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Integration of FGF and TWIST in calvarial bone and suture development

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SUMMARY

Mutations in the FGFR1-FGFR3 and TWIST genes are known to cause craniosynostosis, the former by constitutive activation and the latter by haploinsufficiency. Although clinically achieving the same end result, the premature fusion of the calvarial bones, it is not known whether these genes lie in the same or independent pathways during calvarial bone development and later in suture closure. We have previously shown that *Fgfr2c* is expressed at the osteogenic fronts of the developing calvarial bones and that, when FGF is applied via beads to the osteogenic fronts, suture closure is accelerated (Kim, H.-J., Rice, D. P. C., Kettunen, P. J. and Thesleff, I. (1998) *Development* 125, 1241-1251). In order to investigate further the role of FGF signalling during mouse calvarial bone and suture development, we have performed detailed expression analysis of the splicing variants of *Fgfr1-Fgfr3* and *Fgfr4*, as well as their potential ligand *Fgf2*. The *IIIc* splice variants of *Fgfr1-Fgfr3* as well as the *IIIb* variant of *Fgfr2* being expressed by differentiating osteoblasts at the osteogenic fronts (E15). In comparison to *Fgf9*, *Fgf2* showed a more restricted expression pattern being primarily expressed in the sutural mesenchyme between the osteogenic fronts. We also carried out a detailed expression analysis of the helix-loop-helix factors (HLH) *Twist* and *Id1* during calvaria and suture development (E10-P6). *Twist* and *Id1* were expressed by early preosteoblasts, in patterns that overlapped those of the FGF ligands, but as these cells differentiated their expression dramatically decreased. Signalling pathways were further studied in vitro, in E15 mouse calvarial explants. Beads soaked in FGF2 induced *Twist* and inhibited *Bsp*, a marker of functioning osteoblasts. Meanwhile, BMP2 upregulated *Id1*. Id1 is a dominant negative HLH thought to inhibit basic HLH such as Twist. In *Drosophila*, the FGF receptor FR1 is known to be downstream of Twist. We demonstrated that in *Twist*$^{+/-}$ mice, FGFR2 protein expression was altered. We propose a model of osteoblast differentiation integrating Twist and FGF in the same pathway, in which FGF acts both at early and late stages. Disruption of this pathway may lead to craniosynostosis.

Key words: TWIST, FGF, Craniosynostosis, Suture, ID, FGFR, BMP, Intramembranous bone formation, Mouse, Human

INTRODUCTION

Except for the supraoccipital bone, the majority of the calvarial bones form by intramembranous ossification, directly from mesenchyme without a cartilage preformer. Ossification begins in centres of condensing mesenchymal cells, in which osteoblasts subsequently differentiate. These centres then expand and where two bones confront each other a joint called a suture is formed. Thus a suture consists of two membrane bone ends and interposed mesenchymal tissue. Later in development the sutures are the primary sites of osteoblast differentiation and bone formation. Signalling mechanisms governing this process, as in many other systems in the body, involve conserved growth factors such as FGFs and members of the TGFβ superfamily as well as transcription factors such as MSXs and CBFA1 (Wilkie, 1997 review; Karsenty, 1998 review; Kim et al., 1998). There is evidence that tissue interaction between the underlying brain and the calvarial mesenchyme may be involved (Opperman et al., 1993, 1995, 1998).

Mutations in the genes encoding TWIST and fibroblast growth factor receptors (FGFR) 1-3 as well as MSX2 are known to cause craniosynostosis, premature fusion of the cranial sutures leading to skull deformity (El Ghouzzi et al., 1997; Howard et al., 1997; Paznekas et al., 1998; Muenke et al., 1994; Wilkie et al., 1995; Bellus et al., 1996; Jabs et al., 1993, 1994). *Fgfr*s are expressed at numerous locations during early mouse development including the craniofacial area (Orr-Urtreger et al., 1991; Wilke et al., 1997) and, although *Fgfr*s have been detected in developing bones and sutures (Orr-Urtreger et al., 1991; Iseki et al., 1997; Delezoide et al., 1998; Kim et al., 1998), little is known about their detailed expression during calvarial bone development.

Twist proteins are conserved basic helix-loop-helix transcription factors (bHLH) and Inhibitors of differentiation (Ids) are conserved dominant negative helix-loop-helix

proteins (dnHLH). Both have been implicated as regulators of mesoderm differentiation and myogenesis in both *Drosophila* and vertebrate development (Benezra et al., 1990; Bate et al., 1991) though, in contrast to *Drosophila* Twist, murine Twist is thought to act as a suppresser rather than an activator of myogenesis (Hebrok et al., 1994). Although, Id1 lacks a DNA-binding domain, it inhibits bHLH's function by suppressing their heterodimerization through direct protein-protein interactions (Pesce and Benezra 1993). Early osteoblastic cell cultures have been shown to express both *Twist* and *Id*, with expression decreasing as maturity increases (Ogata and Noda 1991; Murray et al., 1992). We therefore postulate that they may perform similar regulatory functions in osteoblast differentiation as in the myoblast lineage.

Individuals with mutations in either FGFR1-FGFR3 or TWIST have similar craniosynostotic phenotypes. Although most patients with the Saethre-Chotzen syndrome have TWIST mutations, some patients with an overlapping phenotype have a mutation in either FGFR3 or FGFR2 (Paznekas et al., 1998). Interestingly, *Drosophila Twist* is thought to inhibit DFR1, a *Drosophila* FGF-receptor homologue (Shishido et al., 1993). The question then begs whether *Twist* and *Fgf* are in the same or parallel signalling pathways in osteoblast differentiation and calvarial bone development. To this end, we have performed detailed in situ hybridisation analysis to detect the splicing alternatives of *Fgfr1-Fgfr3*, *Fgf2*, *Bone sialoprotein (Bsp)*, *Twist* and *Id* during calvarial bone development. We show that these genes are developmentally regulated. In addition, we have performed in vitro experiments and show that FGF2 upregulates *Twist* and that BMP2 upregulates *Id*. We also demonstrate that FGF2 has different effects on *Bsp* depending on the stage of osteoblast differentiation and that, in $Twist^{+/-}$ mice, FGFR2 protein expression is altered.

We thus present evidence of *Twist*-, *Id*- and *Fgf*-mediated signalling in osteoblast differentiation and calvarial bone formation, and propose a possible model that integrates *Twist* and *Fgf* in this signalling network.

MATERIALS AND METHODS

Preparation of tissues

Whole heads of mouse embryos (CBA × NMRI) aged between E10 and E15 and calvaria from mice aged between E15 and P6 were processed for both sectional and whole-mount in situ hybridisation according to Kim et al. (1998). 7 μm frontal, serial sections were cut of both whole heads and calvaria dissected free from the underlying brain. Calvarial whole mounts were separated from the overlying skin and underlying brain. We therefore studied stages prior to bone initiation until suture morphology has been established.

In vitro experiments

Calvarial explants were prepared from mice aged E15 according to Kim et al. (1998). Affi-Gel agarose beads (Biorad) were incubated in 100 ng/μl recombinant human BMP2 protein (Genetics Institute, MA, USA), heparin-binding acrylic beads (Sigma) were incubated in 25 ng/μl recombinant human FGF2 protein (R&D Systems Ltd, UK), or bovine serum albumin (BSA) (same concentrations as for BMP2 and FGF2) for 1 hour at 37°C. Beads were then placed either between the two parietal bones on the mid-sutural mesenchyme or on the centre of the parietal bone of freshly prepared calvarial explants. These were cultured for 48 hours then processed for either paraffin sections or whole mounts, as previously described by Kim et al. (1998).

Detection of *Twist*, *Id1*, *Bsp*, *Fgfr1b*, *Fgfr1c*, *Fgfr2b*, *Fgfr2c*, *Fgfr3b*, *Fgfr3c*, *Fgfr4* and *Fgf2* mRNA by in situ hybridisation

Preparation of *Fgfr* and *Bsp* mRNA probes has previously been described (Kettunen et al., 1998, Kim et al., 1998, Rice et al., 1999). The *Twist* probes were prepared from a 400 bp fragment of murine *Twist* cDNA in pT7T3 19U, which was digested with *Xba*I and *Eco*RI. *Id1* probes were prepared from a 900 bp fragment of murine *Id1* cDNA in pBS-SK, digested with *Bam*HI and *Hin*dIII. Murine *Fgf2* cDNA in pGEMZ2 was digested with *Sma*I and *Eco*RI producing 579 bp fragments.

In situ hybridisation on tissue sections was performed using [^{35}S]UTP-labelled riboprobes as described previously (Vainio et al., 1991; Kim et al., 1998). Following in situ hybridisation the sections were stained with Delafield's haematoxylin and mounted with DePeX (BDG). Images were taken using a Cohu 4912-5000 CCD (Cohu, SanDiego, CA, USA) camera and a Scion LG-3 Frame Grabber card (Scion, Frederick, MD, USA) with an Olympus BX50 microscope and a Macintosh PPC computer. Images were then processed with the NIH Image 1.61 program (US National Institute of Health, available from the Internet from zippy.nimh.nih.gov) and Adobe Photoshop 4.0 (Adobe Systems, San Jose, CA, USA) software. The silver grains in the dark-field image were selected, coloured red then superimposed onto the bright-field image.

In situ hybridisation on whole mounts was performed using digoxigenin-UTP labelled riboprobes according to the protocol described by Wilkinson and Green (1990), with modifications (Kim et al., 1998).

Detection of FGFR by immunostaining

Whole heads were fixed and sectioned as described (Liu et al., 1999). Primary FGFR2 antibody (Santa Cruz Biotechnology) was allowed to react with tissue sections. A biotinylated, affinity-purified secondary antibody (Zymed Laboratories, San Francisco) was bound to the primary antibody and an HRP-conjugated strepadvidin was added as a signal amplifier. The immunoreactivity was visualized with an AEC chromagen/substrate system that creates a reddish deposit. Sections were counterstained with Haematoxylin. Primary FGFR1 antibody (Santa Cruz Biotechnology) was also used. A biotinylated, affinity-purified secondary antibody, and a Vectastain Elite ABC kit was used to detect immunoreactivity (Vector Laboratories, CA, USA). These sections were not counterstained. Neutralizing peptides, specific for each primary antibody (Santa Cruz Biotechnology), were used to test antibody specificty. In addition, normal rabbit serum IgG (Santa Cruz Biotechnology), of the same concentration as the primary antibody, was used as a control.

RESULTS

Expression of *Twist, Id* and *Bone sialoprotein* during calvarial bone and sagittal suture development

To address the roles of *Twist* and *Id* in calvarial bone development, we examined their mRNA expression patterns in both calvarial whole mounts and serial sections and compared them to *bone sialoprotein* (*Bsp*), a marker of mature osteoblasts. *Bsp* was first expressed at E12 just lateral to the temporal cartilages, in a strip medial and superior to the eye extending occipitally (Fig. 2G). From these ossification centres in the frontal and parietal bones, the expression spread toward the apex of the cranium where the osteogenic fronts approximate to form a suture (E15), two osteogenic fronts and intervening mesenchyme (Fig. 1). Until E17 *Bsp* was expressed throughout the calvarial bones, most notably on their outer surfaces (Figs 2J, 3A,H, 4A,C,E). In contrast, osteoclasts are

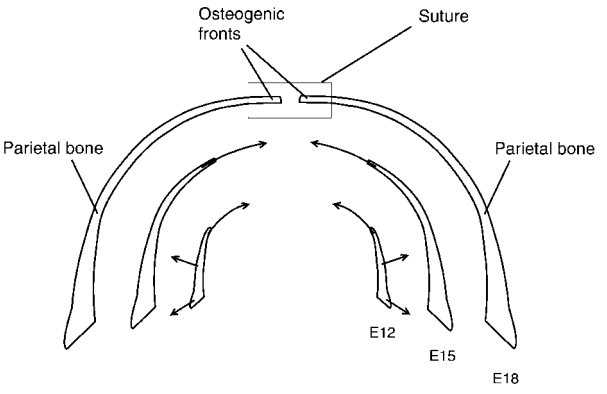

Fig. 1. Schematic diagram to illustrate calvarial bone growth and suture formation. Ossification of the frontal and parietal bones starts on the lateral side of the head. *Bsp* expression is first seen at E12 in osteoblasts just lateral to the temporal cartilages, in a strip medial and superior to the eye extending occipitally (Fig. 2G). From these centres, the process spreads upward toward the apex of the cranium to meet in the midline where a suture is formed (E15), i.e., two osteogenic fronts with intervening mesenchyme (Figs 3A, 4C). Osteoblasts are active mainly on the ectocranial and sutural surfaces, whereas osteoclastic activity is mainly on the endocranial surface (Rice et al., 1997). Growth of the calvarial bones is co-ordinated between the underlying brain and overlying skin.

found mainly on the endocranial surfaces (Rice et al., 1997) and so, as the calvaria expands, there is an intimate balance between bone apposition and resorption, thus maintaining bone thickness and shape. After E17, transcripts became more restricted to areas of high activity, notably the sutures (Figs 3J, 4G). Whole mounts confirmed the findings of sectioned tissue, with *Bsp* expression clearly demarcating the developing calvarial bones and illustrating the approximation of their osteogenic fronts (Fig. 4A,C,E).

At E10, *Twist* was intensely expressed in mesenchyme throughout the first and second branchial arches, as well as in the mesenchyme surrounding the developing eye and cranial mesenchyme just beneath the epithelium (Fig. 2B). Expression then became more restricted so that, by E14, transcripts were seen bordering areas of condensing calvarial mesenchyme (Figs 2E,H,K, 4B). These condensations consist of osteoprogenitors that differentiate into functioning osteoblasts, the temporal, frontal and parietal bones being thereby initiated. *Twist* mRNA was also detected close to developing cartilages. From E15 to P1, *Twist* continued to be expressed in the

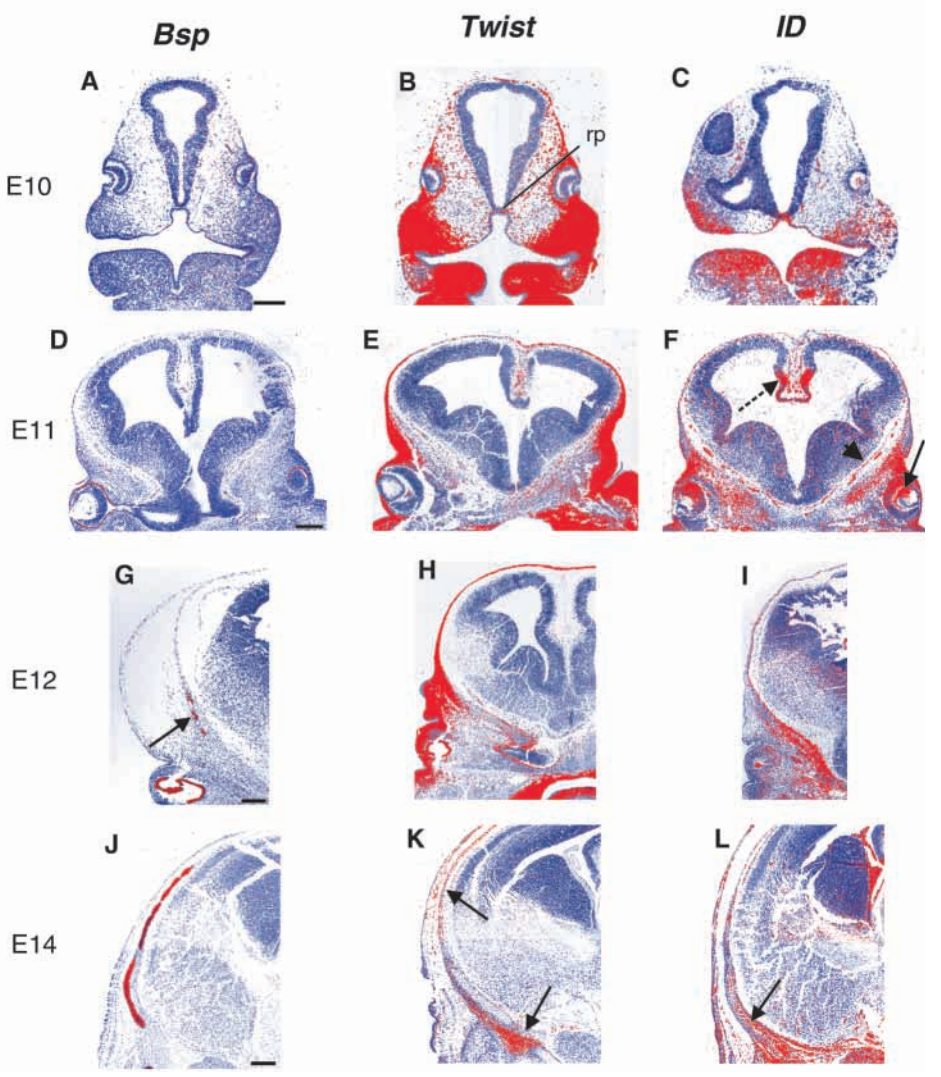

Fig. 2. *Bsp*, *Twist*, and *Id* expression during calvarial bone and sagittal suture development E10-14. (A,D,G,J) *Bsp* is expressed by functioning osteoblasts. Unlike long bones, the calvarial bones form directly from mesenchymal condensations, without a cartilage preformer. Osteoblasts differentiate directly from mesenchyme, and matrix is secreted that then calcifies. In the calvarial bones, these condensations start to appear at E11, so that by E12 (G) *Bsp* transcripts are seen sandwiched between the developing eye and brain (arrow). As the calvarial bones develop *Bsp* expression extends rostrally within the calvarial mesenchyme, between the overlying skin and the underlying meninges (J). (B,E,H,K) *Twist* is intensely expressed in head mesenchyme. At E10 transcripts are seen widely distributed in the first and second branchial arches, the surroundings of the developing eye and cranial mesenchyme below the epithelium, including that around Rathkes poutch (rp) (B). In the calvaria, this becomes confined to mesenchyme from which differentiate osteoblasts (K, arrows). (C,F,I,L) *Id* has a similar expression pattern to *Twist* but is also expressed in epithelia including the neuroepithelium of the developing hippocampus (F, dotted arrow), and in the developing retina (F, arrow), meninges (F, arrowhead) and cartilage (L, arrow). rp, Rathkes pouch. Scale bars, 200 μm, images of the same age are the same scale.

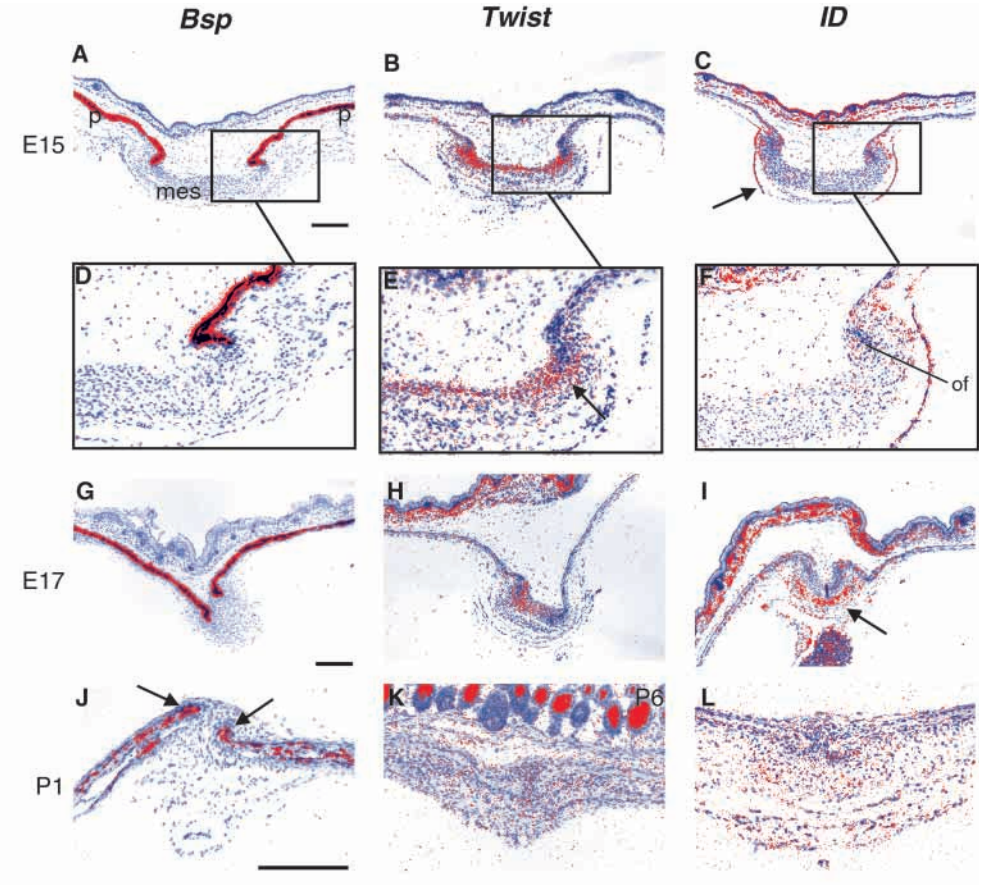

Fig. 3. *Bsp*, *Twist* and *Id e*xpression during calvarial bone and sagittal suture development. Between E15 and P1, the parietal bones approximate but do not fuse. Frontal sections showing the sagittal suture with the two parietal bones (p) and the mid-sutural mesenchyme (mes). The plane of section is illustrated by the dotted arrow in Fig. 4E. (A,D,G,J) At E15, intense *Bsp* expression is seen throughout the parietal bones (A). (D) High magnification of the box marked in A. Postnatally, expression is more restricted to osteoblasts at the bone ends in the sutures (J, arrows). (B,E,H,K) *Twist* is highly expressed in the mid-sutural mesenchyme with highest expression in the osteoprogenitors but not in functioning osteoblasts (B,E arrow), compare to D. *Twist* is also expressed in the lower layers of the skin. *Twist* expression decreases postnatally (K). (C,F,I,L) *Id* expression in the calvarial mesenchyme is less intense than it was in earlier stages (compare Fig. 2). At E15 *Id* is only weakly expressed by mesenchymal cells some distance from the osteogenic front (of). *Id* is still expressed in the meninges (C, arrow) and, as for *Twist*, in the lower layers of the skin. Cartilaginous rods are occasionally and transiently seen in the sutural mesenchyme around the time of birth, *Id* is expressed in this cartilage (I, arrow). *Id* expression decreases postnatally (L). mes, mesenchyme; of, osteogenic front; p, parietal bone. Scale bars, 200 μm, images of the same age are the same scale.

calvarial mesenchyme and, as in earlier stages, not in mature osteoblasts (Figs 3B,E,H, 4D,F). Postnatally its intensity had decreased (Figs 3K, 4H). These findings were again corroborated by whole mounts with *Twist* being expressed in the calvarial mesenchyme between the calvarial bones and most intensely close to the osteogenic fronts (Fig. 4B,D,F). Later, transcripts were confined to areas of high activity, delineating the calvarial bones (Fig. 4H).

Id1, like *Twist*, was initially expressed in the mesenchyme of the first and second branchial arches, but not in such a widespread manner. *Id1* was most notable in the rostral half of the mandibular arch and the lateral section of the maxillary arch (Fig. 2C). Unlike *Twist*, *Id1* was also expressed in epithelia adjacent to these mesenchymal areas and, at E10, in the epithelium of Rathkes pouch, whereas *Twist* was expressed in the surrounding mesenchyme. From E11, transcripts were also seen in the developing hippocampus and retina (Fig. 2F). Similar to the expression of *Fgfr1c*, *Fgfr3b* and *Fgfr3c*, *Id1* was expressed in developing cartilage (compare to Fig. 6E), which mainly does not directly contribute to the calvarial bone. Interestingly, in E11-14 embryos, *Id1* mRNA was detected in the calvarial mesenchyme just prior to and during the condensation of early osteoblasts (Fig. 2F,I,L). By E15, this *Id1* activity in calvarial mesenchyme had reduced (Fig. 3C,F). *Id1* transcripts were also notably detected in the deeper layers of the skin and in the meninges (Figs 2F,I,L, 3C,F,I).

Expression of *Fgfr1b*, *Fgfr1c*, *Fgfr2b*, *Fgfr2c*, *Fgfr3b*, *Fgfr3c* and *Fgfr4* during calvarial bone and sagittal suture development

The FGFRs are high-affinity tyrosine kinase receptors, which together with cofactors mediate the effects of FGFs. They are transmembrane glycoproteins with two or three extracellular immunoglobulin domains. These binding domains differ between alternative splice variants, which are of particular interest as they possess different ligand-binding specificities (Ornitz et al., 1996) as well as exhibiting unique temporospatial expression patterns suggesting unique functions (Orr-Urtreger et al., 1991; Peters et al., 1992; Orr-Urtreger et al., 1993; Kettunen et al., 1998). In addition, many of the human mutations in FGFR1-FGFR3 causing disorders in bone development are found in or close to the third immunoglobulin (III) domain (Wilkie, 1997). We have previously detected the *IIIc* splice variant of *Fgfr2* (*bek*) (Kim et al., 1998) and Iseki et al. (1997) showed the full-length *Fgfr2* in the developing calvaria. Here we have investigated the expression patterns of the *IIIb* and *IIIc* splice variants of *Fgfr1-Fgfr3, as well as Fgfr4*.

The expression pattern of *Fgfr1b* was generally weak compared to the other *Fgfr*s and transcripts were not seen in either the developing calvarial bone or sutures (Fig. 5A-C). Developing teeth were used as positive controls, where *Fgfr1b* mRNA was intensely expressed in the inner enamel epithelium of E16 molar teeth (data not shown; Kettunen et al., 1998).

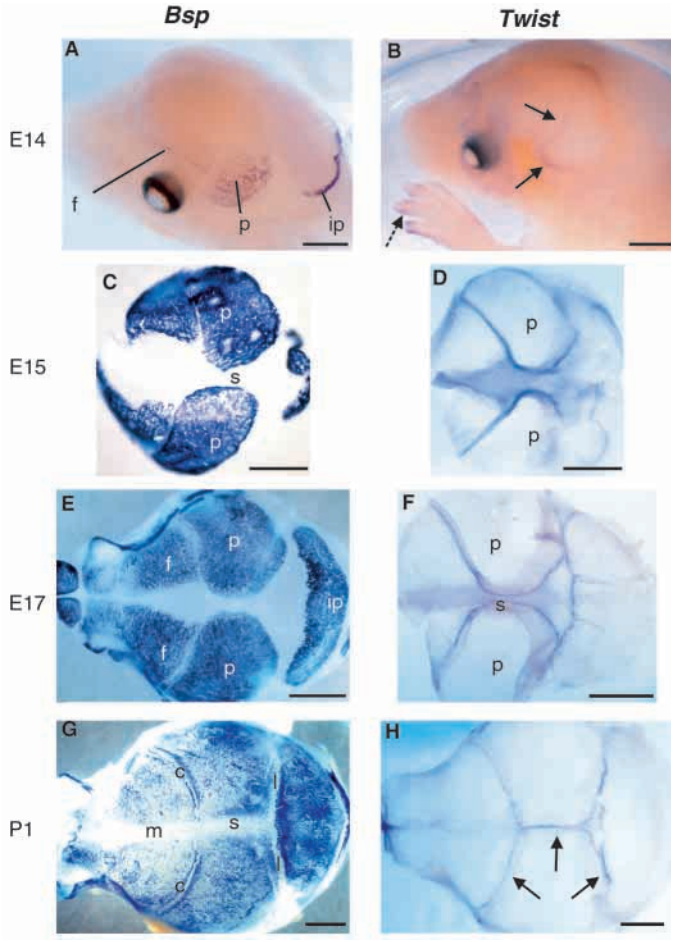

Fig. 4. *Bsp* and *Twist* expression during calvarial bone and suture development, detected by whole-mount in situ hybridisation. (A,B) Whole heads; (C-H) calvariae dissected free from the underlying brain and overlying skin. (A,C,E,G) *Bsp* starts in ossification centres on the lateral and posterior surfaces of the calvaria, these expand so that by E17 they have begun to assume their characteristic bone shapes (E). Thereafter, osteoblast activity and therefore *Bsp* expression is largely concentrated in the sutures (G). (B,D,F,H) *Twist* mRNA is confined to the mesenchyme in between the forming bones, with its strongest expression directly neighbouring the osteogenic fronts (arrows). *Twist* is also expressed in the developing digits (B dotted arrow). c coronal suture; f, frontal bone; fs, frontal suture; ip, interparietal bone; l, lambdoidal suture; p, parietal bone; s, sagittal suture. Scale bars, 1 mm.

Very low levels of *Fgfr1c* expression were detected in the calvarial bones, most notably in the osteogenic fronts between E15 and 17, major sites of osteoblastic condensation and differentiation (Fig. 5D-F). *Fgfr1c* was also expressed in many cartilages in the developing head.

Fgfr2b (*kgfr*) was expressed in the osteogenic fronts of the parietal bones (E15-17). In addition, transcripts were located in developing epithelia, notably the skin including hair follicles (Fig. 5G-I). *Fgfr2c* (*bek)* was found in similar locations to *Fgfr2b* but at generally much stronger intensity (Fig. 5J-L). Transcripts were generally detected in perichondria and periostea, as well as in the superficial layers of skin. Postnatally, expression was at the same locations but diminished in intensity (Fig. 5L). In developing epithelia, transcripts were detected at low intensity, in comparison to *Fgfr2b*.

Fgfr3b was weakly and *Fgfr3c* strongly expressed in many cartilages of the head. The majority of this cartilage does not

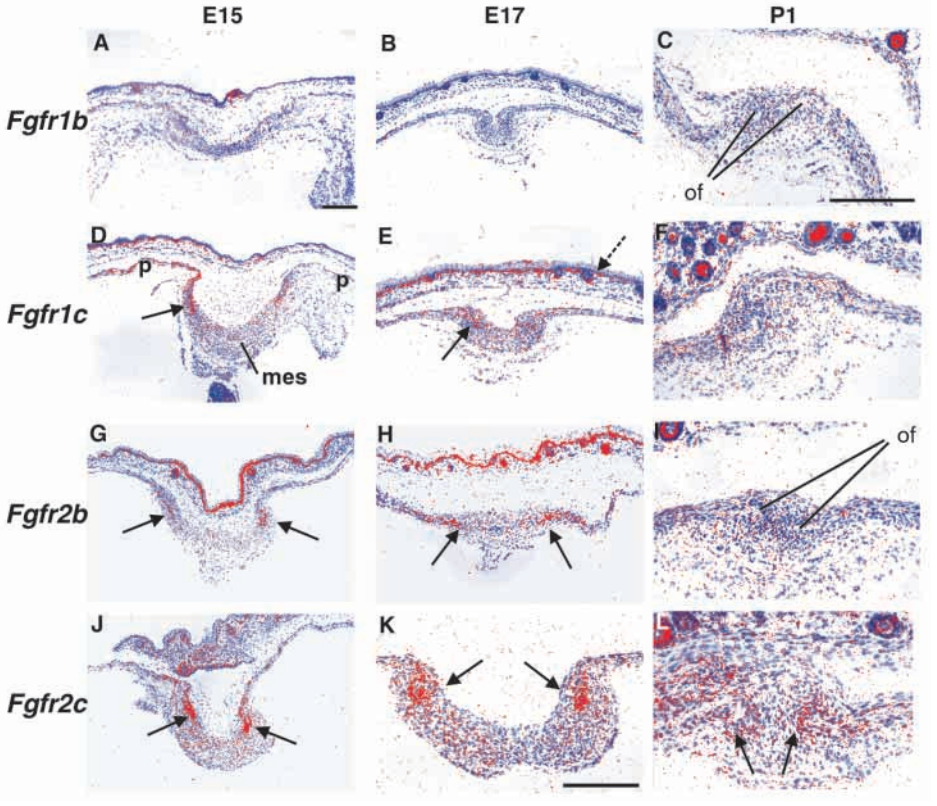

Fig. 5. *Fgfr1b*, *Fgfr1c*, *Fgfr2b* and *Fgfr2c* expression during calvarial bone and sagittal suture development. Frontal sections showing the two parietal bones (p), their osteogenic fronts (of) and the mid-sutural mesenchyme (mes). Transcripts of *Fgfr1b*, are not detected in the developing calvaria studied. At E15, *Fgfr1c*, *Fgfr2b*, *Fgfr2c* and *Fgfr3c* (Fig. 6D) are all expressed in the sutural osteogenic front (arrows), *Fgfr1c* and *Fgfr2b* being expressed with the lowest intensity, *Fgfr2c* with the strongest (compare to Fig. 3D-F). After E15, the intensity decreases with only *Fgfr2c* being expressed postnatally (L). *Fgfr1c*, *Fgfr2b* and *Fgfr2c* mRNAs are also detected in epithelia including hair follicles, with expression commencing at E15; in this regard, *Fgfr2b* shows the strongest expression (G-I). of, osteogenic fronts; mes, mid-sutural mesenchyme; p, parietal bone. Scale bars, 200 μm, Scale in A applies to A,B,D,E,G,H and J; scale in C, applies to C,F,I and L.

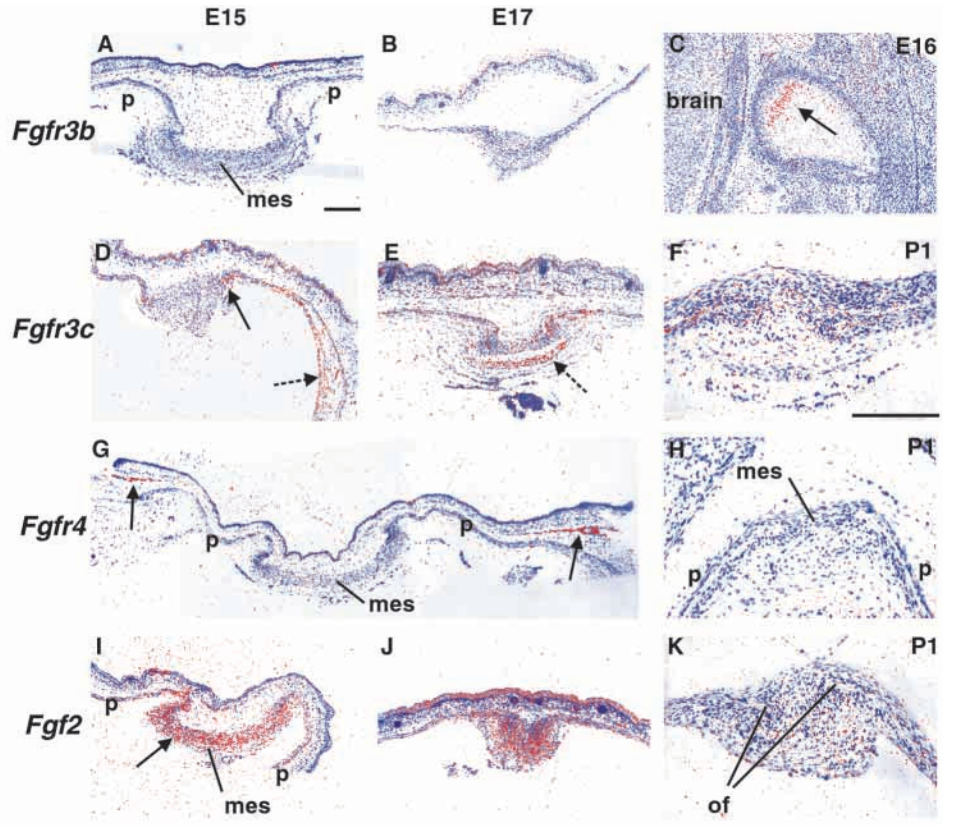

Fig. 6. *Fgfr3b*, *Fgfr3c*, *Fgfr4* and *Fgf2* expression during calvarial bone and sagittal suture development. *Fgfr3b* and *Fgfr3c*, as well as *Fgfr1c*, are expressed in many cartilages in the developing embryonic skeleton of the head. These include those of the cranial base, the condyle of the mandible (C) and cartilages that form on the lateral aspect of the cranial vault, endocranial to the forming intramembraneous bones. Cartilage rods are also seen in the sutural mesenchyme; their appearance is transient, around the time of birth and maybe a tissue reaction to mechanical irritation. This cartilage does not contribute to the calvarial bones that form, in the main by intramembranous and not endochondral ossification. *Fgfr1c*, *Fgfr3b* and *Fgfr3c* are expressed in all these cartilages. *Fgfr3c* mRNA is detected most strongly (E, dotted arrow, compare to Fig. 3I). At E15, *Fgfr3c* is also weakly expressed in the developing calvarial bones (D dotted arrow), notably at the sutural osteogenic front (D, arrow). (G,H) *Fgfr4* mRNA is not detected in the developing calvarial bones or mesenchyme (G, E15; H, P1). Transcripts are found in the developing muscle, on the lateral aspects on the cranium between the epithelium and the calvarial bones (G arrows). (I-K) *Fgf2* transcripts are intensely expressed the mid-sutural mesenchyme (I, arrow), and weakly in the calvarial bones and underlying meninges. This expression is most notable at E15. of, osteogenic fronts; mes, mid-sutural mesenchyme; p, parietal bone. Scale bars, 200 μm, Scale in A refers to A-E,G,I,J; scale if F refers to F,H,K.

contribute to the calvarial bones, which form directly from mesenchyme (Fig. 6C,E). *Fgfr3c* mRNA was also detected with low intensity in the head periostea and sutural osteogenic fronts (Fig. 6D).

Transcripts of *Fgfr4* were not detected in the developing calvarial bone or mesenchyme. However, *Fgfr4* mRNA was detected strongly in developing muscle, notably in the developing temporalis between the epithelium and the underlying calvaria (Fig. 6G,H).

Expression of *Fgf2* during calvarial bone and sagittal suture development

We have previously investigated the expression of potential FGFR ligands and have reported that *Fgf9* was expressed both in the calvarial mesenchyme and the developing bone (Kim et al., 1998). Here we found that *Fgf2* demonstrated a more restricted expression patterns, being associated with osteoblast differentiation in the suture. *Fgf2* was expressed in the mesenchyme of the calvarial sutures and more weakly in the developing calvarial bones and the underlying dura mater (Fig. 6I-K). Expression decreased in intensity after E16. Expression of this potential ligand, although overlapping that of the *Fgfr*s, was not primarily expressed in the osteogenic fronts and was also more extensively expressed in the mid-sutural mesenchyme, suggesting paracrine functions.

Differential regulation of *Twist* and *Id* by FGF2 and BMP2

To test the effect of FGF2 on *Twist* expression, we placed FGF2 beads on the mid-sutural mesenchyme of E15 calvaria. FGF2 stimulated the expression of *Twist* in explants cultured for 48 hours (11 out of 14 explants). This was detected by in situ hybridisation in whole mounts as a halo of expression around the beads, which was confirmed by in situ hybridisation in tissue sections (Fig. 7A,B). BSA beads had no apparent effect (n=7). The effect of BMP on *Twist* expression was also tested. BMP2 did not induce *Twist*. Conversely, one can speculate that BMP2 might inhibit *Twist*, in a similar manner to that demonstrated by RT-PCR in cell culture (Tamura and Noda, 1999); however, conclusions regarding inhibition could not be drawn from our experiment.

*Bmp*s are known to be expressed in the OFs of the developing calvarial bones (Kim et al., 1998; Rice et al., 1999). Also, BMP2 has previously been found, in cell culture, to stimulate *Id* in osteoblast-like cells, in pluripotent fibroblastic cells and transiently in myoblast cells that convert to osteoblasts with BMP2 treatment (Ogata et al., 1993; Katagiri et al., 1994). In addition to stimulating *Id*, Katagiri et al. (1994) found that BMP2 induced alkaline phosphatase activity osteocalcin production, markers of osteoblast maturation, as well as inhibiting *MyoD*. We therefore set out to investigate the effects of BMP on *Id* in the developing calvaria. Beads releasing BMP2 stimulated the expression of *Id* in the mesenchyme of E15 calvarial explants cultured for 48 hours (8 out of 8). This was demonstrated by in situ hybridisation in both whole mounts and sectioned tissue (Fig. 7G,H), while beads releasing BSA had no apparent effect (n=4).

Fgfr and *Twist* are in the same signalling network

To test whether FGFR is a target of Twist, we examined the expression of FGFR1 and FGFR2 protein in the calvaria of mice with a *Twist*$^{+/-}$ background. *Twist*$^{-/-}$ mice were not used as they die before calvarial development has progressed sufficiently The distribution pattern of FGFR2 (Fig. 8) was altered in the sagittal suture of *Twist*$^{+/-}$ mice, as compared to wild type. FGFR2 protein was detected in a discrete central area of the mid-sutural mesenchyme. This area contains undifferentiated mesenchymal cells that will differentiate in osteoblasts, osteoprogenitors. FGFR1 protein was detected in the osteoblasts of the calvarial bones (Fig. 9), in the mid-sutural mesenchyme, as well as in the meninges. No difference in FGFR1 distribution could be distinguished between the wild-type and *Twist*$^{+/-}$ mice. Peptide competition studies, the use of appropriate negative and positive controls confirmed antibody specificity and validity (not shown).

Dual effect of FGF2 on *Bsp* expression

At E15, *Bsp* is highly expressed by mature osteoblasts throughout the developing parietal bones (Fig. 3A) and this expression continues when the calvaria are cultured in vitro (Fig. 7E). However, when FGF2-releasing beads were placed on the parietal bone and cultured for 48 hours, this expression was inhibited (Fig. 7C,D) (n=13 out of 14). This effect was seen in whole mounts as a well-defined clear area of reduced *Bsp* expression around the beads and in sections as an area of reduced expression in the calvarial bone. Interestingly, expression in the osteogenic front, were activity is greatest was maintained (Fig. 7D). An intriguing finding was that, although *Bsp* expression was reduced in cells already differentiated, in other cells in close proximity to the bead *Bsp* expression was induced. This expression was barely evident in whole mounts but verified in sections with *Bsp* being expressed in cells around the beads. These were presumably mesenchymal osteoprogenitor cells (Fig. 7D). BSA beads had no such effects (Fig. 7E,F; n=7).

DISCUSSION

In this study, we have analysed the association of Twist and Id with FGF and BMP signalling during cranial bone and suture development. Based on previous data from several laboratories, including our own, and the findings of this study, we have proposed a model of how they may interrelate (Fig. 10).

Twist and Id in calvarial osteogenesis

Our detailed comparison of the expression patterns showed that *Bsp*, which encodes a bone matrix protein was highly expressed by osteoblasts (Bianco et al., 1991; Chen et al., 1991), whereas *Twist* and *Id* were expressed by mesenchymal and osteoprogenitor cells. In the developing calvarial bones, *Twist* and *Id* are expressed by mesenchymal cells, which directly neighbour *Bsp*-expressing osteoblasts lining the bone matrix. This is consistent with the finding that, in cultured osteoblastic cells, *Twist* and *Id* are expressed very early in osteoblast differentiation and that their expression decreases with maturity (Kawaguchi et al., 1992; Murray et al., 1992). Interestingly, osteoblastic cells overexpressing *Twist* stay in an undifferentiated state, with an increased proliferation rate and change from osteoblast to fibroblast in morphology (Glackin et al., 1997). Our results demonstrate for the first time in vivo that *Twist* and *Id* expression correlate well with early osteoprogenitors. Generally, the expression patterns in the craniofacial region are in accord with previously published data (Füchtbauer et al., 1995; Bourgeois et al., 1998; Jen et al., 1996).

Twist$^{-/-}$ homozygotic mice die at E11.5 with a failure of the cranial neural folds to fuse and defects in head mesenchyme,

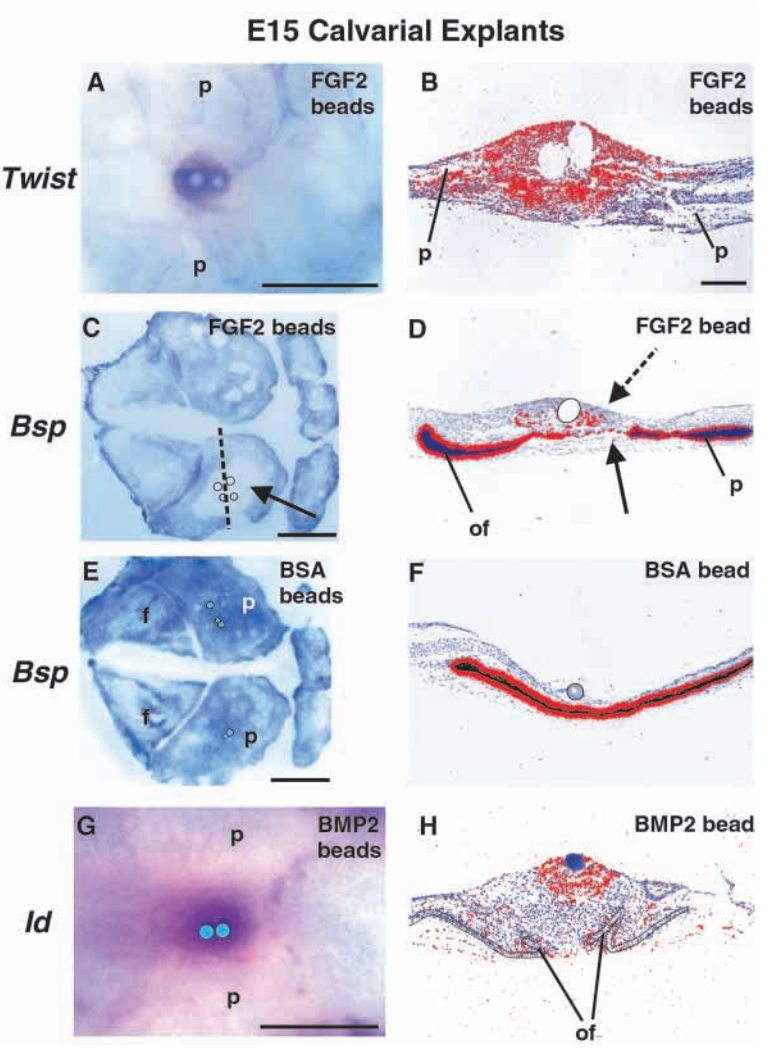

Fig. 7. In vitro effects of FGF2 and BMP beads on E15 calvarial explants. (A,C,E,G) Digoxigenin-UTP labelled in situ hybridisation of whole mounts. (B,D,F,H) [^{35}S]UTP-labelled in situ hybridisation on tissue sections. (A,B) FGF2 beads induce *Twist* in calvarial mesenchyme, (C,D) FGF2 beads inhibits *Bsp* in osteoblasts (arrows) but also stimulates *Bsp* mRNA production in calvarial mesenchyme (osteoprogenitors; dotted arrow), when placed on the parietal bones (p). (E,F) BSA beads have no effect on the normal *Bsp* expression. (G,H) BMP2 beads induce *Id* when placed on calvarial mesenchyme. f, frontal bone; ip, interparietal bone; of, osteogenic front; p, parietal bone. Scale bar in sections 200 μm, all sections same scale. Scale bar in whole mounts 1 mm.

somites and limb buds (Chen and Behringer, 1995). *Twist*$^{+/-}$ mice exhibit limb and calvarial phenotypes reminiscent of Saethre-Chotzen syndrome which is caused by TWIST mutations (El Ghouzzi et al., 1997; Bourgeois et al., 1998). This possibly suggests haploinsufficiency in Saethre-Chotzen patients rather than a dominant negative gene mutation (El Ghouzzi et al., 1997) and is in line with Twist being a negative regulator of osteoblast differentiation.

Others and we have previously shown *Msx1* and *Msx2* to be expressed in the calvarial mesenchyme (Mackenzie et al., 1992; Kim et al., 1998) and we note that their expression patterns overlap with that of *Twist* and at early stages with *Id*. Both MSX1 and MSX2 are known to be intimately involved in osteoblast differentiation (Hodgkinson et al., 1993; Hoffmann et al., 1996) and in the pathogenesis of calvarial bone disorders (Jabs et al., 1993; Satokata and Maas 1994; Liu et al., 1999). Also the osteocalcin promoter contains binding sites for both HLH and MSX proteins (Tamura and Noda 1994; Heinrichs et al., 1993). One can therefore speculate, whether HLHs and MSXs could be either in the same or in parallel signalling pathways.

Role of FGF in calvarial osteogenesis

The expression of *Fgfr1-Fgfr3* in the developing calvarial suture is consistent with mutations in the human FGFR1-FGFR3 genes causing craniosynostosis syndromes. The *IIIc* splicing variants of *Fgfr1-Fgfr3* and *IIIb* variant of *Fgfr2* are all, to some degree, expressed by differentiating osteoblasts at the calvarial bone ends, the osteogenic fronts. Craniosynostosis syndromes, are characterised by early fusion of these bone ends, and this is presumably based on an increase in osteoblast activity possibly as result of precocious osteoblast differentiation.

Interestingly, *Fgfr1-Fgfr3* are also intensely expressed in the cartilages of the cranial base (unpublished observations). Mutations in these genes could therefore lead to a growth defect in the cranial base, which could have the secondary effect of bringing the calvarial bones closer together and therefore increasing the likelihood of premature fusion.

There is evidence indicating that mutations in FGFR1-FGFR3 cause craniosynostosis syndromes by ligand-independent constitutive activation of receptors (Neilson and Friesel 1995; Galvin et al., 1996; Mangasarian et al., 1997). In addition, analysis of the *Bulgy-eye* mouse, which is generated by an insertional mutation at the *Fgf3*/*Fgf4* locus, indicates that ligand overexpression may also cause a craniosynostotic phenotype (Carlton et al., 1998). However, mice ubiquitously overexpressing *FGF2* exhibit chondrodysplasia, with shortened long bones. Interestingly, their occipital bone, a bone formed partly intramembranously and partly from endochondral ossification, appeared to be enlarged (Coffin et al., 1995). Expression of *Fgf2*, although overlapping, differs from the *Fgfr*s; *Fgf2* is expressed primarily in the sutural mesenchyme and *Fgfr*s in the OFs, suggesting paracrine interactions. We have found earlier that FGF4, if placed in vitro on the embryonic osteogenic fronts, will accelerate suture closure, as well as stimulate cell proliferation (Kim et al., 1998). Transgenic mouse models have until now yielded limited information with regard to FGF signalling in intramembranous bone formation and suture fusion. Both knocking out *Fgfr1* and deletion of *Fgfr2's* third Ig loop results in death before start of skeletal development (Deng et al., 1994; Yamaguchi et al., 1994; Xu et al., 1998). Knocking out *Fgfr3* results in long bone overgrowth indicating that *Fgfr3* is a negative regulator of endochondral ossification (Colvin et al., 1996; Deng et al., 1996).

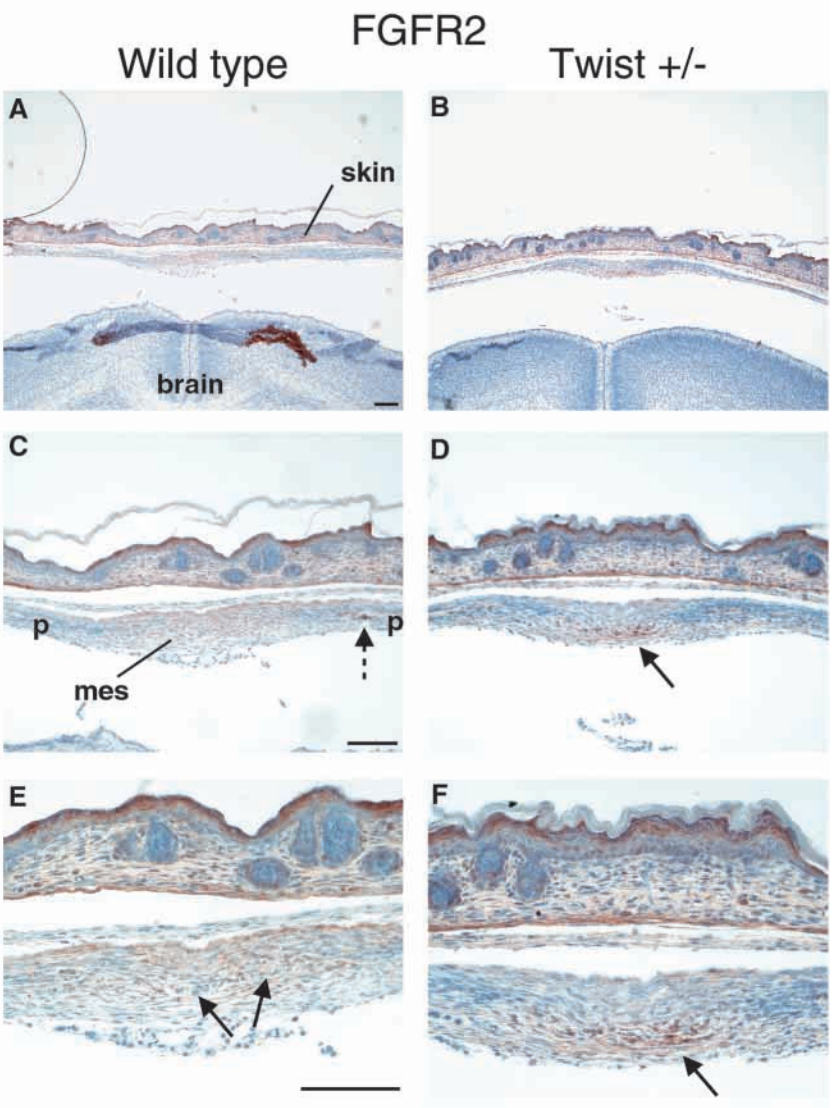

Fig. 8. Immunohistochemical staining for FGFR2 in the, newborn, sagittal suture of wild-type (A,C,E) and *Twist*$^{+/-}$ mice (B,D,F). (C,E) High magnifications of the sections shown in A; (D,F) high magnifications of the sections shown in B. In wild-type mice, FGFR2 protein is detected in the osteoblasts at the osteogenic front (C dotted arrow) as well as weakly and diffusely in the mesenchyme (E arrows). FGFR2 distribution is altered in the *Twist* mutant, being localised more discretely in the mid-sutural mesenchyme (D,F arrows). mes, mid-sutural mesenchyme; p, parietal bone. Scale bars, 100 μm.

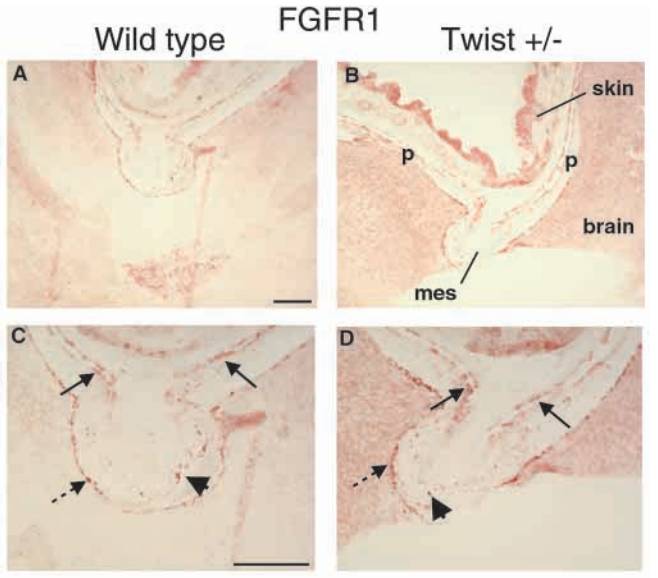

Fig. 9. Immunohistochemical staining for FGFR1 in the newborn sagittal suture of wild-type (A,C) and *Twist*$^{+/-}$ mice (B,D). (C,D) High magnifications of the sections shown in A and B, respectively. FGFR1 protein is detected in the osteoblasts of the calvarial bones (arrows), in the mid-sutural mesenchyme (arrowheads), as well as in the meninges (dotted arrows). No difference in FGFR1 distribution is distinguished between the wild-type and *Twist*$^{+/-}$ mice. mes, mid-sutural mesenchyme; p, parietal bone. Scale bars 100 μm.

Fgf2 knockout mice are morphologically normal with no apparent skeletal phenotype (Zhou et al., 1998).

FGF2 is known to stimulate osteoblast proliferation and inhibit osteoblast differentiation markers (Canalis and Raisz 1980). The effects on bone matrix formation are more confusing, with data suggesting both stimulation and inhibition. Indeed, the effects of FGF2 may be differentiation stage specific with FGF2 causing an increase in matrix mineralization and osteocalcin production in more mature cells (Debiais et al., 1998). Our finding that FGF2 both downregulates *Bsp* mRNA in mature osteoblasts and also induces *Bsp* expression in calvarial mesenchymal cells supports the hypothesis that FGF2 may indeed have different effects at different levels of cell maturity. Interestingly, it has been shown that *Bsp* expression is biphasic, detectable in some early, alkaline phosphatase-negative osteoblastic cells, as well as again later in more mature cells (Malaval et al., 1999).

FGF is associated with Twist signalling

Fgf2 and *Twist* exhibit overlapping expression patterns, both being intensely expressed in the mid-sutural mesenchyme between the calvarial bones, (compare Figs 3B and 6I). We have previously described the expression pattern *Fgf9*, which is also detected at similar locations (Kim et al., 1998). This suggests that FGF and Twist maybe involved in a common signalling network. We therefore studied the effect of FGF on Twist and found that FGF2 upregulates *Twist* expression in calvarial mesenchyme. This is in accordance with an earlier report by McDougall et al. (1997), who found a similar upregulation in osteoblast cell cultures.

Furthermore, we show that in *Twist*$^{+/-}$ mice FGFR distribution is altered, being localised in an ectopic location in the mid-sutural mesenchyme. We have also demonstrated that, in the wild-type suture, *Twist* is expressed at this location, while *Fgfr2* is found here with only weak intensity. Conversely, *Fgfr* is intensely expressed at the osteogenic front, in differentiating osteoblasts, where *Twist* is not; i.e., when Twist is reduced, FGFR alters. These findings, coupled with the knowledge that the TWIST craniosynostosis phenotype is thought to be due to a loss-of-function, and the FGFR craniosynostosis phenotype due to a gain-of-function mechanism, lead us to speculate that Twist's role is to inhibit the terminal differentiation of osteoprogenitors into osteoblasts.

Integration of Twist and Id in FGF-mediated signalling during osteogenesis

In this paper, we have demonstrated, in vivo, that *Twist* and *Id* are is expressed by osteoprogenitors but not by mature osteoblasts. We propose that FGFs have functions at several stages of osteoblast differentiation. FGF2 has both inhibitory and stimulatory effects on osteoblast activity and we present evidence that the inhibitory effects may be via a Twist regulated pathway. In line with Twist having a negative regulatory effect on osteoblast differentiation, the TWIST mutation causing craniosynostosis is thought to be a loss-of-function mutation (El Ghouzzi et al., 1997). Also, we show that Twist regulates FGFR, with *Twist*$^{+/-}$ mice exhibiting altered

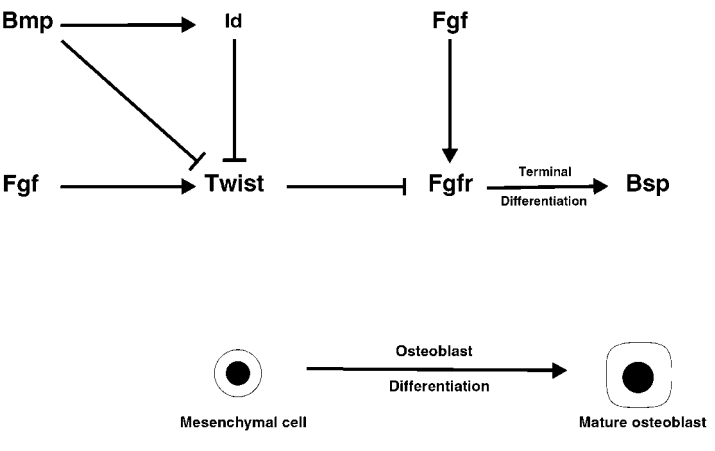

Fig. 10. Schematic model showing how Twist and Id may integrate with FGF signalling during osteoblast differentiation. It is know that BMP2 can induce osteoblast maturation and that Id may inhibit Twist. We have demonstrated that BMP2 can induce *Id* and therefore suggest that the effect of BMP2 on osteoblast maturation maybe via Id/Twist route. Interestingly, it has also been shown that BMP2 inhibits Twist directly. We have demonstrated that FGF both induces *Twist* and inhibits *Bsp*. It is known that a reduction in TWIST/Twist results in craniosynostosis and increased bone growth. An overactivation of FGFR signalling also results in craniosynostosis, and we have shown that FGF can accelerate suture closure and will stimulate *Bsp*. Finally, we demonstrate that Twist alters the expression of FGFRs, thereby directly linking the Twist and FGF pathways.

FGFR protein expression. Thus, Twist would appear to be upstream of FGFR/FGF signalling, though whether it is inhibitory or stimulatory cannot yet be definitively concluded. FGF may also act at a later stage in osteoblast differentiation, with both excess FGF and overactivation of FGF receptors causing an acceleration of suture closure (Carlton et al., 1998; Kim et al., 1998; Neilson and Friesel, 1995).

It is known that Id inhibits bHLH factors such as Twist (Pesce and Benezra, 1993), also that BMP2 induces osteoblast maturation (Katagiri et al., 1994). Here we show that BMP2 stimulates *Id* and we therefore postulate that the effects of BMP2 on osteoblast differentiation may be via Id's inhibition of Twist, thereby promoting cell differentiation instead of proliferation. However, it is known that overexpression of *Id* decreases the activity of the osteocalcin promoter (Tamura and Noda, 1994), also that BMP can cause an increase in calvarial mesenchymal tissue volume (Kim et al., 1998). BMP2 and Id may therefore also act independently, stimulating osteoblast proliferation. This model of osteoblast differentiation is outlined in Figure 10.

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REFERENCES

Bate, M., Rushton, E. and Currie, D. A. (1991). Cells with persistent twist expression are the embryonic precursors of adult muscles in Drosophila. *Development* **113**, 79-89.

Bellus, G. A., Gaudenz, K., Zackai, E. H., Clarke, L. A., Szabo, J., Francomano, C. A. and Muenke, M. (1996). Identical mutations in three different fibroblast growth factor receptor genes in autosomal dominant craniosynostosis syndromes. *Nature Genet.* **14**, 174-176.

Benezra, R., Davis, R. L., Lockshon, D., Turner, D. L. and Weintraub, H. (1990). The protein Id: a negative regulator of helix-loop-helix DNA binding proteins. *Cell* **61**, 49-59.

Bianco, P., Fisher, L. W., Young, M. F., Termine, J. D. and Robey, P. G. (1991). Expression of bone sialoprotein (BSP) in developing human tissues. *Calcif. Tissue Int.* **49**, 421-426.

Bourgeois, P., Bolcato-Bellemin, A. L., Danse, J. M., Bloch-Zupan, A., Yoshiba, K., Stoetzel, C. and Perrin-Schmitt, F. (1998). The variable expressivity and incomplete penetrance of the twist-null heterozygous mouse phenotype resemble those of human Saethre-Chotzen syndrome. *Hum. Mol. Genet.* **7**, 945-957.

Canalis, E. and Raisz, L. G. (1980). Effect of fibroblast growth factor on cultured fetal rat calvaria. *Metabolism: Clinical & Experimental* **29**, 108-114.

Carlton, M. B., Colledge, W. H. and Evans, M. J. (1998). Crouzon-like craniofacial dysmorphology in the mouse is caused by an insertional mutation at the Fgf3/Fgf4 locus. *Dev. Dyn.* **212**, 242-249.

Chen, J. K., Shapiro, H. S., Wrana, J. L., Reimers, S., Heersche, J. N. and Sodek, J. (1991). Localization of bone sialoprotein (BSP) expression to sites of mineralized tissue formation in fetal rat tissues by in situ hybridization. *Matrix* **11**, 133-143.

Chen, Z. F. and Behringer, R. R. (1995). Twist is required in head mesenchyme for cranial neural tube morphogenesis. *Genes Dev.* **9**, 686-699.

Coffin, J. D., Florkiewicz, R. Z., Neumann, J., Mort-Hopkins, T., Dorn, G. W. 2nd, Lightfoot, P., German, R., Howles, P. N., Kier, A., O'Toole, B. A., et al. (1995). Abnormal bone growth and selective translational regulation in basic fibroblast growth factor (FGF-2) transgenic mice. *Mol. Biol. Cell.* **6**, 1861-1873.

Colvin, J. S., Bohne, B. A., Harding, G. W., McEwen, D. G. and Ornitz, D. M. (1996). Skeletal overgrowth and deafness in mice lacking fibroblast growth factor receptor 3. *Nat. Genet.* **12**, 390-397.

Debiais, F., Hott, M., Graulet, A. M. and Marie, P. J. (1998). The effects of fibroblast growth factor-2 on human neonatal calvaria osteoblastic cells are differentiation stage specific. *J. Bone Miner. Res.* **13**, 645-654.

Delezoide, A. L., Benoist-Lasselin, C., Legeai-Mallet, L., Le Merrer, M., Munnich, A., Vekemans, M. and Bonaventure, J. (1998). Spatio-temporal expression of FGFR 1, 2 and 3 genes during human embryo-fetal ossification. *Mech. Dev.* **77,** 19-30.

Deng, C. X., Wynshaw-Boris. A., Shen, M. M., Daugherty, C., Ornitz, D. M. and Leder, P. (1994). Murine FGFR-1 is required for early postimplantation growth and axial organization. *Genes Dev.* **8**, 3045-3057.

Deng, C., Wynshaw-Boris, A., Zhou, F., Kuo, A. and Leder P. (1996). Fibroblast growth factor receptor 3 is a negative regulator of bone growth. *Cell* **84**, 911-921.

El Ghouzzi, V., Le Merrer, M., Perrin-Schmitt, F., Lajeunie, E., Benit, P., Renier, D., Bourgeois, P., Bolcato-Bellemin, A. L., Munnich, A. and Bonaventure, J. (1997). Mutations of the TWIST gene in the Saethre-Chotzen syndrome. *Nature Genet.* **15**, 42-46.

Füchtbauer, E. M. (1995). Expression of M-twist during postimplantation development of the mouse. *Dev. Dyn.* **204**, 316-322.

Galvin, B. D., Hart, K. C., Meyer, A. N., Webster, M. K. and Donoghue, D. J. (1996). Constitutive receptor activation by Crouzon syndrome mutations in fibroblast growth factor receptor (FGFR)2 and FGFR2/Neu chimeras. *Proc. Natl Acad. Sci. USA* **93**, 7894-7899.

Glackin, C. A., Lee, M., Lowe, G., Morales, S., Wergedal, J. and Strong, D. (1997) Overexpressing Human Twist in High SAOS (HSAOS) cells results in major differences in cellular morphology, proliferation rates, and ALP activities. Knocking out human ID-2 greatly reduces the expression of all TWIST family members, indicating that ID-2 may regulate Twist during osteoblast differentiation. *J. Bone Miner. Res.* Abstract **12**, S154.

Hebrok, M., Wertz, K. and Fuchtbauer, E. M. (1994). M-twist is an inhibitor of muscle differentiation. *Dev. Biol.* **165**, 537-544.

Heinrichs, A. A., Banerjee, C., Bortell, R., Owen, T. A., Stein, J. L., Stein, G. S. and Lian, J. B. (1993). Identification and characterization of two proximal elements in the rat osteocalcin gene promoter that may confer species-specific regulation. *J. Cell Biochem.* **53**, 240-250.

Hodgkinson, J. E., Davidson, C. L., Beresford, J. and Sharpe, P. T. (1993). Expression of a human homeobox-containing gene is regulated by 1,25(OH)2D3 in bone cells. *Biochim Biophys Acta* **1174**, 11-16.

Hoffmann, H. M., Beumer, T. L., Rahman, S., McCabe, L. R., Banerjee, C., Aslam, F., Tiro, J. A., van Wijnen, A. J., Stein, J. L., Stein, G. S. and Lian, J. B. (1996). Bone tissue-specific transcription of the osteocalcin gene: role of an activator osteoblast-specific complex and suppressor hox proteins that bind the OC box. *J. Cell Biochem.* **61**, 310-324.

Howard, T. D., Paznekas, W. A., Green, E. D., Chiang, L. C., Ma, N., Ortiz de Luna, R. I., Garcia Delgado, C., Gonzalez-Ramos, M., Kline, A. D., Jabs, E. W. (1997). Mutations in TWIST, a basic helix-loop-helix transcription factor, in Saethre-Chotzen syndrome. *Nat. Genet.* **15**, 36-41.

Iseki, S., Wilkie, A. O. M., Heath, J. K., Ishimaru, T., Eto, K. and Morriss-Kay, G. (1997). Fgfr2 and Osteopontin domains in the developing skull vault are mutually exclusive and can be altered by locally applied FGF2. *Development* **124**, 3375-3384.

Jabs, E. W., Muller, U., Li, X., Ma, L., Luo, W., Haworth, I. S., Klisak, I., Sparkes, R., Warman, M. L., Mulliken, J. B., et al. (1993). A mutation in the homeodomain of the human MSX2 gene in a family affected with autosomal dominant craniosynostosis. *Cell* **75**, 443-450.

Jabs, E. W., Li, X., Scott, A. F., Meyers, G., Chen, W., Eccles, M., Mao, J. I., Charnas, L. R., Jackson, C. E. and Jaye, M. (1994) Jackson-Weiss and Crouzon syndromes are allelic with mutations in fibroblast growth factor receptor 2. *Nature Genet.* **8**, 275-279.

Jen, Y., Manova, K. and Benezra, R. (1996). Expression patterns of Id1, Id2, and Id3 are highly related but distinct from that of Id4 during mouse embryogenesis. *Dev. Dyn.* **207**, 235-252.

Karsenty, G. (1998). Genetics of skeletogenesis. *Dev. Genet.* **22**, 301-313.

Katagiri, T., Yamaguchi, A., Komaki, M., Abe, E., Takahashi, N., Ikeda, T., Rosen, V., Wozney, J. M., Fujisawa-Sehara, A. and Suda, T. (1994). Bone morphogenetic protein-2 converts the differentiation pathway of C2C12 myoblasts into the osteoblast lineage. *J. Cell Biol.* **127**, 1755-1766.

Kawaguchi, N., DeLuca, H. F. and Noda, M. (1992). Id gene expression and its suppression by 1,25-dihydroxyvitamin D3 in rat osteoblastic osteosarcoma cells. *Proc. Natl Acad. Sci. USA* **89**, 4569-4572.

Kettunen, P., Karavanova, I. and Thesleff, I. (1998). Responsiveness of developing dental tissues to fibroblast growth factor – expression of splicing alternatives of FGFR1, -2, -3, and FGFR4 – and stimulation of cell proliferation by FGF-2, -4, -8, and -9. *Dev Gen.* **22**, 374-385.

Kim, H-J., Rice, D. P. C., Kettunen, P. J. and Thesleff, I. (1998). FGF-, BMP- and Shh-mediated signalling pathways in the regulation of cranial suture morphogenesis and calvarial bone development. *Development* **125**, 1241-1251.

Liu, Y-H., Tang, Z., Kundu, R. K., Wu,L., Luo, W., Zhu, D., Sangiorgi, F., Snead, M. L. and Maxson, R. E. (1999). Msx2 gene dosage influences the number of proliferative osteogenic cells in growth centers of the developing murine skull: a possible mechanism for MSX2-mediated craniosynostosis in humans. *Dev Biol.* **205**, 260-274.

Mackenzie, A., Ferguson, M. W. J. and Sharpe, P. T. (1992). Expression patterns of the homeobox gene, Hox-8, in the mouse embryo suggest a role in specifying tooth initiation and shape. *Development* **115**, 403-420.

Malaval, L., Liu, F., Roche, P. and Aubin, J. E. (1999). Kinetics of osteoprogenitor proliferation and osteoblast differentiation in vitro. *J. Cell Biochem.* **74,** 616-627.

McDougall, S., Chen, S., Glackin, C. and Fang, M. A. (1997). The role of basic fibroblast growth factor and *EGR-1* in regulating α2(I) collagen and Twist gene expression in osteoblasts. *J. Bone Miner. Res.* Abstract **12**, S280.

McMahon, A. P., Champion, J. E., McMahon, J. A. and Sukhatme, V. P. (1990). Developmental expression of the putative transcription factor Egr-1 suggests that Egr-1 and c-fos are coregulated in some tissues. *Development* **108**, 281-287.

Mangasarian, K., Li, Y., Mansukhani, A. and Basilico, C. (1997). Mutation associated with Crouzon syndrome causes ligand-independent dimerization and activation of FGF receptor-2. *J. Cell Physiol.* **172**, 117-125.

Muenke, M., Schell, U., Hehr, A., Robin, N. H., Losken, H. W., Schinzel, A., Pulleyn, L. J., Rutland, P., Reardon, W., Malcolm, S., et al. (1994). A common mutation in the fibroblast growth factor receptor 1 gene in Pfeiffer syndrome. *Nature Genet.* **8**, 269-273.

Murray, S. S., Glackin, C. A., Winters, K. A., Gazit, D., Kahn, A. J. and Murray, E. J. (1992). Expression of helix-loop-helix regulatory genes during differentiation of mouse osteoblastic cells. *J. Bone Miner. Res.* **7**, 1131-1138.

Neilson, K. M. and Friesel, R. E. (1995). Constitutive activation of fibroblast growth factor receptor-2 by a point mutation associated with Crouzon syndrome. *J. Biol. Chem.* **270**, 26037-26040.

Ogata, T. and Noda, M. (1991). Expression of Id, a negative regulator of helix-loop-helix DNA binding proteins, is down-regulated at confluence and enhanced by dexamethasone in a mouse osteoblastic cell line, MC3T3E1. *Biochem. Biophys. Res. Com.* **180**, 1194-1199.

Ogata, T., Wozney, J M., Benezra, R. and Noda, M. (1993). Bone morphogenetic protein 2 transiently enhances expression of a gene, Id (inhibitor of differentiation), encoding a helix-loop-helix molecule in osteoblast-like cells. *Proc. Natl Acad. Sci. USA* **90**, 9219-9222.

Opperman, L.A., Chhabra, A., Nolen, A.A., Bao, Y., and Ogle, R.C. (1998). Dura mater maintains rat cranial sutures in vitro by regulating suture cell proliferation and collagen production. *J. Craniofac. Genet. Dev. Biol.* **18**, 150-158.

Opperman, L. A., Passarelli, R. W., Morgan, E. P. Reintjes, M. and Ogle, R. C. (1995). Cranial sutures require tissue interactions with dura mater to resist osseous obliteration in vitro. *J. Bone Miner. Res.* **10**, 1979-1987.

Opperman, L.A., Sweeney, T.M., Redmon, J., Persing, J.A., and Ogle, R.C. (1993). Tissue interactions with underlying dura mater inhibit osseous obliteration of developing cranial sutures. *Dev. Dyn.* **198**, 312-322.

Ornitz, D. M., Xu, J., Colvin, J. S., McEwen, D. G., MacArthur, C. A., Coulier, F., Gao, G. and Goldfarb, M. (1996). Receptor specificity of the fibroblast growth factor family. *J. Biol. Chem.* **271**, 15292-15297.

Orr-Urtreger, A., Givol, D., Yayon, A., Yarden, Y. and Lonai, P. (1991). Developmental expression of two murine fibroblast growth factor receptors, flg and bek. *Development* **113**, 1419-1434.

Orr-Urtreger, A., Bedford, M. T., Burakova, T., Arman, E., Zimmer, Y., Yayon, A., Givol, D. and Lonai, P. (1993). Developmental localization of the splicing alternatives of fibroblast growth factor receptor-2 (FGFR2). *Dev. Biol.* **158**, 475-486.

Paznekas, W. A., Cunningham, M. L., Howard, T. D., Korf, B. R., Lipson, M. H., Grix, A. W., Feingold, M., Goldberg, R., Borochowitz, Z., Aleck, K., et al. (1998). Genetic heterogeneity of Saethre-Chotzen syndrome, due to TWIST and FGFR mutations. *Am. J. Hum. Genet.* **62**, 1370-1380.

Pesce, S. and Benezra, R. (1993). The loop region of the helix-loop-helix protein Id1 is critical for its dominant negative activity. *Molec. Cell. Biol.* **13**, 7874-7880.

Peters, K. G., Werner, S., Chen, G. and Williams, L. T. (1992). Two FGF receptor genes are differentially expressed in epithelial and mesenchymal tissues during limb formation and organogenesis in the mouse. *Development* **114**, 233-243.

Rice, D. P. C., Kim, H. J. and Thesleff, I. (1997). Detection of gelatinase B expression reveals osteoclastic bone resorption as a feature of early calvarial bone development. *Bone* **21**, 479-486.

Rice, D. P. C., Kim, H. J. and Thesleff, I. (1999). Apoptosis in calvarial bone and suture development. *Eur. Oral Sci*. **107**, 265-275.

Satokata, I. and Maas, R. (1994). Msx1 deficient mice exhibit cleft palate and abnormalities of craniofacial and tooth development. *Nature Genet.* **6**, 348-356.

Shishido, E., Higashijima, S., Emori, Y. and Saigo, K. (1993). Two FGF-receptor homologues of Drosophila: one is expressed in mesodermal primordium in early embryos. *Development* **117**, 751-761.

Tamura, M. and Noda, M. (1994). Identification of a DNA sequence involved in osteoblast-specific gene expression via interaction with helix-loop-helix (HLH)-type transcription factors. *J. Cell Biol.* **126**, 773-782.

Tamura, M. and Noda, M. (1999). Identification of DERMO-1 as a member of helix-loop-helix type transcription factors expressed in osteoblastic cells. *J. Cell Biochem.* **72**, 167-176.

Vainio, S., Jalkanen, M., Vaahtokari, A., Sahlberg, C., Mali, M., Bernfield, M. and Thesleff, I. (1991). Expression of syndecan gene is induced early, is transient, and correlates with changes in mesenchymal cell proliferation during tooth organogenesis. *Dev. Biol.* **147**, 322-333.

Wilke, T. A., Gubbels, S., Schwartz, J. and Richman, J. M. (1997). Expression of fibroblast growth factor receptors (FGFR1, FGFR2, FGFR3) in the developing head and face. *Dev. Dyn.* **210**, 41-52.

Wilkie, A. O. M. (1997). Craniosynostosis: genes and mechanisms. *Hum. Mol. Genet.* **6**, 1647-1656.

Wilkie, A. O., Slaney, S. F., Oldridge, M., Poole, M. D., Ashworth, G. J., Hockley, A. D., Hayward, R. D., David, D. J., Pulleyn, L. J., Rutland, P., et al. (1995). Apert syndrome results from localized mutations of FGFR2 and is allelic with Crouzon syndrome. *Nature Genet.* **9**, 165-172.

Wilkinson, D. G. and Green, J. (1990). In situ hybridisation and the three-dimensional reconstruction of serial sections. In *Postimplantation Mammalian Embryos: A Practical Approach*. (ed. A. J. Copp and D. L. Cockroft). pp. 155-171. Oxford: IRL press,

Xu, X., Weinstein, M., Li, C., Naski, M., Cohen, R. I., Ornitz, D. M., Leder, P. and Deng, C. (1998). Fibroblast growth factor receptor 2 (FGFR2)-mediated reciprocal regulation loop between FGF8 and FGF10 is essential for limb induction. *Development* **125**, 753-765.

Yamaguchi, T. P., Harpal, K., Henkemeyer, M. and Rossant, J. (1994). fgfr-1 is required for embryonic growth and mesodermal patterning during mouse gastrulation. *Genes Dev.* **8**, 3032-3044.

Zhou, M., Sutliff, R. L., Paul, R. J., Lorenz, J. N., Hoying, J. B., Haudenschild, C. C., Yin, M., Coffin, J. D., Kong, L., Kranias, E. G., et al. (1998). Fibroblast growth factor 2 control of vascular tone. *Nature Med.* **4**, 201-207.