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Scleraxis genes are required for normal musculoskeletal development and for rib growth and mineralization in zebrafish

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ABSTRACT: Tendons are an essential part of the musculoskeletal system, connecting muscle and skeletal elements to enable force generation. The transcription factor scleraxis marks vertebrate tendons from early specification. Scleraxis-null mice are viable and have a range of tendon and bone defects in the trunk and limbs but no described cranial phenotype. We report the expression of zebrafish scleraxis orthologs: scleraxis homolog (scxa)-a and scxb in cranial and intramuscular tendons and in other skeletal elements. Single mutants for either scxa or scxb, generated by clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated protein 9 (Cas9), are viable and fertile as adult fish. Although scxb mutants show no obvious phenotype, scxa mutant embryos have defects in cranial tendon maturation and muscle misalignment. Mutation of both scleraxis genes results in more severe defects in cranial tendon differentiation, muscle and cartilage dysmorphogenesis and paralysis, and lethality by 2–5 wk, which indicates an essential function of scleraxis for craniofacial development. At juvenile and adult stages, ribs in scxa mutants fail to mineralize and/or are small and heavily fractured. Scxa mutants also have smaller muscle volume, abnormal swim movement, and defects in bone growth and composition. Scleraxis function is therefore essential for normal craniofacial form and function and vital for fish development.—Kague, E., Hughes, S. M., Lawrence, E. A., Cross, S., Martin-Silverstone, E., Hammond, C. L., Hinits, Y. Scleraxis genes are required for normal musculoskeletal development and for rib growth and mineralization in zebrafish. FASEB J. 33, 000–000 (2019). www.fasebj.org

KEY WORDS: zebrafish · tendon · ribs · craniofacial · muscle

The musculoskeletal system is formed by coordinated differentiation and morphogenesis of skeletal muscle, tendon, ligament, cartilage, bone, and associated joint cell types (reviewed in refs. 1 and 2). Recent studies have shown that both signaling between component tissues and physical forces deriving from muscular contraction or passive load can remodel various elements of the system to fit form to function (reviewed in ref. 3). In the integrated musculoskeletal system, resolving the primary cause of defects requires identification of the earliest failures—in muscle, bone, or tendon—and determination of their secondary consequences during development of the entire system. With such detailed understanding, treatments for genetic or environmentally induced musculoskeletal pathologies may be more effective.

Tendons play an essential role in muscular control of the body by connecting muscle and skeletal elements, allowing force transmission. The earliest and most persistent known marker for the tendon cell lineage is the basic helix-loop-helix (bHLH) transcription factor scleraxis (scx) (4–6). Scx expression marks a somitic compartment called the syndetome in mammals and birds, from which the tendon precursors are derived (7). Scx is also expressed in pharyngeal arches and facial tendons of mouse embryos (8–10). Scx-null mice are viable but show a dramatic defect in tendon

ABBREVIATIONS: μCT, microCT; AB, alcian blue; aa, amino acid; AR, alizarin red; bHLH, basic helix-loop-helix; BMD, bone mineral density; BMI, body mass index; bp, base pair; CRISPR, clustered regularly interspaced short palindromic repeats; Cas9, CRISPR-associated protein 9; CT, computed tomography; dpt, days postfertilization; ECM, extracellular matrix; H&E, haematoxylin and eosin; hpf, hours postfertilization; IVD, intervertebral disk; MTJ, myotendinous junctions; MyHC, myosin heavy chain; scx, scleraxis; SHG, second harmonic generation; SL, standard length; tmnd, tenomodulin

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differentiation, resulting in a loss of intermuscular tendons and the tendons responsible for transmitting musculoskeletal force in the limbs, tail, and trunk. However, short-range muscle-anchoring tendons, such as the ones anchoring the intercostal muscles to the ribs, and ligaments, like the cruciate ligaments of the knee, are unaffected (11). Scx is not required for tendon cell specification, as tendon progenitors are present in Scx<sup>−/−</sup> mutant mice, but Scx is necessary for the condensation and differentiation of tendon cell populations (11). Experiments in mice and chicks have shown that Scx is required for secretion of structural extracellular matrix (ECM) components, including colla1a1, other tendon-associated collagens, and tenomodulin (Tnmd) (12–14), for formation of extended cytoplasmic extensions that support matrix organization and in the cross-talk between tenocytes and endotenon cells (11).

It has been suggested that Scx also functions in tendons of lower vertebrates. In frogs, Scx accumulates at the end of muscle fibers in the somites and the limbs and is involved in inducing tendon matrix genes tenascin C and betaig-h3 (19, 20). In trout and zebrafish, the myosepta, sheets of connective tissue that separate the somite muscle blocks, are initially acellular but later contain cells expressing colla1a1 and Scx (21, 22). Zebrafish have 2 Scx genes, scxa and scxb, but only scxa expression has been described (23, 24).

Zebrafish scxa-positive cranial tendons are located between muscles and the craniofacial skeleton and coexpress tendon markers such as tnnmd, colla1a2, and trsp4b (23–26). Interestingly, cranial and fin tendon progenitors can be induced in the absence of muscle or cartilage, whereas myoseptal scxa expression requires muscle for its initiation (23), which suggests that these tendon populations have different origins and regulation. As in mammals, zebrafish have neural crest-derived craniofacial tendons and ligaments (8, 23, 24, 26, 27). However, knockdown experiments in zebrafish with antisense morpholino oligonucleotides against both scxa and scxb were reported to have no effect on tnnmd expression or create any craniofacial defects in the embryos (23). Although expression data implicate Scx in tendon development in various vertebrate groups, functional data derive mostly from mice trunk and limbs. We set out to create a zebrafish loss-of-function model to increase understanding of Scx function across vertebrates.

Here we describe the differential expression of scxa and scxb in embryonic, juvenile, and adult zebrafish. Zebrafish single mutants for scxa or scxb are each viable, allowing assessment of the adult musculoskeletal system. Mutations in scxa lead to embryonic defects in cranial tendon composition and shape as well as muscle misalignment. At juvenile and adult stages, Scxa is essential for growth and mineralization of the ribs and is required for normal swim movement, muscle volume, and body composition. Lack of Scxa in the mutants also results in ectopic growth of bone in neural and haemal arches while also reducing jaw bone mineral density (BMD). Lack of Scxb alone has no obvious phenotype but exacerbates the effect of the lack of Scxa, indicating partially redundant function. Double mutants show severe cranial defects but no obvious defect in somitic myotendinous junctions (MTJs). Double mutant embryos have reduced muscle growth and function and paralysis of the jaw, leading to early juvenile stages.

**MATERIALS AND METHODS**

**Generation of mutant zebrafish lines and maintenance**

Clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated protein 9 (Cas9) genome editing (28) was used to target scxa (zv11, Chr19: 3001919–3001938, GGGGGTGCCGGAGGCTAGT) and scxb (zv11, Chr16: 31,396,781–31,396,801, GCCATATGGTCCTCTGTTAAGCT) and yielded 2 nonsense alleles for scxa (scxa<sup>g141</sup>, scxa<sup>g170</sup>) and 1 for scxb (scxb<sup>g107</sup>), all of which led to premature stop codons upstream of the bHLH domain (Supplemental Fig. S1). scxa<sup>g141</sup> carries a 4 base pair (bp) deletion leading to a frameshift after amino acid (aa) 64, adding a tail of 2 extra incorrect aa followed by a premature stop. scxb<sup>g107</sup> carry a 1-bp insertion also leading to a frameshift after aa 64, adding a 51 wrong aa tail before a premature stop codon in exon 1. scxb<sup>g107</sup> is a deletion of 12 bp combined with a 27-bp insertion, which creates an immediate UAG stop codon after 45 aa of the wild-type protein (Supplemental Fig. S1).

**mRNA in situ hybridization and immunohistochemistry**

In situ mRNA hybridization was performed as previously described (32) and adapted for juveniles, which were cut into 3 or 4 pieces, skinned, bleached, and then treated with 50 μg/ml protease K for 15 min and fixed. Probes for scxa and scxb were made by amplifying from zebrafish cDNA [24 hours post-fertilization (hpf); Thermo Fisher Scientific, Waltham, MA, USA] a 1151 and 847 bp fragment, respectively, and cloning them into pGEM-Teasy vector (Promega, Madison, WI, USA). The following primers were used: 5′-CACAAAGCGCCAGAGTG-TG-3′ and 5′-TGTGATGCCGAAAAATGTGAC-3′ for scxa and 5′-ACACGAGCTGGTTCTCTACCTA A 3′ and 5′-CAGTGTTCGTTCCGTCAA-3′ for scxb. For tnnmd and xirp2a probes, the following primers (containing T3 polymerase site) were used: 5′-TCACTCTCCTCGCAAGAATGC-3′ and 5′-GCACGAGCTGGTTCTCCTA A 3′. For tnnmd and xirp2a probes, the following primers (containing T3 polymerase site) were used: 5′-TCACTCTCCTCGCAAGAATGC-3′ and 5′-GCACGAGCTGGTTCTCCTA A 3′. For tnnmd and xirp2a probes, the following primers (containing T3 polymerase site) were used: 5′-TCACTCTCCTCGCAAGAATGC-3′ and 5′-GCACGAGCTGGTTCTCCTA A 3′. For mRNA hybridization, the following primary antibodies were used: sarcomeric myosin heavy chain (MyHC): A4.1025, 1:10 (35), MP20 (Developmental Studies Hybridoma Bank; DSHB), 1:10, anti–green fluorescent protein, 1:500 (rabbit, Torrey Pines or chicken, ab19390; Abcam, Cambridge, MA, USA), anti-Tsp4 (Thbs4), 1:400 (ab211143, made against N-terminal recombinant fragment within zebrafish Tbs4; Abcam), and anti–α-Actinin, 1:500 (A7811; MilliporeSigma, Burlington, MA, USA). Secondary antibodies were either horseradish peroxidase–conjugated (Vector Laboratories, Burlingame, CA, USA) or Alexa dye–conjugated (Thermo Fisher Scientific). Samples for immunohistochemistry were fixed and stained as scarecrows.
previously described (36). Wholemount pictures were taken on an Olympus DP70 camera (Tokyo, Japan), and dissected samples were flat mounted in glycerol and photographed on a Zeiss Axioskop with Axiocam (Carl Zeiss, Oberkochen, Germany) using Openlab software (Agilent, Santa Clara, CA, USA).

**Alizarin red S and Alcian blue staining**

Staining was performed as previously described (37).

**Microcomputed tomography**

One-year-old fish were fixed in 4% paraformaldehyde for 72 h and dehydrated to 70% ethanol. A total of 24 fish were scanned (7 scans: 3 scans per fish, 14 siblings) using a Nikon XT H225ST computed tomography (CT) scanner (Nikon, Tokyo, Japan) at a voxel size of 21 μm (scan settings 130 kV, 150 μA, 0.5-s exposure, 3141 projections), and selected regions resampled at 5 μm (130 kV, 53 μA, 0.7-s exposure, 3141 projections) without additional filters. Images were reconstructed using CT Pro 3D software (Nikon). Amira 6.0 (Thermo Fisher Scientific) was used to generate 3-dimensional volume renders. Soft tissues were discriminated by treating fixed fish with 2.5% phosphomolybdic acid for 14 d, as previously described (38), followed by microCT (μCT) scanning. Muscle volume was calculated for a single transverse slice in 2 positions in the trunk: the first at the level of the midpoint of the second-to-last rib-bearing vertebra, and the second at the midpoint of the fourth vertebra posterior to the previous position. Trunk musculature was segmented and volume calculated using the Material Statistics module. Nonmuscle volume in that position was calculated by subtracting the muscle volume from the total volume.

Vertebral centrum volumes were calculated for the seventh and eighth thoracic vertebrae using the CT scans of unenhanced fish in Avizo 9.3 (Fei, Hillboro, OR, USA) by segmenting the minimum volume possible around the neural canal, excluding all processes, trabeculae, spaces, and ribs in a transverse view. Volume was calculated using the Material Statistics module. The entire vertebral volume with ribs was measured on the third thoracic vertebra using the aforementioned method but by segmenting the entire vertebra, including all processes, trabeculae, spaces, and ribs. BMD was quantified as previously described (39).

**Second harmonic generation imaging**

Second harmonic generation (SHG) images were acquired using 10 × 0.3 numerical aperture water dipping lens, 880-nm laser excitation, and simultaneous forward and backward detection (440/20) in Leica SP8 AOB5 confocal laser scanning microscope attached to a Leica DM6000 upright epifluorescence microscope with multiphoton lasers and confocal lasers allowing fluorescent and SHG acquisition of the same sample and Z stack. Microscope parameters for SHG acquisition were set as previously described (40). LASX (Leica Microsystems, Buffalo Grove, IL, USA) was used for image acquisition.

**Histology**

Following μCT, fish were rehydrated to PBS with Tween 20 (1X PBS/0.01% Tween 20), decalcified in 1 M EDTA-solution for 20 d, embedded in paraffin, and sectioned at 5 μm. Sections were stained for AB and hematoxylin and eosin (H&E), as previously described (41). Pictures were taken using a GXML3200B with GXCAM camera (GX Vision, Stansfield, Suffolk, United Kingdom).

**Body mass index and standard weight calculation of adult fish**

Adult fish from heterozygote incrosses, grown in tanks together, were anesthetized with tricaine, blotted dry, and weighed nose-to-base of tail fin, length measured with a ruler and fin-clipped for genotyping. Body mass index (BMI) was calculated as weight (g) × length⁻² (cm). Standard weight (K) was calculated using Fulton’s formula: K = weight (g) × 100 × length⁻³ (cm) (reviewed in ref. 42).

**Fish tracking**

Two or 3 fish per movie were recorded in 8 L tanks with a Nikon D3200 camera mounted above the tank at 1920 × 1080 resolution, at 24.96 frames/second (see Supplemental Video and Supplemen
tal Fig. 57). Fish motion was quantified using the Modular Image Analysis plugin (v.0.5.17) (43) in Fiji (44, 45). Initially, the Fiji Color Deconvolution plugin (46) was used to convert the RGB-format video frames into grayscale while also enhancing the contrast of the fish from the background image of the tank. Next, the median time-projection image was subtracted from all frames to enhance the image. This image was subsequently binarized using the intermodes threshold (47) and median-filtered. Identified objects were size-filtered to remove noise spuriously detected as a fish. Individual fish were then tracked between frames using the Apache HBase implementation (Apache Software Foundation, Forest Hill, MD, USA) of the Munkres algorithm, linking costs based on centroid separation (48). From these tracks, instantaneous (frame-to-frame) speeds were calculated. To remove false tracks, tracks lasting less than 50 frames were excluded from further analysis. To measure fish curvature, the binarized objects were skeletonized and a spline curve fitted to this backbone using the Apache Math3 library (49); this permitted measurement of local curvature and backbone length.

The 100 frames in which the fish were most active were selected, and the instantaneous velocity and range of movement was compared between 6 homozygous and 6 heterozygous fish. Range of movement was calculated by subtracting the minimum curvature from the maximum curvature for each fish. Each point on the graphs corresponds to the average value for each fish, and a 2-way ANOVA was performed in GraphPad Prism v.7.04 (GraphPad Software, La Jolla, CA, USA) to compare the mean value from each heterozygous fish with the mean value from each homozygous fish.

The software is available and free to download (Supplemental File S8).

**Statistical analysis**

Statistical analyses were performed using GraphPad Prism 7.00 (GraphPad Software). The tests used n numbers, sample sizes are indicated in the figure legends, and significant P values are shown on the figures. All tests met standard assumptions, and the variation between each group is shown. Sample sizes were chosen based on previous, similar experimental outcomes and were based on standard assumptions. No samples were excluded. Randomization and blinding were not used except where the genotype of zebrafish was determined after experimentation.

**Genomic and protein comparison**

Clustal alignment and sequence pair distances were made using the Lasergene Genomics Suite (DNASTar, Madison, WI, USA). Analysis of syntenie was made using Ensembl zebrafish zv10 and the Genomicc Synteny software v.93.01 (50).
RESULTS

Expression of scxa and scxb during zebrafish development

Zebrafish have 2 orthologs of the mammalian Scx gene, scxa and scxb (23), with Scxa and Scxb showing 68.1 and 63.6% aa identity with mouse Scx and 68.3 and 63.2% with human SCX, respectively (Supplemental Fig. S2A, B and ref. 23). Zebrafish scxa is syntenic to mammals, with the whole scxa gene positioned in the +strand inside intron 3 of bop1 (Supplemental Fig. S2C, Ensembl GRCz11). In contrast, the scxb locus shows more rearrangements (Supplemental Fig. S2C, Ensembl GRCz11). We sought to know where scleraxis genes are expressed in zebrafish and whether this relates to synteny. Expression of scxa, but not scxb, has been reported (23, 24, 26, 51). By 72 hpf, both scxa and scxb mRNAs were detected in tenocytes at the junctions between skeletal elements and head muscles (Fig. 1A, B). scxb mRNA overlapped scxa mRNA in the attachments of the Meckel adductor, the sternohyoideus, and ocular muscles (Fig. 1A, B), similar to expression of tnmd and colla2 (23). However, other tendons, such as the mandidulobuhyoideus tendon and the intermandibularis tendon, showed strong scxa and weak or no scxb expression (Fig. 1A, B). Strong expression of scxb and weak scxa was evident in the ocular muscle attachments (Fig. 1A, B). Both scxa and, to a lesser extent, scxb mRNAs are expressed at 72 hpf and beyond in somitic vertical myosepta (Fig. 1C, D and unpublished data). Thus, scxa and scxb expression partially overlaps in cranial tendons and ligaments and intersomatic MTJs, although scxa mRNA appears more abundant in both during early larval stages.

During juvenile stages, scxa mRNA was detected in various skeletal elements, such as the intermuscular tendons at the vertical myosepta, the fin radials, the joints in the fin bony rays (lepidotrichia) segments at standard length (SL) 8.0–12.0 (Fig. 1E–G). Sections taken from stained juveniles show that scxa is not expressed at muscle ends at this developmental stage. Intriguingly, the chondrogenic marker sox3a mRNA is detected weakly in ribs, although it was observed strongly in fin endoskeletal elements (radials) and weakly in exoskeletal elements (fin rays) (Fig. 1H). scxb was only weakly detected in vertical myosepta (Fig. 1I, J). The head tendons and ligaments expressed strong scxa but little scxb at muscle attachments of the protractor hyoideus and intermandibularis anterior muscles that expressed the muscle marker tmnc (Fig. 1K–M). Thus, expression data show that scxa is the predominant Scx gene expressed at embryonic and juvenile stages.

Lack of Scxa results in defective cranial tendons and ligaments and abnormal musculature

In contrast to the tendon and bone phenotypes that have been reported in mice lacking Scx, morpholino knockdown of scxa and scxb in zebrafish yielded no obvious phenotype (11, 14, 18, 23). To analyze a complete loss of function of scxa and scxb in embryonic and adult fish, we generated stable mutant lines for scxa and scxb using CRISPR/Cas9 genome editing (Supplemental Fig. S1). Scxa<sup>kg141</sup>, scxb<sup>kg870</sup>, and scxb<sup>kg307</sup> have premature stops before the bHLH domain, which is required for DNA binding and dimerization. As we have found no consistent difference between the 2 scxa mutant alleles, henceforth we have used the kg170 allele unless otherwise stated and refer to it as scxa<sup>−/−</sup>. For simplicity, we refer to scxb<sup>kg307</sup> mutants as scxb<sup>−/−</sup>. Analysis of the expression of scxa and scxb mRNA in scxa mutants shows reduced scxa signal in mutants compared with siblings, which is indicative of nonsense-mediated decay (Supplemental Fig. S2D). We observed no change in either the pattern or levels of expression of scxb in the scxa<sup>−/−</sup> mutants, which suggests that there is no compensatory up-regulation of scxb (Supplemental Fig. S2E). To investigate Scxa function, we imaged 7 days postfertilization (dpf) scxa mutants and siblings carrying a col2a1:amCherry transgene by SHG microscopy, which reveals myosin heads in muscle and collagen (mainly collagen I) in tendons and ligaments (40), combined with confocal imaging of the transgene that labels cartilage. No obvious changes to cartilage were observed (Fig. 2A–C). However, SHG revealed decreased signal in certain tendons and ligaments of scxa mutants, such as the sternohyoideus tendon, which is suggestive of poor collagen organization (Fig. 2A, B). To corroborate these results in scxa mutants, we performed in situ hybridization for tnmd at 3 dpf in an incres of scxa<sup>−/−</sup>. Genotyped scxa mutants (9/9) showed reduced tnmd expression levels in cranial tendons, whereas cleithrum expression was largely preserved (Fig. 2D). Using immunostaining for Tsp4b, a marker of tendons and ligaments (25), scxa<sup>−/−</sup> mutant embryos showed disorganization and changes to directionality and shape of cranial tendons and ligaments, which were variable between specific tendons and between individual mutants despite comparable levels of Tsp4b accumulation (8/8 of analyzed mutants, Fig. 2E–G). Muscle fibers visualized with MyHC in scxa mutants showed a range of abnormalities, such as fibers that extended beyond their normal boundaries, marked by Tsp4b, fibers that were misaligned or that crossed the midline, and disorganized junctions (Fig. 2E–G and Supplemental Fig. S3A and Table 1). Similar phenotypes were also seen in scxa<sup>kg141</sup> mutants (Supplemental Fig. S3B–F and Table 1) and occasionally in scxa<sup>−/−</sup> embryos, though at lower penetrance (Supplemental Fig. S3A and Table 1). We found no substantial scxa mutant phenotype in cartilage and bone by analysis of Tg(col2a1:amCherry) and alizarin red (AR)/AB staining at 6 and 13 dpf (Supplemental Fig. S4). Thus, lack of Scxa leads both to disruption of tendon and ligament morphology and to defects in the attachment and orientation of cranial muscle fibers.

**Scxa adult fish are viable but show reduced body size and muscle volume, as well as abnormal swim behavior.**

Growth of zebrafish is dependent on feeding rate (52). To determine whether the cranial musculoskeletal defects in scxa mutants have consequences in later life, we...
examined growth of mutant fish and their co-reared same-sex siblings showed that they weigh ~15% less (Fig. 3A). Overall body length was comparable between the different genotypes, suggesting that underfeeding was not the main cause for lower weight (Fig. 3B). Moreover, mutants also show a significantly reduced BMI and standard weight (K, Fulton’s body condition factor), measures that would compensate for any differences in overall growth rate (Fig. 3C, D). We analyzed contrast-enhanced μCT to allow visualization of soft tissue (Fig. 3I). Muscle volume is clearly smaller in mutants (compare Fig. 3I, J). Quantification of muscle volume from μCT scans (Fig. 3K, L) shows that adult scxa mutant fish have significantly lower (~25% less) muscle volume than their cohabiting siblings (Fig. 3L). Nonmuscle volume did not differ between the groups (unpublished data). To test whether adult scxa mutant fish show altered swim behavior, we developed software to track videos of adult fish (Fig. 3N, see Materials and Methods). Both the range of movement (curvature) and instantaneous velocity of scxa mutants were significantly lower than those of co-reared heterozygotes (Fig. 3O, P). Thus, we conclude that fish lacking Scxa are thin and have reduced muscle and swimming ability compared with their siblings.

**Scxa adult fish lack rib mineralization and show bone growth and composition abnormalities**

Because juvenile zebrafish express scxa mRNA near ribs and in other skeletal elements (Fig. 1), and our data from soft-tissue μCT showed missing ribs (Fig. 3J), we sought to investigate in detail the zebrafish scxa mutant skeleton. We performed μCT on 15-mo adult fixed fish (Fig. 4A–D), which revealed a severe lack of rib growth and mineralization (see below) and multiple bony outgrowths from
neural and haemal arches in the mutants (Fig. 4B, D). AR staining showed this phenotype in more detail (Fig. 4F–I and Supplemental Fig. S5C, D). We also used the μCT to test whether vertebral thickness differs between the groups; we extracted the centrum volume through image segmentation. However, no changes were observed, indicating that Scxa is not essential for vertebral bone thickness in zebrafish (Supplemental Fig. S5A, C, D). However, when the bony structure at the same anteroposterior level is calculated to include rib and arches, the mutants showed significant differences (Supplemental Fig. S5A, C, D). We calculated BMD in the lower jaw (dentine), the parietal skull, and vertebral centrae. Jaw BMD is significantly lower in scxa than in its siblings, whereas skull and vertebral BMD were unchanged (Fig. 4E). Thus, scxa mutants have a range of skeletal and cartilaginous abnormalities in both trunk and skull.

The μCT also showed no mineralization in the thoracic ribs in 7/7 scxa−/− homozygous mutants, whereas 7/7 scxa+/− and 4/4 scxa+/- siblings had normal ribs (Fig. 4A–D). AR staining on similar age adults also revealed a lack of mineralization in ribs in 6/6 scxa mutants, whereas 7/7 scxa+/+ showed normal ribs (Fig. 4F–I). Most juvenile mutants stained with AR also lacked mineralization (7 of 9...
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Some unstained, glossy, rib tissue was present (Fig. 4). The analysis of mutants that lacked mineralization revealed that 17 of 22 analyzed siblings). However, close examination of these mutants showed that some ribs were missing and others displayed residual mineralization defect, with uneven mineralization in which some ribs were missing and others displayed residual mineralization (see Fig. 5). No siblings lacked mineralization (0 of 22 analyzed siblings). However, close examination of these mutants revealed that some stained, glossy, rib tissue was present (Fig. 4J), suggesting that Scxa is required for normal mineralization or growth, rather than formation of ribs per se. Indeed, H&E combined with AB staining on adult sections unveiled rib-like structures between the myotomes (Fig. 4K, L). This histologic analysis also revealed an accumulation of fibrous tissue in the intervertebral disk (IVD), suggesting abnormality with the notochord sheath cell layer (Fig. 4M).

**Scxa mutants have abnormal rib mineralization from patterning stage**

To better understand the nature of the rib growth and mineralization defect, we stained juveniles with AR and AB at various stages around the time when ribs are formed. Ribs develop anteriorly to posteriorly beginning at 5.8 mm SL, as seen by AR or Calcein staining (53, 54). At juveniles of 5.8 mm, although no mineralized ribs were detected in any genotype, the arrangement of the vertical myoseptum and the rib region appeared abnormal in the mutants (Fig. 5A; 2 of 2 scxa mutants analyzed). Juveniles reaching SL 6.5 mm had initiated mineralization in the anterior ribs (ribs 5 and 6), but scxa mutants at that stage lack mineralized ribs. However, the Weberian ossicles located anterior to the ribs developed normally (Fig. 5B; 4 of 4 larvae examined). In SL 10.5-mm juveniles, ribs had formed in siblings (Fig. 5C), but scxa mutants either lacked mineralized ribs (Fig. 5C; 3 of 5 mutants analyzed) or showed a milder phenotype with some ribs missing and others small, bent, and twisted (Fig. 5D; 2 of 5 mutants analyzed) as occasionally found in adults (Supplemental Fig. S5E). These defective ribs are reminiscent of the ribs in mutants in which altered collagen composition causes weak and bent ribs that may reflect a history of repeated fracture repair (55). These observations show that scxa mutants have defects in the tendon-like regions between the myotomes where ribs form already at the patterning stage rather than it being a remodeling in response to later events.

**Scxa mutants maintain normal MTJs in the somites**

During development, muscle fibers from each side of the vertical myoseptal somite border align, connect, and secrete ECM proteins that create a distinctive extracellular MTJ structure. Anchorage to this MTJ allows fibers to transmit and withstand contraction forces (reviewed in ref. 56). Many tendon markers are expressed at the MTJ either by the neighboring muscle cells or by fibroblast-like cells proposed to be tenocytes (22). Indeed, by 4 dpf we observed fibroblast-like cells with the matrix protein Tsp4b surrounding their nuclei and with long processes extending into the myosepta (Supplemental Fig. S6A). Given that scxa is expressed early in the MTJ (Fig. 1A and ref. 23), we tested whether defective early MTJ patterning might underlie the rib and muscle defects. In situ hybridization for xirp2a mRNA, a marker for somitic MTJ, for embryos from a scxa+/− incross at 52 hpf showed reduced

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*Analyzed at 4 dpf in embryos from scxa+/kg170, scxb+kg107, or scxa+/kg170;scxb+kg107 incrosses from immunohistochemistry of Tsp4b and MyHC (A.1025).
Figure 3. Lack of Sexa in adults affects body measurements and swim behavior. A–H) Weight, length, BMI, and standard weight comparison between mutants and sibling adult fish from a sexa−/− incross (13 siblings and 7 sexa−/− males, 18 siblings and 6 sexa−/− females, A–D) and a sexb−/− incross (21 siblings and 5 sexb−/− males, 6 siblings and 2 sexb−/− females, E–H). Males and females are presented separately as were found significantly different. I–J) Contrast-enhanced μCTs to show soft tissue of sexa−/− mutant (J–J') and a +/+ sibling (I–I'). Magnified scans show lack of ribs (black arrows) in the mutant. I'–J') Transverse optical sections at indicated positions, where dashed arrows indicate the vertebrae. K) Myotome volume from co-reared similar-length fish are calculated from scans by creating a virtual steak between 2 ribs (red area, see Materials and Methods). L, M) Quantification of muscle volume in sexa−/− adult mutants (L) and sexb−/− (M) and their respective siblings. N–P) Swimming performance was calculated from videos taken from above the tank [schematic drawing in panel (N), see also Supplemental Video and Supplemental Fig. S7], and the range of movement (curvature, M) and instantaneous velocity (N) were calculated as detailed in the Materials and Methods. Two-way ANOVA statistics with Sidak's post hoc tests were performed (A–H). Unpaired t test with Welch's correction (L, M) and 2-way ANOVA (O, P). Significant P values indicated on graphs.
expression in 9 of 9 genotyped scxa mutants (Fig. 6A) but not in siblings (17/17). At 72 hpf, tmrd mRNA, a marker for maturing tenocytes, was also decreased in scxa mutant larvae (9 of 9 genotyped mutants) but not in siblings from a similar cross (Fig. 6B). In contrast, immunohistochemistry for the Tsp4b protein, which controls matrix assembly in the MTJ (25), yielded no detectable change in level or distribution in scxa mutants (Fig. 6 and Supplemental Fig. S6B; 5 of 5 analyzed mutants). We conclude that some but not all MTJ markers are reduced in scxa mutants.
mineralized ribs (black asterisks) and mineralized rib fragments formed normally (arrows in D) indicated juvenile stages.

Figure 5. Scxa is required for rib mineralization and its patterning. AR staining for fish from a scxa+/- incross at the indicated juvenile stages. A) At SL 5.8 mm, increased differential interference contrast (DIC) shows that the junction region between muscle and rib (yellow arrows) is already abnormal (AA'). B) At SL 6.5 mm, the first anterior ribs (r5 and r6) are lacking (asterisks in B', compared with B). C) A severe lack of mineralized ribs (black asterisks) and mineralized rib fragments (white arrowhead) is seen at SL 10.5 mm (C', compared with C). D) In another mutant (D), some ribs are missing (asterisks in D), whereas others are highly fractured and healed (r5–r9 magnified and marked by red arrowheads in D'). Note that r4 is formed normally (arrows in B–D). All scale bars, 100 μm.

To determine whether MTJ defects were secondary to muscle defects at these early stages, scxa mutants were bred into the transgenic Tg(actc1b:egfp)zf13. Somite muscle architecture appeared normal as seen by MyHC, α-actinin, and green fluorescent protein distribution (Fig. 6C and Supplemental Fig. S6D). The ECM protein laminin and the fiber-end–associated cytoskeletal link protein dystrophin also did not distinguish mutants from their siblings (Supplemental Fig. S6D and unpublished data). Thus, early myogenesis appears normal in scxa mutants.

Scxb mutants are viable and show no obvious defects

We also examined scxb homozygous mutants at embryonic, juvenile, and adult stages. During embryonic stages, scxb mutants show neither tendon or muscle craniofacial abnormalities (Fig. 2C and Supplemental Fig. S3G and Table 1) nor difference in AR/AB staining at 6 dpf (unpublished results). Somitic MTJ of scxb mutant embryos also developed normally as seen by normal Tsp4b distribution in the myosepta (5 of 5 mutants and 13 of 13 genotyped sibling larvae), and somitic muscle volume and structure was unchanged (MyHC; Fig. 3M and Supplemental Fig. S6C). Adult scxb mutants are viable and survive in normal numbers (9 of 39; 23% mutants from a heterozygote incross). Measurement of 4- and 12-mo-old scxb mutants showed no significant differences between scxb mutants and siblings in weight, length, BMI, and standard weight (Fig. 4D–F and unpublished results). The skeleton was evaluated by μCT (3 of 3) and AR (4 of 4, Supplemental Fig. S5F), and the mutants were shown to be normal and indistinguishable from siblings (Supplemental Fig. S5F, G and unpublished results). Thus, the lack of Scxb has no detectable effect on the development of the zebrafish musculoskeletal system.

Lack of Scxa and Scxb leads to lethal jaw defects

We generated double mutants from incrosses of scxa+/kg170, scxb+/-. Double mutants were indistinguishable from their siblings before 4 dpf and were viable in normal Mendelian numbers up to early juvenile stages (7 of 138 from total number of genotyped embryos at 6–13 dpf, χ² test P = 0.567). Immunostaining for Tsp4b and MyHC showed no phenotypic abnormality in the MTJ (Fig. 7D compared with Fig. 6C), showing that scxa and scxb combined function is not essential for early somite MTJ development.

In embryos from incrosses of scxa+/kg170;scxb+/-. a subset had abnormal lower jaw, which hung open from 4 dpf, (Fig. 7A, B). This phenotype showed in 22 of 533 embryos (4.1% of all embryos), of which there were scxa+/--;scxb+/-. (16 of 22) and scxa+/--;scxb+/- (6 of 22, ~10% penetrance). No normal embryos (25 genotyped) were double mutant, but 1 embryo was scxa+/--;scxb+/--. The jaw morphology defect caused reduced jaw movement, although they were motile and able to swim (unpublished results). At 13 dpf, scxa+/--;scxb+/- larvae had a similar jaw phenotype and severe growth retardation (3 of 45, 6.6% from all embryos; Fig. 7C), and by 34 dpf, no surviving scxa+/--;scxb+/- fish were obtained (0 of 41, 0% from all embryos). This was confirmed by an incross of scxa+/kg14;scxb+/- that yielded no double mutants (0 of 63, 0% from whole surviving incross, tested at 12 mo of age). Overall, lack of scxa+/--;scxb+/- fish is significant (χ² = 0.008), indicating that they die in the period between 2 and 5 wk of age. scxa+/--;scxb+/- fish were found in expected Mendelian numbers for both crosses.

To further investigate the hanging jaw phenotype, we stained 6 dpf larvae from an incross of scxa+/kg170;scxb+/- for AR/AB (Fig. 7E–G). scxa+/--;scxb+/- show a clear change of position of the Meckel’s cartilage (Fig. 7B, E). The joint at the anterior tip of the Meckel’s cartilage contains many rounded cells that are undifferentiated as opposed to elongated mature cartilage in siblings (compare Fig.
All double mutants (6 of 6) showed a severe reduction in Tsp4b and disorganization in cranial tendons and ligaments, most severely in the mandibulohyoid junction between 4 and 13 dpf (Fig. 7I). Functional muscle has been shown to be required for normal jaw morphology (57, 58). We found that scxa<sup>-/-</sup>;scxb<sup>-/-</sup> larvae had more severe defects in jaw muscles, particularly in the intermandibularis posterior and interhyoideus muscles. A large proportion of the intermandibularis posterior muscle fibers from either side of the midline extended beyond the mandibulohyoid junction, where they normally end, until their displaced meeting, whereas others appeared to change angle and also be part of the interhyoideus muscle (compare Fig. 7H, I and Table 1). Thus, lack of both Scx genes in zebrafish cause substantial tendon, muscle, and cartilage defects that result in paralysis of the jaw with lethal consequences.

**DISCUSSION**

The findings described here provide genetic demonstration of 3 major points. Firstly, that scxa is required for correct skeletal development, including rib growth and mineralization, morphology of vertebral arches, normal swimming behavior, and trunk muscle composition. Secondly, scxa mutation leads to embryonic defects in cranial tendon formation and muscle misalignment. Thirdly, whereas loss of scxb alone does not lead to severe phenotypes, scxb is required in the absence of scxa because loss of both leads to lethal jaw paralysis. From this we conclude that scxa and scxb have overlapping functions in tendon formation.

**scxa and scxb expression and function during embryonic stages**

In addition to confirming the expression of scxa in the craniofacial tendon precursors and the MTJ (23, 24), we demonstrate that scxa mRNA is expressed in the full extent of the vertical myosepta at juvenile stages. Loss of Scxa affects the structure and shape of various tendons, most notably ones connecting the jaw muscles to the jaw. This leads to abnormal connections, ectopic growth, and misalignment of fibers of the craniofacial musculature. scxa mutants are viable, however, surviving to adulthood despite a range of phenotypes. Although craniofacial cartilage and bone appear normal in embryos, our μCT data show significantly lower BMD in jaws of adult scxa mutants. The jaw bones mineralize much later than in our larval analyses. This may reflect changes to muscle activity...
that is due to the above tendon and muscle phenotypes leading to changes in the mechanical load of certain areas. Mechanical loading has been previously shown in humans and fish to affect bone properties, specifically BMD (59, 60). Mechanical loading has been previously shown in humans leading to changes in the mechanical load of certain areas.

Our data show that scx function in tenoblasts contributes to the maturation of cranial tendons. None of the described mouse loss-of-function models reported head phenotypes (11, 14). However, Scx is expressed in pharyngeal arches and facial tendons of mouse embryos (8–10), and other mutations affecting mouse tongue muscle tendons resulted in tongue muscle abnormalities and dysmorphogenesis (63, 64). Facial tendons in mice, chicks, and zebrafish have a common origin from cranial neural crest (63, 64). Similarly, we show that tendon malformation can affect the muscle and the morphogenesis of the jaw, indicating synergy in development of the cranial musculoskeletal system. Some of the defects are reminiscent of the zebrafish cyp26b1 mutant tendon phenotypes (24). In cyp26b1 mutants, tenoblasts fail to condense into nascent scxa-expressing tendons, affecting muscle projection and misdirecting it. We, and others, have previously shown that periods of larval immobility affect the formation of jaw skeletal elements and joints (57, 58, 61, 62). Similarly, we show that tendon malformation can affect the muscle and the morphogenesis of the jaw, indicating synergy in development of the cranial musculoskeletal system. Some of the defects are reminiscent of the zebrafish cyp26b1 mutant tendon phenotypes (24). In cyp26b1 mutants, tenoblasts fail to condense into nascent scxa-expressing tendons, affecting muscle projection and misdirecting it. Our data show that scx function in tenoblasts contributes to the maturation of cranial tendons. None of the described mouse loss-of-function models reported head phenotypes (11, 14). However, Scx is expressed in pharyngeal arches and facial tendons of mouse embryos (8–10), and other mutations affecting mouse tongue muscle tendons resulted in tongue muscle abnormalities and dysmorphogenesis (63, 64). Facial tendons in mice, chicks, and zebrafish have a common origin from cranial neural crest cells (8, 23, 27). They are also similar in function, although different fish, birds, and mammals have varied feeding strategies and mandibular morphology (65, 66) such that cranial phenotypes stemming from tendon defects may differ between species.

Figure 7. Scxa;scxb double mutants have a jaw phenotype and severe musculoskeletal defects. A–C) Live transmitted light and red fluorescent images in lateral view, anterior to left of genotyped scxa-/-;scxb-/- double mutants (A–C, shown is scxa-/- scxb-/-). Mutants show a hanging open jaw. The col2a1:mCherry transgene (B) shows the dropping Meckel’s cartilage (mc). At 13 dpf, fish are much smaller than siblings (whole-fish insets in C). D) Confocal stacks of immunodetection of MyHC (A4.1025) and Tsp4b in 4 dpf embryos of scxa-/- scxb-/- showing normal distribution of Tsp4b and normal muscle structure (compare with Fig. 6C). E–G) AB/AR staining for cartilage and bone for scxa-/- scxb-/- (E–G) and sibling from the same cross (E–G) shown in lateral (E) and ventral (F, G) views that show the hanging jaw phenotype. The magnified area from mc shows many less differentiated rounded cells at its most anterior tip, near the joint (arrow, G) compared with siblings (whole-fish inset in G).
The role that Scxa and Scxb has in the somitic MTJs seems to be limited at embryonic stages. We detected mild down-regulation of tendon markers and downstream targets, such as tnmd and collagens, which is comparable with mammals and birds (11–14). However, we found no evidence for down-regulation of key components of the ECM, such as thbs4b and laminin and functional embryonic phenotype, neither did we detect damaged muscle, loss of sarcomeric structure, or somitic boundary compromise in either the single or double mutants at larval stages. This contrasts with the phenotype observed upon loss of the dystrophin-associated glycoprotein complex components (reviewed in refs. 56, 67). This may reflect low levels of expression of scxa and scxb at embryonic stages, but other genes, likely in the fibers themselves, could control these ECM components at the somitic MTJs. It suggests that the muscle-dependent-dystrophin-associated glycoprotein complex and integrin complexes are independent from tendon development and are sufficient to connect the somitic muscle blocks even when the tendons are impaired, thus preventing damage at least during embryonic stages.

**Scleraxis function in rib mineralization**

Our data show that Scxa is strongly expressed in the intramuscular tendons adjacent to the developing ribs and is essential for rib growth and mineralization. In scxa mutants, we see severe defects in rib structure, such that mutants lack mineralized ribs. The tissue appears to become fibrous rather than bony. scxa mutants display changes to the structure of the vertebral arches, which are wide and irregular despite the normal myotome pattern seen at larval stages.

Many studies have indicated that all parts of the ribs are derived from the sclerotome compartment of the somites (68–71), whereas other studies have suggested that the ribs can be divided into 3 regions and that rib development also depends on the dermomyotome (72, 73). In addition, manipulations in chicks, which led to loss of Scx expression, as well as separating the ectoderm physically from somites or changes to MKP3 levels affecting ERK signaling strength, resulted in defective distal rib development (74, 75). Although in mice Scx is expressed in rib primordia (8, 11, 13), the ribs and the tendons that connect them to the intercostal muscles were unaffected in 1 Scx−/− allele (11), and the rib cage was decreased in size for the Scxcre/cre allele (14). Conditional inactivation of Sox9 in Scxcre/cre Sox9* cells in ScxCre;Sox9flox/flox mice, caused a loss of all but the proximal rib cage (76). Mammalian tendon-bone attachments, including the patella, deltoid tuberosity, olecranon, and other eminences, express both Sox9 and Scx (16, 76, 77). It is unclear if scxa is expressed in rib precursors in fish and whether it has a similar role in mineralization of the ribs as in mineralization of these mammalian eminences (11, 14, 16, 17, 76, 77). Function may also be maintained in the distal parts of the ribs in some amniotes. Ribs protect internal organs in fish and amniotes. The development of lungs and the requirement to protect the respiratory system with a strong bony rib cage may have shifted rib development to be more dependent on Sox9 in land-living animals, and so affecting rib composition and strength.

Interestingly, we found that zebrafish lacking rib bone are viable, but their swimming performance is altered. This may indicate that the ribs play a mechanical role in swimming. Indeed, some studies have highlighted correlations in intramuscular ossification in fish that differ in their swimming modes (78, 79). The reduced volume of trunk musculature and body weight in scxa adult mutants could be linked to the altered swim behavior seen in the mutants. This, in turn, could be due to musculoskeletal attachments to the ribs and other intramuscular bones between the myomeres that are not capable of transmitting the full force from muscle contractions. Alternatively, altered intramuscular attachments in the trunk or abnormal fin attachments could alter both swim performance and preclude rib development. Although scxa;scxb double mutants are smaller in length and have paralyzed jaw, both linked to reduced feeding, scxa mutants have normal standard length, and their jaw movement seemed normal. However, we cannot rule out the possibility that reduced feeding affects the lower weight of scxa mutants, which in turn may be due to the mutants being outcompeted by their siblings.

Both our expression and functional data points to a greater role for scxa than for scxb in both head and trunk development, especially at juvenile stages. This likely reflects the high synteny of scxa, but not scxb, to the mammalian orthologs, likely keeping ancestral regulatory elements intact. However, Scb protein is very similar to Sca protein: a 70.8% identity between the 2 proteins, almost identical bHLH domain (Supplemental Fig. S2A, B), overlapping expression, and the ability to replace the function of the other to some extent.

In summary, we have shown that Scx has an essential role in the normal development of the musculoskeletal system in fish. Its essential function in differentiation and maturation of tendons, and in ossification of skeletal elements that express Sox9 and Scx, are conserved with other vertebrates. Zebrafish are thus a useful model to study the close relationship of muscle, tendon, and bone in development and disease of joints.

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**AUTHOR CONTRIBUTIONS**

E. Kague, E. A. Lawrence, S. Cross, E. Martin-Silverstone, C. L. Hammond, and Y. Hinits performed and analyzed experiments and wrote the manuscript; S. M. Hughes and...
Y. Hnits conceived the study; and C. L. Hammond and Y. Hnits managed the workplan.

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