Vertebrate Sprouty genes are induced by FGF signaling and can cause chondrodysplasia when overexpressed

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Summary

The \textit{Drosophila sprouty} gene encodes an antagonist of FGF and EGF signaling whose expression is induced by the signaling pathways that it inhibits. Here we describe a family of vertebrate Sprouty homologs and demonstrate that the regulatory relationship with FGF pathways has been conserved. In both mouse and chick embryos, Sprouty genes are expressed in intimate association with FGF signaling centers. Gain- and loss-of-function experiments demonstrate that FGF signaling induces Sprouty gene expression in various tissues. Sprouty overexpression obtained by infecting the prospective wing territory of the chick embryo with a retrovirus containing a mouse Sprouty gene causes a reduction in limb bud outgrowth and other effects consistent with reduced FGF signaling from the apical ectodermal ridge. At later stages of development in the infected limbs there was a dramatic reduction in skeletal element length due to an inhibition of chondrocyte differentiation. The results provide evidence that vertebrate Sprouty proteins function as FGF-induced feedback inhibitors, and suggest a possible role for Sprouty genes in the pathogenesis of specific human chondrodysplasias caused by activating mutations in \textit{Fgfr3}.

Key words: Chondrodysplasia, FGF8, FGF signaling, Limb development, Sprouty, \textit{Drosophila}

INTRODUCTION

Fibroblast Growth Factors (FGFs) are vital intercellular signaling molecules that regulate numerous processes (reviewed by Basilico and Moscatelli, 1992; Szebenyi and Fallon, 1999). They signal by binding to and activating specific transmembrane receptor tyrosine kinases (reviewed by Johnson and Williams, 1993). At least 18 different FGF and 4 FGF receptor (FGFR) genes are known in vertebrate species (reviewed by Coulier et al., 1997; see Ohbayashi et al., 1998 and references therein). Genetic studies in the mouse have demonstrated that FGF signaling is required for cell proliferation/survival at the time of embryo implantation (embryonic day [E] 4.0; Feldman et al., 1995; Arman et al., 1998) and for cell migration during gastrulation (beginning at ~E6.5; Ciruna et al., 1997; Sun et al., 1999). At later stages of embryogenesis FGFs regulate development of the brain, limb, lung, tooth and many other organs (reviewed by Goldfarb, 1996; Szebenyi and Fallon, 1999). FGF and FGFR genes have also been identified in \textit{Drosophila}, and are required for migration of mesoderm and glial cells and for the control of branching events in the tracheal system (reviewed by Skaer, 1997). In worms, FGF signaling is required for migration of sex myoblasts (reviewed by Chen and Stern, 1998).

FGF signaling has been extensively studied in the vertebrate limb, where it is thought to provide the signals that induce limb formation and maintain initial outgrowth of the limb bud (reviewed by Martin, 1998). Subsequent outgrowth of the bud and specification of the limb skeletal elements is thought to depend on FGFs produced by cells in a specialized epithelium at the limb bud distal tip, known as the apical ectodermal ridge (AER). This conclusion is based on the observation that surgical removal of the AER results in limb truncation (Saunders, 1948; Summerbell, 1974), but an FGF-bead can substitute for it to provide all of the AER-derived signals necessary for limb development (Niswander et al., 1993; Fallon et al., 1994).

The AER regresses after the precursors of the skeletal elements have been specified, but FGF signaling continues to play a role in limb skeletogenesis. Mice with loss-of-function mutations in \textit{Fgfr3} have abnormally long limb bones (Colvin et al., 1996; Deng et al., 1996), whereas mice overexpressing \textit{Fgf2} have short limb bones (Coffin et al., 1995), and both
phenotypes are due to abnormalities in the growth plate of the skeletal elements. In addition, overexpression of Fg8 in chick embryos causes a complex phenotype, including short limb skeletal elements (Vogel et al., 1996). Furthermore, several of the most common human dwarfism syndromes are due to dominant activating mutations in Fgfr3 (reviewed by Webster and Donoghue, 1997; Burke et al., 1998). Together these data indicate that FGF signaling controls the rate of endochondral ossification, and thereby determines the length of the skeletal elements.

In view of the importance of FGF signaling in limb formation and many other developmental processes, it was intriguing when a gene that modulates FGF signaling was identified in a screen for mutations that affect tracheal branching in Drosophila (Hacohen et al., 1998). In wild-type embryos, FGF signaling guides outgrowth of primary tracheal branches and induces cells closest to the FGF signaling center to form secondary branches (Sutherland et al., 1996). In spry (spry) null mutants, the FGF pathway is overactive and ectopic secondary branches are induced in cells farther from the FGF signaling center. Overexpression of spry during primary branch outgrowth causes the opposite effect, inhibiting the FGF inductive pathway and blocking all secondary branching. Thus, spry antagonizes FGF signaling in the developing trachea. Importantly, expression of spry is induced by FGF signaling. Therefore, the FGF pathway regulates the expression of its own antagonist, thereby limiting the range over which FGF signaling is active.

Recently, spry was found to inhibit EGF and possibly other RTK signaling pathways (Bergmann et al., 1998; Casci et al., 1999; Kramer et al., 1999).

spry encodes a novel protein with a unique cysteine-rich domain, which localizes to cell membranes (Hacohen et al., 1998; Casci et al., 1999), but the biochemical mechanism by which it antagonizes FGF and other signaling pathways is not fully understood. Studies in cultured Drosophila cells and in vitro binding experiments have led to the proposal that it is localized at the inner surface of the plasma membrane and antagonizes RTK signaling pathways by direct binding of the signal transduction components Gap1 and the Grb2 homolog Drk (Casci et al., 1999). However, endogenous SPRY protein in developing wing discs is found in punctate structures that resemble secretory vesicles or endocytic uptake vesicles, and it has also been suggested to function as an extracellular antagonist to explain its cell non-autonomous actions in the tracheal system (Hacohen et al., 1998; Kramer et al., 1999).

Three human genes have been identified with sequence similarity to Drosophila spry (Hacohen et al., 1998), and a fourth family member has been identified in mouse (de Maximy et al., 1999). Here we have investigated the relationship between Sprouty genes and FGF pathways in vertebrates, and have begun to explore Sprouty gene function in vertebrate embryogenesis. Our data indicate that FGF signaling regulates expression of Sprouty genes in the mouse and chick embryo, and suggest that in turn, Sprouty gene expression antagonizes FGF signaling. In addition, we show that overexpression of Sprouty genes in the chick limb leads to inhibition of chondrocyte differentiation that results in a chondrodysplasia resembling that observed in individuals with activating mutations in Fgfr3. This raises the possibility that induction of Sprouty gene expression plays a role in these human skeletal malformation syndromes.

MATERIALS AND METHODS

Cloning and chromosome mapping

Fragments of the cysteine-rich domains of human (h)Spry1, hSpry2, hSpry3 and mouse (m)Spry4 were amplified by PCR using primers derived from EST sequences and either hSpry1 and hSpry2 EST plasmids or mouse genomic DNA as template. The amplification products were used to screen a neonatal mouse brain cDNA library in the AZAP vector (Stratagene; La Jolla, CA) for mSpry1, mSpry3 and mSpry4, an E11 mouse embryo cDNA library (Clontech; Palo Alto, CA) for mSpry2, a stage 14-16 chick embryo cDNA library (kindly provided by C. Tabin) for chick (c)Spry1, and an E10 chick embryonic brain cDNA library (kindly provided by T. Kennedy and M. Tessier-Lavigne) for cSpry2. Hybridizations were performed at 55°C for 16 hours (1% BSA, 0.2 M sodium phosphate, 15% formamide, 1 mM EDTA, 7% SDS), followed by three 20 minute washes at 55°C in 2× SSC/1% SDS, and three 20 minute washes at 55°C in 0.2× SSC/0.1% SDS. For mSpry1 both strands of a 2.5 kb clone representing the major transcript were sequenced. For mSpry2 and mSpry4 both strands of a single clone containing the complete coding region were sequenced. The cSpry2 sequence was compiled from three overlapping partial cDNAs. GenBank accession numbers: mSpry1, AF176903; mSpry2, AF176905; mSpry4, AF176906; cSpry1, AF177875; cSpry2, AF176904.

Chromosome mapping was performed using The Jackson Laboratory (Bar Harbor, ME) interspecific backcross panels BSB ([C57BL/6J × M. spreitus]F1 × C57BL/6J), and BSS([C57BL/6J/Ei × SPRET/Ei]F1 × SPRET/Ei) (Bowen et al., 1994). Restriction site polymorphisms were identified between parental strains. The backcross panels were genotyped and the data were submitted to the Jackson Laboratory for analysis. The data are available at www.jax.org/resources/documents/cmdata.

RNA in situ hybridization, BrdU labeling, skeletal preparations and histology

Embryos were obtained by mating CD1 mice (Charles River Laboratories; Hollister, CA) or mice heterozygous for an Fg8 null (−) allele, Fg8−/− (Meyers et al., 1998). Noon of the day of plug detection was considered E0.5. Fg8−/− embryos were identified by their characteristic morphology (Sun et al., 1999). White Leghorn chick embryos (California Golden Eggs; Sacramento, CA), were staged by the criteria of Hamburger and Hamilton (1951). Whole-mount and paraffin section in situ hybridization analyses were performed as previously described (Neubüser et al., 1997). Probes were prepared from plasmids containing the complete protein coding region and 3′UTR (mSpry1, mSpry2, mSpry4) or sequences extending 5′ from the 3′UTR into the region encoding the cysteine-rich domain (mSpry3, cSpry1, cSpry2). The cDNA sequences used as probes for mouse and chick Fg8 were described previously (Crossley and Martin, 1995; Crossley et al., 1996b) and the chick Sox9 probe was kindly provided by C. Tabin. BrdU labeling and analysis were performed as described by Zou et al. (1997).

For cartilage staining, embryos were fixed overnight in 5% trichloroacetic acid, rinsed in water, stained with Alcian blue and stained with hematoxylin and eosin (H&E).
RESULTS

Isolation and evolutionary conservation of vertebrate Sprouty genes

cDNAs representing four mouse genes with sequence homology to Drosophila and human spry genes, and the chick orthologs of Spry1 and Spry2 were isolated. Sequence analysis indicated that all contained full coding regions except the mSpry3 and cSpry1 cDNA clones, which were partial cDNAs encoding only the C-terminal region of the proteins. The predicted mSpry1, mSpry2, and mSpry4 proteins are similar in size (34, 34.6 and 32.6 kDa, respectively), and each contains an ~125 amino acid (aa) residue cysteine-rich C-terminal domain with at least 23 cysteines (Fig. 1). mSpry3 contains a similar cysteine-rich domain (not shown). Throughout the C-terminal domain the four mouse proteins share 56-70% aa sequence identity. In the N-terminal domain mSpry1 and mSpry2 are more similar to one another (~37% aa identity) than mSpry1 is to mSpry4 (~25% aa identity) or mSpry2 is to mSpry4 (~25% aa identity). Comparison of the mouse, chick, and previously described human SPRY2 sequences demonstrates that the Spry2 gene has been highly conserved during vertebrate evolution (m/h, 97% aa identity; m/c, 84% aa identity; h/c, 86% aa identity); most of the differences among species are in the N-terminal domain.

The similarity between the vertebrate and Drosophila sprouty (dSpry) protein sequences (Fig. 1 and data not shown; Hacohen et al., 1998) is limited mostly to the cysteine-rich domain, with each vertebrate protein showing ~44-52% aa identity to dSpry in this region. The cysteine residues are particularly highly conserved, with 18 or more of the 22 cysteines in the Drosophila protein present in each vertebrate gene. Outside the cysteine-rich domain there are two short regions that show similarity between dSpry and all three mouse proteins (Fig. 1). There are also short stretches of sequence similarity between dSpry and individual vertebrate Sprouty proteins, such as the region containing residues 345-356 in dSpry and residues 80-91 in the human (Hacohen et al., 1998), mouse and chick SPRY2 proteins (data not shown). The many stretches of repeated or alternating amino acid residues found in dSpry are not present in any of the vertebrate Sprouty family members. None of the vertebrate SPRY proteins contains a predicted signal peptide, whereas dSpry has a signal sequence predicted by the GCG SPScan program near its N-terminal end. Thus, if the vertebrate SPRY proteins are secreted it may be by a signal peptide-independent mechanism (reviewed by Muesch et al., 1990; Friesel et al., 1995).

The chromosomal map locations of mSpry1, mSpry2, and mSpry4 genes were determined by standard backcross analysis. mSpry1 mapped to proximal chromosome 3 and mSpry2 to distal chromosome 14. Their human orthologs have been mapped to the syntenic regions of human chromosomes 4 and 13, respectively (Deloukas et al., 1998). mSpry4 mapped to central chromosome 18. mSpry3 was not mapped, but its human ortholog maps to the X chromosome (Rogner et al., 1996), suggesting that mSpry3 might also be X-linked. None

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Fig. 1. Sequence comparison of three mouse and Drosophila Sprouty proteins. The deduced amino acid sequences of mouse Spry1, SPRY2 and SPRY4 are aligned with portions of the Drosophila SPRY sequence (dSpry residue numbers from Hacohen et al., 1998). Dashes represent gaps inserted to maximize alignment. Amino acids conserved in two or more Sprouty family members are highlighted in light gray. Cysteine residues are highlighted in dark gray. Asterisks indicate the residues conserved in all three mouse proteins.
of the mapped mouse Sprouty genes co-localize with a known mouse mutation.

**Vertebrate Sprouty genes are expressed near FGF signaling centers in the embryo**

Sprouty expression in mouse embryos and adult tissues was initially surveyed by northern blot analysis of poly(A)* RNAs. mSpry1, mSpry2 and mSpry4 RNAs were detected in the embryo and in many adult tissues including heart, brain, lung, kidney and skeletal muscle. For both mSpry1 and mSpry2, there was a major ~2.5 kb transcript and a minor ~6.5 kb form, whereas for mSpry4 there was a major ~6 kb, a minor ~2 kb, and an additional ~7.2 kb transcript in skeletal muscle (data not shown). Although mSpry1 expression was not detected in the embryo by northern blot (E7-E18) or whole-mount in situ hybridization (E7.0-E11.5) analysis, transcripts of ~6.5 kb and ~1 kb were detected in adult brain and testis, respectively (data not shown).

Whole-mount in situ hybridization analysis demonstrated that at stages when organogenesis is commencing in the mouse embryo (E8.5-E9.5), Spry1, Spry2 and Spry4 are expressed in similar, highly localized domains. At E8.5 expression of all three genes was detected in the primitive streak, in the rostral forebrain, and in cells lateral to the posterior hindbrain (Fig. 2A,D,G). At E9.5, expression continued to be detected in the rostral forebrain and primitive streak, and was also detected in the branchial arches and the forelimb bud (Fig. 2B,E,H, and data not shown). At E10.5, expression of the three genes was also detected in the somites, branchial arches, hindlimb bud (Fig. 2C,F,I, and data not shown). In addition to
these common expression domains, mSpry1 and mSpry2, but not mSpry4 RNAs were detected throughout the developing midbrain and in the anterior hindbrain at E8.5, and subsequently in a transverse domain that encompassed the prospective caudal midbrain, isthmus, and cerebellum (Fig. 2A-I), as well as in a distinct stripe that appeared to mark the region of presomitic mesoderm in which the next somite will segment (Fig. 2E, and data not shown). Thus, at least up to midgestation stages, Spry1, Spry2 and Spry4 are expressed in highly restricted patterns and appear to be co-regulated in most tissues. The chick Spry1 and Spry2 genes displayed similar expression patterns at comparable developmental stages (data not shown).

One important aspect of these expression patterns is that in both mouse and chick each of the Sprouty expression domains overlapped with or was immediately adjacent to the known expression domains of one or more FGF genes, with the possible exception of cells adjacent to the posterior hindbrain. This correlation was particularly evident when Sprouty and Fgf8 gene expression patterns were compared (Fig. 2J-O). In some domains the Sprouty genes and Fgf8 appeared to be co-expressed in the same cells, as for example, in the rostral forebrain and at the mid/hindbrain junction. However, in the latter region the Sprouty expression domains extended both rostral and caudal to the Fgf8 expression domain (compare Fig. 2C,F with O). In other regions Sprouty gene expression was detected exclusively in cells adjacent to cells expressing Fgf8. For example, mFgf8 RNA is detected in the ectoderm of the mandibular and maxillary arches (Fig. 2K) and mSpry1 RNA in the subadjacent mesenchyme (Fig. 2L). In the limb bud, mFgf8 RNA is detected in the AER (Fig. 2M) and mSpry1 RNA in the underlying mesenchyme (Fig. 2N). In these tissues, there appeared to be a gradient of Sprouty gene expression, with the highest levels in cells closest to the FGF signaling center. These results suggest that FGFs act as inducers of Sprouty gene expression.

**FGF signaling induces Sprouty gene expression**

To determine if FGF signaling can induce Sprouty gene expression we examined the effects of adding or removing FGF signals in various developmental settings on the expression of the Sprouty genes. We first tested whether FGF signaling was sufficient to induce ectopic Sprouty gene expression in two tissues in the chick embryo known to be responsive to addition of FGFs (Cohn et al., 1995; Crossley et al., 1996a), but in which Spry1 and Spry2 are not normally expressed. When a heparin bead soaked in recombinant FGF4 (FGF4-bead) was implanted in the prospective caudal diencephalon at ~stage 11, Spry2 RNA was detected in the neuroepithelium surrounding the bead in most (9/11) cases (Fig. 3A), whereas no such induction occurred with control beads soaked in PBS (PBS-beads) (n=3; data not shown). Similarly, both Spry1 (n=5) and Spry2 (n=8) expression were induced in cells near an FGF4-bead implanted in the lateral plate mesoderm (LPM) of the chick interlimb region at stage 14, (Fig. 3B, and data not shown). FGF2-beads (n=3) and FGF8-beads (n=3) also induced Sprouty gene expression, whereas PBS-beads had no effect (Fig. 3C, and data not shown). A time course analysis showed that Spry2 expression could be induced within one hour after implantation of an FGF4-bead (data not shown). Thus FGF signaling can rapidly induce Sprouty gene expression, suggesting it is a primary response to the signal.

To determine the relationship between FGF signaling and endogenous Sprouty gene expression, we first examined Sprouty expression in explant cultures of the mouse mandibular arch (Neubüser et al., 1997). All three Sprouty genes are normally expressed in mandibular arch mesenchyme.
in the region immediately underlying ectoderm that expresses Fg8 (see Fig. 2K) and Fgf9 (Kettunen and Thesleff, 1998). When the mandibular ectoderm was left in place (n=5) or removed and then immediately replaced (n=10), Spry1 RNA was detected in the underlying mesoderm (n=13/15; Fig. 3D). In contrast, when the mandibular ectoderm was removed and a PBS-bead was implanted, Spry1 RNA was not detected (n=9; Fig. 3E), indicating that signals from the overlying ectoderm are required to maintain Spry1 expression. However, when an FGF4-bead was implanted in the isolated mesenchyme, Spry1 RNA was detected in all cases (n=10), but only in the region surrounding the FGF4-bead (Fig. 3F). These data indicate that FGF signaling is sufficient to maintain Sprouty gene expression in the mandibular arch. Since Fgf4 is not expressed in the mandibular arch ectoderm (Kettunen and Thesleff, 1998), it is likely that Fgf8 and/or Fgf9 expressed there provide the endogenous signals that regulate Sprouty gene expression.

We next examined Sprouty gene expression in Fg8 null mutant mouse embryos at E7.5. At this stage Fg8 RNA is detected in the primitive streak (Crossley and Martin, 1995), where ectodermal cells undergo a transition from an epithelial to mesenchymal morphology and generate the mesodermal and endodermal lineages. Spry2 and Spry4 but not Spry1 RNAs are also detected in the primitive streak at this stage (Fig. 3G,H), with the highest levels localized in the nascent mesoderm (Fig. 3I). Spry2 and Spry4 expression appear to be rapidly downregulated as the cells migrate away from the streak (Fig. 3I, and data not shown). Fg8−/− embryos fail to gastrulate normally, but the primitive streak forms and nascent mesoderm cells are apparently present (Sun et al., 1999). However, neither Spry2 (n=5) nor Spry4 (n=5) RNA was detected in the nascent mutant mesoderm (Fig. 3J,K). Together, the data from these experiments demonstrate that expression of all three Sprouty genes is dependent on FGF signaling.

Ectopic Sprouty gene expression inhibits limb bud outgrowth and causes chondrodysplasia

To explore vertebrate Sprouty gene function, we expressed Sprouty genes throughout the chick limb and analyzed the effects at various stages of limb development. In the normal limb bud, all three Sprouty genes are expressed in the distal mesenchyme underlying the AER, which expresses Fg8 (Fig. 2). The AER also expresses Fgf4 (Niswander and Martin, 1992), Fgf9 and Fgf17 (M. Lewandoski and G.R.M., unpublished observations). If Sprouty functions as an antagonist of FGF signaling in vertebrates as it does in Drosophila, then one might expect excess Sprouty gene expression to interfere with FGF-mediated outgrowth and patterning of the limb.

The prospective forelimb territory was infected at stages 9-10 (E1.5) with a replication-competent avian retrovirus containing an mSpry2 cDNA, and the infected embryos were allowed to develop for up to 4.5 days after infection (up to stage 28; E6). In 56 embryos (52%), there was a modest reduction and in 8 embryos (7%) a dramatic reduction in limb bud size compared to the contralateral uninjected wing (Fig. 4A-D). In the remaining 45 embryos there was no obvious effect on wing bud size (data not shown). Similar results were obtained with mSpry4 virus: 17 of the 26 infected limb buds (65%) were modestly reduced in size (data not shown). No effect was observed in the uninfected limb, or in limbs infected with a control retrovirus containing a GFP cDNA (GFP virus; n=20). The affected wing buds were assayed for expression in the distal mesenchyme of genes that are dependent on FGF signals from the AER, such as Shh, Fgf10, Msx1, Bmp2 or Bmp4 (reviewed by Martin, 1998). Expression of each of these genes was detected in all the infected limb buds examined (Fig. 4B, and data not shown). In most affected wing buds, AER morphology and gene expression patterns (Fgf4, Fgf8, Bmp2 and Bmp4) appeared normal (data not shown), although in some cases Fg8 expression was patchy (Fig. 4C). This suggests that Sprouty misexpression can interfere with a signal from the mesenchyme that maintains Fg8 expression, possibly Fgf10 (Min et al., 1998; Sekine et al., 1999).

The effects of excess Sprouty expression on the patterning processes that occur during the bud stages of development were determined by examining skeletal preparations of embryos incubated for approx. 5-12 days after retroviral infection (to stages 30-39; E6.5-E13.5). In 44 of 60 (73%) embryos infected with the Spry2 virus, but in none of the embryos infected with the control GFP virus (n=9), the injected wing was much smaller than the un.injected one. In 2 of the 44 cases (5%), the stunted wing lacked the normal complement of skeletal elements: the only skeletal element present was a small humerus (Fig. 4E). The absence of skeletal elements distal to the humerus is similar to what is observed when the AER is removed at early stages of limb bud outgrowth. As discussed below, these data support the conclusion that excess Sprouty expression in the limb can antagonize FGF signaling from the AER.

The remaining 42 (95%) affected wings, although not lacking any skeletal elements, had a striking phenotype: the skeletal elements were considerably shorter and usually thicker than those in the uninjected limb (Fig. 4F). In 31 cases (70%) all the elements were thus affected, and in 11 cases (25%) only some were affected, presumably because the limb was only partially infected (data not shown). To determine whether the decreased size of the skeletal elements could be attributed to reduction in the size of the mesenchymal condensations from which they developed, we examined the expression of Sox9, an early marker of such condensations (Wright et al., 1995), in embryos which they developed, we examined the expression of Sox9, an early marker of such condensations (Wright et al., 1995), in stage 23-28 infected embryos. In most cases (n=15) the condensations in the infected wing were indistinguishable or only modestly reduced in size compared with those in the uninjected wing (Fig. 4D). This result suggested that the reduction in skeletal element size was due to abnormalities in the orderly progression from proliferating to hypertrophic chondrocytes that is essential for normal endochondral bone elongation.

Hypertrophic chondrocytes are normally localized towards the center of a skeletal element and are readily detected by their characteristic morphology (Fig. 4G-I). Analysis of serial sections showed that affected wings at stages 34-39 contained no cells with the distinctive histological characteristics of hypertrophic chondrocytes (Fig. 4H, and data not shown). Consistent with this observation, ColX expression, a marker for hypertrophic chondrocytes (Vortkamp et al., 1996), was not detected in the affected skeletal elements (data not shown). Furthermore, no evidence of bone formation was detected after staining with Alizarin red, even in embryos incubated to stage 39 (Fig. 4F), approximately 6.5 days after ossification begins.
in the normal chick limb. This is consistent with studies indicating that differentiation of hypertrophic chondrocytes is required for invasion of cartilage by osteogenic cells (Karsenty, 1998). To determine whether chondrocytes progressed to the prehypertrophic stage, we assayed for Ihh expression (Vortkamp et al., 1996). Although Ihh was readily detected in the skeletal elements of the contralateral uninfected limb (Fig. 4K), Ihh RNA was not detected in the affected skeletal elements of the infected limb (Fig. 4L). This suggests that overexpression of Spry2 prevents differentiation of proliferating chondrocytes. Consistent with this conclusion, proliferating cells, as detected by BrdU labeling, which are normally restricted to the ends (Fig. 4M), were found scattered throughout the affected skeletal elements (Fig. 4N). Thus, excess expression of Sprouty during chick skeletal development causes a severe chondrodysplasia in which cartilage cell differentiation is inhibited.

**DISCUSSION**

In *Drosophila*, FGF signaling induces expression of its own antagonist, sprouty. By isolating mouse Sprouty genes and their chick orthologs and studying their expression in normal embryos and various experimental settings we have demonstrated that this regulatory relationship has been conserved. In many embryonic tissues, Sprouty genes are expressed in intimate association with FGF signaling centers. Evidence that Sprouty expression is dependent on FGF signaling was obtained from studies showing that Spry1 expression is not maintained in branchial arch mesenchyme deprived of FGF-expressing ectoderm unless an FGF-bead is applied, and that Spry2 and Spry4 are not detected in the primitive streak of Fgf8−/− embryos. Moreover, Spry1 and Spry2 are ectopically expressed in the chick brain and interlimb region in response to an FGF-bead. In *Drosophila*, FGF induction of sprouty expression appears to be a primary response mediated by a MAP kinase cascade (Hacohen et al., 1998). In vertebrates, FGF induction of Sprouty gene expression is very rapid, suggesting it is also a primary response to the signal. Evidence that Sprouty genes antagonize FGF signaling was obtained from studies of excess Sprouty expression in the developing limb. We observed a reduction in limb bud size and in some cases limb truncation consistent with inhibition of the FGF signal required for limb bud outgrowth and patterning. In addition, overexpression of Sprouty inhibited chondrocyte terminal differentiation. This caused a chondrodysplasia similar to that observed in patients with mutations in FGFR3, raising the possibility that Sprouty plays a role in some human chondrodysplasias.

**Regulation of Sprouty gene expression by FGF signaling**

Our data show that from gastrulation through mid-gestation stages of development, Spry1, Spry2 and Spry4 have remarkably similar and highly specific expression domains, suggesting that these three genes may be coordinately regulated. We have observed a striking correlation between the expression domains of the Sprouty genes and Fgf8 during this period of development, suggesting that FGF8 may regulate Sprouty gene expression. The absence of Sprouty gene expression in the primitive streak of Fgf8−/− embryos supports this hypothesis. However, other FGF family members are also expressed in each domain and could participate in the regulation of Sprouty genes. For example, Fgf4 expression, which is detected in the primitive streak of normal but not Fgf8−/− embryos (Niswander and Martin, 1992; Sun et al., 1999), might be required for Sprouty gene expression. On the other hand, since Fgf8−/− embryos express Fgf5 (Sun et al., 1999), it appears that not all FGFs induce Sprouty gene expression. At later stages of development Sprouty gene expression is detected in specific cell types in virtually every organ, including the eye, lung, gut, brain, kidney and bone (data not shown; de Maximy et al., 1999), and the correlation between Sprouty and Fgf8 gene expression does not always hold.

Although there is extensive overlap in the expression domains of the individual Sprouty genes up to mid-embryogenesis, there are significant differences among them. For example, Spry2 and Spry4 are expressed in the primitive streak whereas Spry1 is not, and Spry 1 and Spry2 are expressed in the midbrain and anterior hindbrain region whereas Spry4 is not. Such differences might be due to differences among Sprouty genes in their sensitivity to FGF signaling or perhaps differences in other factors required for individual Sprouty gene expression.

The functional significance of multiple Sprouty gene expression in a given domain remains to be determined. One possibility is that different Sprouty genes have different effects on FGF signaling pathways or possibly other RTK signaling pathways active in the domain. Alternatively, the effects of different Sprouty proteins may be similar, perhaps serving to restrict the range of FGF signaling activity as in the *Drosophila* tracheal system, and the requisite amount of Sprouty activity in a domain may be achieved by co-expression of several different Sprouty genes. Excess mSpry2 or mSpry4 in the developing chick limb bud caused similar phenotypes, indicating that these two genes have similar effects, at least when overexpressed.

**Sprouty can antagonize FGF function in the limb bud**

We assessed the function of Sprouty gene products in the chick limb bud at stages 18-28, when its development is dependent on FGFs produced in the AER, by using a retroviral vector to express Spry2 or Spry4 genes and examining the effects of Sprouty overexpression on limb bud outgrowth, marker gene expression, and skeletal element specification. In the infected limb buds, we observed a modest to severe reduction in bud outgrowth, but the continued expression of genes known to be dependent on FGF signaling. These results are different from the effects observed when all FGF signaling is eliminated by removing the AER. However, they are similar to what has been observed when the Fgf8 gene is specifically inactivated in the AER of the mouse embryo limb bud (M. Lewandoski and G. R. M., unpublished observations). On the basis of these similarities, we suggest that the Sprouty expression obtained by retroviral infection of chick limb buds was in most cases sufficient to antagonize but not to eliminate FGF signaling. However, Sprouty expression levels may have been close to the threshold needed to eliminate FGF signaling, since a small proportion of the limbs ultimately displayed a skeletal phenotype similar to that obtained when the AER is removed.
at stages 18-19: development of the humerus but not more distal skeletal elements (Saunders, 1948; Summerbell, 1974). These effects might be due to interference with either FGFR1 or FGFR2 signaling pathways, since both of these receptor genes are expressed in limb bud mesenchyme (Peters et al., 1992; Xu et al., 1998).

In the normal limb bud, Sprouty genes are expressed in the mesenchyme underlying the AER, consistent with their induction by FGF signaling from the AER. This region contains the “progress zone,” in which the cell division responsible for limb bud outgrowth and the specification of limb skeletal elements occurs (Summerbell et al., 1973). If Sprouty proteins inhibit FGF signaling from the AER, as our overexpression studies suggest, then Sprouty genes may serve as FGF feedback inhibitors during normal limb bud development, modulating the rate of cell proliferation or perhaps limiting the range of FGF signaling from the AER to the progress zone, much as dSPRY limits the range of FGF signaling in Drosophila tracheal development. This model predicts that in Sprouty loss-of-function mutants limb bud outgrowth and skeletal element patterning will be perturbed.

The effects of Sprouty overexpression were first observed during the bud stages of limb development (stages 18-28). We did not observe effects on limb induction and initiation of limb bud formation, processes that are also thought to depend on FGF signaling (reviewed by Martin, 1998) but which occur at stages 13-17. This was not surprising because the recombinant virus was introduced at stages 9-10, and retroviral gene expression does not become robust until 18-24 hours after infection (stage 17-18) (Morgan and Fekete, 1996).
**Sprouty overexpression causes chondrodysplasia**

Analysis of limbs overexpressing Sprouty at stages when skeletal element elongation and ossification normally occur (stages 30-39; E6.5-E13.5), revealed that approximately two-thirds of the infected limbs display a striking chondrodysplasia. All skeletal elements are present but each is dramatically shorter than normal. This is apparently due to a block in the differentiation of proliferating chondrocytes, which results in the lack of chondrocyte hypertrophy and subsequent bone formation.

FGF signaling is known to be a negative regulator of endochondral bone formation. In Fgfr3−/− mice, the hypertrophic zone is enlarged and there is excessive bone elongation (Colvin et al., 1996; Deng et al., 1996). If Sprouty always functions as an antagonist of all FGF signaling, one would predict that Sprouty overexpression in skeletal elements would mimic the effects of loss of FGF3 signaling. However, the effects of Sprouty overexpression in the chick limb mimicked or were more severe than those caused by excess FGF signaling (Coffin et al., 1995; Vogel et al., 1996). The gross morphologic and histologic features of the affected limbs were similar to those seen in several human chondrodysplasias caused by mutations in Fgfr3 that result in ligand-independent signaling activity by the receptor (Horton and Hecht, 1993; Webster and Donoghue, 1997; Burke et al., 1998). Fetuses heterozygous for the most strongly activating mutations are afflicted with type I Thanatophoric Dysplasia (TD), the most common form of lethal congenital dwarfism, and have short, thick, excessively curved femurs, and a paucity of hypertrophic chondrocytes. Heterozygosity for less strongly activating mutations in Fgfr3 are associated with the most common form of congenital dwarfism, Achondroplasia (Ach). Fetuses homozygous for such mutations have a phenotype that closely resembles type I TD. Recent studies show that the skeletal elements in transgenic mice overexpressing an Fgfr3 mutant allele, similar to the one that causes Ach, display a decrease in the hypertrophic and proliferative zones, and a modest reduction in bone length (Naski et al., 1998). One possible explanation for our results is that in developing bone, and perhaps other developmental settings, Sprouty might function as an enhancer rather than an antagonist of FGF3 signaling.

Alternatively, Sprouty overexpression may have no effect on signaling via FGF3, but instead may antagonize other FGF signaling pathways that function as positive regulators of endochondral bone formation. Presently, there is no genetic evidence that FGF signaling positively regulates chondrocyte differentiation, but Fgfr1 is expressed in osteoblasts and hypertrophic chondrocytes, and Fgfr2 is expressed in the perichondrium (Peters et al., 1992). Their potential roles in skeletal development are not known because severe loss-of-function Fgfr1 and Fgfr2 mutations cause lethality before the bones form (Deng et al., 1995; Yamaguchi et al., 1995; Arman et al., 1998; Xu et al., 1998). FGFR4 is an unlikely candidate because loss-of-function studies indicate that it is not required for bone development (Weinstein et al., 1998). It is also possible that the chondrodysplasia that we observed is due to Sprouty-mediated inhibition of EGFR or some other RTK signaling pathway (Bergmann et al., 1998; Casci et al., 1999; Kramer et al., 1999) that positively regulates endochondral ossification (Fig. 5). Tests of this hypothesis will require analysis of skeletal tissue from individuals with FGFR3-mediated chondrodysplasias, as well as a better understanding of the expression and functions of Sprouty and FGF receptor genes in normal skeletal development.

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