Negative regulation of Hedgehog signaling by the cholesterogenic enzyme 7-dehydrocholesterol reductase

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Cholesterol regulates Hedgehog (Hh) signaling during early vertebrate development. Smith-Lemli-Opitz syndrome (SLOS) is caused by defects in 7-dehydrocholesterol reductase (DHCR7), an enzyme catalyzing the final step of cholesterol biosynthesis. Many developmental malformations attributed to SLOS occur in tissues and organs where Hh signaling is required for development, but the precise role of DHCR7 deficiency in this disease remains murky. We report that DHCR7 and Sonic Hedgehog (Shh) are co-expressed during midline development in Xenopus embryos. DHCR7 has previously been implicated to function as a positive regulator of Hh signaling that acts to regulate the cholesterol adduction of Hh ligand or to affect Hh signaling in the responding cell. We present gain- and loss-of-function analyses suggesting that DHCR7 functions as a negative regulator of Hh signaling at the level or downstream of Smoothened (Smo) and affects intracellular Hh signaling. Our analysis also raises the possibility that the human condition SLOS is caused not only by disruption of the enzymatic role of DHCR7 as a reductase in cholesterol biosynthesis, but may also involve defects in DHCR7 resulting in derepression of Shh signaling.

KEY WORDS: Xenopus, Midline, Cholesterol, Floor plate, Smith-Lemli-Opitz syndrome (SLOS), Sonic hedgehog

INTRODUCTION

The members of the Hedgehog (Hh) family are involved in a wide variety of processes, including establishment of midline structures, somite development and digit formation. After translation, Hh preproteins autoproteolytically cleave their ~45 kDa precursor to generate two mature proteins, a N-terminal ‘signaling’ ligand and a C-terminal cleavage product (Lee et al., 1994). Autoproteolysis occurs concomitantly with the covalent attachment of cholesterol to the C terminus of the Hh ligand (Porter et al., 1996). Hh ligands are also palmitoylated at a highly-conserved Cys residue (Chamoun et al., 2001; Pepinsky et al., 1998) and these lipid modifications lead to production of a soluble multimeric protein complex that is essential to ensure effective potency and range for Hh signaling (Chen et al., 2004; Lewis et al., 2001; Zeng et al., 2001).

Hh proteins bind to their receptor Patched (Ptc), a 12-pass transmembrane protein (Ingham and McMahon, 2001; Lum and Beachy, 2004). This binding relieves the inhibitory effect of Ptc on the seven-pass transmembrane protein Smoothened (Smo), thereby transducing the Hh signal to the interior of the cell. Once Smo activity is triggered, Gli/Ci transcription factors are activated that induce downstream target genes. At present, the details of the Hh signaling cascade between the relief of Smo inhibition and the activation of Gli/Ci are not well understood. However, in vertebrates, the activity of the Gli protein is negatively regulated by protein kinase A (PKA) (Hammerschmidt et al., 1996).

Involvement of cholesterol in Hh signaling was further suggested by sensitivity of the response to perturbation of cholesterol homeostasis. A number of reagents known to inhibit cholesterol transport, such as cyclopamine, jervine, progesterone and U1866A, block Hh signaling in chick neural plate explants (Cooper et al., 1998). Among these agents, cyclopamine has also been shown to specifically bind to Smo (Chen et al., 2002). Additionally, AY-9944, an inhibitor of cholesterol biosynthesis, also blocks Shh signaling in vitro (Cooper et al., 1998; Incardona et al., 1998). Together, these results point to the importance of cholesterol regulation during embryogenesis, with the implication that disturbance of this process could result in the types of developmental defects known to be associated with abnormal Hh signaling.

Aberrant Hh signaling underlies a number of human diseases and congenital defects, including basal cell carcinoma, polydactyly and holoprosencephaly (HPE) (Ingham and McMahon, 2001). HPE is a patterning defect characterized by incomplete separation of the two halves of the forebrain at the midline. Similarly, HPE is also observed in the offspring of pregnant rats treated with AY-9944, which inhibits cholesterol biosynthesis by inhibiting the enzymatic activity of 7-dehydrocholesterol reductase (DHCR7) (Roux and Aubry, 1966). DHCR7 is a nine-pass membrane protein that catalyzes the final cholesterogenic step in the endoplasmic reticulum by reducing 7-dehydrocholesterol (7-DHC) to cholesterol (Fitzky et al., 1998; Wassif et al., 1998). Milder manifestations of HPE have been observed in ~5% of individuals with Smith-Lemli-Opitz Syndrome (SLOS), which is an autosomal recessive human disorder that results from mutations in DHCR7 (Kelley et al., 1996). In addition to midline defects, individuals with SLOS also suffer from malformations in the limbs, heart, kidneys, pancreas and genitals (Kelley and Hennekam, 2000). Explanations of how blockade of the cholesterol biosynthetic pathway leads to these malformations include (1) low levels of cholesterol and/or (2) the accumulation of sterol precursors in tissues, either of which are proposed, in turn, to affect the development of various tissues and organs during embryogenesis.

Several groups have shown that cholesterol deficiency can interfere with normal Hh signaling, and have proposed that this deficiency is the root cause of some of the developmental abnormalities seen in individuals with SLOS (Cooper et al., 2003; Guy, 2000). However, direct evidence demonstrating that impaired
DHCR7 function leads to cholesterol deficiency that, in turn, blocks Hh signaling is notably lacking. Because cholesterol can be supplied to early embryos maternally, it is difficult to assess the requirement of DHCR7 activity during early development. Additionally, although some correlations exist between decreased levels of plasma cholesterol and increased levels in the clinical severity of SLOS, there are also inconsistencies between the acuteness of the SLOS phenotype and the plasma levels of cholesterol and its precursor 7-DHC (Witsch-Baumgartner et al., 2000). Finally, neither treatment of cells with HY-9944 nor deletion of DHCR7 in mouse embryonic fibroblasts has proven effective in blocking sterol addition of Shh (Cooper et al., 1998; Cooper et al., 2003).

In order to uncover the function of DHCR7 during mouse embryogenesis, two DHCR7 mutants have been generated in this animal model. In the first, exon 8 was removed, generating the mutation DHCR7ΔEx8, which resembles DHCR7IVS8-1G>C, a mutation frequently encountered in individuals with SLOS (Fitzky et al., 2001). Another mutant, DHCR7Δ3-5, was produced by deleting exons 3, 4 and 5, thus eliminating most of the transmembrane-spanning region (Wassif et al., 2001). Both of these alterations inactivated the reductase activity of DHCR7, resulting in impaired conversion of 7-DHC to cholesterol. Further characterization of the mutant mice also revealed an overall accumulation of sterol precursors and reduction in tissue cholesterol levels; importantly, similar changes have been observed in human SLOS. However, neither mutant displayed morphological defects in the developing central nervous system or limbs, tissues where Shh is known to play crucial roles. Therefore, the precise relationships between DHCR7 activity, Hh signaling and SLOS need to be clarified.

We identified *Xenopus* DHCR7 in a microarray-based screen to uncover genes involved in chordamesodermal specification during gastrulation. To characterize the role of DHCR7 during early vertebrate development, we have performed both loss- and gain-of-function analyses in early *Xenopus* embryos. We report that DHCR7 functions contrarily to previously held notions. DHCR7 acts as a negative regulator of the response to Shh signaling during early embryogenesis, and its inhibitory affects appear to impinge on the Hh signaling pathway at the level of smoothened (Smo).

**MATERIALS AND METHODS**

**Embryo manipulations**

*Xenopus* embryos were fertilized in vitro and processed as described (Blitz and Cho, 1995). Embryos were microinjected and maintained with or without 5-100 μM HY-9944. Embryos were treated with cycloheximide continuously from the blastula stage (Perron et al., 2003). Capped mRNAs were prepared using an Ambion mMessage Machine kit. Animal cap explants were dissected and cultured as described (Cho et al., 1991). For luciferase reporter assays, Gli-luciferase reporter (0.2 ng) (Sasaki et al., 1997) was microinjected into two-cell stage embryos alone or with combinations of *Chordin*, *Shh*-N and DHCR7 mRNAs. Animal caps were dissected (stage 8), cultured until control embryos reached stages 12-18 and subjected to luciferase assays. All reporter gene experiments were repeated a minimum of three times. Animal cap conjugation experiments were conducted by recombining two animal caps expressing indicated mRNAs and a reporter gene. The conjugates were prepared by digesting the DNAs with EcoRI and transcribing with T7 RNA polymerase.

**Microarray analysis**

Total RNA was isolated from microdissected notochordal and presomitic mesodermal tissue fragments from early neurulae. Fluorescent labeled probes were generated based on a T7-based RNA amplification method (Wang et al., 2000). Four micrograms of amplified RNA were reverse transcribed in the presence of amine-modified random hexamers, and subsequently fluorescent labeled using a Cy3- and Cy5 labeling kit (Amersham). Generation of microarray slides, slide hybridization and scanning were as described previously (Shin et al., 2005). A GenePix Pro image acquisition program and Expressionist software (GeneData) were used for array data analyses.

**Plasmids**

*Xenopus* DHCR7 was subcloned into pCS2+ (Turner and Weintraub, 1994) to generate DHCR7 mRNA transcripts. A DHCR7 rescue construct was created by inserting a PCR fragment between the EcoRI and Ascl sites of pCS2 AT+ (Tsujii and Hashimoto, 2005). Primers used were DHCR7wt-F (5'-GGAGGTACTCCCACTCAGGAGGACATGAC-3') and DHCR7wt-R (5'-GGCGGAGCCAAGAGTGGAGAGGGAAGG-3') and DHCR7wt-F and DHCR7IVS8-1G>C-R (5'-GGCGGAGCCAAGAGTGGAGAGGGAAGG-3') for DHCR7IVS8-1G>C; DHCR7wt-F and DHCR7IVS8-1G>C-R (5'-GGCGGAGCCAAGAGTGGAGAGGGAAGG-3') for DHCR7IVS8-1G>C; and DHCR7wt-F, DHCR7wt-R, DHCR7IVS8-1G>C-R (5'-GGCGGAGCCAAGAGTGGAGAGGGAAGG-3') for DHCR7IVS8-1G>C. All DHCR7 templates were digested with NotI and transcribed using SP6 polymerase. Full-length *Shh* and *Shh*-N mRNA were synthesized with T7 polymerase using EcoRI-linearized XshhTST and XshhTST-N templates (Ekker et al., 1995a). NotI-linearized pCS2+GPKA (Ungr and Moon, 1996) and pCS2+XSmoM2-FLAG (Koebenick et al., 2003) templates were transcribed with SP6 polymerase. *chordin* RNA was synthesized as described (Blitz et al., 2000).

**Morpholinos and RT-PCR**

Morpholino oligos (GeneTools) used to inhibit DHCR function were DHCR7a-MO (5'-TACTACCTTCTGGATGACCATCT-3') and DHCR7b-MO (5'-TACTACCTTCTGGATGACCATCT-3'). A large-scale cDNA microarray screen was conducted to identify genes specifically expressed in developing notochord (Fig. 1). Among these, DHCR7 (7-2396/2557) was subcloned into pCS2+ as a probe. 4 Micrograms of amplified RNA were reverse transcribed in the presence of amine-modified random hexamers, and subsequently fluorescent labeled using a Cy3- and Cy5 labeling kit (Amersham). Generation of microarray slides, slide hybridization and scanning were as described previously (Shin et al., 2005). A GenePix Pro image acquisition program and Expressionist software (GeneData) were used for array data analyses.

**RESULTS**

**Isolation of Xenopus DHCR7 using cDNA microarrays**

A large-scale cDNA microarray screen was conducted to identify genes specifically expressed in *Xenopus* notochord. RNAs isolated from notochord, and left and right presomitic mesoderm of neurula stage embryos (stage 14-15) were hybridized to cDNA microarrays consisting of 21,000 clones representing ~8500 transcripts (Shin et al., 2005). Hierarchical clustering analysis identified several genes, including *Pentraxin, Caveolin-1, FoxA1, Chordin, Kox1, FK506BP, FoxA4A* and *DHCR7*, which are differentially expressed in the developing notochord (Fig. 1). Among these, DHCR7 (7-dehydrocholesterol reductase, EC 1.3.1.21) was particularly interesting as this enzyme has a presumed role in Hh signaling. Whole-mount in situ hybridization confirmed the expression of DHCR7 in the midline of early neurula stage embryos (Fig. 1).
Two related DHCR7 cDNAs were identified from the Xenopus EST (http://Xenopus.nibb.ac.jp/) and TIGR databases (see Fig. S1 in the supplementary material). The predicted amino acid sequences of these Xenopus DHCR7 cDNAs were 95% identical, and the activities of these gene products appeared to be identical in all the assays performed (T.K., T.H. and K.W.Y.C., unpublished). Therefore, we conclude that these similar cDNAs represent duplicated forms of DHCR7 arising from the pseudotetraploidy of Xenopus laevis, and are hence designated as DHCR7a and DHCR7b. The predicted Xenopus DHCR7 protein consists of 473 amino acids and the percentage of identity at the amino acid sequence level against its mouse, human, rat and zebrafish counterparts is 77% (see Fig. S1 in the supplementary material). Xenopus DHCR7 possesses a conserved 180 amino acid sterol-sensing domain (SSD) (residues 179-360) that is 86% identical to that of human DHCR7 (residues 181-362). The significance of the possession of an SSD in DHCR7 that is related to SSDs in other proteins is currently unknown.

**DHCR7 expression in Xenopus embryos**

As DHCR7 has been implicated in Hh signaling, we looked for clues to its relationship with Shh during Xenopus embryogenesis. Temporally, DHCR7 transcripts are first detected at the blastula stage (stage 9). As Shh is initially transcribed at the early gastrula stage (stage 10) (Ekker et al., 1995a), DHCR7 expression precedes that of Shh. Both DHCR7 and Shh transcripts continue to be expressed during early embryogenesis at least until tadpole stages (Fig. 2A).

Whole-mount in situ hybridization revealed that shortly after the onset of gastrulation, DHCR7 is expressed in the organizer and extends broadly along the marginal zone (Fig. 2B, part a), whereas Shh is first detected weakly in the organizer with expression restricted to the dorsal midline of the gastrula (Fig. 2B, part e). As neurulation proceeds, expression of both DHCR7 and Shh mRNA extend along the embryonic dorsal midline (Fig. 2B, parts b, f). By late neural stages (stage 20), DHCR7 is expressed in the presumptive telencephalon and anterior ventral endomesoderm (ave) with weak expression in the neural plate, epidermis and notochord (Fig. 2B, parts c,d,j), while Shh is expressed in the floor plate, prechordal plate and notochord (Fig. 2B, parts g,h,n). At the tailbud stage, both DHCR7 and Shh are similarly expressed in the notochord, ventral central nervous system, floor plate, branchial arches, frontonasal region, and presumptive anterior gut endoderm, and in a very limited region of the ave (Fig. 2B, parts k,l,o,p). In conclusion, although there are differences in the details of their expression, the overall patterns are similar for Shh and DHCR7, allowing for the existence of a functional link between their activities.

We then used assays in animal cap (ectodermal) tissue explants to examine how the expression of DHCR7 is controlled. Overexpression of Shh, BMP or Wnt in animal caps did not induce DHCR7 (data not shown). However, treatment with activin protein, a member of the TGFβ superfamily, induced DHCR7 expression, and this induction was direct as DHCR7 was upregulated even in the presence of the protein synthesis inhibitor cycloheximide (Fig. 2C). These results implicate a potential role for TGFβ signaling in the regulation of the Shh signal cascade during early Xenopus embryogenesis.

**Gain-of-function analysis suggests DHCR7 is an inhibitor of Shh signaling**

Sterol modification of Shh appears to be obligatory for proper Shh signaling in the processing of the precursor to produce the Hh ligand, suggesting that DHCR7 is an important enzyme positively influencing the activity of Shh. To explore the function of DHCR7 during early embryogenesis, we examined the effects of DHCR7 overexpression. Embryos overexpressing DHCR7 mRNA appeared to develop relatively normally until tailbud stages (data not shown). At the swimming tadpole stage, however, embryos overexpressing DHCR7 developed ectopic pigmentation in the optic stalk (Fig. 3A; 63%, n=46). This is a surprising observation as this phenotype resembles that reported in mice deficient in Shh in retinal ganglion cells (Dakubo et al., 2003) and suggests that DHCR7 may function as a negative regulator of Hh signaling. We therefore examined whether DHCR7 is capable of reversing phenotypes induced by Shh overexpression. To accomplish this, we injected Shh mRNA alone or together with DHCR7 mRNA, and examined the expression of genes influenced by Shh. Previous work has shown that enhancement of Shh signaling promotes the expression of Pax2 at the expense of Pax6 expression in optic vesicles (Hammerschmidt et al., 1996; Macdonald et al., 1995; Unger and Moon, 1996). Pax6 expression, which is inhibited by Shh, is rescued by co-injection of DHCR7 mRNA (Fig. 3B). Likewise, the expression of Pax2, Gli1 and Ptc1, which is stimulated by Shh overexpression, can be rescued by co-expression of DHCR7 mRNA.

Next, we examined the behavior of DHCR7 in a more defined system: animal cap assays. When the BMP antagonist Chordin is expressed in animal cap ectodermal explants, the caps are converted to a neural fate (Sasai et al., 1994). Chordin expression in the presence of Shh effectively induces Shh targets such as Gli1 (Tsuda et al., 2002) (Fig. 3C, lane 2). However, expression of DHCR7 significantly reduced the expression of Gli1, Ptc1 and FoxA2 (Fig. 3C, lane 3) consistent with an inhibitory role for DHCR7 in Shh signaling. To examine whether this inhibitory behavior of DHCR7 is independent of the cholesterol addition of Shh, we examined the effect of DHCR7 on a Shh-N–mediated Hh response. Shh-N, a N-terminal Shh ligand produced from recombinant Shh mRNA lacking...
reporter activation is due to Hh signaling, as mGli-BS (a reporter activation is blocked in the presence of DHCR7 (Fig. 3D). This Gli activated in animal caps expressing Chordin and Shh-N, and this was shown to respond to Hh signaling directly. The Gli reporter is vesicle. (k,l,o,p) stages. (a,b,d,e,f,h) Dorsal views. (c,g) Anterior views. (i-p) Lateral views with anterior towards the left and dorsal upwards. dl, dorsal lip; fp, floor plate; arc, archenteron; tel, telencephalon; ave, anterior ventral endoderm; ba, branchial arches; fnr, frontonasal region; age, presumptive anterior gut endoderm; nd, notochord; ov, otic vesicle. (C) Induction of DHCR7 by activin in animal cap explants. CHX, cycloheximide; WE, whole embryos.

Fig. 2. Developmental expression profiles of DHCR7 and Shh. (A) RT-PCR analysis of DHCR7 and Shh expression during Xenopus development. H4, histone H4. (B) Whole-mount in situ hybridization of DHCR7 and Shh at gastrula (a,e), neurula (b-d,f-h,i,j,m,n), tadpole (k,l,o,p) stages. (a,b,d,e,f,h) Dorsal views. (c,g) Anterior views. (i-p) Lateral views with anterior towards the left and dorsal upwards. dl, dorsal lip; fp, floor plate; arc, archenteron; tel, telencephalon; ave, anterior ventral endoderm; ba, branchial arches; fnr, frontonasal region; age, presumptive anterior gut endoderm; nd, notochord; ov, otic vesicle. (C) Induction of DHCR7 by activin in animal cap explants. CHX, cycloheximide; WE, whole embryos.

the C-terminal domain, does not require cholesterol adduction for its activity, but is as active as full-length Shh construct in overexpression studies (Ekker et al., 1995a; Lai et al., 1995). DHCR7 efficiently blocked Shh-N-induced Gli1, Ptc1 and FoxA2 expression in both animal caps (Fig. 3C, lanes 4 and 5) and embryos (data not shown), suggesting that the role of DHCR7 in antagonizing Shh signaling does not occur at the level of cholesterol modification of Shh ligand.

To determine whether DHCR7 impinges on Hh signaling, we used a Gli reporter gene (8×3’-Gli-BS) (Sasaki et al., 1997), which was shown to respond to Hh signaling directly. The Gli reporter is activated in animal caps expressing Chordin and Shh-N, and this activation is blocked in the presence of DHCR7 (Fig. 3D). This Gli reporter activation is due to Hh signaling, as mGli-BS (a reporter gene with mutations in Gli-binding sites) was not induced by Shh-N. We observed the effect of Shh-N on Gli transcription as early as stage 12 embryos.

We also wished to determine whether DHCR7 inhibits Hh signaling by blocking responding cells from reacting to the signal. To address this issue, we used an animal cap conjugation assay (Fig. 3E). Animal caps expressing Chordin with or without Shh-N mRNA were used to provide the Shh protein to conjugated animal caps injected with Gli-reporter in the presence or absence of DHCR7. The recombined caps were then incubated and subjected to a luciferase assay. We found that induction of Gli-BS reporter was effectively blocked by DHCR7 (Fig. 3F), indicating that DHCR7 inhibits signaling in Hh responding cells and not at the level of production of the ligand.

Loss-of-function analysis: DHCR7 is an inhibitor of Shh signaling

Antisense morpholino oligonucleotides (MOs) designed to recognize both DHCR7a and DHCR7b were injected into developing Xenopus embryos. DHCR7-MO-injected embryos had developed small eyes with reduced retinas and pigmented epithelia in the ventral half of the eye (Fig. 4B,E; 90%, n=48). This phenotype was efficiently rescued by co-expression of DHCR7 mRNA lacking the MO-binding sequence (Fig. 4C,F; 78%, n=40). Combined injection of MOs designed against both DHCR7a and DHCR7b gave stronger phenotypes than injection of the individual MOs alone (data not shown). Interestingly, this DHCR7 phenotype is similar to loss-of-function phenotypes for the known Hh antagonists Rab23 and FKBP8, which result from an inappropriate activation of Shh signaling within the optic vesicle (Bulgakov et al., 2004; Eggenschwiler et al., 2001). The similarities between these phenotypes are consistent with the notion that DHCR7 functions as a negative, rather than a positive, regulator of Shh signaling. To address whether the defects in optic vesicle patterning are due to the effect of DHCR7 on Shh signaling, rather than by other indirect effects, we injected DHCR7-MO into Xenopus embryos and examined the expression patterns of marker genes known to be regulated by Shh signaling. Expression of Pax6 was reduced in DHCR7 MO-injected embryos (compare Fig. 4G with H; 70%, n=30), accompanied by slightly expanded expression of Pax2 in the ventral eye (Fig. 4K,L; 60%, n=28). Gli1 was also broadly upregulated in MO-injected embryos (Fig. 4O,P; 58%, n=22). Thus, the DHCR7 loss-of-function effects resemble the phenotypes observed after Shh overexpression or PKA inhibition in Xenopus and zebrafish (Ekker et al., 1995b; Macdonald et al., 1995; Perron et al., 2003).

As loss-of-function suggests that DHCR7 is an inhibitor of Shh signaling, we examined whether loss of DHCR7 enhances responsiveness towards Hh signaling. Therefore, we coinjected DHCR7-MO with low doses of Shh-N mRNA that, alone, only weakly alter the expression of Pax2, Pax6 and Gli1 expression. Stimulation of Hh signaling by injecting 50 pg of Shh-N mRNA alone resulted in a reduction of Pax6 (Fig. 4I; 80%, n=28) with concomitant expansion of Pax2 (Fig. 4M; 80%, n=22) in the ventral half of the eye. Importantly, embryos co-injected with DHCR7-MO and Shh-N mRNA showed complete suppression of Pax6 expression (Fig. 4J; 80%, n=16) and expansion of Pax2 in the entire optic vesicle (Fig. 4N; 80%, n=16). These effects were similar to those of embryos receiving high Hh signaling (Lupo et al., 2005), suggesting that the loss of DHCR7 enhances the cellular response towards Hh signaling during optic vesicle patterning.
DHCR7 functions as a Shh inhibitor in neural tube patterning

Shh plays an important role in patterning the ventral neural tube. Therefore, we wished to know whether DHCR7 also acts as a negative regulator of Shh in that region. Whole-mount in situ hybridization analysis of DHCR7 MO-injected embryos showed significant increases in the expression levels of both Hnf3β/FoxA2 (Fig. 5A,B; 78%, n=28) and Shh (Fig. 5D,E,J,K,M,N; 92%, n=26), which are the markers for the midline. To test further the effect of DHCR7 MO on ventral neural patterning, we then performed unilateral injection of DHCR7 MO (Fig. 6A). Expression of ventral neural tube markers such as Shh, FoxA2 and Nkx2.2 expanded dorsally in MO-injected side (Fig. 6). Expression of Dbx1, which marks the intermediate region of the spinal cord, is also narrowed (Fig. 6H,I), in agreement with the previous finding that high levels of Shh signaling repress Dbx1 expression (Pierani et al., 1999; Briscoe et al., 2000). All these phenotypes were effectively rescued by overexpression of DHCR7 mRNA (Fig. 5C,F,I,L,O; Fig. 6D,G,J). These phenotypes are consistent with the notion that DHCR7 loss-of-function causes partial ventralization of the neural tube owing to upregulation of Shh signaling.

De novo cholesterol synthesis is not essential for Shh signaling during Xenopus early embryogenesis

We next examined how DHCR7 might function together with an inhibitor of cholesterol biosynthesis, in particular AY-9944, a pharmacological inhibitor of the enzymatic activity of DHCR7 (Roux and Aubry, 1966). When Xenopus embryos were continuously treated with AY-9944 (up to 100 μM) from the early gastrula stage onwards, no obvious morphological defects were noted (compare Fig. 7C with 7D). Similarly, when animal cap explants were treated with 10 μM AY-9944, a fivefold higher concentration than that necessary to inhibit completely FoxA2 induction by Shh-N in chick neural plate explants (Cooper et al., 1998), induction of the Gli-reporter by Shh-N was largely unaffected (Fig. 7B). These results suggest that inactivation of the enzymatic activity of DHCR7 by AY-9944 alone may not be sufficient to inhibit Shh signaling in Xenopus embryos. However, as the knockdown of DHCR7 clearly shows its requirement in Shh signaling, we considered the possibility that a non-enzymatic activity of DHCR7 is responsible for its inhibition of Shh activity.

Therefore, we treated DHCR7 mRNA-injected embryos with AY-9944. The embryos developed noticeable microcephaly and a shortened body axis when compared with DHCR7 alone or with AY-
944 alone (compare Fig. 7C-F; 76%, n=58). We also assessed the effects of AY-9944 on Gli reporter activity. Induction of Gli reporter was suppressed more strongly in DHCR7-expressing embryos treated with AY-9944 than that of either AY-9944 or DHCR7 alone (Fig. 7B). These data support the idea that AY9944 augments the antagonistic activity of DHCR7 towards Shh by influencing an activity other than its reductase activity.

SLOS-associated mutations reveal dispensability of the sterol-sensing domain for Shh inhibition

In light of our findings both that DHCR7 can act as a Shh inhibitor in Xenopus early embryos, and that the reductase activity of DHCR7 is dispensable, we wished to examine the effects of Xenopus DHCR7 mutants corresponding to human counterparts found in SLOS (Fig. 7A). One human mutation is DHCR7R350W (corresponding to R350W in Xenopus DHCR7), which results in abrogation of 95-97% of enzyme activity (Fitzky et al., 2001; Witsch-Baumgartner et al., 2000). Another mutation, DHCR7IVS8-1G>C, is the most frequently encountered DHCR7 mutation in individuals with SLOS. This defect causes aberrant splicing of exon 8, generates a truncated protein that is missing part of the sterol sensing domain (SSD; amino acid residues 318-471), and is also significantly reduced in its reductase activity (Fig. 7A). Several missense mutations mapped within the DHCR7 SSD have also been identified among some individuals with SLOS. Overexpression of either DHCR7R350W or DHCR7IVS8-1G>C resulted in blockade of induction of Gli reporter in the animal cap conjugation assay (Fig. 7L), despite the fact that the mutant proteins have presumably lost essentially all of their reductase activity. Additionally, embryos expressing either DHCR7IVS8-1G>C or DHCR7R350W displayed severe microcephaly and a shortened body axis (Fig. 7G;H; 90%, n=44 and 78%, n=44, respectively). When such severely affected embryos were stained for the eye marker, Pax6, a single small ‘cyclopic’ eyespot was detected (Fig. 7K). It is noteworthy that cyclopa is frequently observed in mouse embryos deficient in Shh and in individuals with holoprosencephaly (HPE) (Chiang et al., 1996; Cohen, Jr and Shiota, 2002). The experiments presented in the current study suggest that mutant DHCR7 proteins associated with SLOS are still capable of inhibiting Shh signaling despite their lack of reductase activity.

Next, in order to determine the contribution of the SSD on Hh signaling, we generated a Xenopus counterpart (DHCR7W149X) of human DHCR7W151X, which completely lacks the SSD. Additionally, DHCR7AN lacking most of the N terminus of DHCR7 was generated. When DHCR7W149X was expressed, it caused microcephaly in Xenopus embryos (Fig. 7I; 70%, n=20), and effectively blocked the induction of the Gli-reporter in the animal cap conjugation assay (Fig. 7L), despite the fact that the entire SSD is missing in the mutant protein. Importantly, expression of DHCR7AN did not affect cephalic development (Fig. 7J; 100%, n=30) but instead moderately upregulated the expression of the Gli-reporter gene (Fig. 7L). Altogether, these results show that the inhibition of Hh signaling by DHCR7 is mediated via the N-terminal domain of DHCR7.

Epistasis analysis: DHCR7 acts at the level of Smoothened

At what level does DHCR7 inhibit Hh signaling? The inhibition by DHCR7 of Hh signaling does not appear to be at the level of cholesterol adduction of the ligand, as loss of reductase activity does not appear to be essential and as Shh-N, which is not cholesterol modified, is also inhibited by DHCR7. Using an animal cap conjugation assay, we also showed that DHCR7 inhibits signaling in Hh responding cells and not at the level of production of the Shh ligand. To determine where in the signal transduction pathway DHCR7 acts, we performed epistasis experiments. First, we examined whether the cyclopic phenotype caused by the expression of DHCR7R350W was due to a defect in Shh signaling. The expression patterns of FoxA2, Shh and Ptc1 in these embryos were
examined. Injected embryos (Fig. 8) exhibited significant reductions of FoxA2 (100%, n = 20), Shh (100%, n = 34) and Ptc1 (92%, n = 38) transcripts. We also examined whether dominant-negative Protein Kinase A (dnPKA) could block the midline defects induced by DHCR7R350W. dnPKA reversed the microcephalic/cyclopic phenotype caused by DHCR7R350W (Fig. 8G-J; 96%, n = 46), demonstrating that DHCR7 acts as an inhibits Shh signaling by acting upstream of PKA.

Previous studies have demonstrated that the Hh dependent optic vesicle patterning is inhibited in X. laevis embryos treated with the Hh signaling inhibitor cyclopamine, which is known to inhibit the function of Smo (Perron et al., 2003). In order to determine whether DHCR7 functions upstream or downstream of Smo, embryos injected with DHCR7 MO were treated with cyclopamine and its effects on eye development were examined. Cyclopamine blocked both the inhibition of Pax6 and induction of Foxa2 and Gli1 by DHCR7-MO or Shh-N overexpression (Fig. 4G-J,K,L,N-R).

One interpretation of these observations is that DHCR7 functions to inhibit Hh signaling by acting either at the level of, or upstream of, Smo.

To confirm this possibility, we performed an epistasis experiment using an activated form of Smo (Smo-M2). When embryonic rescue experiments as shown in Fig. 8G-J were performed using Smo-M2, the rescue was only partially successful (data not shown). Similarly, animal cap assays revealed that Smo-M2 partially rescued the
DHCR7-mediated suppression of Hh signaling (Fig. 8K). These observations are consistent with the notion that DHCR7 acts upstream of Smo or at the level of Smo. As DHCR7IVS8-1G>C is a potent inhibitor of Hh signaling, we next addressed whether DHCR7IVS8-1G>C could block the activity of Smo-M2. As shown in Fig. 8L, DHCR7IVS8-1G>C effectively blocked the activation of the Gli reporter gene by Smo-M2, suggesting that DHCR7 affects Hh signaling by impinging on Smo.

**DISCUSSION**

We identified *Xenopus* DHCR7 in a microarray screen for genes regulating chordamesodermal development during vertebrate early embryogenesis. Contrary to the prevailing view that DHCR7 functions as a positive regulator of Shh signal transduction, the data presented here instead suggest a novel function for DHCR7 as a negative regulator of Shh signaling. We provide multiple lines of evidence demonstrating that DHCR7 negatively modulates the Shh signaling pathway during early embryogenesis, and suggest that it exerts this action at the level of Smo.

**Requirement for DHCR7 activity during early development**

The fact that DHCR7 is a key enzyme in cholesterol biosynthesis, responsible for the final step in the process, would suggest that DHCR7 stimulates Hh signaling through increased production of cholesterol. However, results of our current loss- and gain-of-function analyses do not support this view. Instead, our data indicate that DHCR7 serves to inhibit Hh signaling during early *Xenopus* development. Overexpression of DHCR7 inhibits the effects of ectopic expression of Shh, as well as endogenous Shh activity (Figs 3, 7 and 8), whereas knockdown of DHCR7 by morpholino antisense oligonucleotides leads to enhancement of Shh activity in both the eye and neural tube (Figs 4-6). Importantly, inhibition of the enzymatic activity of DHCR7 either by treatment of embryos with the pharmacological inhibitor AY-9944 or by overexpression of mutant DHCR7 proteins deficient in reductase activity, both still lead to inhibition of Shh signaling (Fig. 7), suggesting that some of the observed effects of DHCR7 on Shh signaling are independent of the enzymatic properties of DHCR7.

Previous work using DHCR7-deficient mouse fibroblasts has suggested that DHCR7 is required for cellular response to Shh (Cooper et al., 2003). This is in contrast to our finding that DHCR7 knockdown promotes Shh signaling (Figs 3, 4), and the reason for this discrepancy is unclear at present. However, it is important to note that the Shh response of fibroblast cells lacking DHCR7 was impaired only when residual endogenous cholesterol was depleted. As embryos from many non-placental vertebrates, including *Xenopus*, stockpile cholesterol maternally [in contrast to mammals, where cholesterol is supplied by yolk sac/placental transfer (Fitzky et al., 2001; Wassif et al., 2001)], differences in cellular cholesterol content may contribute to the difference in DHCR7 loss-of-function phenotypes.

**DHCR7 and Shh signaling in midline development**

Shh secreted from the notochord and floor plate forms a concentration gradient along the dorsoventral (DV) axis of the neural tube, thereby controlling the expression of specific homeodomain transcription factors (Ericson et al., 1997). Shh signaling is also negatively regulated by the Hh antagonists Patched1, Rab23, Pka, Hip1 and FKBP8 (Bulgakov et al., 2004; Eggenschwiler et al., 2001; Goodrich et al., 1997; Hammerschmidt et al., 1996; Jeong and McMahon, 2005). Defects in these components lead to
Negative regulation of Hh signaling by DHCR7

ventralization of the neural tube. In the present study, a similarly ventralized neural tube phenotype was also observed in Xenopus embryos when DHCR7 activity was inhibited (Figs 5 and 6). We note that mice deficient in DHCR7 do not display obvious defects in the developing central nervous system (Fitzky et al., 2001; Wassif et al., 2001), but our findings are consistent with the recent observation that the formation of serotonin (5-HT) neurons, which is dependent on high Shh signaling, showed a threefold increase in the number of neurons in the ventral CNS of DHCR7<sup>R350W</sup> mutant mice (Waage-Baudet et al., 2003). In addition to its role in the CNS, Shh is also required in the formation of the notochord and for maintenance of Shh signaling in that tissue once formed (Chiang et al., 1996). That DHCR7 is expressed both in the notochord and ventral CNS, and that the loss of DHCR7 enhances the transcription of Shh and FoxA2 in these tissues (Fig. 5), lead us to surmise that DHCR7 functions to negatively regulate levels of Shh signaling in both these structures.

What is the molecular mechanism underlying Shh inhibition by DHCR7?

We propose that DHCR7 inhibits Hh signaling at the level or downstream of Smo based on the following observations. First, the primary effects of DHCR7 do not appear to occur at the level of regulating the transcription of the Shh because DHCR7 was able to inhibit the effects of overexpression of Shh. Second, the inhibition of Hh signaling by DHCR7 appears to be independent of cholesterol adduction of the ligand, as Shh-N, which is not cholesterol modified, is also inhibited by DHCR7. Third, an animal cap conjugation assay demonstrated that DHCR7 inhibits signaling in Hh-responding cells and not at the level of production of the ligand. Fourth, epistasis analysis using Smo-M2 and DHCR7<sup>IVS8-1G>C</sup> is consistent with the notion that DHCR7 regulates Shh signaling either at the level of Smo or impinges downstream of the Smo. We also observed that dnPKA reversed the microcephalic/cyclopic phenotype caused by DHCR7<sup>R350W</sup>, demonstrating that DHCR7 acts as an inhibitor of Hh signaling by acting upstream of PKA.

DHCR7 functions intracellularly at the level or downstream of Smo and possesses a conserved sterol-sensing domain (SSD) that is found predominantly among proteins involved in vesicular trafficking (Kuwabara and Labouesse, 2002). Ptc1 and Disp1 are implicated in the vesicular trafficking of Hh, whereas SCAP, NPC1 and NPC1L are involved in sterol trafficking. Accordingly, fibroblasts isolated from many individuals with SLOS show abnormal storage of sterols, presumably resulting from defects in sterol trafficking (Wassif et al., 2002). Given that the Ptc protein is largely detected within intracellular vesicles (Incardona et al., 2000), and that both Ptc and Smo appear to shuttle between the plasma membrane and cytoplasmic vesicles in response to the presence/absence of Hh ligand (Denef et al., 2000), it is tempting to speculate.
that DHCR7 participates in the regulation of vesicular trafficking of Hh signaling components. However, our current DHCR7 mutational analyses confound this simple interpretation, as a DHCR7 mutant containing an intact N terminus (but lacking the SSD) is sufficient to inhibit the action of Hh signaling. It is currently unclear what the role of this N-terminal region might be, and further work will be required to fully understand the function of each domain of DHCR7.

The role of DHCR7 in the pathogenesis of SLOS

One curious aspect of SLOS is the wide range of symptoms seen in this disease. Individuals appear to display opposing phenotypes for the same underlying genetic condition. For example, some individuals are polydactyl (extra digits), while others are monodactyl (a single digit); some show holoprosencephaly, while others are macrocephalic (Kelley and Hennekam, 2000). How can mutations in a single gene cause such seemingly divergent phenotypes? As DHCR7 appears to have two distinct activities, a Hh antagonistic activity and a reductase enzymatic activity, perhaps, depending on the precise nature of the specific mutations, the activity of DHCR7 is oppositely modulated to bring phenotypes of opposing directionality. Additionally, mutations in DHCR7 can have the effect of altering intracellular sterol concentrations, which may affect cellular responses to Hh signaling (Cooper et al., 2003).

An important topic to address in the future is the biochemical nature of the DHCR7 mutants, especially how point mutations in the SSD domain or deletions affect the antagonistic activity of Shh relative to its reductase activity. Additionally, it is important to address how DHCR7 expression is regulated and its relationship to the occurrence of SLOS as proper expression of DHCR7 is essential for normal midline development.

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Supplementary material

Supplementary material for this article is available at http://dev.biologists.org/cgi/content/full/133/12/2395/DC1

References

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