Evolution of a Core Gene Network for Skeletogenesis in Chordates

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Abstract

The skeleton is one of the most important features for the reconstruction of vertebrate phylogeny but few data are available to understand its molecular origin. In mammals the Runx genes are central regulators of skeletogenesis. Runx2 was shown to be essential for osteoblast differentiation, tooth development, and bone formation. Both Runx2 and Runx3 are essential for chondrocyte maturation. Furthermore, Runx2 directly regulates Indian hedgehog expression, a master coordinator of skeletal development. To clarify the correlation of Runx gene evolution and the emergence of cartilage and bone in vertebrates, we cloned the Runx genes from hagfish as representative of jawless fish (MgRunxA, MgRunxB) and from dogfish as representative of jawed cartilaginous fish (ScRunx1–3). According to our phylogenetic reconstruction the stem species of chordates harboured a single Runx gene and thereafter Runx locus duplications occurred during early vertebrate evolution. All newly isolated Runx genes were expressed in cartilage according to quantitative PCR. In situ hybridisation confirmed high MgRunxA expression in hard cartilage of hagfish. In dogfish ScRunx2 and ScRunx3 were expressed in embryonal cartilage whereas all three Runx genes were detected in teeth and placoid scales. In cephalochordates (lancelets) Runx, Hedgehog and SoxE were strongly expressed in the gill bars and expression of Runx and Hedgehog was found in endo- as well as ectodermal cells. Furthermore we demonstrate that the lancelet Runx protein binds to Runx binding sites in the lancelet Hedgehog promoter and regulates its activity. Together, these results suggest that Runx and Hedgehog were part of a core gene network for cartilage formation, which was already active in the gill bars of the common ancestor of cephalochordates and vertebrates and diversified after Runx duplications had occurred during vertebrate evolution. The similarities in expression patterns of Runx genes support the view that teeth and placoid scales evolved from a homologous developmental module.

Introduction

The skeleton is one of the hallmark features of vertebrates and has been widely used over the past decades for phylogenetic analyses [1]. However, little is known about its molecular evolution.

Descriptive data are available for the matrix proteins produced by the cells that constitute the skeleton in jawless vertebrates (epitomized by hagfish and lampreys, collectively termed agnathans). Beside species specific proteins [2] they possess little is known about its molecular evolution.

Abstract data are available for the matrix proteins produced over the past decades for phylogenetic analyses [1]. However, little is known about its molecular evolution.

From the three members of the Runx family Runx2 is most likely responsible for the secretion of an acellular cartilage. Such an endodermal secretion was postulated to be primarily the ancestral mode of making pharyngeal cartilage in deuterostomes [5].

Up to now no Runx gene expression has been described in skeletal elements of lancelets, agnathans and jawed cartilaginous fish in spite of the fact that Runx transcription factors (Runx1–3 synonyms: Ami1–3/Cbfa1–3/Pebp2a–c) are central regulators of skeletal development in higher vertebrates [6,7]. They are characterized by a highly conserved DNA binding Runx domain and the presence of two promoters [8]. Each Runx gene has two isoforms with different N-termini starting with a MASNS-like motif under the distal P1 promoter and a MRIPV sequence under the proximal Promoter P2. Furthermore the 3' end has a conserved WVRP-fmotif [8]. Runx2 is indispensable for osteogenesis as mice bearing a homozygous mutation in Runx2 completely lack bone [7], and Runx2 is together with Runx3 essential for cartilage differentiation [9,10]. Furthermore Runx2 directly regulates the key signaling molecule Indian hedgehog (Ihh), which coordinates cartilage differentiation, endochondral ossification and limb outgrowth [10]. From the three members belonging to the mammalian Hedgehog (Hh) family (Ihh, Sonic hedgehog,
Important molecular mechanisms underlying mammalian skeletogenesis have been described but knowledge about the evolutionary origin of these gene networks is limited. The Runx gene family (Runx1–3) is of extraordinary importance for skeletogenesis. Runx2 deficient mice completely lack bone. Runx2 and Runx3 are essential for cartilage development and Runx2 regulates the key factor Indian hedgehog, which coordinates skeletogenesis. Here, we reconstructed Run gene evolution in correlation to skeletal evolution. By analyzing lancelets, one of the closest living relatives of vertebrates, we revealed that the single Run and Hedgehog family founder genes were co-expressed in primitive skeletal elements of the chordate stem species. Interestingly, at this stage the Run and Hedgehog pathways were already directly linked to one another. Furthermore we isolated two Run genes from a representative of jawless cartilaginous fish (hagfish) and three Run genes from jawed cartilaginous fish (dogfish) which were all expressed in cartilage. The dogfish Run genes were also found in teeth and placoid scales. This study suggests that Run genes were involved in all ancient processes of chordate skeletogenesis. Furthermore the analysis supports the theory that most likely the gut was the tissue that originally secreted an acellular gill gut skeleton in the chordate ancestor.

Desert hedgehog also Sonic hedgehog (Shh) signaling is influenced by Runx2 during tooth morphogenesis [11]. Runx2 haploinsufficiency causes the human bone disease cleidocranial dysplasia, further substantiating its importance for skeletal development [12]. Importantly, all three mammalian Run genes are expressed in cartilage and have been shown to play a role in the formation and differentiation of skeletal elements [6,10,13]. Furthermore, all Run genes in the mouse are involved in tooth formation [14].

In contrast to the extensively studied Hox genes, which are important for patterning, Run genes are essential for features that represent evolutionary innovations of vertebrates such as bone [1]. Such innovations result from tinkering with existing processes, from the flexibility that arises from modifications to existing gene networks, and from selective advantage provided by gene duplications or modifications [15]. As simply as this theory explains an important evolutionary process, it is difficult to functionally analyze how the genetic networks underlying innovations like the vertebrate skeleton evolved. Based on the central role of Run genes for skeletogenesis in higher vertebrates we hypothesized that these genes played a role in the evolution of cartilage, bone and teeth and thus might be instrumental to understand skeletal evolution in chordates. We therefore analyzed number and expression of Run genes in hagfish (Myxine glutinosa) as a representative of jawless vertebrates, in dogfish (Scyliorhinus canicula) as a representative of cartilaginous fish and lancelets (Branchiostoma lanceolatum and B. floridae) as representatives of cephalochordates to reconstruct if Run genes were already expressed in the developing skeleton of the chordate, vertebrate and jawed vertebrate stem species. In addition, we tested if Run and Hh are co-expressed in lancelets and if a functional interaction between the Run and Hh pathways might have evolved before the cellular cartilage of vertebrates evolved.

In this study we show that the stem species of chordates harboured a single Run gene, whereas three Run genes were present before the emergence of gnathostomes. Run genes are expressed in developing cartilage, teeth and placoid scales of cartilaginous fish and cartilage of jawless vertebrates. In adult lancelets the Run gene is expressed together with Hh, in the endo- and ectoderm of the gill bars. Furthermore, we demonstrate that the lancelet Run protein can directly bind to and activate the lancelet Hh promoter. This suggests that beside SoxE and fibrillar collagen two other key factors for vertebrate skeletogenesis (Run and Hh) were part of an ancient gene network for skeletogenesis in the gill gut stabilizing the gill bars of the common ancestor of vertebrates and lancelets approximately 700 million years ago. Our finding that the gut is an ancient Run expression domain of deuterostomes is in accordance with the hypothesis that endodermal secretion was the ancestral mode of making pharyngeal cartilage [5].

Results

Isolation of hagfish and dogfish Run genes

We used a PCR-based approach using cDNA as well as genomic DNA to identify Run genes in lower vertebrates. This led to the detection of two Run genes in hagfish (MgRunx2, MgRunx3) and three Run genes in dogfish (ScRunx1–3). All of these newly detected Run genes had a 3’ end with the characteristic VWRPY-motif. The two different 5’ ends of the Run genes amplified from embryonal dogfish cDNA were homologous to the 5’ mammalian promoter variant-1 (MASSN-like) and variant-2 (MRIP-like) motifs, respectively. In the two hagfish Run genes amplified from adult hagfish cDNA only a single 5’ gene end was detected. According to our Blast searches against the Ensembl pre-genome sequences of lamprey (Petromyzon marinus) the two hagfish 5’ ends represent most likely the promoter variant 2. Because of the unavailability of hagfish embryos it could not be clarified if two Run gene promoter 1 variants are expressed during early hagfish development.

Blast searches in whole genome databases (NCBI, JGI, Ensembl) revealed that there are most likely two Run genes in the lamprey genome, and one Run gene in cnidarians (Nematostella vectensis), nematodes (Caenorhabditis elegans), cephalochordates (B. floridana), and tunicates (Ciona intestinalis, Oikopleura dioica) [16,17]. We detected two Run genes in sea urchin (Stronglyocentrotus purpuratus) [18,19], which were located on the same genomic contig, two partial Run genes in skate (Raja eglanteria) [20], three Run genes in mammals [6,7] and four in pufferfish (Takifugu rubripes) [21,22] and also four in zebrafish (Danio rerio) including a duplicated Run2 gene [23]. In chicken (Gallus gallus) three Run genes were found. An alignment of all newly detected Run genes together with other deuterostome Run genes is provided as supporting information (Figure S1) and the GeneBank accession numbers are given in the footnote.

Conserved synteny of Run and the chloride intracellular channel (Clic) genes in human, chicken and tunicate genomes

Comparable to the human Run loci [24], the three orthologous chicken Run genes are followed by a Clic gene on the complementary strand. The chicken Runx1 on chromosome 1 is followed by a Clic6 homologous gene, the chicken Runx2 on chromosome 3 by a Clic3 homologous gene and the chicken Runx3 on chromosome 23 is followed by a Clic4 homologous gene. In lancelet the Run and Clic genes are located on different scaffolds [JGI assembly vers 1.0]. However, in the genome of the tunicate C. intestinalis a Clic homologous gene was found in proximity to Run on chr_12q (JGI, Assembly vers 2.0). This strongly suggests that the entire Run locus was triplicated during the evolution of chordates.

The last common ancestor of chordates harboured a single Run gene

Our phylogenetic analysis (Figure 1) suggests that the stem species of chordates harboured a single Run gene, whereas the last...
common ancestor of jawed vertebrates harboured three Runx genes. In addition, our results indicate that the English Sea Runx1–3 genes are orthologous to the human Runx1–3 genes. In contrast to this, the two hagfish Runx genes did not cluster with any of the three paralogous Runx genes from higher vertebrates. As outlined in Figure 2, several lineage-specific Runx gene duplications have occurred: (a) in the sea urchin lineage, (b) in the stem species of bony fish and (c) probably also in hagfish. But there is a need for further data e.g. from whole genome comparison, to determine if the two hagfish Runx genes are a result of a Runx gene duplication in the stem species of vertebrates or evolved by a separate gene duplication event in the hagfish lineage.

Figure 1: Phylogenetic tree (Bayesian inference) of chordate Runx genes. Numbers refer to branch support (Bayesian posterior probability). Sea urchin Runx genes were used to root the tree. Branch length reflects the number of substitutions per alignment site (compare scale bar).
To determine a possible role for Runt genes in the skeleton we asked the question if Runt genes are expressed in skeletal elements of hagfish. Using quantitative Reverse Transcriptase PCR (qRT-PCR) from dissected tissues we found that the MgRunxA gene had its highest expression in hard cartilage, followed by the gill region and soft cartilage (Figure 3). Compared to the MgRunxA gene the MgRunxB gene was only weakly expressed with the strongest expression in the gill region. In situ hybridizations confirmed the high expression of MgRunxA in hard cartilage (Figure 3B and 3C).

In adult dogfish the Runt genes show ubiquitous expression but it is noteworthy that all Runt genes had their third highest expression in the gill gut cartilage. For all three dogfish Runt genes the highest expression was found in the skin (Figure 4). We performed in situ hybridization to characterize the distribution of Runt expression in the skin (Figure 4A–4C). All three Runt genes were expressed in the placoid scales in the skin of dogfish embryos. ScRunx1 and ScRunx3 were expressed in the basal epidermis cells of the stratum germinativum, whereas ScRunx2 was found at the site where later the basal plate will develop. Based on the similarities between scales and teeth we performed expression analysis of Runt genes in the developing teeth of dogfish embryos. In the developing teeth

Figure 2. Overview of the Runt gene evolution in chordates. The stepwise evolution of cartilage and bone and the most likely time intervals of Runt gene duplications (Dup) are indicated. The position of tunicates is contentious [31] which is indicated by a dashed line. In this context it is of interest that pre-neural crest cells have been observed in tunicates [60].

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Figure 3. Analysis of hagfish MgRunxA and -B expression in different tissues of adult animals. Quantification of MgRunxA and -B expression by qRT-PCR (A). Whereas MgRunxB was only weakly expressed in all tissues analyzed, MgRunxA showed a strong expression in calcified cartilage gills and soft cartilage. Expression of MgRunxA was also detected by radioactive in situ hybridisation in hard cartilage tissue (B, C). Insert of (B) is shown at higher magnification in (C) displaying the silver grains of the autoradiography emulsion indicating MgRunxA expression. B: Brain, C-h: Hard cartilage, C-s: Soft cartilage, Cho: Chorda, G: Gills, Gb: Gall bladder, G-a: Anterior gut, G-m: Midgut, G-h: Hindgut, H: Heart, L: Liver, Mu: Muscle, Sk: Skin.

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Expression of Runt during lancelet (*B. floridiae*) development in the notochord, gut and neural tube

To be able to reconstruct the Runt expression domains in the chordate stem species and to see if Runt was expressed in ancient skeletal elements such as the notochord, we analyzed Runt gene expression in lancelets, the putative sistergroup of vertebrates. Using whole mount in situ hybridization of early developmental stages (early and late gastrula) a diffuse Runt staining, indicating a maternal Runt expression, was detected, comparable to the description of maternal *Runx1, −2b*, and −3 expression in zebrafish. [25–27]. Two different probes were used, corresponding to the Runt gene variant starting with exon 1 (transcribed from the distal promoter P1) and the Runt gene variant starting with exon 2 (transcribed from the proximal promoter P2). These two probes showed overlapping staining patterns (Figure 7).

The Runt gene variant P1 was expressed at the 8 somite stage (16 h) in the posterior part of the gut, the notochord and the developing neural tube (Figure 7A). At 26 h Runt expression can be predominantly seen in the middle part of the notochord, the midgut and foregut (Figure 7C). An inconsistent staining pattern was also detected at this stage in about 50% of the larvae immediately below the preoral pit (Figure 7C insert). At 33 h the larvae showed persistent expression of the *Runt* exon 1 variant in the notochord and neural tube, but also in the midgut region (Figure 7E).

The Runt gene variant P2 was exclusively expressed in the hindgut at 16 h (Figure 7B). At 26 h the expression domain extended throughout the entire gut and a signal was also found in a confined region of the foregut (Figure 7D). At 33 h Runt expression was found throughout the entire larvae with the most intense signals in the tailbud and in the anterior gut region (Figure 7F).

**Discussion**

**Runt gene evolution in chordates**

In order to get insight into the molecular mechanisms underlying the evolution of the skeleton we analyzed the evolution of the Runt gene family in various representative species. Runt genes are important regulators of neurogenesis and hematopoiesis [29,30] and they are essential for mammalian skeletogenesis [7,10]. Our analysis revealed that the stem species of chordates harboured most likely only a single Runt gene and as outlined in Figure 2 independent Runt duplications occurred in the clades of sea urchin (*SpRunt1, SpRunt2*), and bony fish (duplication of *Runx2*).
A chordate stem species with only a single Runt gene is the most parsimonious assumption since the genomes of cnidarians, nematodes, cephalochordates and tunicates harbour also only a single Runt gene. The presence of two Runt genes in sea urchin is most likely a result of a tandem duplication, as we found both genes on a single genomic contig and they cluster together in our phylogenetic analysis (Figure 1). It was recently postulated that tunicates and not cephalochordates are the sistergroup of vertebrates [31,32]. Focusing on our aim to reconstruct the framework for Runt gene evolution, both alternative taxonomic

Figure 5. ScRunx1–3 expression analysis by in situ hybridization in placoid scale (A–C) and tooth development (D–F). Bright field is given on top, dark field below. ScRunx1 (A, D) and –3 (C, F) are expressed in the basal epidermis cells of the stratum germinativum, which forms the enamel organ, whereas ScRunx2 (B, E) is found at the site of the developing basal plate. These expression patterns were identical in teeth and placoid scales. (G) Scheme of Runt expression in placoid scales and teeth with overlapping expression of ScRunx1 and –3 in the stratum germinativum (light grey) and ScRunx2 in the developing basal plate (dark grey). Dotted lines represent section planes of transverse sections in (A, C–F). Section in (B) is a longitudinal section.

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positions of tunicates and lancelets would be consistent with our hypothesis that the stem species of chordates harboured only a single Runt gene.

In accordance with the evidence for at least one genome wide duplication, 350 to 650 million years ago [33,34] we detected in dogfish (as a representative of the jawed cartilaginous fish) three Runt genes, orthologous to Amniota Runx1, –2 and –3 genes, whereas only two Runt genes (MgRunxA and MgRunxB) were identified in hagfish (as a representative of jawless vertebrates). The phylogenetic tree (Figure 1) identifies the MgRunxA and MgRunxB genes as being closely related to the Runx1–3 genes. However, it is unknown if these evolved by a hagfish specific duplication or by a Runt gene duplication in the stem species of vertebrates. The phylogenetic analysis of the divergent Runt genes does not give satisfactory high support and a comparative analysis of the Runt gene loci will be needed to resolve this problem.

In the pufferfish (T. rubripes) genome, an enigmatic fourth Runt domain gene (FrRunt) was detected in addition to the orthologs of the Runx1, –2 and –3 genes, which appeared to represent either a pufferfish-specific fast evolving derivative of Runx2 or a direct descendant of the ancestral chordate Runt gene [22]. According to our data it is unlikely that the FrRunt gene represents a direct descendant of the ancestral chordate Runt gene which evolved in parallel with the vertebrate Runt genes [22] since we did not detect a FrRunt orthologous gene in tunicates, lancelets, hagfish and dogfish. Instead our phylogenetic analysis (Figure 1) and a comparison of the genomic environment of the FrRunt locus with the genomes of other bony fish (supporting information Figure S2).

Figure 6. Expression of ScRunx2 and –3 in developing dogfish cartilage. Expression of ScRunx2 was detected in developing cranial and gill bar cartilage (A) and in the proximal cartilage elements of the pectoral fin (B). Expression of ScRunx3 was detected in developing visceral cartilage (C). Cc: cranial cartilage, gb: gill gut cartilage, fc: fin cartilage.

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Figure 7. Runt gene expression in lancelet larvae (B. floridæ). Anterior site is located to the left and the dorsal site towards the top. Whole mount in situ hybridization at stages of 16 h (A, B), 26 h (C, D) and 33 h (E, F), A), C) and E) Runt gene exon 1 variant. B), D) and F) Runt gene exon 2 variant. Note that the primary pigment spot, indicated by an arrow, lays in the nerve chord and does not represent a Runt expression domain. An: Anterior notochord, Nt: Neural tube, Nc: Notochord, Hg: Hindgut, Pp: Primary pigment spot, Ppi: Preoral pit.

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suggests that the FrRunt gene represents a fast evolving Runx2 orthologous gene. Such an accelerated evolution within duplicated genes is a common phenomenon [35].

Our findings that beside the human [24] also the chick and tunicate (C. intestinalis) Runx genes are followed by Clx genes together with the evidence that the FrRunt gene represents a fast
evolving Runx2 gene suggests that during chordate evolution the entire Runx locus wastriplicated.

Runx genes and the evolution of cartilage and bone in vertebrates

Cartilage has evolved multiple times in metazoa [1]. Here we focus on the vertebrate cellular cartilage expressing Col2α1 as the predominant matrix protein. Differentiation of this cartilage is regulated by a molecular network including Sox9, a transcription factor that directly regulates Col2α1 expression [36]. Furthermore Sox9 is a target of PTH related protein (PTHrP) that controls chondrocyte differentiation through a negative feedback loop with Indian hedgehog (Ihh). Runx2 in turn directly regulates Ihh [10]. Besides Runx2 also Runx1 and Runx3 genes are expressed during murine and zebrafish cartilage formation. However Runx2 and Runx3 appear to be the most important Runx genes for skeletogenesis [6,23].

In hagfish soft and hard cartilage can be distinguished [2] and a Col2α1-homologous protein is expressed only in soft cartilage [4]. It is unknown if a protein homologous to Col2α1 is expressed in hard cartilage as it is the case in mammalian bone. As shown in Figure 3 the hagfish MgRunxB gene is only weakly expressed in both types of cartilage. However, the MgRunxA gene had its strongest expression in hard cartilage and its third highest expression in soft cartilage (Figure 3A). We only analyzed tissues from adult hagfish of medium size (30–40 cm). The fact that hagfish grow up to a length of 80 cm suggests that the Runx gene expression in hagfish cartilage is also of importance for the growth of the skeleton.

The view that Runx genes have a conserved functional role in skeletogenesis is also supported by our finding of Runx gene expression in the developing cartilage of dogfish. We detected a strong expression in visceral cartilage for all three dogfish Runx genes by qRT-PCR (Figure 4). Furthermore we performed in situ hybridizations on dogfish embryos and found ScRunx2 to be expressed in the cartilage of the fin and together with ScRunx3 in the gill gut cartilage (Figure 6).

In lamprey (another representative of jawless vertebrates) the Col2α1 gene is expressed in cartilage along with Sox9 and PTHrP, indicating that they were already a part of the chordrogenic gene repertoire in early vertebrate evolution [3]. Our finding of dogfish and hagfish Runx expression in cartilage together with the well-known role of Runx genes in skeletogenesis, suggests that Runx genes can now be considered to be a part of the ancient molecular machinery for cartilage formation in the stem species of vertebrates.

ScRunx1–3 gene expression in teeth and placoid scales

Placoid scales are small conical structures in the skin of cartilaginous fish. We found that all three dogfish Runx genes are expressed in the developing placoid scales (Figure 5A–5C). Interestingly, the basal plate of scales and teeth is initiated by osteoblasts which continue to secrete bone matrix in a basal direction, while slightly later, the odontoblasts secrete dentine on the pulpar side on the basal plate [37]. Since ScRunx2 is expressed in the developing basal plate it is an interesting speculation that the expression of Runx2 at this site might reflect the origin of bone as a dermal tissue in early vertebrate evolution. The dermoskeleton is the first to show mineralization in vertebrate phylogeny [38]. This mineralized dermoskeleton was composed of odontodes (dermal “teeth”) supported by extensively developed bone, imposing mineralization upon the collagenous layer of the dermis [38].

In placoid scales as well as in the developing teeth ScRunx1 and ScRunx3 were expressed in the stratum germinativum, whereas ScRunx2 was found at the site where later the basal plate will develop (Figure 5A–5F). In mammals teeth develop as epithelial appendages in which sequential and reciprocal interaction between the ectoderm and underlying neural crest derived mesenchyme constitute a central developmental mechanism [1,14]. The dental epithelial cells differentiate into ameloblasts and mesenchymal cells into odontoblasts, secreting the matrices enamel, and dentin respectively [1]. Runx2 and Runx3 expression is confined to mesenchymal tissues, whereas Runx1 was found to be restricted to epithelia [14].

According to a classical view teeth evolved secondarily from skin denticles moving into the mouth (reviewed in [39]). However, this model was recently challenged by the proposal that sets of denticles on the pharyngeal (gill) arches and not external denticles were the precursors of the organized tooth families [39]. This alternative theory was based on the observations of homologous arrays of denticle whorls occurring within the pharyngeal region of jawless fish such as the theldont Loganellia [40]. In this model the endoderm played an important role in the patterning process involved in the production of denticles on the postbranchial lamina [39]. It was assumed that the denticles on the postbranchial...
lamina have been formed in the presence of an inductive endoderm as one part of the internal visceral skeleton. This would be remarkably different to the development of external denticles, which are only under the influence of an inductive ectoderm [39].

Our Runt expression pattern supports the classical view that teeth and placoid scales have a common evolutionary origin, at least on the level of the molecular pathway underlying their development. In other words, the hypothesis that teeth and placoid scales evolved from a common developmental module, which might have been shifted and extended in its expression topology [41] is supported by the striking similarity of the Runt expression patterns in teeth and placoid scales.

Conservation of molecular pathways in skeletogenesis

The gut appears to be an ancient expression domain of Runt. This expression in the chordate stem species can be reconstructed as Runt genes are expressed in the gut in representatives of the outgroup (sea urchins, nematode [16,17] and the lancelet (this study, Figures 7 and 8). The Runt expression in the gill bars, structures that stabilize the gill gut, might be linked to the later role of Runt genes in the evolution of the pharyngeal skeleton. In zebrafish Runx3 was shown to promote cartilage formation via the endodermal expression of Runx3 in pharyngeal pouch cells [23].

However, in vertebrates most of the branchial arch cartilage, the cranial bone forming cells (ostoblasts), as well as the cells that deposit dentin (odontoblasts) are derived from the neural crest [42]. It was previously proposed that the neural crest acquired chondrogenic ability by recruiting proto-chondrogenic gene programs from the notochord, neural tube and gill gut [4,5,28,43–45] Strikingly, we found high Hh expression together with high Runt expression in exactly these three sites indicating that the described interaction between the Runt and Hh pathways is of relevance for chordate cartilage evolution.

Whereas the homology of the gill gut in lancelets and vertebrates is well established [28] little is known about the molecular machinery necessary for development and maintenance of the skeletal-like structures of the pharyngeal gill slits in lancelets. The gill bars are stabilized by 15 nm thick filaments aligned parallel to the long axis of the rods, and are covered by a single layered epithelium, that can be morphologically distinguished into atrial, lateral and pharyngeal epithelium [46]. Gill bars gave a positive signal when stained with an antibody against type II collagen [29] indicating a cartilage-like structure, which appears to be acellular.

To get deeper insights into the molecular machinery underlying the early evolution of the skeleton we analyzed Runx and SoxE gene expression in adult lancelets. Our analyses revealed that both genes were highly expressed in the gill bar region (Figure 8). Furthermore our in situ hybridization results revealed that the lancelet Runt gene is expressed in atrial, lateral, and pharyngeal epithelium of ectodermal and endodermal origin (Figure 8D and 8E), but not in the mesodermal coelomic cells of the primary gill bars. It has recently been reported that the lancelet gills contains lymphocyte-like cells most likely located between the cells of the lateral and pharyngeal epithelia [47]. We cannot resolve these cells in our in situ hybridizations and thus cannot detect if Runt is expressed in these cells of the gill bars (Figure 8D and 8E). The finding of endodermal Runt expression supports the model in which endodermal secretion was the ancestral mode of making cartilage [3]. Since in deuterostomes the endoderm is a plesiomorphic Runt expression domain, Runt is likely to be present also in the endoderm of the gill gut in hemichordates.

Other crucial genes for mammalian skeletogenesis are Ihh and Shh. For Ihh a direct regulation by Runx2 has been shown and Runx2 influences Shh signaling in tooth development [10,11]. Furthermore, Runt and Ihh genes are coexpressed during skeletogenesis in zebrafish [23,25,48]. We observed Runt expression in the midgut and foregut of lancelet larvae, similar to a recent study [49]. The exon 1 variant, however, showed additional expression in the notochord and neural tube (Figure 7A, 7C, and 7E). These expression domains were still detected in adult lancelets together with high Hh expression (Figure 8A and 8B). The observation that the single Runt and Hh genes of lancelets are coexpressed in the notochord, neural tube and in the adult lancelet gill gut (Figures 7 and 8 and reference [50]) prompted us to investigate if also the lancelet Runt protein might regulate lancelet Hh gene expression. In our Hh promoter studies the lancelet Runt protein bound directly to Runt binding sites in the lancelet Hh promoter and regulated the reporter gene driven by this promoter (Figure 9). The highest Hh expression together with Runt coexpression was found in the notochord, the neural tube, and the gill gut, all of which were previously proposed to be involved in the evolution of chordate cartilage [4,5,28,44,45]. It is thus likely, that the direct regulation of Hh by Runt was a relevant mechanism in chordate evolution. This suggests that the core gene network involved in vertebrate cartilage, bone and tooth formation was present prior to the divergence of cephalochordates and vertebrates and the duplication of the Runt and Hh genes.

Further research is needed to determine if a small cell group directly adjacent to both sites of the acellular matrix, with high Runt and Hh expression (arrows in Figure 8D–8G), is of special importance for cartilage formation in lancelets. Another interesting aspect will be to determine if a direct regulatory interaction between the Runt and Hh pathways is also present in hemichordates and whether a direct interaction between Runt and Hh pathways was maintained during vertebrate evolution in other important developmental processes, such as vertebrate hematopoiesis [29,51].

Materials and Methods

Materials

Lancelets (B. floridus) were collected by shovel and sieve in water of 1 m in depth in Tampa Bay, Florida and in vitro fertilization, embryo culture and fixation were performed as previously described [32]. Adult B. lanceolatum were obtained from the Biologische Anstalt Helgoland. Hagfish (M. glutinosa) were collected by S.E. Material from adult dogfish (S. canicula) was obtained from the Biologische Anstalt Helgoland and dogfish embryos from the Aquazoo (Düsseldorf).

Oligonucleotides

All primers and oligonucleotides employed in our study are given as supporting information. Primers for dogfish sequences can be found in Table S1. Primers for hagfish sequences are given in Table S2, and primers for amphioxus are listed in Table S3. Oligonucleotides employed for EMSAs are given in Table S4.

Analysis of Runx gene sequence and number

Total RNA was isolated as described previously [17] from B. floridus (larvae), B. lanceolatum (adult), M. glutinosa (adult), S. canicula (embryos 4.5 cm, 6.5 cm, and 9.5 cm as well as adult animals). Runx genes were amplified by a strategy reported previously, using degenerated primers to amplify the conserved Runx domain followed by RACE PCRs to amplify the full length Runx genes [17]. The only exception was the amplification of the hagfish Mr25 end which was obtained by inverse PCR with gene specific primers [53].
Phylogenetic analysis

Alignments were obtained with ClustalW from 28 full length Runt amino acid sequences [54]. Ambiguously aligned proportions were omitted using Gblocks ver. 0.91b [55] with the following parameters: minimum number of sequences for a conserved/ flanking position (15/15), maximum number of contiguous nonconserved positions (8), minimum length of a block (5), allowed gap positions (all). The phylogenetic analysis was performed using MrBayes 3.1.5 [56], employing JTT+G+I as substitution model and running eight chains for 1.000.000 generations. Trees were sampled every 1000 generations and according to a saturation curve of likelihood values the first 500 trees were discarded as burn-in. Analysis was performed with Runt sequences from O. dioica (AAS21356.1), C. intestinalis (c0100131551, c010013155, ci010310, cinc013i02 and cies003n20), B. lanceolatum and B. floridanus (AAN08567.1, AAN08565.1). M. glutinosa (DQ990008, DQ990009), S. canicula (DQ990010, DQ990012, DQ990014), D. rerio (NP_571678.1, AAS02047.1, AAG93399.1, AAO55550.1), T. rubripes (BAF36011.1, BAF360011, AB280005.1, NP_001092121), G. aculeatus (Ensemble Gene Id: ENSGACG00000020145, EN- SGACG00000012322, ENSGACG00000011721, EN- SGACG00000007301), M. musculus (EDL03777.1, BAA03485.1, EDL29993.1) and H. sapiens (NP_001001890.1, EAX04278.1, NP_004341.1), while using the sea urchin Runt genes from S. purpuratus (U41512.2, XM_776533.1) as an outgroup.

In situ hybridizations

Whole mount in situ hybridizations with lancelet larvae were performed as previously described [43]. Radioactive in situ hybridizations on paraffin embedded tissue sections were performed as reported in [57] with the exception of using lower hybridization and washing temperatures of 50°C, and using 0.2× SSC instead of 2× SSC for washing of B. lanceolatum tissue sections. Non-radioactive in situ hybridization on cryo-sections of B. lanceolatum was carried out using the GenePaint System [58]. Probes for MmIhh and ScRunx3 were used as hybridization controls for B. lanceolatum.

Expression profiling of Runt genes in M. glutinosa, S. canicula and B. lanceolatum by qRT-PCR

QRT-PCR was performed on an ABIPrism 7900HT Cycler (Applied Biosystems, Forster City, USA) using SYBR Green PCR Master Mix (Applied Biosystems), TaqMan Reverse Transcription Reagents (Applied Biosystems) were used to synthesize the cDNA and primers were generated using the Primer Express software (Applied Biosystems). Quantification was performed using the standard curve method with dilutions of plasmids containing the sequence to be amplified in a known copy number as a standard. For the analysis of SoxE expression by qRT-PCR first a SoxE cDNA fragment was amplified by employing primers which were designed according to a SoxE sequence of B. floridanus. Expression of target genes was normalized using 18S rRNA as reference.

Immunohistology

For immunohistochemistry on paraffin sections citrate antigen retrieval was performed. Anti-human Ihh antibody (Santa Cruz) was applied 1:50 over night. Secondary antibody (biotinylated anti-goat, Sigma-Aldrich) was applied 1:500 for one hour. Subsequent staining was performed with the Vectastain ABC kit from Vector laboratories according to the manufacturers’ instructions.

EMSA

Electrophoretic mobility shift assays for putative binding sites were performed as described in [39] with nuclear extracts from chicken DF-1 cells infected with a RCAS-virus expressing the Runt cDNA from B. lanceolatum. Specific binding was confirmed with a labeled oligo containing the putative binding site and using either wild type oligos or oligos with mutated binding sites as competitors.

Luciferase reporter assays

PCR amplification fragments of the B. floridanus Hh promoter (AC150424) were cloned into the pGL3-basic reporter vector. NIH3T3 cells were transfected in 24-well plates with the reporter constructs (250 ng per well) together with an expression vector containing either the cDNA for BrRunt or MmRunx2 or an empty vector as control (100 ng per well). 5 ng per well of pRL-CMV were co-transfected for normalization. Cells were lysed with 100 µl passive lysis buffer (Dual Luciferase Assay Kit; Promega, Madison, USA). 5 µl of the lysate were measured using the Dual- Glo Luciferase Assay Kit (Promega) with 25 µl of the assay reagents each. Measurements were performed on a 1450 MicroBeta Scintillation and Luminescence Counter (Perkin Elmer, Waltham, USA). The result of a representative experiment is shown which was confirmed five times independently.

Data deposition

The sequences reported in this paper have been deposited in the GenBank databases. Dogfish: MASNS-like-promoter variant 1, ScRunx1 Acc-Nr DQ990011, ScRunx2 DQ990013, ScRunx3 DQ990015 and MRIPV-like-motifs promoter variant 2, ScRunx1 DQ990010, ScRunx2 DQ990012, ScRunx3 DQ990014. Hagfish: MgRunxA DQ990008, MgRunxB DQ990009. Lancelet: SoxE EF051347.

Supporting Information

Figure S1 Alignment used for Phylogenetic Analysis. Alignment (ClustalW, BioEdit: http://www.mbio.ncsu.edu/BioEdit/bioedit.html) of newly detected Runt genes in hagfish (MgRunxA and B, DQ990008, DQ990009) and dogfish (ScRunx1-3, DQ990010, DQ990012, DQ990014) with other deuterostome Runt genes. The conserved sequence blocks used for the phylogenetic analysis are underlined with #. Parameters used with Gblocks 0.91b were: Minimum number of sequences for a conserved / flanking position: 15/15; Maximum number of contiguous nonconserved positions: 8; minimum length of a block: 5; allowed gap positions: all. 338 (52%) of the original 645 alignment positions were used in the phylogenetic analysis. Abbreviations: B.l.: Branchiostoma lanceolatum, C.i.: Ciona intestinalis, D.r.: Danio rerio, G.a.: Gasterosteus aculeatus, H.s.: Homo sapiens, M.m.: Mus musculus, M.g.: Myxine glutinosa, O.d.: Oikopleura dioica, S.p.: Strongylocentrotus purpuratus, S.c.: Scolosinus canicula, T.r.: Takifugu rubripes.

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Figure S2 Synteny Analysis. A search for cross-species conserved gene orders was performed as previously described [1]. We compared a larger contig of the BrRunt locus (Ensemble: Scaffold 39) than previously analyzed (Ensemble: Scaffold 833[2]) to the zebrafish genome and detected a synteny region between the 3’ genomic region of the BrRunt gene and chromosome 1 of zebrafish comprising Est1 and Gja5 (A). Furthermore we detected in the stickleback (G. aculeatus) genome a BrRunt orthologous gene with a genomic environment almost identical to the BrRunt gene locus (B). The gene orthologous to Clic 5 located 3’ of the BrRunt locus was expressed in a RCAS-virus expressing the Runt cDNA from B. lanceolatum. Specific binding was confirmed with a labeled oligo containing the putative binding site and using either wild type oligos or oligos with mutated binding sites as competitors.

Runt Gene Evolution
and chromosome 1 had occurred in the common stem species of pufferfish and stickleback.

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Table S1  Dogfish Primers. Primers employed to amplify and analyze the expression of Runt genes in dogfish. PA: Primary amplification, RA: Reamplification.

Table S2  Hagfish Primers. Primers employed to detect Runt genes and analyze Runt gene expression in hagfish. PA: Primary amplification, RA: Reamplification.

Table S3  Amphioxus Primers. Primers employed to analyze Sox9, Hedgehog and Runt genes in lancelets.

Table S4  EMSA Oligos. Oligos employed for the electrophoretic mobility shift assays.

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Author Contributions
Conceived and designed the experiments: JH SS VS. Performed the experiments: JH SS VS. Analyzed the data: JH SS UW ACS GP LP CD SE SM VS. Contributed reagents/materials/analysis tools: SE. Wrote the paper: JH SS LP SM VS.

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