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An Evolutionarily Conserved Enhancer Regulates Bmp4 Expression in Developing Incisor and Limb Bud

Dolrudee Jumlongras1,2,*, Salil A. Lachke3,9, Daniel J. O’Connell1, Anton Aboukhalil1,4, Xiao Li5, Sung E. Choe1*, Joshua W. K. Ho1,6, Annick Turbe-Doan1, Erin A. Robertson1, Bjorn R. Olsen2, Martha L. Bulyk1,7,8, Brad A. Amendt2, Richard L. Maas1*

1 Division of Genetics, Department of Medicine, Harvard Medical School, Brigham and Women’s Hospital, Boston Massachusetts, United States of America, 2 Department of Developmental Biology, Harvard School of Dental Medicine, Boston, Massachusetts, United States of America, 3 Department of Biological Sciences, Center for Bioinformatics and Computational Biology, University of Delaware, Newark, Delaware, United States of America, 4 Department of Aeronautics and Astronautics, Massachusetts Institute of Technology (MIT), Cambridge, Massachusetts, United States of America, 5 Institute of Biosciences and Technology, Texas A&M Health Science Center, Houston, Texas, United States of America, 6 Center for Biomedical Informatics, Harvard Medical School, Boston, Massachusetts, United States of America, 7 Department of Pathology, Harvard Medical School, Brigham and Women’s Hospital, Boston, Massachusetts, United States of America, 8 Harvard-MIT Division of Health Sciences and Technology, Harvard Medical School, Boston, Massachusetts, United States of America

Abstract

To elucidate the transcriptional regulation of Bmp4 expression during organogenesis, we used phylogenetic footprinting and transgenic reporter analyses to identify Bmp4 cis-regulatory modules (CRMs). These analyses identified a regulatory region located ~46 kb upstream of the mouse Bmp4 transcription start site that had previously been shown to direct expression in lateral plate mesoderm. We refined this regulatory region to a 396-bp minimal enhancer, and show that it recapitulates features of endogenous Bmp4 expression in developing mandibular arch ectoderm and incisor epithelium during the initiation-stage of tooth development. In addition, this enhancer directs expression in the apical ectodermal ridge (AER) of the developing limb and in anterior and posterior limb mesenchyme. Transcript profiling of E11.5 mouse incisor dental lamina, together with protein binding microarray (PBM) analyses, allowed identification of a conserved DNA binding motif in the Bmp4 enhancer for Pitx homeoproteins, which are also expressed in the developing mandibular and incisor epithelium. In vitro electrophoretic mobility shift assays (EMSA) and in vivo transgenic reporter mutational analyses revealed that this site supports Pitx binding and that the site is necessary to recapitulate aspects of endogenous Bmp4 expression in developing craniofacial and limb tissues. Finally, Pitx2 chromatin immunoprecipitation (ChIP) demonstrated direct binding of Pitx2 to this Bmp4 enhancer site in a dental epithelial cell line. These results establish a direct molecular regulatory link between Pitx family members and Bmp4 gene expression in developing incisor epithelium.

Introduction

Bmp4, a member of the TGF-β superfamily, is a secreted signaling molecule essential for embryogenesis [1–9]. It is expressed in a variety of tissues and organs throughout embryonic and postnatal life [4]. Evidence from mutations in mice and humans indicates that Bmp4 regulates several developmental processes including patterning, proliferation, differentiation and apoptosis [15]; http://omim.org/entry/112262).

The study of conditional Bmp4 or Bmp receptor knockout alleles has shed light on the spatiotemporal functions of Bmp4 in epithelial-mesenchymal interactions during early craniofacial and limb morphogenesis [6–9]. For example, inactivation of Bmp4 or Bmp4r1a in the facial primordia leads to isolated cleft lip or bilateral cleft lip and palate and deficient tooth development [10]. Furthermore, conditional deletion of Bmp4 in distal mandibular arch ectoderm results in mandibular truncation and lack of incisors, indicating essential functions of epithelial Bmp4 in these ectodermal organs [7]. Bmp4 has also been implicated as one of the earliest signaling molecules secreted from the oral ectoderm that is capable of inducing dental mesenchymal genes that are necessary for tooth formation [7,11–13].

Bmp4 also plays an important role in regulating limb development, as suggested by its strong expression in the apical ectodermal ridge (AER), an important epithelial signaling center at the distal end of the limb bud, and in the anterior and posterior limb mesenchyme. Moreover, conditional inactivation of Bmp4, alone or in combination with other Bmps, or inactivation of its receptors, in limb bud AER or mesenchymal domains, has revealed roles in AER induction and maintenance respectively, as well as anteroposterior and dorsoventral limb patterning, and digit specification [9,14–16], and chondrogenesis and osteogenesis [17].


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* E-mail: maas@genetics.med.harvard.edu

† Current address: Agios Pharmaceuticals, Cambridge, Massachusetts, United States of America

These authors contributed equally to this work.

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In the developing limb, Bmp signaling has been shown to function in the context of an interconnected Bmp/Grem1 signaling module and a Shh/Grem1/Egf feedback loop [18]. While in the developing molar tooth, Bmp4 interacts with canonical Wnts as part of a feedback circuit that couples the development of the dental epithelium and mesenchyme [19].

As a step towards defining the gene regulatory networks (GRNs) that control Bmp4 expression in vivo, we searched for Bmp4 CRMs (cis-regulatory modules) using a transgenic reporter assay. Previously, Chandler et al. (2009) used a BAC reporter-based transgenic approach and identified a Bmp4 lateral plate mesoderm (LPM) enhancer ~46 kb upstream of the Bmp4 transcription start site. We independently identified the same highly conserved, developmentally active Bmp4 regulatory region, but have extended the prior characterization by Chandler et al. (2009) of a 4.3 kb CRM and of a smaller 467 bp subregion to reveal several important new attributes [1].

We refined this CRM to an essential 396-bp minimal enhancer that confers reporter gene expression in developing distal mandibular and incisor epithelium and the limb bud, tissues that require Bmp4 for proper morphogenesis. We also used TF (transcription factor) DNA binding specificity motif data from the UniPROBE database [20,21] to analyze the Bmp4 enhancer and identified a high-affinity binding sequence for Pitx homeobox TFs, which are strongly expressed in the developing mandible, tooth and limb, and which have been implicated in human and mouse odontogenic defects and lower limb malformations [22–24]. Pitx1 may activate gene expression in dental epithelium [25], while Pitx2 null mutants exhibit an early stage arrest in tooth development [26,27]. In hindlimb development, Pitx1−/− and Pitx2−/− double mutants exhibit altered signaling molecule expression in the AER, which is proposed to account for the proximal limb reduction defect in these mutants [28]. However, the molecular regulatory relationship between Pitx1, Pitx2 and Bmp4 remains unclear. We show here that Pitx homeoprotein family members bind a specific site in the Bmp4 incisor epithelium limb bud ("IE/LB") enhancer that is necessary for its activity in vivo. These results define a minimal, highly conserved Bmp4 enhancer and identify Pitx homeoproteins as key TFs that regulate its embryonic expression.

## Results

### Identification of Putative Bmp4 CRMs by Phylogenetic Footprinting

To identify candidate Bmp4 enhancers, we conducted a phylogenetic footprinting analysis [29–31] on the genomic region surrounding the mouse Bmp4 gene. The mouse Bmp4 transcription unit is located on chromosome 14qC1, and spans ~7 kb with five exons and two alternative TATA-less promoters [32,33]. We focused our search on a 159 kb region consisting of two 76 kb non-genic regions upstream and downstream of Bmp4, and the 7 kb Bmp4 transcription unit itself. We compared this 159 kb mouse genomic sequence, obtained from the UCSC genome database and devoid of other known genes and ESTs, with homologous genomic sequences of human and pufferfish (Takifugu rubripes, or Fugu) using the local alignment program BLASTZ which displays homology as blocks of sequence conservation [34,35]. The Fugu sequence, although distantly related, was used in the analysis based on the assumption that non-coding sequences that have tolerated selective pressure for hundreds of million years of evolution are likely to be functionally significant and to play important roles in gene regulation [36–38]. While not all morphogenetic programs in which Bmp4 plays a critical role (e.g., limb and tooth development) are likely to be fully conserved in fish, we reasoned that certain core regulatory sequences might be. Moreover, we hypothesized that the compactness of the Fugu genome could further filter the relatively high degree of conservation between human and mouse, thereby prioritizing putative regulatory regions for further analysis.

The BLASTZ alignment identified several discrete blocks of sequence conservation between mouse and human, using parameters of >75% identity over >50 bp, which have similar stringency to parameters previously used for identification of functional mammalian regulatory elements [39,40]. In addition to highly conserved sequences representing Bmp4 exons IA, IB, II, III and IV, 87 blocks of sequence conservation (31 blocks located 5’ and 56 blocks located 3’ to the Bmp4 transcription start site) between mouse and human were identified and considered as candidate Bmp4 regulatory sequences (Figure 1). While several of these blocks cover long genomic regions, others are smaller and reside in clusters. Previous studies indicate that conserved non-coding regions of developmental genes frequently cluster together [38,41]. Therefore, we grouped closely residing conservation blocks of 200 bp or longer into larger conserved or "CONS" regions. Based on human-mouse sequence conservation analyses, we selected four highly conserved regions and their immediate flanking sequences upstream and within the Bmp4 gene as high priority candidate regulatory sequences. These sequences were designated as CONS1, CONS2, CONS3 and CONS4, with their respective 5’ boundaries located 11 kb, 30 kb, and 47 kb upstream, and 4.6 kb downstream of the Bmp4 transcription start site; the latter region resides within an intron in the Bmp4 gene (Figure 1).

When the orthologous Fugu genomic sequence was included in the analysis, only two blocks of conservation, located ~46 kb 5’ upstream and ~80 kb 3’ downstream of the mouse Bmp4 transcription start site, were conserved in all three genomes. Both blocks are embedded within larger regions of human-mouse conservation, and the ~46 kb upstream block is located within the CONS3 sequence, but only the ~46 kb upstream block contained conserved regions exceeding our 200 bp cut-off (Figure 1). To verify that these conserved regions represented non-coding sequences, we performed a BLAST search and re-confirmed that they did not match any known coding regions, mRNAs or ESTs. We refer to the previously described 2.4 kb proximal Bmp4 promoter also shows high human-mouse conservation (Figure 1) and that in transgenic mice, this region in isolation has been shown to drive Bmp4 expression in epithelial-derived ameloblasts and hair shaft keratinoocytes and matrix [43,44]. In addition, the mammalian proximal promoter region does not show conservation with Fugu under the stringency used in this analysis (Figure 1). Collectively, these results suggest that other more distant elements regulate the full repertoire of Bmp4 developmental expression.

### CONS3 Recapitulates Bmp4 Expression in Multiple Tissues during Development

To determine if these candidate regulatory regions harbored transcriptional regulatory activity, we tested the ability of each individual CONS region to drive expression of a lacZ reporter gene in transgenic mouse embryos at embryonic day (E) 11.5
and compared them to E11.5 embryos heterozygous for a Bmp4lacZneo reporter allele [45] (Figure 2A, B). Transient transgenic analysis of CONS1 (n = 10), which spans 4.7 kb and includes 4 highly conserved blocks, and CONS4 (n = 13), which extends approximately 1.7 kb over the intronic region between exons III and IV, showed no reporter activity in any of the known Bmp4 expression domains at E11.5 (Figure 1 and Figure 2C). Transgenic embryos carrying the 4.3 kb CONS2 transgene, which consists of six conserved blocks, showed consistent expression in the developing forebrain (n = 17). Although not a domain where endogenous Bmp4 is normally expressed, this validates the functional competence of the CONS2 construct. It is also possible that CONS1, 2 ands 4 are expressed in the adult animal, or at developmental times different from the E11.5 time point assayed here.

In contrast, transient transgenic analysis of the 4.3 kb CONS3 region, which includes one of the two human-mouse-Fugu conserved blocks and has 94% overall human-mouse homology, revealed that a subset (n = 11/20) of embryos exhibited transgene expression in the oral epithelium overlying the maxillary process and mandibular arch, a pattern similar to that of endogenous Bmp4 (Figure 2C; Figure 3). The epithelial incisor dental lamina placodes also exhibited transgene expression in a pattern similar to that of endogenous Bmp4 (Figure S1). We also detected transgene expression specific to the limb bud apical ectodermal ridge (AER), and in forelimb and hindlimb posterior mesenchyme (n = 16/20), with weaker expression in anterior limb mesenchyme, similar to that of endogenous Bmp4 (Figure 3). Transgene expression was also observed in the proximal limb where endogenous Bmp4 is normally expressed (Figure 2C, Figure 3). Thus, CONS3 contains cis-regulatory sequences that are capable of acting on a heterologous beta-globin promoter to direct gene expression to the orofacial region, the AER, and limb bud mesenchyme in a pattern similar to that of endogenous Bmp4.
While CONS3 contains epithelial bud, until at least E13.5 (Figure 3B). This indicates that pre-maxilla, nasal pits, distal mandible, and in the incisor domains at these stages (Figure 3A).

Further deletion of the 5' ends of CONS3.8 to generate a 396-bp CONS3.8 sequence, which overlaps CONS3.6 and CONS3.7, exhibited reporter activity in the same domains as CONS3 (Figure 4A, B), albeit at lower levels. Further deletion of the 5' and 3' ends of CONS3.8 to generate a 300-bp CONS3.9 construct yielded no enhancer activity in any of the CONS3 expression domains (Figure 4A, B).

Thus, the 396-bp CONS3.8 sequence represents the minimal enhancer element necessary for Bmp4 expression in the AER and limb bud mesenchymal domains, and in mandibular arch and incisor dental lamina epithelia. Although its full expression properties remain to be explored, we have provisionally denoted this cis-regulatory module the Bmp4 incisor epithelium/limb bud, or "IE/LB", enhancer. In addition, since the entire 396 bp IE/LB enhancer is contained within the 467 bp LPM (lateral plate mesoderm) enhancer previously characterized by Chandler and coworkers [1], the 467 bp sequence likely functions as a composite IE/LB and LPM, or "IE/LB/LPM" enhancer, although this was not tested directly by comparing the behavior of both the 396 and CONS3 and endogenous Bmp4 (Figure 2B and Figure 4A, B). CONS3.1, which covers 500-bp of the 3' end of CONS3, did not confer any activity of the reporter gene; however, CONS3.2, which spans 3.8 kb of the 3' portion of CONS3 reproduced expression of the entire 4.3 kb CONS3 construct (Figure 4A, B).

The 1.5 kb CONS3.3 fragment, a subset of CONS3, also retained CONS3 activity (Figure 4A, B). We then generated and tested CONS3.3, which covers 757 bp with the highest sequence conservation within CONS3.3, and found that it also retained enhancer activity similar to that of CONS3 (Figure 4A, B). We also noted consistent ectopic expression in the midbrain of CONS3.5 transgenic embryos (data not shown), which suggests that sequences outside CONS3 and within CONS3.3 may possess repressive activity for Bmp4 reporter transgene expression in midbrain. Lastly, the CONS3.3 fragment was tested in an orientation opposite to that of the endogenous locus, which establishes its orientation independence.

We further investigated CONS3.5 activity during incisor morphogenesis. At E14.0, CONS3.5 expression was maintained in cap-stage dental epithelium, but absent from the dental mesenchyme and enamel knot; the latter is an epithelial signaling center that expresses endogenous Bmp4 and controls tooth cusp patterning [47]. Endogenous Bmp4 is normally expressed in the enamel knot, and downregulated in the surrounding dental epithelium. Thus, in contrast to its activity in mandibular ectoderm and lamina stage incisor epithelium, which is faithful to endogenous Bmp4 expression, at the cap-stage CONS3.5 directs epithelial expression in the developing incisor in a complementary pattern to that of endogenous Bmp4 (Figure S2). While beta-galactosidase perdurance cannot be entirely excluded, it seems much more likely that genomic regions outside of CONS3.5 are required for the repression of Bmp4 in the dental epithelium after the lamina stage. Moreover, the results indicate that sequences outside CONS3.5 are required for the activation of Bmp4 expression in the dental mesenchyme and enamel knot.

To further define the minimal genomic region required for Bmp4 enhancer activity, we subcloned overlapping 3' and 5' halves of CONS3.5, designated CONS3.6 (392-bp) and CONS3.7 (424-bp) respectively, into reporter vectors and tested their ability to confer expression. Although a few CONS3.7 embryos exhibited reporter gene activity in the proximal limb, neither construct gave detectable reporter activity in the AER, mandibular arch or incisor dental lamina (CONS3.6, CONS3.7); hence these were scored as negative (Figure 4A, B). In contrast, CONS3.8, a 396-bp sequence from the approximate mid-region of CONS3.5 that overlaps CONS3.6 and CONS3.7, exhibited reporter activity in the same domains as CONS3 (Figure 4A, B), albeit at lower levels. Further deletion of the 5' and 3' ends of CONS3.8 to generate a 300-bp CONS3.9 construct yielded no enhancer activity in any of the CONS3 expression domains (Figure 4A, B).

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467 bp sequences at the time point at which LPM activity was detected [1].

The Minimal \textit{Bmp4} CONS3.8 Enhancer Contains a Conserved \textit{Pitx} and \textit{Msx} Binding Motif

To identify potential direct regulators of the \textit{Bmp4} enhancer, we searched the UniPROBE database (http://thebrain.bwh.harvard.edu/uniprobe/) for putative transcription factor (TF) binding sites within the minimal 396-bp \textit{Bmp4} enhancer (CONS3.8) sequence. To further restrict the list of candidate TF regulators, we generated and analyzed microarray gene expression datasets from tissues with CONS3.8 enhancer activity. Epithelial gene expression analysis, using laser capture microdissection (LCM) of E11.5 mouse incisor tooth germs (Figure S3), and previously published E12.5 fore- and hindlimb microarray datasets, were used in combination to identify genes whose transcripts were consistently expressed (i.e., ≥ 2 of 3 replicates). This list of expressed genes was then intersected with the list of TF families having conserved putative binding sites in the minimal CONS3.8 \textit{Bmp4} enhancer (see Materials and Methods). In summary, fourteen TF families, which included the Pitx and Msx TF families, exhibited conserved
potential binding sites in the minimal CONS3.8 Bmp4 enhancer (Table S1).

The CONS3.8 Enhancer Supports Pitx and Msx Protein Binding in vitro

Among these candidates, we chose to focus only on those TFs previously implicated in limb, tooth or mandible development [18,19,24,48]. The above analyses yielded strong candidate binding sites for the Pitx (5'-TAATCC-3') and Msx (5'-GTAATTG-3') TF families within the minimal 396-bp enhancer (Figure S4). We next performed Electrophoretic Mobility Shift Assays (EMSA) to determine whether Pitx or Msx proteins can specifically bind to their respective predicted binding sites in the CONS3.8 enhancer. We generated full-length Pitx1 and Msx2 GST-fusion proteins and incubated them with 25-mer sequences taken from within CONS3.8 that encompassed either the Pitx or Msx binding sites, and compared DNA-protein complex formation to that with probes consisting of canonical DNA recognition sequences for each protein [49,50]. Both Pitx1 and Msx2 proteins specifically bound the wild type Bmp4 enhancer (WT-PitxBS-CONS3 or WT-MsxBS-CONS3) and their canonical sequences (Bicoid or MBS, respectively) (Figure 5A and Figure S5; lanes 3, 6–8). In addition, these complexes were specifically competed by excess (50-fold or 100-fold) unlabeled wild type Bmp4 enhancer oligonucleotide competitor (WT-PitxBS-CONS3 or WT-MsxBS-CONS3) (Figure 5A and Figure S5; lanes 12–15), confirming the binding specificity of each TF with its respective binding site.

To ascertain the necessity of these intact DNA sites for protein binding, we introduced mutations into each site that were predicted to abolish binding (see Materials and Methods). As expected, EMSA demonstrated that the proteins could not bind the respective mutant oligomers (Figure 5A and Figure S5). In addition, unlike their wild type counterparts, unlabeled mutant oligomers at 50- to 100-fold excess did not compete with wild type

Figure 4. Deletion analysis of the Bmp4 enhancer CONS3. (A) Schematic of the four regions (CONS1-4; black boxes), each containing multiple human-mouse sequence conservation blocks, tested in a transient transgenic mouse reporter assay in the same reporter shown in Figure 2. The CONS3 enhancer was systematically narrowed down to 758 bp region, CONS3.5, which contains the Fugu-Mouse upstream conservation block, and then to a minimal 396 bp minimal enhancer. (B) The number of E11.5 transgenic mouse embryos showing endogenous Bmp4 orofacial and limb expression (in the AER and mesenchyme region of fore- and hindlimbs) is reported over the total number of transgenic embryos analyzed (No. Stained/No. Tg). doi:10.1371/journal.pone.0038568.g004
oligomer binding. Thus, the CONS3.8 396-bp Bmp4 minimal enhancer sequence contains specific, high affinity Pitx and Msx binding sites that support binding of these proteins in vitro. This is also in agreement with the prediction from PBM analysis, in which both Pitx and Msx displayed strong sequence preference for their respective putative binding sites (PBM enrichment (E) score = 0.45).

**CONS3 Enhancer Activity in vivo Requires an Intact Pitx Motif**

To test the functionality of the Pitx and Msx binding sites in CONS3 in vivo, we assayed the activity of CONS3 enhancer sequences that contained clustered point mutations in the respective binding sites in transient transgenic mice. The introduced mutations fulfilled the criteria of completely abolishing TF binding in EMSAs, and insofar as could be determined, did not generate an adventitious site that could bind other TFs.

Transient transgenic mice carrying MutPitxCONS3 and MutMsx-CONS3 reporter transgenes with mutations in Pitx and Msx binding sites respectively, displayed significantly reduced reporter activity compared to wild type (Figure 5B and Figure S6). When each of the CONS3 limb and orofacial expression domains was examined for β-galactosidase expression in forelimbs, hindlimbs, or orofacial tissue. Asterisk indicates statistically significant differences (p<0.05) compared to wild-type CONS3 by Fisher’s exact test.

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![Figure 5. Pitx binds to the minimal Bmp4 enhancer CRM in vitro and the Pitx binding site is necessary for enhancer activity. (A) Electrophoretic Mobility Shift Assay (EMSA) exhibits robust binding of Pitx1 protein to both a positive control bicoid DNA sequence and to the consensus Pitx1/2 binding site in with a 25 bp probe sequence in the CONS3.8 sequence. Competition with specific or non-specific unlabelled probes indicates sequence-specific binding of GST:Pitx1 fusion protein to the consensus Pitx1/2 DNA binding motif. (B) Number of transient transgenic embryos that supported β-galactosidase expression in forelimbs, hindlimbs, or orofacial tissue. Asterisk indicates statistically significant differences (p<0.05) compared to wild-type CONS3 by Fisher’s exact test.](image-url)
type CONS3 embryos (Figure 5B and Figure S6). Moreover, when transgenic embryos were stringently scored for expression in all CONS3 expression domains, only one embryo for each mutant construct exhibited lacZ expression in all domains. This reduction in mutant CONS3 enhancer activity is statistically significant (p<0.05, Fisher’s exact test) when compared to the 53% of wild type CONS3 transgenics that were lacZ-positive in all domains (Figure 5B and Figure S6). To test whether the Pitx and Msx binding sites might cooperate to activate the CONS3 enhancer, we engineered a construct, MutPitxMsxCONS3, which carried mutation in both Pitx and Msx binding sites and assayed it in transient transgenic mouse embryos which carried mutation in both Pitx and Msx

**Discussion**

**Pitx Homeoproteins as Potential Regulators of the Bmp4 IE/LB Enhancer**

We identified a 396 bp minimal ‘incisor epithelium/limb bud’ (IE/LB) Bmp4 enhancer that contains putative binding sites for members of the Pitx and Msx homeoprotein families, which are expressed with Bmp4 in these developing tissues. The Pitx and Msx binding sites reside 152 bp apart, and may represent part of a combinatorial code essential for Bmp4 expression in early craniofacial and limb development. Both the Pitx and Msx binding motifs were present in all Bmp4 IE/LB enhancer deletion constructs that exhibited reporter expression in transgenic assays, and mutation of either motif dramatically reduced expression. Interestingly, the entirety of the 396 bp Bmp4 IE/LB enhancer, including the Pitx and Msx binding motifs, is also contained within the 467 bp lateral plate mesoderm (LPM) element described by Chandler and coworkers [1]. These data suggest specific possibilities about the regulatory circuitry that governs Bmp4 expression in tooth and limb development. First, the presence of a required Pitx1/2 binding site in the Bmp4 IE/LB enhancer supports a direct, positive regulatory relationship between Pitx1/2 and Bmp4 gene expression. Interestingly, however, Bmp4 expression is expanded in Pitx2-deficient mandibular ectoderm at E10.5, suggesting a repressive regulatory relationship [26,52]. A similar expansion of Bmp4 craniofacial expression is not observed in Pitx1 null mutants [53], which exhibit defective mandibular development [49]. These data could be reconciled if, for example, Pitx1 and Pitx2, which are both expressed in initiation stage mandibular and incisor epithelium, functioned at slightly different times with a combination of activating and repressive capacities. Notably, Pitx1 expression at the bud and cap stages of tooth development, including its exclusion from the enamel knot at the cap stage, mimics the persistent ectopic expression of the Bmp4 IE/LB enhancer at these stages of tooth development (see Figure 1 and Figure S2, [19]). Conversely, at the cap stage, Pitx2 expression is enriched in the enamel knot, from which Bmp4 enhancer activity is absent. These data are consistent with a model whereby Pitx1 activates and Pitx2 represses the Bmp4 enhancer in non-enamel knot dental epithelium and in enamel knot respectively, potentially through the same Pitx binding site in the Bmp4 enhancer.

Although Pitx2 has been shown to function as a transcriptional activator, at least four known isoforms of Pitx2 exist via alternative splicing; these may have different regulatory properties. In addition, existing data indicates that Pitx2 can interact with any of several co-factors to regulate gene transcription [54–58]. It is therefore possible that co-factor choice may dictate whether the Pitx site in the Bmp4 enhancer functions as a positive or negative regulatory input. For example, Pitx2 activation of the Dlx2 promoter is attenuated by the direct interaction of Dlx2 with Pitx2 [58]. In another scenario involving the Dlx2 promoter, Msx2 binds to the same Bicoid element as Pitx2, and antagonizes the activation of Dlx2 transcription by Pitx2 [50]. These examples highlight the spectrum of possibilities that could account for the unique expression properties of the Bmp4 IE/LB enhancer in developing incisor epithelium.

Thus, in early dental epithelium (mouse stage E9.5 - E11.5), Pitx1 or Pitx2 may activate the Bmp4 enhancer directly by binding to the Pitx site. At later stages from E13.5, Bmp4 protein may establish a self-regulatory circuit, by negatively regulating Pitx1 expression, as suggested by the observation of Bmp4-mediated Pitx1 repression in dental epithelium [25], and by the transient repression of Pitx2 by Bmp4 in mandibular epithelium [53]. Such a feedback loop could potentially explain the downregulation of Bmp4 expression in the dental epithelium that normally occurs after the initiation stage. However, the Pitx site in the Bmp4 enhancer itself is not a candidate to mediate this feedback since the Bmp4 IE/LB enhancer fails to exhibit the normal downregulation observed for Bmp4 expression in the incisor epithelium (Figure S2). Nonetheless, such a negative feedback loop might help ensure the correct regulation of Pitx1/2 mediated Bmp4 expression. Indeed, Pitx2 gene dosage is critical, because Axenfeld-Rieger patients carry PTTX2 haploinsufficiency, and Pitx2+-/- mouse embryos exhibit oligodontia, along with other phenotypes [59].

Less is known about the relationship between Bmp4 expression and Pitx1/2 in developing limb bud and lateral plate mesoderm, although similarly complex regulatory relationships may exist. Pitx1 and 2 are differentially expressed in posterior and left sided lateral plate mesoderm, respectively, where Pitx1 specifies hindlimb identity in LPM and Pitx2 helps determine laterality [29]. Both Pitx1 and Pitx2 expression overlap in early LPM and they cooperate in hindlimb specification [28]. Bmp4 expression is unaffected in the phenotypically affected hindlimbs of Pitx1 null embryos [60], suggesting that other TFs, possibly Msx1/2 homeoproteins, regulate Bmp4 expression in this tissue.
Finally, since mouse CONS3 has strong sequence homology with human, we performed bioinformatic analyses on the human sequence orthologous to mouse CONS3 to determine if it exhibits features of a regulatory enhancer. After aligning the mouse CONS3 to human sequence, we identified a 243-bp region of sequence homology located 45 kb upstream of the human BMP4 gene. This region was compared against various epigenomic profiles in ENCODE human cell lines [61,62]. Indeed, profiles of DNase I hypersensitivity, histone modification, and transcription factor binding all suggest that this region can function as an enhancer in human (Figure S7). Thus, public epigenomic data from ENCODE or other consortia can help corroborate potentially homologous enhancers in human.

In sum, one of the most interesting aspects of the present work is that a single enhancer can regulate the expression of a key developmental signaling gene such as BMP4 in craniofacial, limb and potentially lateral plate mesoderm tissues. This result furthers the view that while the fine details of gene regulatory networks may differ from case to case, the central features of these regulatory circuits are conserved, not only in evolution, but also in multiple developmental contexts within an organism.

Materials and Methods

Phylogenetic Footprinting (Comparative Genomic Analysis of Conserved Sequences)

To generate human, mouse and pufferfish alignments, mouse genomic sequence surrounding the BMP4 gene (76 kb upstream and 76 kb downstream of the BMP4 gene) from public database (GenBank accession X56848.1) was compared against orthologous human and pufferfish sequences using BLASTZ (http://bio.csc.psu.edu/pipmaker/), a local alignment program that generates graphical outputs by PipMaker as blocks of sequence conservation [34,35]. Repetitive DNA of the reference mouse sequence was masked using RepeatMasker (http://www.repeatmasker.org/cgi-bin/WEBRepeatMasker).

Generation of DNA Constructs for Microinjection

The blocks of conserved non-coding sequences (CONS regions) were amplified by polymerase chain reaction (PCR) using either MasterAmp PCR amplification or Extralong PCR amplification kit with proofreading DNA polymerase (Epicentre Biotechnologies, Madison, WI). The PCR primers were designed to contain a restriction site and an additional 3–6 nucleotides at their 5' ends for subsequent restriction enzyme digestion and directional cloning of the PCR product. All constructs CONS3.1, 3.2, 3.3, 3.4, 3.5 were subcloned directly from CONS3 construct using restriction enzyme digestion.

The PCR products were purified using QIAquick PCR Purification Kit (QIAGEN, Valencia, CA), restriction enzyme-digested and subcloned into a multiple cloning site of GLKS plasmid which contains an E. coli lacZSV40pA reporter cassette under the control of a minimal human β-globin promoter [63]. Correct clones were confirmed by either restriction enzyme digestion or direct sequencing methods. Constructs were released.
from GLKS vector backbone using appropriate restriction enzymes, purified using QIAGEN Gel Extraction kit (QIAGEN, Valencia, CA) and eluted with microinjection buffer (10 mM Tris pH 8.0, 0.25 mM EDTA).

**Generation and Genotyping of Transgenic Mice**

The constructs were diluted in microinjection buffer to a concentration of 1–2 ng/µl and injected into fertilized mouse oocytes derived from FVB/N matings using standard procedures [64]. The injected oocytes were then transferred into oviducts of pseudopregnant Swiss female mice. Transgenic embryos were collected, fixed and stained for β-galactosidase activity. Yolk sacs were carefully dissected away from maternal tissues and avoided cross contaminations between littersmates. Crude yolk sac genomic DNA was extracted by overnight digestion in 200 µl of yolk sac lysis buffer (50mM potassium chloride, 1.5mM magnesium chloride, 10mM Tris pH8.3, 0.01% gelatin, 0.45% Nonidet P-30, 0.45% Tween-20) supplemented with 0.1mg/ml proteinase K at 55°C. For tail biopsies, genomic DNA was extracted by boiling the tissue for 20 minutes in 200 µl of 25mM Sodium hydroxide, followed by neutralization with 50 µl of Tris-HCl pH 8.0. Transgenic embryos and transgenic founder mice were identified by the presence of the lacZ transgene using PCR with primers wacZ-F 5’-TTGATGGCGCCGTGTTTTACAACGTCG-3’ and wacZ-R 5’-ATGTGAGCGAGTAACAACC CGTCGGA-3’. Permanent transgenic lines were established by crossing the founder animal with FVB/N wild type mice. Age-matched Tg(wacZ-Tg)-1/2 mice with FVB/N were used as controls.

**Cryosections and Whole Mount β-galactosidase Staining**

Staining for β-galactosidase activity in whole embryos and on cryosections was performed according to standard protocols [64]. Heads of selected transgenic embryos were removed and the lower jaws were separated to allow direct visualization of the intraoral cavity and to facilitate penetration of X-gal staining solution. For cryosections, embryonic heads were processed as described and sectioned at 10 µm thickness. After staining for β-galactosidase activity, the sections were counterstained with 0.5% Eosin Y solution, dehydrated through an ascending series of ethyl alcohol, cleared in xylene and mounted with Permount (Sigma, St. Louis, MO).

**Laser Capture Microdissection (LCM) and Gene Expression Analysis**

Embryonic tissue was dissected in ice-cold RNase-free phosphate buffered saline (PBS) and the E11.0 heads were frozen immediately in Tissue Tek OCT (Andrew Scientific, Schaumburg, IL). Fresh-frozen tissue was cryosectioned and collected on PEN membrane slides (Molecular Devices, Sunnyvale, CA). The slides were immediately refrozen and maintained on dry ice before staining and dehydrating with Histogene Staining Kit (Molecular Devices, Sunnyvale, CA). Discrete incisor epithelial tissues were isolated using a Leica laser capture microdissection (LCM) LMD 6000 microscope. The tissue was isolated directly into the extraction buffer provided with Pico Pure Isolation Kit (Molecular Devices, Sunnyvale, CA). RNA purification was performed according to the Pico Pure Isolation Kit and included an on column treatment with RNase-free DNase 1 (Qiagen, Valencia, CA). Eluted RNA quality was determined using the Agilent Bioanalyzer 2100. 10 to 25 ng of total RNA was then amplified to yield 7–10 µg of single-stranded DNA using a poly-dT based Ovation RNA Amplification System V2 (NuGEN, San Carlos, CA). The quality and size distribution of amplified DNA were confirmed using an Agilent Bioanalyzer 2100. Biotinization was achieved through abasic site creation in the single stranded DNA with Uracil N-Glycosylase (Epigenic Biotechnologies, Madison, WI), and reaction with Aldehyde-Reactive Probe (ARP) N-(a-minooxyacetyl)-N’- (D-biotinoyl) hydrazine, trifuluroacetic acid salt (Invitrogen). 1.5 µg of biotinylated DNA was hybridized according to the NuGEN manufacture note to the Illumina Mouse Ref-6 whole genome expression array. For expression profiling of the developing limb, Affymetrix microarray datasets were obtained from Gene Expression Omnibus (GEO) reference series GSE2560. Probe datasets were called “Present” if at least two of the three replicates had a detection p-value less than 0.05. The E11.0 tooth germ microarray data is deposited in the GEO database [http://www.ncbi.nih.gov/geo/].

**Analysis of the CONS3.8 CRM for Putative TF binding sites**

Custom MATLAB scripts were written to map ungapped 8-mers from the UniPROBE database for mouse TFs [20], http://thebrain.bwh.harvard.edu/uniprobe/ to the CONS3.8 CRM. The Mouse July 2007 (NCBI37/mm9) assembly was used along with the 46-way multiz vertebrate alignment from Galaxy (http://main.g2.bx.psu.edu/). A putative binding site in CONS3.8 was selected for further analysis when at least two consecutive overlapping un ungapped 8-mers scored above an enrichment score (ES) of 0.35 (medium affinity binding site) and 0.45 (high affinity binding site). We focused on TF families whose members had binding sites that were conserved in at least 90% of the vertebrate alignment within CONS3.8. TFs were grouped into families based on their names and their common DNA binding domain (DBD) annotation from the InterPro database [65]; e.g., since the TFs Msx1, Msx2, and Msx3 each have the same name, Msx, and the same three DBD annotations of IPR000047 (helix-turn-helix), IPR001356 (homeodomain), and IPR009057 (homeodomain-like), we grouped these three TFs into the family “Msx IPR000047; IPR001356; IPR009057”. We further restricted our candidate TF families based on the expression of at least one of their members in the tissues of interest. Microarray datasets were used from mouse tissue of E11.5 tooth germ (this study) and E12.5 fore- (GEO datasets GSM48648, GSM48912, GSM48913) and hindlimb (GEO datasets GSM48914, GSM48915, GSM48916). Transcription factors were retained if they were called present in at least 2 out of the 3 replicates, in all three tissues, and had conserved binding sites in CONS3.8.**

**Generation of Pitx1 and Msx2 Plasmid Constructs**

Full-length Pitx1 and Msx2 expression plasmids were constructed in pGEX3X by PCR-based cloning of the Pitx1 and Msx2 coding regions. Each reaction contained template, 4 pmoles of each primer, 2.5 U of PfuTurbo® DNA polymerase (Stratagene, La Jolla, CA), and 2 x FailSafe Premix A (Epigenic Biotechnologies, Madison, WI) which contains 1.5 mM Mg2+ and 1 x Betaine. PCR conditions were as follows: 95°C for 2 minutes, 95°C for 30 seconds, 60°C for 30 seconds, and 72°C for 1 minute with a final extension of 10 minutes after 30 cycles in PCR thermocyclers (MJ Research, Reno, NV). We purified the PCR products using Gel Extraction kit (QIAGEN, Valencia, CA). Approximately 1 µg of the purified PCR products was subjected to double digestion. The digested products were then ligated into the
expression vector (pGEX3X). Both Pitx1 and Msx2 constructs were directly sequenced with forward and reverse primers designed from plasmid sequences flanking the cloning site (pGEX3X-F: 5′-ATGGCCCTTGACCGCTGCTGACAGC-3′ and pGEX3X-R: 5′-TCGCCGGAGCTGTGAT-3′) to ensure the absence of mutations.

**Pitx1 and Msx2 Glutathione S-Transferase Fusion Protein Preparation**

Cells of Escherichia coli strain BL21 (DE3) was transformed using the plasmids selected after confirming the sequences. Bacterial cultures were induced with 1.0 mM isopropyl-1-thio-β-D-galactopyranoside (IPTG) for 3 hours. Cells were collected after centrifugation at 5000×g for 30 minutes at 4°C. The cultures were resuspended in ice-cold phosphate buffered saline (PBS). Cells lysis was performed by adding lysozyme to a final concentration of 1 mg/ml and incubation on ice for 30 minutes. Triton X-100, DNase I and 5 µg/µl RNase A and 1 mM PMSE were added to the lysates. After incubation at 4°C for 30 minutes, lysates were spun at 3000×g for 30 minutes. Supernatants were removed and adjusted to 1 mM DTT and 1 mM PMSE. Fusion proteins were purified using glutathione agarose beads (Sigma, St. Louise, MO) and performed by adding increasing amounts of purified fusion proteins to fresh bacterial lysates. Bacterial lysis was performed by adding lysozyme to a final concentration of 1 mg/ml and incubation on ice for 30 minutes. Triton X-100, DNase I and 5 µg/µl RNase A and 1 mM PMSE were added to the lysates. After incubation at 4°C for 30 minutes, lysates were spun at 3000×g for 30 minutes. Supernatants were removed and adjusted to 1 mM DTT and 1 mM PMSE. Fusion proteins were purified using glutathione agarose beads (Sigma, St. Louise, MO) according to standard protocols.

**Preparation of Double Stranded DNA Targets**

Two control target DNA sequences used for Pitx1 and Msx2 EMSA were Bicoid: 5′-TATGGCCCTTGAACTCCGGACT-3′ and MBS: 5′-ATGCCCACTAATTGAGG-3′, respectively [49,50]. Target DNAs for Pitx1-CONS3 EMSA and Msx2-CONS3 EMSA were WTpitxBSCONS3: 5′-AGTTCCCTACAATTCCTTACGGTTG-3′, MutpitxBSCONS3: 5′-AGTTCCCTACACCGGTATTGTGAGT-3′, WTmsxBSCONS3: 5′-GACCTGTATGAATTCAGTCTTTGGA-3′ and MutmsxBSCONS3: 5′-GACCTGTATGAAATTCAGTCTTTGGA-3′. Four micrograms of each of the above synthetic oligonucleotide pairs were annealed by boiling for 5 min. in annealing buffer (10 mM Tris, pH 7.5, 50 mM NaCl, 1 mM MgCl2) followed by cooling. They were then labeled in a 20 µl reaction volume using 20 ng of annealed oligonucleotide in polynucleotide kinase (PNK) buffer (New England BioLabs, Inc., Beverly, MA), 10 units of T4 polynucleotide kinase (New England BioLabs, Beverly, MA) and 5 µCi of γ-32P-ATP. Reactions were incubated at 37°C for 1 hour. To remove unincorporated oligonucleotides, the labeled probe reactions were loaded onto Micro Bio-Spin P-30 Tris Chromatography columns (Bio-RAD, Hercules, CA) and centrifuged according to the manufacturer’s instructions and diluted with protein binding buffer to ~2×10^4 cpm/µl.

**Electrophoretic Mobility Shift Assay (EMSA)**

Protein-DNA binding reactions of 20 µl total volume were performed by adding increasing amounts of purified fusion proteins in final reaction of 1X phosphate buffer, 10% glycerol, 0.3 mg/µl BSA and 0.1 µg/µl DNAasel digested poly[dG-dC], incubated on ice for 10 minutes and then further incubated with addition of 1 µl of [32P]-labeled annealed probe on ice for 20 minutes. One microliter of loading dye was added to a free probe reaction (no protein) to assist in locating free probe in the gel. Protein-DNA complexes were separated on a pre-cooled 6% non-denaturing polyacrylamide gel. Electrophoresis was performed at 4°C with 1X Tris-Borate-EDTA (TBE) buffer at 200 volts for 2 hours. Gels were transferred to Whatman paper and dried at 80°C for 2 hours before being subjected to autoradiography at ~80°C.

**In vitro Mutagenesis**

We used a QuikChange Lightning Site-Directed Mutagenesis Kit (Clontech, Mountainview, CA) and the following primer pairs to perform mutagenesis of Pitx or Msx binding sites in the CONS3 construct - SDMpsxBs-F: 5′-GAGGCCCTTCAAGGGTGAAG TAaangggTGAAGGGG-3′, SDMpsxBs-R: 5′-CTTCTTTTTTAAAGTCCCTGACaccaTTACCG TGAAGAGGCGCTC-3′ and SDMMsxBs-F: 5′-GGGCTTGTTACCTTACAGGAATG aggceggATAGGGTTCAAATAAACAATG-3′, SDMMsxBs-R: 5′-CATGTGG TATTGGAACCTGATCgccCAATCGGAAG-AGT-GAGGACCATGGCC-3′. The mutated constructs were sequenced to confirm the introduced mutation prior to purification for pronuclear microinjection. E11.5 transgenic embryos were collected and tested for reporter activity as described above.

**Chromatin Immunoprecipitation (ChIP) Assay**

The ChIP assays were performed as previously described [56] using the ChIP Assay Kit (Upstate/Millipore, Billerica, MA) with the following modifications. LS-8 cells were fed for 24 hours, harvested and plated in 60 mm dishes, then cross-linked with 1% formaldehyde for 10 minutes at 37°C the next day. All PCR reactions were done under an annealing temperature of 61°C. The antibodies for amplifying the Pitx2 binding site in the Bmp4 CONS3 are as follows: forward 5′-CGACCCACAGATTCCAACCT-3′ and reverse 5′-CAGGAAGGAAT-TCGCTGGAA-3′ (chr14:47,056,511–47,056,642). The two control primers are as follows: forward 5′-AGACCAACAGGGCATCATTGG-3′ and reverse 5′-GGAACTGTGGTAAGGTCTTTGGA-3′ (chr14:47,056,304–47,056,390); forward 5′-TGACTGTGGGT-CAGTCAGTCA-3′ and reverse 5′-TGCTTCACCAAGGTCTCG-3′ (chr14:47,058,298–47,058,653). All PCR products were evaluated on a 2% agarose gel in 1X TBE for appropriate size. Quantitative real-time PCR was performed using the same annealing temperature but extending the number of cycles. Identical amounts of the IP DNA and IgG DNA were loaded as template. All of the regular PCRs and real-time PCR products were confirmed by sequencing.

**Supporting Information**

**Figure S1** Bmp4Δneo and TgCONS3 β-gal activity in initiation stage incisor. Whole mount and sagittal sections of Bmp4Δneo and TgCONS3 transgenic upper incisors. Abbr: NP, nasal pit; MNP, medial nasal process; Mxp, maxillary process; MdDp, mandibular process; OC, oral cavity; UI, upper incisor; M, mesenchyme; DL, dental lamina; D, dorsal; V, ventral; A, anterior; P, posterior. (TIF)

**Figure S2** Bmp4Δneo and TgCONS3 β-gal activity in cap-stage incisors. Sagittal sections of cap stage Bmp4Δneo and TgCONS3 transgenic upper and lower incisors. Note persistent inappropriate expression of TgCONS3 in non-enamel knot dental epithelium and surrounding ectoderm, and its failure to be expressed in the dental papilla and adjacent mesenchyme, as is observed in the control Bmp4Δneo heterozygotes. Abbr: EK, enamel knot; DP, dental papilla; EO, enamel organ; T, tongue; UL, upper lip; LL, lower lip; VL, vestibular lamina. (TIF)

**Figure S3** Laser capture microdissection (LCM) of epithelial incisor region. Sagittal sections of an E11.5 initiation stage incisor pre- and post-LCM. The captured
epithelium was identified by bright field microscopy. Scale bar: 100 μm.

Figure S4 Pitx and Msx binding sites in the Bmp4 IE/LB enhancer. Sequence of the 758 bp region (chr14:47,056,171–47,056,928) containing the 396 bp Bmp4 minimal enhancer double underlined (chr14:47,056,283–47,056,678). The Pitx1/2 binding site (5’-TAATCC-3’) and Msx1/2 binding site (5’-GTAATTG-3’) are indicated, and the location of the 467 bp enhancer (chr14:47,056,226–47,056,692) described by Chandler and coworkers [1] containing the 396 bp minimal enhancer sequence contained is underlined.

Figure S5 In vitro binding of Msx to the minimal Bmp4 enhancer. Electrophoretic Mobility Shift Assay (EMSA) exhibits robust binding of Msx2 protein to both a positive control MBS DNA sequence and to the consensus Msx1/2 binding site in the CONS3 sequence. Competition with specific or non-specific cold probes indicates sequence-specific binding of GST-Msx2 fusion protein to the consensus Msx1/2-binding motif.

Figure S6 Transgenic mutational analysis of Pitx and Msx binding sites. Graphical representation of the transgenic mutational results presented in Fig. 3B indicates that Pitx binding site is necessary for reporter expression in forelimb and hindlimb AER and mesenchyme and orofacial tissues.

Figure S7 Integrative epigenomic analysis suggests that the human orthologous sequence of mouse CONS3 likely functions as an enhancer. Using public epigenomic data from the University of California at Santa Cruz (UCSC) Genome Browser, we analyzed the human homolog of CONS3 (labeled CONS3 at the upper right hand corner of the top genome browser view; genome assembly hg18). This region is enriched for an enhancer associated histone mark H3K4me1, is DNase hypersensitive, is a binding site for transcription factors Max and c-Fox in human embryonic stem cells, and is annotated to be in “enhancer state” in multiple human cell lines by ChromHMM [62]. These multiple lines of evidence suggest CONS3 homolog may also function as an enhancer in human.

Table S1 Families of Transcription Factors (TFs) with their InterPro (IPR) DNA binding domain annotation number that have potential binding sequences in the minimal Bmp4 enhancer. Transcription factors families with binding sites (BS) in the minimal Bmp4 enhancer in >75% and >90% of aligned vertebrates are indicated.

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Author Contributions

Conceived and designed the experiments: DJ SAL BAA RLM. Performed the experiments: DJ SAL IJO XL AT EAR. Analyzed the data: DJ SAL AA SEC JWKH MLB BAA RLM. Contributed reagents/materials/analysis tools: BRO MLB BAA RLM. Wrote the paper: DJ SAL IJO RLM.

References

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