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Chapter 6 - General Conclusions

As detailed anatomical descriptions of coral development are still some way off, there is no morphological framework to aim the interpretation of expression patterns. Indeed, even comparing expression patterns of what should be orthologous genes within the Cnidaria is not a trivial task; for example, while *ind/Gsh* orthologs (*cnox2/anthox2* genes) are restricted along the O/A axis in all cnidarians investigated, in some expression is biased towards the oral end, in others to the aboral end (Schummer *et al.*, 1992; Shenk *et al.*, 1993a; Shenk *et al.*, 1993b; Cartwright *et al.*, 1999; Gauchat *et al.*, 2000; Hayward *et al.*, 2001; Yanze *et al.*, 2001). It is also difficult to interpret the very different expression patterns of *ems*-related genes seen in *Acropora* and *Hydractinia*; in *Acropora*, *ems* is expressed in a subset of presumed neurons (i.e. in the ectoderm) that is spatially restricted along the O/A axis (Hislop, 2003), while in *Hydractinia*, the corresponding gene is expressed in the endodermal digestive cells of the hypostome (Mokady *et al.*, 1998). This thesis describes the isolation and preliminary characterisation of 6 novel homeobox genes (*vnd1Am*, *vnd2Am*, *vnd3Am*, *msx3Am*, *cnox1Am* and *barhAm*) from *Acropora*, as well as extending what is known about 3 other coral homeobox genes (*cnox-2Am*, *PaxBam* and *PaxCam*). From the results presented, it is clear that members of most of the homeobox gene families known from higher animals are represented in cnidarians, and there are some intriguing hints that aspects of gene function may be conserved.

In general, cnidarian genes show surprising levels of similarity with their vertebrate (rather than their invertebrate) counterparts. A preliminary EST project revealed that 10% of those genes with clear database matches corresponded to mammalian genes that have been lost from the model invertebrates *Drosophila* and *Caenorhabditis* (Kortschak *et al.*, 2003). Moreover, those *Acropora* sequences that correspond to genes present across the Metazoa resembled much more closely human sequences than any *Drosophila* or *Caenorhabditis* sequences (Kortschak *et al.*, 2003). The picture that is emerging is that cnidarian genomes are much more complex at the level of gene complements than was previously thought.

An additional aspect of the genetic complexity of cnidarians is that many of the genes likely to play key roles in development have been independently duplicated (Hayward *et al.*, unpublished; Go *et al.*, unpublished; Ball *et al.*, 2004 and Hislop *et al.*, DGE in press; Samuel *et al.*, 2001). Analysis of a larger EST dataset using the INPARANOID software implies that at least 5% of *Acropora* genes have been independently duplicated (Technau *et al.*, submitted). In addition, more data is required before it can be ascertained if duplication is shared amongst all cnidarians; the duplication of the *nanos* genes is common to both *Hydra* and *Acropora* (Mochizuki *et al.*, 2000), (Go *et al.*, unpublished), while in other cases (for example *Acropora Dmbx1/2*) it would seem that the duplication is anthozoan specific (Hislop *et al.*, DGE in press). In any case, it is clear that cnidarians in general possess a greater genetic complexity than was previously thought; best estimates suggest that the anthozoans *Acropora* and *Nematostella* have more genes than the model invertebrates *Drosophila* (~14,000 genes) and *Caenorhabditis* (~17,000 genes) and that their gene numbers are in the same range as vertebrates (Technau *et al.*, submitted). Gene duplications clearly contribute to this complexity, but their significance in cnidarian evolution is unknown.

The identification of members of the *vnd* and *msx* families (described in Chapter three) demonstrates that *Acropora* possesses at least one ortholog of each of the genes of the *vnd/ind/msh* cascade. Each of the newly isolated genes is expressed in a spatially restricted manner along the O/A axis. Together with data for *cnox-2Am*, the expression patterns of these genes are consistent with the hypothesis of a conserved repressive cascade also functioning in the Cnidaria. However, unlike the situation in higher animals, the expression of *vnd* and *msx* is not restricted to the nervous system; expression in putative neurons is only seen with *cnox-2Am*. Assigning possible functions to the *barhAm* and *cnox1Am* genes identified in this project has also been difficult. Generally speaking, *Bar* genes are important in specifying the cells (including neurons) surrounding the eye, craniofacial features and in the CNS. The *Chlorohydra Bar* gene (*cnox3*) is expressed in the head region, suggesting a role in head regeneration, and this is consistent with an ancestral role in the specification of anterior embryonic structures (Schummer *et al.*, 1992). *Acropora barhAm* is also expressed in the oral region, but is highly restricted both in its spatial and temporal expression pattern. In addition, the transcript is not restricted to specific cell types, complicating the interpretation of the expression pattern.

The work described in this thesis clearly indicates how informative anthozoan cnidarians can be with respect to the evolution of function in gene families. Genes that are clearly related to those known to play key roles in specification of both A/P and D/V axes in the Bilateria are present in the ‘radially-symmetric’ cnidarians. A number of these A/P and D/V patterning genes are differentially expressed along the single overt axis of the anthozoan planula, but a few, such as *Dpp*, are expressed in what seems to define a second axis. Clearly we are still some way off understanding how cnidarians use these genes to specify their body plans, but the work described in this thesis represents a substantial contribution towards this goal. Ultimately, the information gained from work on cnidarians will be a major contributing factor to our understanding of the evolution of body plans, as cnidarian research becomes an essential component of the growing field of evo-devo.

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Appendix A – Abbreviations

aa	amino acid
Ab	antibody
amp	ampicillin
AP	alkaline phosphatase
arm	armadillo
A/P	anterior/posterior
BCIP	5-bromo-4-chloro-3-indolyl phosphate
bp	base pair
°C	degrees Celsius
cDNA	complementary deoxyribonucleic acid
Ci	Curie(s)
cm	centimetre
CNS	central nervous system
cpm	counts per minute
DAB	3,3-diaminobenzidine
ddH ₂ O	double distilled water
DEPC	diethyl pyrocarbonate
DIG	digoxygenin
DNA	deoxyribonucleic ac id
DNase	dexyribonuclease
dATP	deoxyribo-adenine triphosphate
dCTP	deoxyribo-cytosine triphosphate
dGTP	deoxyribo-guanine triphosphate
dNTP	deoxyribo-nucleotdie triphosphates (dATP, dCTP, dTTP, dGTP)
dTTP	deoxyribo-thymine triphosphate
dUTP	deoxyribo-uracil triphophate
D/V	dorsal/ventral
<i>E. coli</i>	<i>Escherichia coli</i>
EDTA	ehylenediamine tetraacetic acid
F1	fluorescein
g	gram
HD	homeodomain
HEPES	N-2-hydroxyethylpiperazine-N]-2-ethane sulphonic acid
h	hour(s)
HRP	horseradish peroxidase
I	inosine
kan	kanamycin
kb	kilobase pair(s)
LB	Luria-Bertani Media
M	molar
min	minutes(s)
μg	microgram (10^{-6} g)
μL	microlitre (10^{-6} L)
μM	micromolar (10^{-6} M)
mg	milligram(s)

mL	millilitre(s)
mol	mole(s)
MOPS	3-(N-morpholino)propanesulphonic acid
mm	millimetre (10^{-3} m)
mM	millimolar (10^{-3} M)
mRNA	messenger ribonucleic acid
NBT	nitro blue tetrazolium
ng	nanogram(s) (10^{-9} g)
O/A	oral/aboral
OP	octapeptide
ORF	open reading frame
PBS	phosphate-buffered saline
PCR	polymerase chain reaction
PD	paired domain
PEG	polyethylene glycol
pfu	plaque forming unit(s)
pH	unit of acidity/alkalinity
RNA	ribonucleic acid
RNase	ribonuclease
RNAi	ribonucleic acid interference
SEM	scanning electron microscope
TE	Tris.HCl-EDTA buffer
Tris	tris(hydroxymethyl)aminomethane
tRNA	transfer ribonucleic acid
U	unit(s)
UAS	upstream activator sequence
UTR	untranslated region
UV	ultraviolet
VNC	ventral nerve cord
v/v	units volume per units volume
w/v	units weight per units volume

Appendix B – Creation of an *ind*-GAL4 driver line

Although *ind* was cloned as a direct target of Vnd and the motif likely to mediate this interaction is known (Weiss *et al.*, 1998), no enhancers have been identified and its promoter has not been characterised. This lack of information on *ind* regulation represents a major problem in terms of construction of an *ind*-GAL4 line.

The strategy adopted was to generate constructs containing different portions of the region immediately 5' of the likely transcription start site (promoter); in addition, the intention was to generate additional constructs in which promoter fragments were fused (using the technique of splicing by overlap extension - see section 2.4.15) to an 80bp candidate regulatory region located downstream of the *ind* coding sequence. This region contains several Vnd binding sites, and is hereafter referred to as the Weiss fragment (Weiss *et al.*, 1998). Each of the constructs were designed to include *KpnI* and *NotI* restriction sites on their 5' and 3' ends respectively to enable directional cloning into the equivalent sites of the pG4PN vector (which was kindly supplied by Dr Coral Warr, Monash University). Constructs were generated by Mr Niko Frank under my direct supervision. The constructs for this work are summarised schematically as Fig 7.1.

Each of the fragments was initially amplified from genomic DNA extracted from wild type *Drosophila*. A common reverse primer was used in all constructs (6_prom_rev 5'-aaggaaaaagcggccgcctgggttctgggta) while additional primers used in the production of each construct varied and occasionally overlapped depending upon the particular requirements (Construct 1: 1_Weiss_for 5'-gggttaccagttcctgctcaagtgtgc; 2_Weiss_rev 5'-cgagtgttgcggcctacctgctgacctcag; 5_prom_for 5'-ctgggtcagcaggtaggccgaacacactcgctc; Construct 2: 1_Weiss_for; 4_prom_for 5'- ctgggtcagcaggtaaatcgccagacaaaaacggaa; 3_Weiss_rev 5'-ttttgtctgcgattcacctgctgacctcag; Construct 3: 7_prom_for 5'-gggttaccaatcgccagacaaaaacggaa). Each construct was subcloned into pGEM-T and sequenced before being isolated by restriction digest and cloned into the pG4PN vector. Plasmids were purified using a QIAGEN midprep purification kit before being injected into white *Drosophila* embryos. Each of the constructs was injected into the dechorionised eggs of 100 – 120 *Drosophila* and allowed to develop. Of these, for

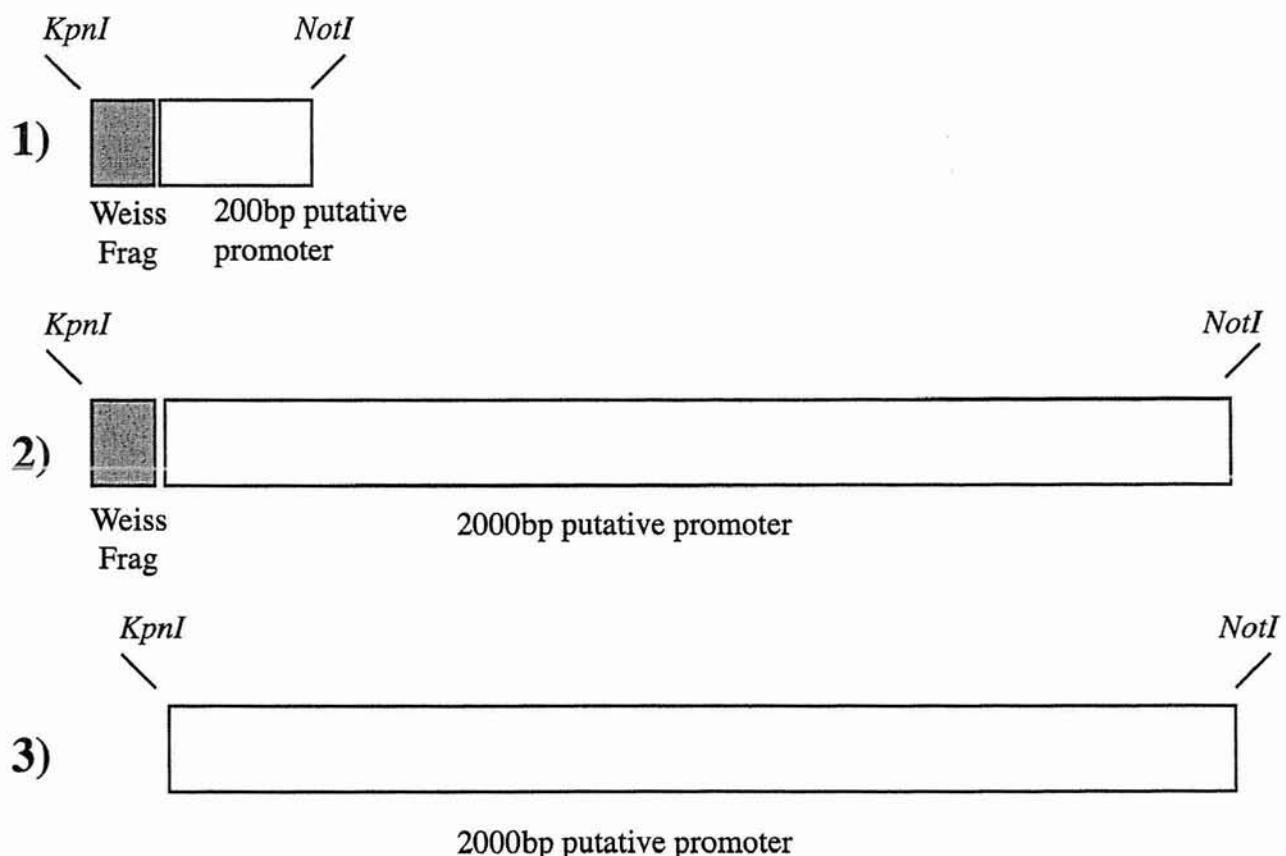


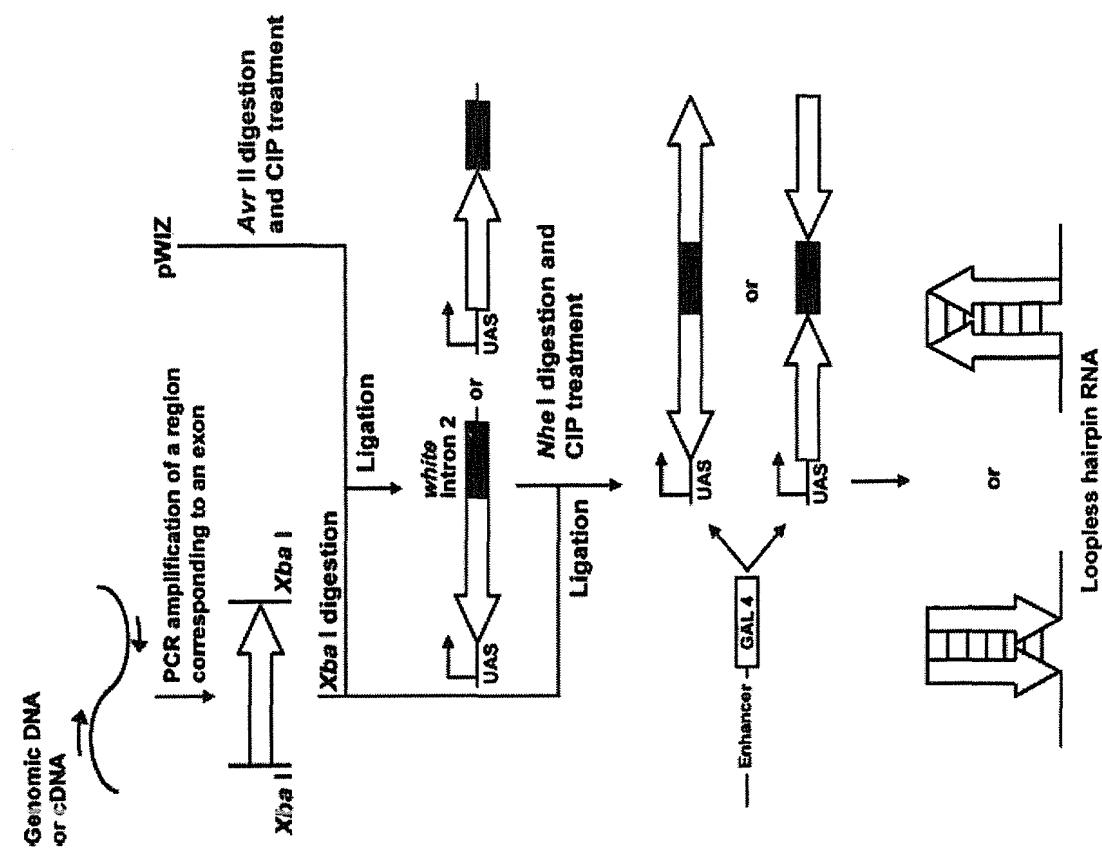
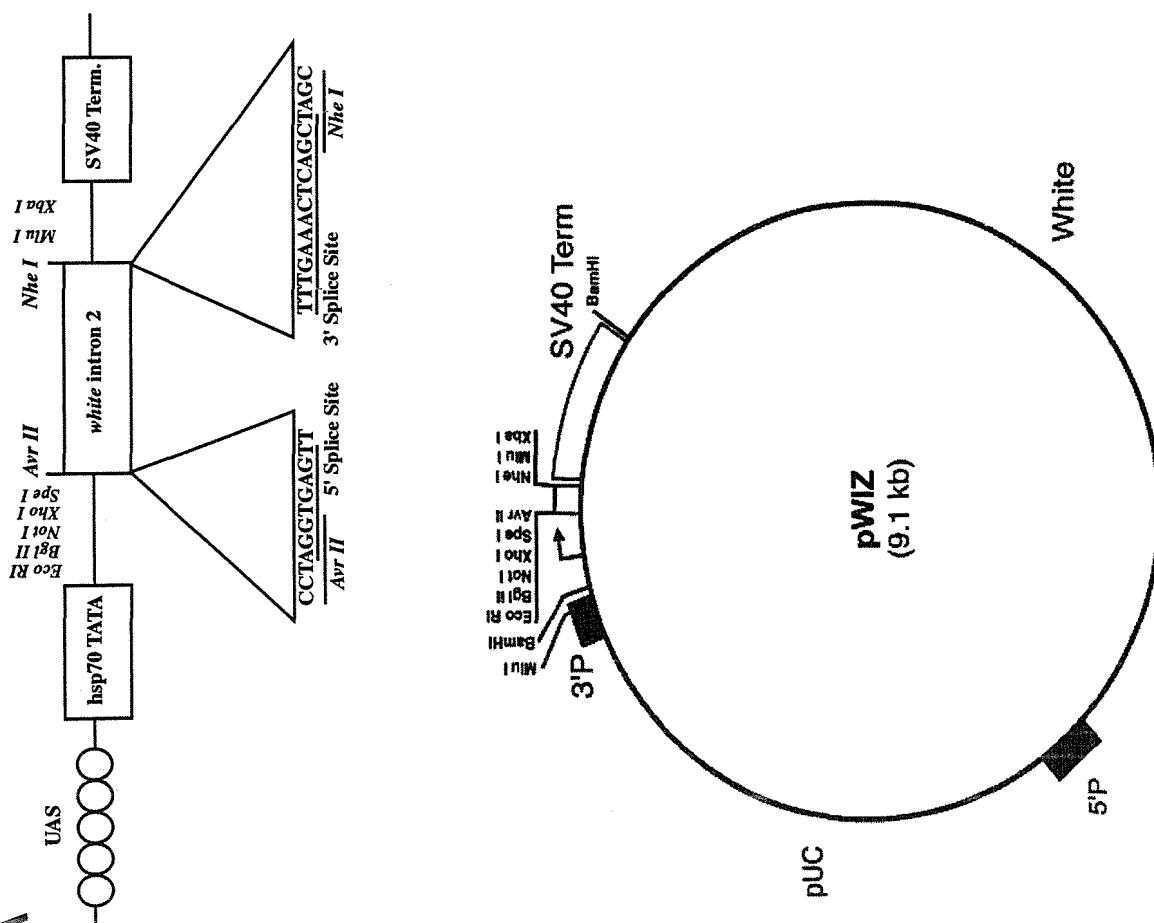
Figure 7.1: Schematic representation of *ind*-GAL4 constructs. The grey shaded box indicates the Weiss Fragment (see appendix B), while the open box indicates either 200bp or 2000bp *ind* promoter fragment as indicated. Constructs were generated via splicing by overlap extension and *KpnI* and *NotI* restriction sites engineered onto the 5' and 3' ends respectively to enable cloning into the pG4PN vector, upstream of the GAL4 activator. The numbers beside the constructs correspond to how they are referred to in the text. Note that constructs shown are not to scale.

construct (1) (see Fig 7.1) 60 flies hatched, and only 10 of these had successfully integrated the construct into their genome. For construct (2) and (3), approximately the same proportion of larvae hatched, however none of these had integrated the construct into their genomes. However, crossing the lines which had successfully integrated construct (1) with UAS-lacZ lines did not give any significant lacZ expression, so the experiment must be regarded as a failure. The generation and characterisation of additional *ind*-GAL4 constructs is continuing in collaboration with the laboratory of Prof G Technau at the University of Mainz.

Appendix C - RNAi as a tool to silence genes in Drosophila

Until fairly recently, targeted gene knockouts in *Drosophila* on the basis of sequence or position were difficult. Although *P*-element mutagenised fly lines are available from various stock centres, for many genes no mutant alleles or deficiency stocks are available. RNA interference (RNAi) is a powerful method for silencing genes at the post-transcriptional stage. Introduction of double-stranded RNA (dsRNA) triggers degradation of the mRNA bearing the same sequence and has been shown to be effective in a variety of organisms (Fire *et al.*, 1998; Kennerdell and Carthew, 1998; Baulcombe, 1999). Injection of a gene specific dsRNA into the early *Drosophila* embryo results in interference persisting throughout embryonic development (Kennerdell and Carthew, 1998; Misquitta and Paterson, 1999; Tsuda *et al.*, 1999), however effects on adult gene expression can be inconsistent and greatly reduced (Kennerdell and Carthew, 1998). However, the introduction of a genomic DNA/cDNA hybrid that is predicted to form hairpin dsRNA molecules following splicing was shown to effectively induce silencing of target genes in adult transgenic animals and could be stably expressed in transgenic *Drosophila* (Kalidas and Smith, 2002). Cloning of these fusions into a vector such as pUAST would allow targeted expression of the dsRNA hairpin via the GAL4-UAS system. For this reason, four cg13424 RNAi constructs were designed which were predicted to form differently sized dsRNA hairpins after splicing with differently sized loop regions between the hairpin. The constructs were designed to ensure that splice donor sites (GTNNGT) were not present in either orientation in the cDNA portion of the hybrid, encoded regions of homology between 190 and 450bp, and constructed so that the genomic DNA portion of the hybrid contained at least one intron. The genomic DNA and cDNA portions were spliced together using the PCR mediated technique, splicing by overlap extension, with outer primers designed to enable cloning into the *NotI* and *KpnI* sites of pUAST. Unfortunately, inverted repeat constructs such as these proved difficult if not impossible to clone, even with the presence of the intron in the genomic DNA portion of the construct and the use of SURE cells (Stratagene) which are deficient in *recBC sbcBC* and thus eliminate all known restriction systems which excise inverted repeats during replication of plasmid DNA. In addition, amplification of the genomic section of DNA required for the RNAi fusion often resulted in non-specific amplification products.

Recently, a simpler method of cloning inverted repeats for the production of an RNAi construct has become known, using the pWiz vector (WIZ for white intron zipper) (Lee and Carthew, 2003). Gene fragments are cloned upstream and downstream of the 74-nucleotide *white* intron, which is flanked by various restriction sites to facilitate cloning. The entire cassette is downstream of the UAS enhancer-promoter and upstream of the SV40 transcription termination site. The system is designed so that a single PCR fragment (as long as it doesn't contain consensus splice sites in either orientation as before) derived from only two PCR primers can be inserted on each side of the *white* intron. In addition, the vector includes *P*-element sites and a UAS sequence (as with pUAST) which allows for targeted expression of the dsRNAi hairpin loop in *Drosophila* (Lee and Carthew, 2003). The pWiz vector and cloning strategy is shown as Fig 7.2. Even with this vector, cloning proved difficult, and attempts were made to clone four cDNA fragments ranging from 230bp to 700bp of *cg13424*. Eventually, one of these (a 250bp inverted repeat) was cloned on either side of in pWiz in a 'tail-to-tail' manner (ie. with the 3' ends of the fragments on either side of the *white* intron), and verified by restriction mapping. Sequencing of the construct in pWiz could not be achieved, possibly due to the formation of a hairpin loop within the vector. Due to time constraints, this construct has not yet been transgenically expressed in *Drosophila*, however with time this will be achieved and expression of the RNAi hairpin driven by an appropriate GAL4 line. Production of additional *cg13424* RNAi/pWiz constructs will also be completed in order to determine which is most efficient in knocking out *cg13424* expression.

B**A**

Appendix D

**Tandem organization of independently duplicated homeobox genes
in the basal cnidarian Acropora millepora**

Submitted to Sequence Corner, *Development, Genes and Evolution*

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Sequence corner**Tandem organization of independently duplicated homeobox genes
in the basal cnidarian *Acropora millepora***

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ABSTRACT

A number of examples of independently duplicated regulatory genes have been identified in cnidarians, but the extent of this phenomenon and organization of these duplicated genes are unknown. Here we describe the identification of three pairs of independently duplicated homeobox genes in the anthozoan cnidarian, *Acropora millepora*. In each case, the pairs of paralogous genes are tightly linked, but the extent of sequence divergence implies that these do not reflect recent duplication events. Cnidarians have recently been shown to contain a number of genes previously assumed to have been vertebrate innovations; the presence of independently duplicated paralogs of a substantial number of regulatory genes adds a quantitative dimension to the likely complexity of cnidarian genomes.

INTRODUCTION

During vertebrate evolution, the Hox clusters and many other regulatory genes have been duplicated; hence regulatory genes that are present in single copies in *Drosophila* or amphioxus often have a number of vertebrate paralogs (Furlong and Holland, 2002). Although specific regulatory genes have been independently duplicated in other animal phyla (e.g. Minguillon et al., 2002), there has been an assumption that this phenomenon has been much more extensive in vertebrates and may have contributed to their evolutionary success.

Although limited data are presently available, it is clear that a significant number of regulatory genes have been independently duplicated in the Cnidaria. The *Hydra* nanos genes (Mochizuki et al., 2000) are the best-characterised example of this phenomenon, but

other cases include Smad-1/5 (Samuel et al., 2001) and nuclear receptor (Grasso et al., 2001) genes in *Acropora*, snail and mox genes in *Nematostella* (Martindale et al., 2004), and paired-like genes in *Hydra* (Gauchat et al., 1998). Independent duplication of some genes is perhaps to be expected, as the Cnidaria may have been distinct from the bilaterian stem since deep in Pre-Cambrian time (Conway-Morris, 2000). However, the extent of gene duplication within the Cnidaria is unknown, as is the organization of these duplicated genes.

In the course of characterising the homeobox gene complement of *Acropora*, we have identified several cases of tightly linked paralogs, three of which are described here. Whilst one of these pairs may consist of pseudogenes, the other two pairs of genes are expressed and are therefore likely to be functional. The tandem duplicates are highly divergent, suggesting that their origins may not be recent. No comparable genomic data are yet available for any other cnidarian, but it is likely that independently duplicated genes are a common feature of cnidarian genomes, and may have contributed to the large genome sizes estimated for some members of the phylum. In addition to the duplication phenomenon described here, cnidarians share a surprising number of genes with vertebrates (Kortschak et al., 2003). The traditional assumption that a simple morphology correlates with a small transcriptome is therefore unlikely to hold; cnidarians are likely to have at least as many genes as *Drosophila* and *Caenorhabditis* and, in some cases, many more.

RESULTS AND DISCUSSION

Tandemly-organised NK2 genes related to *Drosophila vnd*

The *Acropora* genome contains a tandem pair of NK class homeobox genes related to the *Drosophila* vnd and the vertebrate Nkx2.1 type (see Fig. 1). The pair of genes was discovered during primer walking on a single genomic clone from the 5' end of vnd1am. The two genes (vnd1-Am and vnd2-Am) are organised 'head-to-head' (Fig. 1a) with the start codons and homeoboxes only 7.4kb and 9kb apart respectively. Neither vnd1-Am nor vnd2-Am is likely to be a pseudogene as northern analysis indicates that both genes are expressed in planula larvae and adult *Acropora* colonies (data not shown). Complete or near-complete cDNAs for both vnd1-Am and vnd2-Am have been isolated using either 5'/3' RACE (vnd1-Am) or by screening an adult *Acropora* cDNA library (vnd2-Am). In addition to the homeodomain (HD), both *Acropora* genes encode an Eh1 domain and vnd1-Am also contains an NK2SD; the former mediates interactions with Groucho class corepressors (Smith and Jaynes, 1996; Cowden and Levine, 2003) and is present in a range of different homeodomain proteins, whereas the latter is characteristic only of NK2 proteins and its function *in vivo* is unclear (Watada et al., 2000). The HDs encoded by vnd1-Am and vnd2-Am are 77% identical, and both are most closely related to an NK2 sequence from the sea anemone *Nematostella vectensis*. The closest non-cnidarian match for both vnd1-Am and vnd2-Am is *Branchiostoma floridae* Nkx2.2 (accession# AAD01958).

Unlike the other cases discussed here, there are bilaterian precedents for the pattern of organization of NK genes observed in *Acropora*, suggesting the possibility of synteny. In mouse and man, the four vnd/Nkx2.1-type genes are organised as two linked paralogous pairs; Nkx2.2/Nkx2.4 and Nkx2.1/Nkx2.9, reflecting an ancient duplication in which an ancestral NK2-type gene was duplicated to form a tandem gene pair, and the pair then duplicated to another chromosomal locus at a later time. Thus, genes are more

similar to their duplicated partner on another chromosome than to their linked partner (Wang *et al.*, 2000). On the basis of phylogenetic analysis (Fig. 1B) however, the *Acropora* NK2/vnd genes have been independently duplicated within the Cnidaria, thus their organisation does not reflect synteny between cnidarians and mammals. Both *Acropora* sequences fall into a clade that includes mouse and human Nkx2.2 and Nkx2.9 and *Drosophila* vnd, but within this the cnidarian sequences form a clearly distinct monophyletic group.

Acropora has two genes related to vertebrate Dmbx1.

Two paired-like genes of the K50-type (Galliot *et al.*, 1999) are tightly linked and organised in tandem in the *Acropora* genome (see Fig. 2). The two genes are expressed, although in both cases only incomplete cDNA clones have so far been isolated. Database comparisons indicate that the HDs encoded by the two genes are closely related to the vertebrate Dmbx1-type, (Takahashi *et al.*, 2002; Gogoi *et al.*, 2002; Broccoli *et al.*, 2002; Ohtoshi *et al.*, 2002), and *Hydra* manacle (Bridge *et al.*, 2000). Note that Dmbx1 has also been known as mbx (Kawahara *et al.*, 2002), Atx (Martinez-Barbera *et al.*, 2001), PaxB and otx3 (Zhang *et al.*, 2002) in the literature. As in the case of a significant number of other *Acropora* genes (Kortschak *et al.*, 2003), no clear orthologs of Dmbx1 appear to be present in either *Drosophila* or *Caenorhabditis*, reflecting secondary losses of this gene. The vertebrate Dmbx1 sequences are remarkably similar; the HDs in the zebrafish, chicken, mouse and human proteins are identical. The cnidarian and chordate Dmbx-related sequences appear to define a distinct family of K50 HD proteins that are closely related to, but distinct from, the Otx- and Ptx-types (see Fig. 2B).

The two *Acropora* Dmbx loci appear to represent a cnidarian specific duplication, as we could find no evidence for paralogous genes in any of the complete metazoan genomes (human, mouse, rat, zebrafish, pufferfish, *Ciona*, sea urchin). This duplication event presumably occurred in the deep past, as the corresponding proteins are highly divergent; the HDs have 65% identity, and the remainder of the sequences are virtually unalignable. Of the two coral proteins, Dmbx2-Am is more closely related to the chordate Dmbx1 type in the HD (77% vs 60% identity). On the basis of phylogenetic analysis, Dmbx1-Am appears to be the *Acropora* ortholog of manacle, although it is not yet clear whether both genes are present in *Hydra*.

Although the HDs of the Dmbx group are closely related (> 60% identity), the overall domain structures of the proteins differ significantly. In addition to the HD, the only other recognisable motif in the Dmbx2-Am protein is an octapeptide; it is not clear whether this is also present in Dmbx1-Am, as the sequence is incomplete. By contrast, the mouse and human Dmbx1 proteins contain OAR domains at their C-termini but no octapeptides, and manacle contains neither of these additional motifs.

A pair of Msx loci – genes or pseudogenes?

Two Msx-related homeobox genes are tightly linked in the genome of *Acropora millepora* – the linkage was discovered during the course of a primer walk from one of the genes (see Fig. 3). The genes are organised in a 'tail-to-tail' manner, the homeoboxes being a little under 3 kb apart. Single Msx genes have previously been cloned from two hydra species – *Chlorohydra viridissima* (Schummer et al., 1992) and *Hydra vulgaris* (Gauchat et al., 2000). The mammalian Msx loci are not linked.

Phylogenetic analysis (Fig. 3B) clearly groups the HDs in both of these *Acropora* sequences with the Msx class, but the sequences are highly divergent and, although no stop codons are present in the homeoboxes, we suspect that these might be pseudogenes, on the following grounds. Firstly, no evidence could be obtained that the genes are expressed. Screening several million plaques from cDNA libraries corresponding to various developmental stages failed to identify cDNAs corresponding to Msx1-Am or Msx2-Am.

Furthermore, quantitative RT-PCR using mRNA from all major developmental stages did not yield signals significantly above background. Secondly, the predicted amino acid sequences of the *Acropora* Msx HDs, particularly that of Msx2-Am, are highly derived and feature some dramatic amino acid substitutions at positions likely to be structurally significant. For example, the phenylalanine residue at HD position 16 (Phe16) in Msx2-Am appears to be unique; in all other HDs a leucine residue at this position is involved in HD core stabilisation. Residues known to be involved in DNA-binding specificity in the case of MSX1 (Hovde et al., 2001), but differing in the *Acropora* sequences, include Arg2 (Ser in Msx2-Am, Gly in Msx1-Am) and Arg58 (Lys in both *Acropora* sequences). In addition, the Glu30/Lys23 and Glu42/Arg31 salt bridges known to stabilise the MSX1 HD core (Hovde et al., 2001) are not possible in either of the *Acropora* HDs.

The cases described above imply that many regulatory genes have been independently duplicated in *Acropora*; of the 13 distinct classes of homeobox genes thus far identified in *Acropora* (excluding Pax genes), at least three exist as duplicated pairs that are tightly linked. Two highly similar Not loci are also tightly linked in *Acropora* (Hayward et al., unpublished) and the possibility of linked duplicates for many other genes cannot be ruled out. The

paucity of genomic data for cnidarians means that the true extent of duplication events may be much greater than the cases documented here, and may have contributed significantly to the large genome sizes estimated for some cnidarians (David and Campbell, 1972; Zacharias et al., in press).

It is also unclear whether the specific duplications seen in *Acropora* occur throughout the Cnidaria. The degree of divergence between paralogs in *Acropora* (e.g. 77%, 65% and 53% identity in the Nkx, Dmbx and Msx HDs respectively) implies that the duplication events that gave rise to them are unlikely to have been recent. The divergence of the cnidarian classes is thought to have occurred deep in Pre-Cambrian time (Chen et al., 2002); hence some genes that are duplicated in *Acropora* may not be in (for example) *Hydra*. However, at least some cnidarian-specific duplication events precede the Anthozoa / Hydrozoa divergence; for example, duplicated nanos genes are present in both *Hydra* (Mochizuki et al., 2000) and *Acropora* (Go et al., unpublished). In other cases, such as that of the Msx genes, patterns of relatedness imply that the duplication events that gave rise to them may have post-dated the Anthozoa / Hydrozoa split. In the case of the Dmbx1-related genes, phylogenetic analyses reveal that one of the *Acropora* sequences (Dmbx1-Am) is likely to be orthologous with *Hydra* manacle (Bridge et al., 2000), whereas the other is more closely related to the vertebrate Dmbx sequences (Fig. 2B). This relationship, between related pairs of genes in a basal cnidarian and vertebrates, may indicate that the duplication of Dmbx genes predated the Anthozoa / Hydrozoa split. Hence, it is likely that a second Dmbx gene is, or was, present in the derived hydrozoan lineage.

Cnidarians share a surprising number of genes with vertebrates (Kortschak et al., 2003); hence cnidarian genomes are qualitatively

complex. The independent duplication of a significant number of regulatory genes adds another dimension of complexity to cnidarian genomes. The traditional assumption that the morphological simplicity of cnidarians corresponds to a small transcriptome is therefore clearly incorrect; cnidarians are likely to have at least as many genes as the model invertebrates *Drosophila* and *Caenorhabditis* and, in some cases, many more.

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Figure Legends

Fig. 1. Sequence comparisons and genomic organization of vnd-related genes in *Acropora*. (A) Structure of the genomic region containing the *vnd1-Am* and *vnd2-Am* loci. The arrows indicate the direction of transcription, and the boxes indicate exons. (B) The *vnd1-Am* and *vnd2-Am* homeodomains were subjected to Maximum-Likelihood phylogenetic analyses in MolPhy version 2.3 (Adachi and Hagesawa, 1996) using the Dayhoff model of protein evolution and local rearrangement of the NJ trees (1000 bootstraps). In these analyses, *Xenopus* Xnot (accession # CAA79629) served as outgroup. The shaded area indicates the clade

consisting of the cnidarian vnd-related sequences. (C) A Boxshade alignment of the homeodomain sequences used in the phylogenetic analyses. Database accession numbers of the sequences are:

Nematostella vectensis NK2 (AAP88430), *Drosophila melanogaster* vnd (NM 057438), *Brachiostrongylus floridiae* NK2.2 (AF032999), human TTF1 (NM 003317), human NKX2.2 (NM 002509), human NKX2.9 (AF000297), *Strongylocentrotus purpuratus* Nk2.2 (AAS58444), *Caenorhabditis elegans* ceh24 (NM 074018), *Hydra vulgaris* CnNK2 (AAB67611), *D. melanogaster* tinman (AAQ75417), *D. melanogaster* bagpipe (AAQ74415), *D. melanogaster* scarecrow (AAF26436) and *B. floridiae* NK2.1 (AF077840).

Fig. 2. Sequence comparisons and genomic organization of *Dmbx1*-related genes in *Acropora*. (A) Structure of the genomic region containing the *Dmbx1-Am* and *Dmbx2-Am* loci. The arrows indicate the direction of transcription, and the boxes indicate exons. (B) Maximum-Likelihood phylogenetic analyses of *Dmbx1*-related homeodomain sequences, as described in Fig. 1B, using the *Drosophila aristaleless* sequence (accession # NP 523834.1) as outgroup. The light shaded area indicates the clade consisting of the cnidarian *Dmbx1*-related sequences; the more darkly shaded area defines the *Dmbx* group. (C) A Boxshade alignment of the homeodomain sequences used in the phylogenetic analyses. Database accession numbers of the sequences are: *Hydra vulgaris* manacle (AF126249_1), mouse *Dmbx1* (AAM78514.1), *Ciona intestinalis* CiDmbx (AAT66432.1), *Branchiostoma floridiae* BfDmbx (AAT66431.1), *Drosophila melanogaster* Ptx1 (O18400), mouse Ptx2 (NP 035228.2), *D. melanogaster* orthodenticle (A35912), mouse Otx2 (AAH29667.1), human OTX1 (NP 055377.1), *H. vulgaris* Alx (AF295531), *H. vulgaris* prdla (CAA75668.1) and *H. vulgaris* prdlb (CAA75669.1).

Fig. 3. (A) Structure of the genomic region containing the *Msx1-Am* and *Msx2-Am* loci. The arrows indicate the direction of transcription, and the boxes indicate exons. (B) Maximum-Likelihood phylogenetic analyses of *Msx1-Am* and 2-Am homeodomains, as described in Fig. 1B, using the mouse *Dlx1* sequence (accession # AAH79609) as outgroup. The shaded area indicates the clade consisting of the cnidarian Msx-related sequences. (C) A Boxshade alignment of the homeodomain sequences used in the phylogenetic analyses. Database accession numbers of the sequences are: *Hydra vulgaris* Msh (CAB88390), *Chlorohydra viridissima* Msh (CAA45912), *Drosophila melanogaster* Msh (NM 057976), mouse *Msx2* (NP 038629), mouse *Msx1* (AAH16426), *Danio rerio* mshE (NP 571348), *D. rerio* mshD (NP 571351), mouse *Msx3* (AAH51983), *Branchistoma floridae* Msx (CAA10201), *D. rerio* mshB (U16311) and *Ciona intestinalis* MshA (M38581).

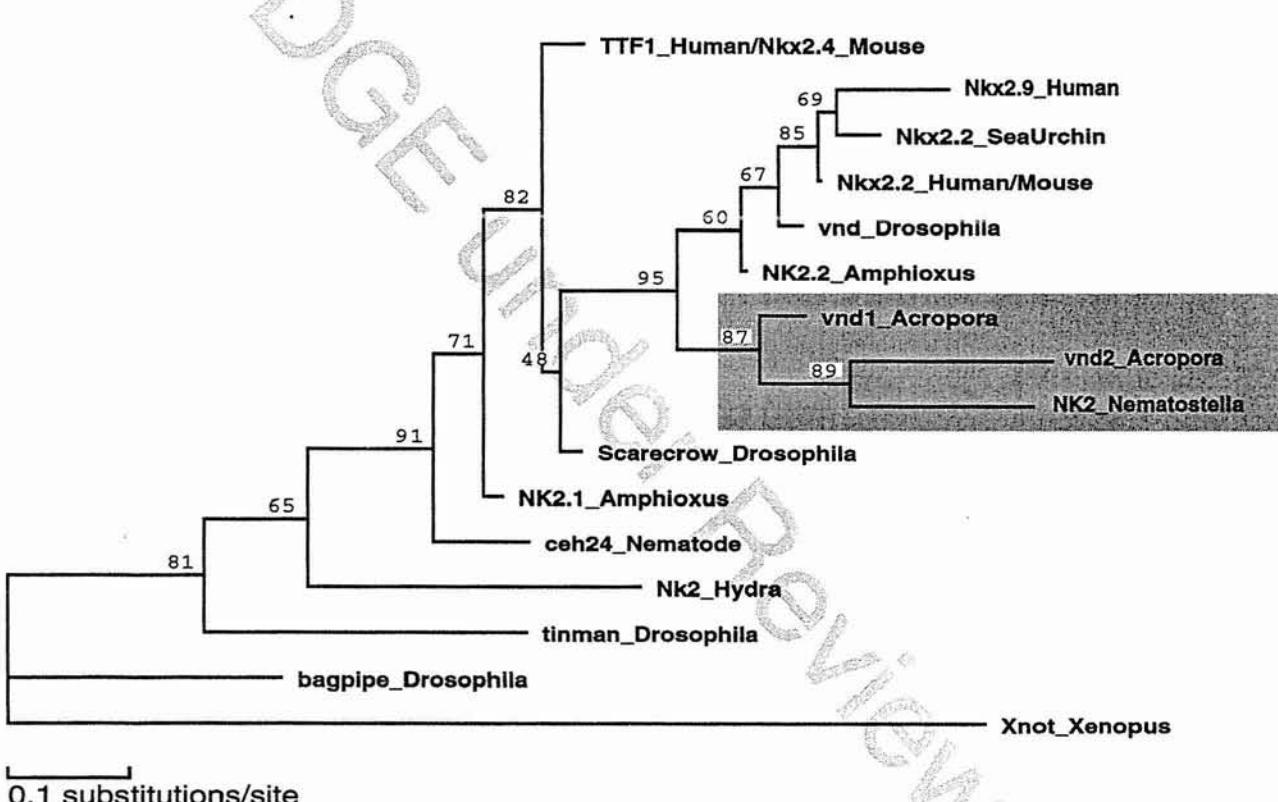
vnd2am

Homeodomain Eh1 domain

vnd1am

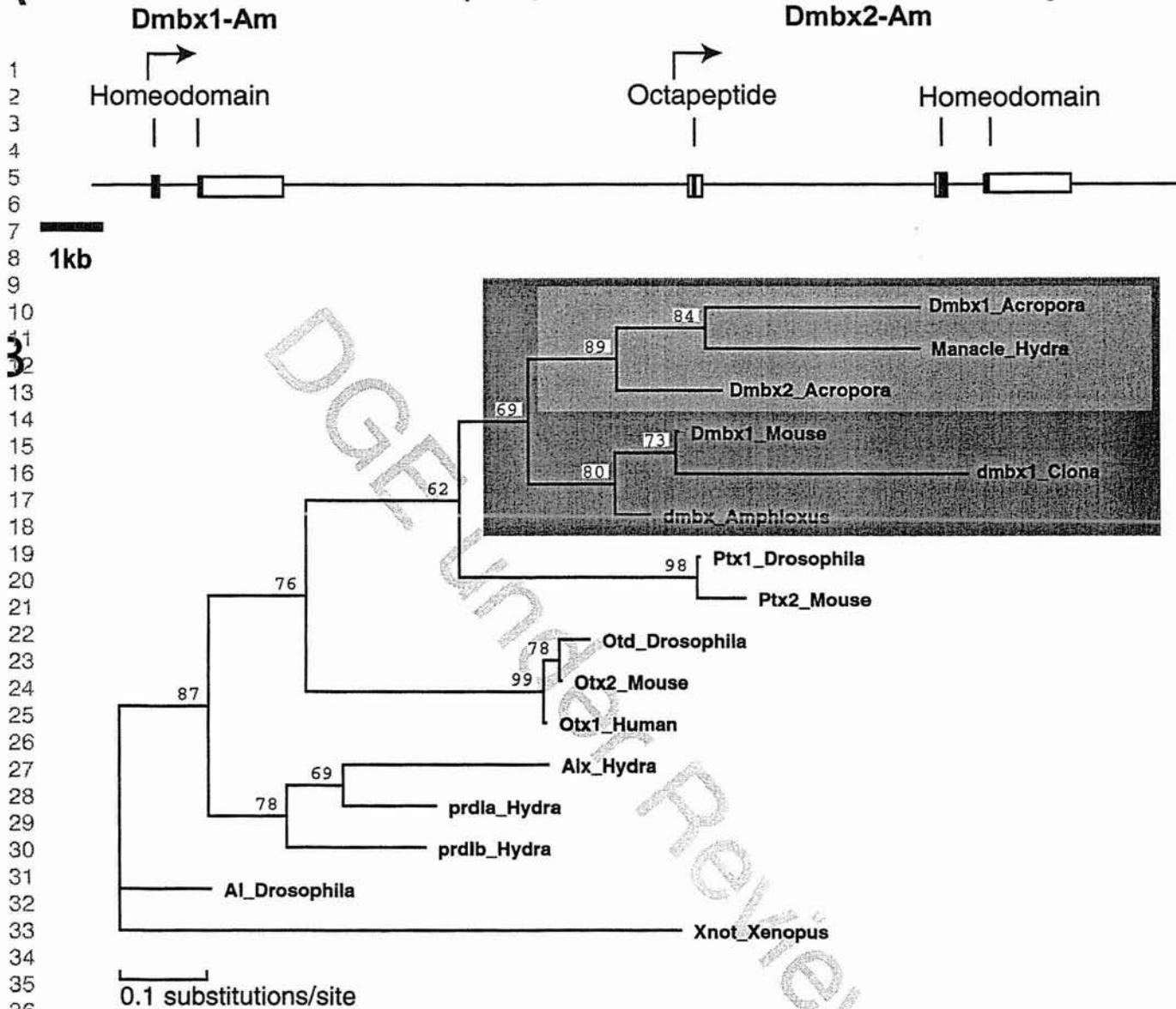
Eh1 domain Homeodomain
Nk2-SD

1kb



1 Acropora vnd1
2 Acropora vnd2
3 Nematostella NK2
4 Drosophila vnd
5 Amphioxus Nk2.2
6 Human TTF1/Mouse Nkx2.4
7 Human/Mouse Nkx2.4
8 Human Nkx2.9
9 Sea Urchin Nkx2.2
0 Nematode ceh24
1 Hydra CnNK2
2 Drosophila tinman
3 Drosophila bagpipe
4 Drosophila scarecrow
5 Amphioxus Nk2.1

	Identity/ Similarity %
KRKRRVLFSAQTYELEERRFRQQRYLSAPEREQLARIINLSPTQVKIWFQNHRYKCKKQS	77/88
KRKRRVLFTKAQTEVLEKRFQQRYLSAPEREELARIVHLTPAQVKIWFQNHRYKTKRQI	80/93
KRKRRVLFTKAQTYELEERRFRQQRYLSAPEREHLASILIRLTPTQVKIWFQNHRYKFKKQI	83/90
KRKRRVLFSKAQTYELEERRFRQQRYLSAPEREHLASILIRLTPTQVKIWFQNHRYKTKRAQ	88/93
RRKRRVLFSSAQVYELERRFKQQKYLSSAPEREHLASIMIHLTPTQVKIWFQNHRYKMKRQA	78/90
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RKRRVLFSSAQTYELEERRFRQQRYLSAPEREQLASILIRLTPTQVKIWFQNHRYKLKRAR	80/90
KRKRRVLFSKAQTYELEERRFRQQRYLSAPEREHLASILIRLSPTQVKIWFQNHRYKLKRAR	88/90
RRKRRVLFSSAQVYELERRFKQQAKYLTAPEREQLANSIRLTPTQVKIWFQNHRYKCKRQE	78/88
RKRRVLFSSAQVYELERRFKQQKYLSDQIANKINLTPTQVKIWFQNHRYKCKKQI	62/85
KRPVLFSSAQVLELECRFRLKKLTGAEREITIAQKLNLSATQVKIWFQNHRYKSQRD	63/75
KKRSRAAFSHAQVYELERRFAQQRYLSGPERSEMAKSIRLTTETQVKIWFQNHRYKTKRKQ	60/80
RRKRRVLFSSAQVYELERRFKQQVYLSAPEREHLASILHLPPTQVKIWFQNHRYKCKRQA	80/92
RRKRRVLFSSAQVYELERRFKQQKYLSSAPEREHLAQIINLTPTQVKIWFQNHRYKCKRQD	82/92



<i>Acropora Dmbx2</i>	QRRSRTAFTLQQQLRLESTFSKTHYPDVAMREQLASWTNLPESRIVQWFKNRRAKHRKQD	65/78
<i>Acropora Dmbx1</i>	PRRMRTCFSPRQLQILEQAFSKTHYPDVLIREQLSNEANLPESRIVQWFKNRRAKYRKHQ	67/73
<i>Hydra Manacle</i>	HRRVRVTAFTHHQLTTLERTFETSHYPDVVLRERLASFTGLAESRIQVWFKNRRAKYRKHQ	75/80
<i>Mouse Dmbx1</i>	QRRSRTAFTAQQLEALEKTFKQKTHYPDVMVRERLAMCTNLPEARVQWFKNRRAKFRKQ	68/70
<i>Clona dmbx1</i>	HRRSRRTAFTAMQDALARTEFTFKDQYQPDVFETRESLATCTNLAEARIQVWFKNRRAKWRKQO	78/79
<i>Amphioxus dmbx</i>	QRRSRTAFTSQQLAALEKCFQKTHYPDVMVRERLAMCTNLPESRVQWFKNRRAKWRKQ	63/78
<i>Drosophila Ptx1</i>	QRRQRRTHTFTSQQLQELEHTFSRNRYPDMSTREEIAMWTNLTEARVRFWFKNRRAKWRKRE	62/78
<i>Mouse Ptx2</i>	QRRQRRTHTFTSQQLQELEATFQRNRYPDMSTREEIAVWTNLTEARVRFWFKNRRAKWRKRE	65/77
<i>Drosophila Otd</i>	QRERRTTFTTRAQLDVLEALFEAKTRYPDIFMREEVALKINLPESRVQWFKNRRAKCRQQQ	65/78
<i>Mouse Otx2</i>	QRERRTTFTTRAQLDVLEALFEAKTRYPDIFMREEVALKINLPESRVQWFKNRRAKCRQQQ	65/78
<i>Human Otx1</i>	QRERRTTFTRSQLDVLEALFAKTRYPDIFMREEVALKINLPESRVQWFKNRRAKCRQQQ	58/70
<i>Hydra Alx</i>	LRRNRRNTFTTYQLHQLERSFDKTYQPFDPVTRENLAKKLDLSEARVQWFKNRRAKWRKRE	62/70
<i>Hydra prdla</i>	ERRYRRTTFTQFQDLDELERAFDKTHYPDVFMRMEELAVRVHLTEARVQWFKNRRAKWRKRE	57/68
<i>Hydra prdlb</i>	KRRYRRTTFTTHQLDELERVEMRTHYPDMEELREEMAVKLGLTEARIQVWFKNRRAKWRKRN	60/72
<i>Drosophila Al</i>	QRRIRTTFTSNQNLNELEKIELETHYPDLYTREERIASKLHLTEARVQWFKNRRAKWRKQD	

