were both located within a conserved acyl transferase domain (Fig. 2C). Furthermore, a deleterious mutation in vns (G239R) was serendipitously found to be linked to a neighboring gene during a separate study. The deleterious point mutation was identified by Sanger sequencing of the pks1 locus and confirmed by relatively high penetrance of otolith agenesis (95%).

3.4 Japanese medaka pks1 mRNA or plasmid DNA rescues otolith biomineralization in csr, nco, and vns

While the last common ancestor of Japanese medaka and zebrafish was estimated to be 150 million years ago [30], we sought to assess if the function of pks1 within the inner ear is conserved. We injected Japanese medaka pks1 mRNA or DNA into single-cell embryos of csr, nco, and vns heterozygous incrosses. Microinjection of Japanese medaka pks1 mRNA (300 ng/μL) rescued otolith biomineralization in both csr ($p{=}0.0001; \chi^2{=}0.0001; n=93$) and nco ($p{=}0.0032; \chi^2{=}0.0022; n=84$) mutants (Fig. 3B; Table S1). Additionally, microinjection of the Japanese medaka pks1 plasmid (20 ng/μL) provided by Dr. Takeda rescued otolith biomineralization in vns ($p{=}0.0001; \chi^2{=}0.0004; n=39$). Using
the non-synonymous mutation (A911P) in csr to the Japanese medaka mRNA construct (L905P). We repeated injections into single-cell embryos and failed to rescue otolith biomineralization in csr and nco. WT medaka pks1, but not pks1<sup>L905P</sup>, rescued otolith biomineralization in csr and nco embryos (Fig. 3C; Table S1).

### 3.5 Ingenuity pathway analysis of nco embryos

While pks1 is thought to produce an otolith nucleation factor [25], its broader role during inner ear development is unknown. Ingenuity Pathway Analysis of nco at 24 hpf identified eNOS and Endothelin-1 signaling as the top up- and down-regulated pathways, respectively (Fig. 4A). Among the down regulated genes was rdh12l, a gene adjacent to pks1, suggesting that there is local control of transcription at that locus. mir-92a, the top down-regulated gene, has a predicted binding site in the 3'UTR of rdh12l (Fig. S2) [31]. In addition, several genes listed in the top ten up- or down-regulated lists are also enriched in adult mechanosensory hair cells such as il11b, fosab, fosb, fosl1a, socs3a, scg5, and dnaaf3 (Figs. 4B-C) [32]. Of these genes, il11b is up-regulated during neuromast hair cell regeneration [33]. Notably, dnaaf3 causes primary ciliary dyskinesia and morpholino knockdown of dnaaf3 causes abnormal otolith growth [34]. While its role in inner ear development is unknown, scg5 is expressed within the anterior and posterior poles of the otic placode during the critical period of otolith nucleation [35].

### 3.6 Aberrant expression of proteins involved in otolith development in csr and nco

In mammalian inner ear development, Oc90 is necessary for otoconial seeding and nucleation [13, 14]. Similarly, the role of Oc90 is evolutionarily-conserved in zebrafish and has been previously thought to be necessary for otolith nucleation [18]. Using immunofluorescence (IF), we saw diffuse expression of Oc90 in csr and nco otocysts (Figs. 5B-D), which demonstrated that Oc90 expression within the otocyst is not sufficient for otolith biomineralization in zebrafish. Similarly, normal localization of Ototelin (Otog), a protein required for otolith tethering in the otolithic membrane is not sufficient for Oc90 attachment. Additionally, other otoconins that are important for calcium deposition and growth were detected with diffuse expression within the otocyst such as Starmaker and Keratan Sulfate (data not shown) [36, 37].

### 3.7 Polyketide synthase as an otolith precursor binding factor?

Otolith nucleation is thought to be mediated by a tether-cell specific otolith precursor binding factor (OPBF), which lays the foundation for the successive biomineralization of the otolith [9, 11, 38]. The presence of an OPBF was proposed almost two decades ago and its identification proves to be elusive [38]. Recent studies suggest that one or more OPBFs are expressed by tether-cells and help to mediate otolith nucleation by binding other OPPs [9, 11, 39].

We sought to assess if pks1 or its enzymatic product is a tether-cell specific nucleation factor. While medaka has diffuse pks1 mRNA expression in the otic epithelium [25], we hypothesized that the expression might be restricted to hair cells. First, using publicly available RNA-seq data, we found that pks1 mRNA is enriched (7.46-fold increase) in adult mechanosensory hair cells compared to support cells within the zebrafish inner ear (Table S2). Additionally, this data suggests pks1 mRNA to be transcriptionally regulated in support cells. Support cells predominantly express a 300bp region of the 5'UTR of the pks1 transcript while hair cells express the full open reading frame [32]. A search
for transcriptional regulatory motifs in the 5' UTR of pks1 found a predicted binding site for TCF-3 [40], a transcription factor highly expressed in adult mechanosensory hair cells [32]. While the role of TCF-3 in the inner ear is unknown, it is expressed within the otic vesicle during the critical period of otolith nucleation [35].

Then, we demonstrated that the total number of hair cells remain unchanged during early development in nco, suggesting there are no differences in tether cell maturation and maintenance (Figs. 5E-G). Using RT-PCR, we detected pks1 mRNA during the critical period of otolith nucleation (Fig. S3). However, in situ data showed ubiquitous expression of pks1 in the otic vesicle of zebrafish [25]. While pks1 might be enriched in adult hair cells, early expression shows that it is ubiquitously expressed in the otic vesicle and, therefore, not the tether-cell specific OPBF.

4. Discussion

The homozygous recessive mutants csr, nco, and vns were chosen for this study because each lack the necessary factors such as an OPBF for otolith seeding and biomineralization. To determine the genes responsible for otolith agenesis in these mutants, we used two complementary approaches. The first approach was Whole Genome Sequencing of the csr mutant genome to identify regions of high homology. This indeed was difficult as the csr background strain was heavily inbred, resulting in multiple peaks of high homology. Since we demonstrated csr and nco are genetically-linked, we sought to further clarify the responsible locus using a second method (i.e. RNA-seq of the nco transcriptome) for comparison. This result pinpointed a region of high homology near the end of the 24th chromosome. While deciphering potentially deleterious mutations within that region, we focused on pks1 following evidence that it is responsible for otolith nucleation in Japanese medaka [25]. While these species are evolutionarily divergent, the shared phenotype between medaka and our mutants suggested that the role of pks1 is conserved. As a result, we chose to use medaka pks1 nucleic acid to rescue otolith formation in csr, nco and vns mutants. Similarities can also be drawn with other zebrafish mutants such as keinstein, which has diffused expression of Starmaker within the otocyst and exhibits similar circling swimming behaviors [41, 42]. Furthermore, keinstein may be another pks1 allele due to its predicted chromosomal location [43].

While WT medaka pks1 rescues otolith biomineralization in csr and nco, differences in penetrance of exogenous ions on otolith formation suggested the nature of each mutation is fundamentally different. This was confirmed by Sanger sequencing that nco has a premature stop codon while csr likely makes a defective protein that may be stabilized by exogenous ions. This defective protein may be the explanation for the differences in Mitotracker localization in csr. Due to its surface stain expression, we hypothesize that Mitotracker was localized to mitochondria-rich ionocytes [44]. Ionocytes have previously been implicated in otolith formation as mutations in gcm2, which is responsible for ionocyte maturation, leads to otolith agenesis [20, 45]. We hypothesize that the endolymph in csr and nco mutants has the necessary components for otolith nucleation [2] but lack a trigger factor produced by pks1. The absence of pks1 does not visibly appear to affect hair cell development that are required for otolith nucleation either [9]. It has been previously suggested that apolipoprotein could potentially bind polyketide synthase [4, 25]. Given our RNA-seq analysis of nco, we see no significant change in any apolipoprotein expression. Publicly-available in situ data does not support Apolipoprotein expression within the inner ear [35]. Additionally, IF of csr and nco
embryos demonstrated that expression of a critical otoconial seeding protein, Oe90, within the otocyst is not sufficient for otolith biomineralization in the presence of the otolithic membrane.

One caveat is that the penetrance of otolith formation is influenced by the genetic background of zebrafish. When treated with the small molecule 31N3, WT embryos in the AB/EKW background fail to develop otoliths [10]. However, 31N3 fails to inhibit otolith formation in the TL and TU strains, suggesting that there are potential genetic modifiers that influence otolith nucleation in these backgrounds. While the csr mutation (A911P) leads to otolith agenesis in the AB background, homozygosity at the locus is compatible with proper development in the AB/TL background (data not shown). This suggests csr may be a hypomorphic allele and the AB background can overcome the loss of Pks1 function with enhanced ion flux. Ironically, the mutant phenotype was lost when csr was outcrossed to the WIK background. It was only until csr was backcrossed to the AB background that the mutants were recovered. Altogether, we suggest that the AB background heavily influences the penetrance of otolith formation.

While pks1 likely acts as an enzyme whose expression is enriched in adult mechanosensory hair cells [32], its product is required for otolith nucleation in zebrafish. However, the molecular function of pks1 remains unknown. Using nco RNA-seq data, we performed an Ingenuity Pathway Analysis, which identified eNOS and Endothelin-1 signaling as the most up- and down-regulated pathways, respectively. eNOS signaling could be impacted by pks1 metabolites such as iromycin, which has been shown to inhibit this pathway [46]. Both eNOS and Endothelin-1 have been implicated in inner ear development and function. Notably, it has been demonstrated that these pathways are inversely related in sensorineural hearing loss [47]. An example of this is Waardenburg syndrome, caused by mutations in endothelins, which cause abnormal pigmentation and sensorineural hearing loss [48]. During early development, Endothelin-1 mRNA turns on during the critical period of otolith nucleation [35, 49] and is detected in the otic vesicle at 24 hpf [50]. Endothelin-1 and its receptor (ednraa) are both enriched in adult zebrafish inner ear support cells [32]. Additionally, Endothelin-1 has been identified as a potential modifier of osteoblast function to increase bone mineralization [51]. Furthermore, Endothelin-1 has been implicated with the FOS-family of genes (fosab, fosb, and fosl1a) and socs3a, which are all differentially expressed in nco at 24 hpf. These genes are all part of a regulatory network during hypergravity-mediated bone formation [52]. Furthermore, the presence of osteoblast-associated proteins within teleost otoliths suggest a common mechanism between bone mineralization and otolith biomineralization [4]. Future studies will attempt to clarify the roles of Endothelin-1 and eNOS signaling pathways during biomineralization events.
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**Conflicts of Interest:** The authors declare no conflict of interest.

### References


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Figure 1: (A-D) The csr, nco, and vns mutant phenotypes fail to form otoliths within the inner ear. However, semicircular canal formation appears to be normal. (A’-D’) All mutants fail to inflate their swim bladders, which is lethal. Imaged at 5 days post fertilization (dpf). Magnification 6.3X. (*) indicates swim bladder.
Figure 2: Complementary approaches for causative gene discovery. MMAPPR analysis of RNA sequencing data for \textit{nco} (A) and whole genome homology mapping for \textit{csr} (B) identified regions of high homology on the 24th chromosome near the \textit{pks1} locus (~33 Gb). (C) Deleterious mutations were identified in \textit{pks1} for \textit{nco} and \textit{csr} within the acyl transferase (AT) domain and \textit{vns} within the polyketide synthase (PKS) domain. Sanger sequencing confirmed SNPs in \textit{csr}, \textit{nco}, and \textit{vns} mutants. Other domains include Ketoacyl Synthetase (KS), Medium Chain Reductase (MDR), NAD(P)-dependent dehydrogenase (NDD), and Phosphopanthetheine-Binding (PP).
WT pks1 nucleic acid rescues otolith formation in csr, nco, and vns. (A) Normal frequencies of mutant phenotypes in each uninjected strain. All four pairings follow homozygous recessive mode of inheritance. (B) Results of injected embryos show that Japanese medaka pks1 mRNA (300 pg) rescues both csr and nco mutants and pks1 DNA (20 pg) rescues vns mutants. (*, p < 0.0001, paired t-test)(**, p < 0.0032, paired t-test)(***, p = 0.0001, paired t-test). Site-directed mutagenesis was used to introduce a conserved mutation in csr (A911P) into the Japanese medaka construct (L905P) (C) Injection of pks1<sup>L905P</sup> (300 pg) fails to rescue csr or nco mutant phenotypes.
Figure 4: Gene expression and pathway analysis of nco embryos. (A) Ingenuity Pathway Analysis shows the top up-regulated and down-regulated pathways, which are eNOS Signaling and Endothelin-1 Signaling, respectively. Positive z-score indicated increased mRNA levels. Negative z-score indicates decreased mRNA levels. No change in mRNA levels results in a z-score of zero. (B) Differential gene expression in the top up-regulated genes. (C) Differential gene expression in the top down-regulated genes. (**, expressed in adult zebrafish mechanosensory hair cells) [32].
Figure 5: Aberrant expression of proteins involved in otolith development in csr and nco. (A) Schematic of anterior macula (AM) tethered to otolith at 27 hpf. (B) In WT, Otoconin-90 (Oc90) is expressed within the mineralized otolith, which is situated atop the otolithic membrane (Otogelin, or Otog), at 27 hpf. Scale bar = 5 μm. (C-D) Oc90 has diffuse expression within the otocyst of csr and nco. In csr and nco, Otog is localized near the apical surface of hair cells. (E-F) Expression showing hair cells in WT and nco larvae at 5dpf. Scale bar = 25 μm. (G) Quantification of hair cell numbers in the posterior and anterior macula of WT and nco (n = 4).
**Figure S1**: Spatial differences in mitochondrial membrane potentials. (A) While Mitotracker marks active mitochondria in WT, (B) *csr* embryos show a lack of Mitotracker expression during early development. Arrow indicates otic vesicle.
**Figure S2:** miR-92a binding site in the 3’ UTR of *rdh12l*. TargetScanFish 6.2 of *rdh12l* in zebrafish shows potential microRNA binding sites including miR-92a, which is the most down-regulated gene in *nco* embryos at 24 hpf.
Figure S3: pks1 expression during early inner ear development. Using primers from distinct exons and total RNA from several developmental stages, RT-PCR was used to assess expression of pks1 and actb1 as a control. Amplification of pks1 cDNA is predicted to produce a 602bp product, while genomic contamination should produce a 789bp product. actb1 cDNA should yield a 249bp product, while gDNA should yield a 349bp product.
Table S1. Frequency of WT and mutant phenotypes for uninjected and injected csr, nco, and vns embryos.

<table>
<thead>
<tr>
<th>Strain</th>
<th>Wild-type</th>
<th>Otoliths absent</th>
<th>Total (n)</th>
</tr>
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<tbody>
<tr>
<td>csr</td>
<td>83.81%</td>
<td>16.19%</td>
<td>105</td>
</tr>
<tr>
<td>nco</td>
<td>80.70%</td>
<td>19.30%</td>
<td>57</td>
</tr>
<tr>
<td>csr x nco</td>
<td>77.37%</td>
<td>22.63%</td>
<td>137</td>
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<tr>
<td>vns</td>
<td>60.71%</td>
<td>39.29%</td>
<td>56</td>
</tr>
<tr>
<td>csr + WT mRNA</td>
<td>100.00%</td>
<td>0.00%</td>
<td>93</td>
</tr>
<tr>
<td>nco + WT mRNA</td>
<td>96.43%</td>
<td>3.57%</td>
<td>84</td>
</tr>
<tr>
<td>csr + L905P mRNA</td>
<td>79.35%</td>
<td>20.65%</td>
<td>92</td>
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<tr>
<td>nco + L905P mRNA</td>
<td>76.60%</td>
<td>23.40%</td>
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</tr>
<tr>
<td>vns + WT DNA</td>
<td>94.87%</td>
<td>5.13%</td>
<td>39</td>
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Table S2. Differential expression of pks1 in adult zebrafish hair and support cells.

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<tr>
<th></th>
<th>Total Reads</th>
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<th>ORF RPKM</th>
<th>5' UTR Read Counts</th>
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<td><strong>Support cells (SRA)</strong></td>
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</tbody>
</table>

|                      |             |                   |          |                    |
| **Hair cells RPKM average - ORF** | 0.44963989   | -1.1531           |          |                    |
| **Hair cells SD**    | 0.082651371 |                   |          |                    |
| **Support cells RPKM average - ORF** | 0.002556894  | -8.611            |          |                    |
| **Support cells SD** | 0.00442867  |                   |          |                    |
| **Fold Change**      |             |                   | 7.4579   |                    |