

Mouse embryo Hox gene enhancers assayed in cell culture: *Hoxb4, b8* and *a7* are activated by Cdx1 protein

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ABSTRACT Mouse Hox gene enhancer elements have typically been identified and characterized using *Hox/lacZ* transgenic mouse embryos. Such studies have, for example, identified Cdx responsive binding motifs in the enhancers of *Hoxb8* and *Hoxa7*. Production of transgenic mouse embryos involves issues of cost, welfare, and considerable technical skill. It would be of benefit if these studies could be performed, or advanced, in cell culture. It is shown here that Cdx1 activation of mouse *Hoxb4*, *b8* and *a7* embryo-active enhancers can be detected using a HepG2 cell culture model system. The technique employed uses co-transfection of an inducible Cdx1 expression construct together with a Hox enhancer/*luciferase* reporter construct. Cultures to be compared receive identical DNAs and differ only in whether or not they also receive inducer (doxycycline). Response of all three Hox enhancers to Cdx1 protein is inhibited by mutation of Cdx binding motifs which are conserved in sequence from fish or *Xenopus* to mammals. The magnitude of transfected chick *Hoxa7* activation by Cdx1 is increased by multiple copies of its enhancer, but for maximum effect these must contain intact Cdx binding motifs. Cdx1 protein was found not to activate *Hoxb4*, *b8* or *a7* enhancers in P19 mouse pluripotential cells.

KEY WORDS: transgenic embryo, HepG2, Tet-On, transfection

Introduction

Gene expression is regulated to a large extent by transcription factors that bind to specific DNA sequence motifs located within *cis*-regulatory elements (Cho, 2012, Gaunt and Paul, 2012, Long *et al.*, 2016). These elements are also known as enhancers. Enhancers of vertebrate Hox genes may be 1) local, positioned inside the gene cluster and usually regulating only nearby genes (Gould *et al.*, 1997, Sharpe *et al.*, 1998), or 2) long range, usually positioned outside the gene cluster and regulating multiple Hox genes over longer distances (Spitz *et al.*, 2003).

Analysis of Hox gene enhancers in transgenic mouse embryos

Enhancers regulating Hox gene expression during mouse embryogenesis have typically been identified in some or all of the following steps (Charite *et al.*, 1998, Marshall *et al.*, 1994, Tabaries *et al.*, 2005). 1) Identify a fragment of DNA that when positioned upstream of a promoter and *lacZ* reporter gene is able to confer a Hox-like pattern of lacZ expression in transgenic embryos. 2) Perform deletions and mutations upon the enhancer-active fragment to narrow-down the specific DNA sequences necessary for its function. 3) Check whether these sequences are conserved between different vertebrate species, as is commonly the case for essential regulatory regions. 4) Examine these sequences for presence of any known transcription factor binding motifs. 5) Test whether these candidate transcription factors do indeed bind to the sequences. 6) Test whether these transcription factors activate the gene. Use of these steps has, for example, identified gene-activating Cdx binding motifs within enhancers of both *Hoxb8* (Charite *et al.*, 1998) and *Hoxa7* (Gaunt *et al.*, 2004, Knittel *et al.*, 1995).

The above experiments can provide direct evidence about the sites and regulation of mouse Hox gene enhancers during embryo development. The approach does, however, involve substantial technical skill, cost, and animal welfare issues that are associated with the production of large numbers of transgenic mouse embryos. Furthermore, the extents of *lacZ* reporter activity detected in transgenic embryos are only weakly quantitative since many uncontrolled factors affect expression levels, such as number of transgene copies, sites of integration, and transgene methylation. Also problematic may be the testing of candidate transcription factors. In practice, this has been achieved *in vivo* in a few cases by electroporation of expression constructs into chick embryos main-

Abbreviations used in this paper: Dox, doxycycline.

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Hoxb4

Tetraodon Stickleback Coelocanth Xenopus

Anole Turtle

Mouse Hoxb8

Fuqu Turtle Zebrafinch Mouse

Hoxa7

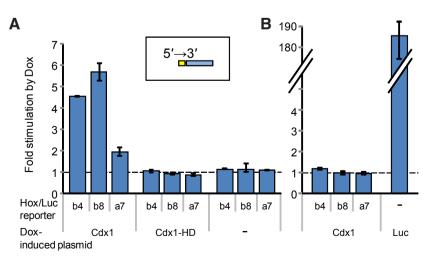
Xenopus Turtle Zebrafinch Chicken Platypus Mouse

tained in culture. For example, a Xenopus Xcad3 (Cdx4) construct electroporated into chick neural tube induced ectopic expression of Hoxb4 (Bel-Vialar et al., 2002). However, the electroporation procedure is itself technically demanding, poorly quantitative, and of low success rate.

Analysis of Hox gene promoters in cell culture

In attempt to find an alternative and more quantitative approach we have sought to obtain activation of Hox gene enhancers transfected into cultured cells. The enhancer fragments used are those which have already been reported in published studies to be expressed in a Hox-like pattern when tested in transgenic mouse embryos. Development of successful in vitro enhancer assays should facilitate future progress on the analysis of Hox gene regulations.

Candidate extracellular Hox activators such as Gdf11 can be tested simply by their addition to the culture medium after transfection of Hox enhancer/luciferase reporter plasmids (Gaunt et al., 2013). However, to add candidate intracellular transcription factors it is necessary to co-transfect the cells with expression plasmid.



luciferase reporter construct and doxycycline-inducible Cdx1 expression construct. Bar at right shows cultures transfected only with an inducible luciferase control vector. Data are plotted as fold stimulation relative to replicate cultures not given doxycycline (dotted baseline). Throughout, each bar shows average values for three replicate cultures, and range bars are shown. Dox, doxycycline; Luc, luciferase; Cdx1-HD, Cdx1 minus homeodomain.



Fig. 1. Conservation between species in Cdx binding motifs within Hoxb4, b8 and a7 enhancers. Sequences shown are the most highly conserved regions of enhancer fragments previously found to be active in Hox/lacZ transgenic embryos (Brend et al., 2003; Charite et al., 1995; Knittel et al., 1995). Confirmed or putative Cdx binding motifs are boxed in green. The sequences, from Ensembl, are aligned by Clustal Omega. Asterisks show sequence identity.

A recent protocol (Gaunt, 2017) successfully demonstrated that the Hoxc8 early enhancer (Shashikant and Ruddle, 1996) is activated in HepG2 cells by the combined (synergistic) action of Cdx proteins and Gdf11/Smad signalling. This protocol, which is also used in the current work, utilises the doxycycline-inducible Tet-On system (Clontech).

In the present study, it is shown that Cdx1 protein is able to activate embryo-active enhancers of Hoxb4 (Brend et al., 2003, Gilthorpe et al., 2002), Hoxb8 (Charite et al., 1995) and Hoxa7 (Knittel et al., 1995) in HepG2 cells, though not in P19 mouse pluripotential (embryonal carcinoma) cells (McBurney, 1993). Cdx responsive motifs conserved from fish or Xenopus to mammals are identified in mutation studies.

Results and Discussion

Conserved Cdx binding motifs in Hoxb4, b8 and a7 enhancers

Cdx proteins bind optimally to the [A/T] [T] [A/T] [A] [T] [A/G] sequence motif, or its reverse complement (Margalit et al., 1993). Fig. 1 shows such motifs found to be conserved from fish or Xenopus

> Fig. 2. Doxycycline-induced Cdx1 protein activates mouse Hoxb4, b8 and a7 enhancers transfected into HepG2 but not P19 cells. (A) HepG2 Tet-On cells. All cultures were transfected with a Hox/luciferase reporter construct, either Hoxb4, Hoxb8 or Hoxa7 (insert: yellow box is Hoxb4, b8, or a7 enhancer; blue box is SV40 minimal promoter/luciferase/SV40polyA). Three bars at left show cultures co-transfected with doxycycline-inducible Cdx1 expression construct. Three bars in middle show cultures co-transfected with inducible Cdx1-minus-homeodomain expression construct. Three bars at right show cultures not given Cdx1 expression construct. (B) P19 Tet-On cells. Three bars at left show cultures co-transfected with Hox/

to mice within the embryo-active enhancers of *Hoxb4*, *b8* and *a7*. These sequences in the *Hoxb8* enhancer have already been identified as Cdx binding sites by electrophoretic mobility shift assays (Charite *et al.*, 1998). For *Hoxb8* (Charite *et al.*, 1998) and *Hoxa7* (Gaunt *et al.*, 2004) they have also been shown by mutation studies to regulate position of *Hox/lacZ* transgene expression boundaries in mouse embryos. However, it is not yet clear whether Cdx proteins operate alone, or must co-operate with other factors to activate the *Hoxb8* and *Hoxa7* enhancers. For *Hoxb4*, the conserved Cdx motifs shown in Fig. 1 have not, apparently, been previously noted.

Mouse Hoxb8, b4*and*a7 *enhancer activation by Cdx1 in HepG2 but not P19 cells*

In preliminary studies (not shown), experimental cultures were co-transfected with Hox enhancer/*luciferase* reporter together with constitutive promoter/Cdx expression plasmids. Luciferase levels were compared with those from control cultures that received only the reporter plasmid. The comparison was difficult to interpret since experimental cultures acquired not only Cdx expression but also twice the overall amount of transfecting DNA. It was concluded that two cultures could only be validly compared if transfected with identical DNAs. To enable this, the doxycycline-inducible Tet-On system (Clontech) is used. Cultures to be compared receive replicate DNAs and differ only in whether or not they receive doxycycline. Data are expressed as 'fold stimulation' (luciferase value for doxycycline-induced cultures divided by value for replicate non- induced cultures). This gives results that are consistent between different experiments and DNA preparations.

Fig. 2A (three bars at left) shows activation of mouse *Hoxb4*, *b8* and *a7* enhancer/*luciferase* reporters in HepG2 Tet-On cells by Cdx1 protein produced from a *pTRE3G-Cdx1* doxycycline-inducible

expression construct. As controls, doxycycline given in the presence of a *pTRE3G-Cdx1*-minushomeobox construct (three bars in middle), or in absence of *pTRE3G-Cdx1* (three bars at right) does not activate the *Hox/luciferase* reporters in HepG2 Tet-On cells.

Fig. 2B, in contrast, shows that there is little or no activation of the Hox enhancer/*luciferase* reporters when Cdx1 is induced in P19 Tet-On cells. As a positive control, a transfected *pTRE3G-Luc* plasmid is abundantly activated in these cells, showing that they are fully able to host doxycycline-activation of *pTRE3G* vectors (Fig. 2B, right). The reason why P19 Tet-On cells fail to show Cdx1 activation of transfected Hox enhancers is not clear, and is currently under investigation. Possible explanations include lack of an essential co-factor or presence of an inhibitor. P19 pluripotential cells represent a cell type in embryogenesis (inner cell mass, about 3-4 days) that appears earlier in time than those that first express Cdx1 and Hox genes (about 7.5 days).

Mutations in Cdx binding motifs inhibit response to Cdx1

Functional transcription factor binding motifs within enhancers are commonly, though not always, conserved between species (Cho, 2012). Mutations were therefore introduced into the species-conserved (Fig. 1), putative Cdx binding motifs of the mouse Hox enhancers as shown in Fig. 3A. Fig. 3B shows how, for all three Hox enhancers, the mutations result in inhibitions of their responses to Cdx1 protein, suggesting that Cdx1 protein exerts a direct stimulatory effect via these motifs. The inhibitions are, however, incomplete, raising the following possibilities. First, Cdx1 protein might activate canonical binding motifs (Margalit et al., 1993) which are not conserved between species but which are located in the mouse Hox enhancer DNAs outside the conserved regions shown in Fig. 3. Second, Cdx1 protein might activate noncanonical binding motifs in the Hox enhancers. Third, the possibility is not excluded of an indirect effect, where Cdx1 may induce some other transcription factor(s) which then, in turn, activate the Hox enhancers via alternative sequence motifs.

Hoxa7 response to Cdx1 is increased by multiple copies of the enhancer

The level of expression from an enhancer/promoter/reporter construct is typically increased, with retained tissue specificity,

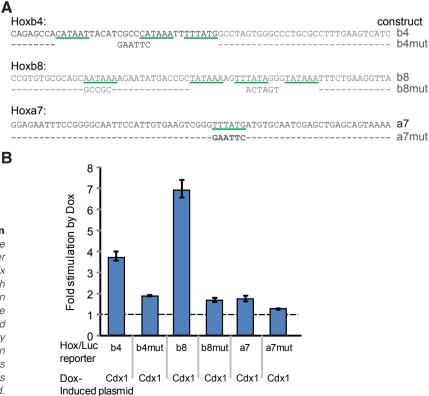


Fig. 3. Cdx1 stimulatory effects inhibited by mutations in Cdx binding motifs. (A) For each mouse Hox gene, wild-type enhancer DNA (upper sequence) was mutated (mut; lower sequence) in its species-conserved (Fig. 1), putative Cdx binding motifs (green underline). Dashes indicate identity with wild-type sequence. (B). Mutated constructs are inhibited in their response to doxycycline-induced Cdx1protein relative to their corresponding wild-type constructs. Transfected plasmids are as indicated. Bars show fold stimulation by doxycycline relative to results for replicate cultures not given doxycycline (shown as dotted baseline). Each bar shows average values for three replicate cultures, and range bars are shown. Dox, doxycycline; Luc, luciferase; mut, mutated.

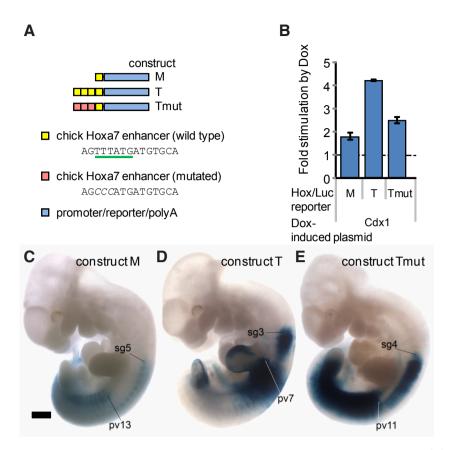


Fig. 4. *Hoxa7* response to Cdx1 is increased by multiple copies of the enhancer. (A) Chick Hoxa7 reporter constructs. The promoter/reporter (blue bar) is either SV40 promoter/ luciferase for cell transfection, or chick Hoxa7 promoter/acZ for transgenic embryos (Gaunt et al., 2004). (B) Expression of luciferase reporter constructs in HepG2 cells. Transfected plasmids are as indicated. (C-E) Expression of lacZ reporter constructs in 10.5 day transgenic mouse embryos. Four copies of the enhancer results in higher fold-stimulation by Cdx1 (Doxycycline) in HepG2 cells (B), and more anterior embryonic expression (D) than does only one copy (B,C). These effects are partially inhibited when three copies of the enhancer tetramer are mutated in their species-conserved (Fig. 1) Cdx binding motifs (green underline in A) (B,E). Embryos shown in (C,D) are transient transgenic embryos derived independently from embryos shown previously (Gaunt et al., 2004). Bars in (B) show fold stimulation by doxycycline relative to results for replicate cultures not given doxycycline (shown as dotted baseline). Abbreviations: Dox, doxycycline; Luc, luciferase; M, monomer; pv, prevertebra; sg, spinal ganglion; T, tetramer; Tmut, tetramer mutated in three copies. Bar, 0.5 mm.

by incorporating multiple tandem copies of the enhancer element (Blain *et al.*, 2010, Wang *et al.*, 2008).

Cdx1 enhancer activation in HepG2 Tet-On cells is modest for mouse Hoxa7: up to about two-fold (Fig. 2A, 3B). It is now shown that a tetramer (T) of the chick Hoxa7 enhancer provides a more substantial quantitative response to Cdx1 (doxycycline) than does monomer (M) (Fig. 4A,B), and much of this is overcome when three copies of the enhancer are mutated in their species-conserved (Fig. 1) Cdx binding motifs (Fig. 4B).

In earlier published work (Gaunt *et al.*, 2004) we compared these monomers (M) and tetramers (T) of the chick *Hoxa7* enhancer (Fig. 4A) in their ability to drive *lacZ* transgene expression in mouse embryos. Tetramer produces a forward shift in the anterior boundaries of lacZ expression (Fig. 4D) when compared with monomer (Fig. 4C). It may also shift forward the posterior boundaries, though this is not seen consistently in all independently-

derived transgenic embryos: compare Fig. 4D with our earlier Fig. 2C (Gaunt *et al.*, 2004). Much, but not all, of the tetramer effect is overcome if three copies of the enhancer are mutated in their Cdx binding motif (Tmut) (Fig. 4A,E). The full tetramer effect therefore depends upon an overall increase in the number of Cdx binding motifs, both *in vitro* (Fig. 4B) and *in vivo* (Fig. 4 C-E).

Role of Cdx proteins in positioning of Hox gene expression boundaries

It is suggested that Cdx proteins provide activation, and are essential for opening the chromatin structure, of the central group of Hox genes (*Hox4* to *Hox9*) (Neijts *et al.*, 2017, Neijts and Deschamps, 2017). Cdx binding sites are reported within the central Hox cluster region but not around more posteriorly-expressed Hox genes. Anteriorlyexpressed Hox genes (*Hox1* to *Hox3*) are activated independently of Cdx (Neijts *et al.*, 2017, Neijts and Deschamps, 2017).

It has been proposed that Cdx proteins in the vertebrate embryo may be instructive in the positioning of Hox gene expression boundaries (Bel-Vialar *et al.*, 2002, Charite *et al.*, 1998, Schyr *et al.*, 2012), and that this may be by their acting as graded morphogens (Gaunt *et al.*, 2004, Gaunt *et al.*, 2008). This is consistent with observations that Cdx proteins are expressed in posterior-to-anterior gradients along the tail-to-head axis (Gamer and Wright, 1993, Gaunt *et al.*, 2008, Marom *et al.*, 1997) and that, as indicated below, Hox expression boundaries are regulated by Cdx proteins in a dose-dependent way.

Dose-dependency in Hox activation by Cdx proteins is shown by the following. 1) Knockout of some or most Cdx gene activity results in posterior shifts in the anterior limits of Hox expressions in embryos (Subramanian *et al.*, 1995, van den Akker *et al.*, 2002). 2) Increased Cdx protein dosage causes forward shift in Hox expressions and homeotic activities in embryos (Gaunt *et al.*, 2008). 3) Increase in the number of enhancer elements in

both *Hoxb8/lacZ* and *Hoxa7/lacZ* transgenes causes forward shifts in their embryo expressions, and this depends upon the increased number of Cdx binding motifs (Charite *et al.*, 1998, Gaunt *et al.*, 2004). In the latter report, forward shift in *Hoxa7/lacZ* expression is associated with an earlier time of initial expression (Gaunt *et al.*, 2004). Similarly, manipulating Cdx1 protein concentrations in *Xenopus* embryos can change the timing of *Hoxc8/lacZ* first expressions (Schyr *et al.*, 2012).

Hoxa7/lacZ and Hoxb4/lacZ expressions in transgenic mouse embryos show some caudal regression in mid-gestation stages (Brend *et al.*, 2003, Gaunt *et al.*, 2004). This coincides in time with caudal regression of the Cdx protein gradient (Bel-Vialar *et al.*, 2002, Gamer and Wright, 1993). A similar regression is not reported for expression of endogenous *Hoxb4* (Bel-Vialar *et al.*, 2002). This suggests a two-step mechanism: Cdx gradients may regulate the early position of a Hox expression boundary, and then this is subsequently maintained by Cdx-independent mechanisms (Gaunt *et al.*, 2008, Schyr *et al.*, 2012), such as autoregulation in the case of *Hoxb4* (Gould *et al.*, 1997).

Concluding remarks

An inducible expression system in HepG2 cells allows Cdx1 activation of Hoxb4, b8 and a7 enhancers that previously had only been shown to function in transgenic embryos. Compared with the embryo approach, the in vitro technique now described offers the relative advantages of requiring low cost and skill, of avoiding animal welfare issues, of allowing greater quantitation, and of potentially identifying enhancers active in both embryonic and adult tissues. However, it has the relative disadvantages of not specifically showing that an enhancer is embryo-active, and of not providing information about spatial patterns of embryonic expression. The in vitro approach cannot therefore fully replace in vivo work. However, it may provide a useful early screen for enhancer-active DNA regions that can subsequently be tested in transgenic embryos. It can also permit rapid deletion analyses to narrow-down enhancer fragment size. The essential binding motifs within an enhancer, once identified, can more easily be analysed by the in vitro approach. To maximise the numbers of Hox enhancers detectable, it will be of value to conduct screens on additional cell lines.

Materials and Methods

DNA constructs

Luciferase reporter constructs were prepared using enhancers known to regulate Hox-like patterns of reporter (lacZ) expression in transgenic mouse embryos. Each of the enhancers was inserted, in 5' to 3' orientation, upstream of the minimal SV40 promoter and luciferase reporter gene in pGL3-promoter (Promega) (Fig. 2A insert). Mouse Hoxb4 intron enhancer was the 1.4kb Sall/BglII fragment (Brend et al., 2003, Gilthorpe et al., 2002). Mouse Hoxb8 upstream enhancer was 555bp of DNA cloned by PCR using oligos GCGAAGGAAGTCCCAGTTTC (5') and CCAGCTGCTAGCTTCTT-TAG (3'). This includes the essential EcMs79 fragment within the larger BH1100 fragment, both of which fragments regulate lacZ expression in at least part of the Hoxb8-like expression pattern (Charite et al., 1998, Charite et al., 1995). Mouse Hoxa7 upstream enhancer was 469bp of DNA cloned by PCR using oligos CTATTTTAGAATTTTATTTCTC (5') and AGGCCATGCTGGAAGACTGGCGAC (3') (Knittel et al., 1995). Various mutations were introduced by PCR into putative Cdx binding motifs of the Hox enhancers as shown in Fig. 3A. The chick Hoxa7 enhancer (271bp) and its tetramers (Fig. 4A) were described earlier (Gaunt et al., 2004). For luciferase assays these were inserted into the *pGL3-promoter* vector.

Cdx1 protein expression construct (pTRE3G-Cdx1) and a control derivative expressing Cdx1 protein without the homeodomain (pTRE3G-Cdx1-minus-homeobox), both inducible by doxycycline, were prepared in pTRE3G-IRES plasmid (Clontech) and were described earlier (Gaunt, 2017). A control plasmid pTRE3G-Luc (Clontech) was used to test the responsiveness of transgenic Tet-On cell lines to doxycycline.

Cell culture and luminometry

HepG2 is an established line of hepatocellular carcinoma (HCC) cells (Aden *et al.*, 1979). HCC cells, unlike normal liver cells, typically express a wide variety of Hox genes (Kanai *et al.*, 2010), though this is not specifically documented for HepG2 cells. HepG2 cells do not normally express Cdx genes (Gautier-Stein *et al.*, 2003), but do express Gdf11 receptors making them a useful model system for induction of posterior Hox genes (Gaunt, 2017, Gaunt *et al.*, 2013). The HepG2 Tet-On Advanced transgenic

cell line (Clontech, cat. 631150) is designed for use with the doxycyclineinducible pTRE3G plasmids. A stable P19 Tet-On cell line was prepared by transfection of P19 cells (McBurney, 1993) (obtained from ATCL) with linearized pCMV-Tet3G plasmid (Clontech) followed by selection for a transgenic clone in 1.6 mg/ml G418.

Cell culture conditions, transfections using Lipofectamine 2000 (Invitrogen), treatment with doxycycline (10 μ M), luciferase assays (Promega cat. E1500) and luminometry were all as described earlier (Gaunt, 2017, Gaunt and Paul, 2011), and were in accordance with manufacturers' instructions. Cultures were transfected for 5 hours, followed by change of medium with or without doxycycline. After a further 18 hours monolayers were rinsed in phosphate buffered saline then lysed for luminometry. As is usual in cell culture transfection assays, plasmids were transfected as closed circular DNA, including vector sequences. Plasmids for transfections were prepared using Sigma GenElute HP Plasmid Midiprep kits.

Each bar on each bar chart shows the mean value obtained from three replicate cultures (n=3). Range bars show the values obtained from the highest and lowest of these three biological replicates. Range bars are preferred to statistical error bars where n is small, including n=3 (Krzywinski and Altman, 2013).

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