A tyrosine-rich domain within homeodomain transcription factor Nkx2-5 is an essential element in the early cardiac transcriptional regulatory machinery

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Homeodomain factor Nkx2-5 is a central component of the transcription factor network that guides cardiac development; in humans, mutations in Nkx2.5 lead to congenital heart disease (CHD). We have genetically defined a novel conserved tyrosine-rich domain (YRD) within Nkx2-5 that has co-evolved with its homeodomain. Mutation of the YRD did not affect DNA binding and only slightly diminished transcriptional activity of Nkx2-5 in a context-specific manner in vitro. However, the YRD was absolutely essential for the function of Nkx2-5 in cardiogenesis during ES cell differentiation and in the developing embryo. Furthermore, heterozygous mutation of all nine tyrosines to alanine created an allele with a strong dominant-negative-like activity in vivo: ES cell–embryo chimaeras bearing the heterozygous mutation died before term with cardiac malformations similar to the more severe anomalies seen in Nkx2.5 mutant families. These studies suggest a functional interdependence between the NK2 class homeodomain and YRD in cardiac development and evolution, and establish a new model for analysis of Nkx2-5 function in CHD.

KEY WORDS: Heart, Homeodomain, Nkx2-5, Congenital heart disease

INTRODUCTION

Genetic studies over the past decade have defined a cardiac regulatory network that is used for heart formation in both vertebrates and invertebrates (Cripps and Olson, 2002; Harvey, 1996). This network probably evolved for specification of a visceral muscle type specialised for pulsatile contraction (Harvey, 1996), and the cardiac-like contractile properties of body wall muscles in primitive diploblastic metazoa have long been appreciated (Fye, 1987).

Nkx2-5/Csx is a vertebrate member of the NK2 class of homeodomain transcription factors that sits high in the cardiac regulatory hierarchy (Cripps and Olson, 2002). Murine Nkx2-5 was first identified in screens for relatives of the Drosophila gene tinman, expressed immediately downstream of mesodermal specification genes during fly development and absolutely required for formation of precursor cells of the heart and gut muscle lineages (Bodmer, 1993; Azpiazu and Frasch, 1993). Numerous vertebrate cognates of Nkx2-5 have now been described, with related genes expressed in the simple heart tube of amphioxus (Holland et al., 2003), in the pulsatile muscular pharynx of C. elegans (O’Kema et al., 1997) and in the contractile foot of hydra (Shimizu and Fujisawa, 2003). Transgenic rescue experiments testify to the functional homology that exists between cognates of this gene family in distantly related species (Haun et al., 1998; Park et al., 1998; Ranganayakulu et al., 1998).

Nkx2-5 is expressed in the earliest recognizable cardiac precursor cells in all models examined (Harvey, 1996), including cells of the heart morphoregulatory field in Xenopus (Raffin et al., 2000), and the second heart precursor field of annelids (Stanley et al., 2002). In Xenopus, dominant-negative inhibition of Nkx2-5 and its close relative Nkx2-3 leads to total loss of all cardiac progenitors (Gowe and Krieg, 1998). In homozygous Nkx2-5 knockout mouse embryos, a simple beating myogenic heart tube is able to form, although differentiation and morphogenesis of specialised chamber myocardium is blocked (Lyons et al., 1995). A remarkable diversity of structural and functional abnormalities of the heart occur in human families and individuals carrying heterozygous Nkx2.5 mutations (Benson et al., 1999). Atrioventricular (AV) conduction block, present in most individuals, results from hypoplasia and progressive postnatal loss of AV nodal tissue, and requires a pacemaker (Jay et al., 2004; Pashmforoush et al., 2004). Structural malformations requiring surgery include atrial septal defect (ASD), tetralogy of Fallot, ventricular septal defect (VSD) and hypoplastic left heart syndrome (Benson et al., 1999; Elliott et al., 2003; McElhinney et al., 2003).

Among the earliest Nkx2-5-dependent genes are those encoding other cardiac transcription factors (Biben and Harvey, 1997; Bruneau et al., 2000; Molkentin et al., 2000; Ueyama et al., 2003; von Both et al., 2004; Yoshioka et al., 1998). Nkx2-5 physically interacts with several transcription factors, including members of the GATA and T-box factor families, serum response factor (SRF) and Fox1, and collaborates with them to regulate target promoters (Chen and Schwartz, 1996; Durocher et al., 1997; Bruneau et al., 2001; Hiroi et al., 2001; von Both et al., 2004). Recent data show that competition between Nkx2-5 and different members of the T-box family of transcription factors drives formation of chamber and non-chamber myocardium (Habets et al., 2002; Stennard and Harvey, 2005).

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also activates negative regulatory circuits controlled by transcriptional repressors CARP and HOP (Chen et al., 2002; Zou et al., 1997).

Despite these advances, the central question of how broadly expressed transcription factors, such as Nkx2-5, control the temporal and spatial specificity of lineage and morphogenetic events during heart development remains unanswered. Region-specific signalling inputs that influence the nuclear localisation and/or the chromatin-modifying activity of transcription factors are likely to play key roles (Charron et al., 2001; McKinsey et al., 2000). Members of the cardiac Nkx2 family are known to function as both transcriptional activators and repressors (Choi et al., 1999), and two conserved domains, the N-terminal TN-Domain and C-terminal NK2-specific domain (NK2SD) appear to act as negative regulatory domains, the former through association with the Groucho family of co-repressors (Muhr et al., 2001; Watada et al., 2000).

In this paper, we genetically define a novel, conserved and essential transcriptional domain within the C-terminus of murine Nkx2-5. The tyrosine-rich domain (YRD) has co-existed with the NK2 class homeodomain since before radiation of vertebrate and invertebrate evolutionary lines. The apparent absolute functional inter-dependence between the YRD and NK2 homeodomains can explain the similar phenotypic manifestations arising from mutations in different regions of the NKX2.5 protein in individuals with CHD.

MATERIALS AND METHODS
Expression constructs and culture assays
Plasmids for G5E1b-luciferase, pGAL, FLAG-Nkx2-5, 3xHA-luciferase and Nippal and Gja5 promoters, and transient transfection protocols were as described previously (Ranganayakulu et al., 1998; Sadowski et al., 1992; Stennard et al., 2003). Neonatal rat cardiomyocytes were cultured (Engelmann, 1993) and transfected using Lipofectamine and Lipofectamine PLUS (GIBCO BRL).

Western blotting and EMSA
Nuclear extracts were prepared (Stennard et al., 2003) and proteins separated by SDS-PAGE. Western blotting was performed using anti-FLAG mouse mAb (1:1000; AMRAD) or anti-GAL4 (BD) mouse mAb (RK5C1) (1:1000; Santa Cruz) with anti-mouse IgG-HRP (1:2000; Silenus). Proteins were detected using ECL reagent (Pharmacia Amersham Biotech). Nkx2-5 proteins for EMSA (Stennard et al., 2003) were translated using TNT Rabbit reticulate lysates (Promega). The oligonucleotide contained three high-affinity Nkx2-5-binding sites (5’ ctcaagtggg 3’).

Nkx2-5 homologues
Systemic or branchial hearts from adult O. kaurna, S. officinalis and L. peelei were dissected into RNAlater (Ambion). RNA was extracted using Trizol (Invitrogen). RT-PCR was performed using 200 ng of NK2 homeodomain-specific degenerate oligonucleotides (5’ cgccttctcagc 3’, and 5’ rtaagctcgaagcc 3’, r=t or g; a=deoxynosine), 0.5 mM dNTPs, 1×PCR buffer (Boehringer) and 2U of TAQ (Boehringer). Cycling conditions were: 95°C for 2 minutes followed by 35 cycles of 95°C for 20 seconds, 50°C for 30 seconds and 72°C for 1 minute. Homeobox sequences were used to design specific primers for 5’ and 3’ RACE using Ambion and Clontech kits, respectively, and a modified oligonucleotide (5’ aagcagttgtaacagagttggttt 3’).

ES cells and gene targeting
Gene targeting was performed using standard methods. The IRESlacZHygro cassette was adapted from IRESCreHygro (Stanley et al., 2002). Embryoid body (EB) culture was adapted from the hanging drop method (Bader et al., 2001). GFP expression was analysed on a FACS Calibur (BD Biosciences). A sort gate was established on the basis of forward scatter, side scatter and propidium iodide staining. A second gate was established based on GFP fluorescence intensity (FL-1) and side scatter that excluded most auto-fluorescent cells. Animal experiments were approved by the St Vincent’s Hospital/Garvan Institute for Medical Research Animal Ethics Committee.

RT-PCR analysis
RNA from FACS-isolated GFP-positive cells was extracted using Trizol (Invitrogen). After RNA extraction, cDNA was prepared and linearly amplified (Baugh et al., 2001). Results were confirmed by RT-PCR without amplification. Real-time PCR used the LightCycler-FastStart DNA master SYBR Green I kit (Roche) on a LightCycler (Roche). PCR protocols: 95°C for 10 minutes; followed by 35 cycles of 95°C for 10 seconds; 60°C for 10 seconds; 72°C for 10 seconds.

TUNEL assay
TUNEL was performed on sections from three 14.5 dpc control Nkx2-5+/−wild-type and two similarly staged Nkx2-5+/−wild-type chimaeric hearts using the DeadEnd fluorometric TUNEL system (Promega). TUNEL was assessed on a total of 8-16 sections from the mid-region of chimaeric hearts. Statistical significance was assessed using nested analysis of variance.

RESULTS
A tyrosine-rich domain in the C-terminus of Nkx2-5 is required for its transcriptional activity in vitro
We have previously shown that C-terminal amino acids 232-318 of murine Nkx2-5 possess positive transcriptional activity in a heterologous assay in C3H10T1/2 fibroblasts (Ranganayakulu et al., 1998). This activity does not require the conserved NK2SD implicated in transcriptional repression. To define the region(s) essential for positive activity, the C-terminal fragment and progressively smaller sub-fragments were fused to the yeast GAL4 DNA-binding domain (DBD) and tested for transcriptional activity in a GAL4-dependent luciferase reporter gene (GST-luc) in C3H10T1/2 cells (Fig. 1A,B). Only the full-length fragment [Nkx(232-318)] showed activity, with deletion of 30 or more N-terminal amino acids reducing activity to background levels. This finding suggests that the conserved C-terminal GIRAW motif and Nkx2-5 Box (Evans, 1999), the functions of which are unknown, have no autonomous transcriptional activity in this assay. To confirm this finding, we tested whether the GIRAW motif and Nkx2-5 Box were essential in the context of the full-length C-terminal fragment. Mutation of GIRAW to GIRAG, GIGAW or merely GI failed to diminish transcriptional activity significantly (Fig. 1C). An alanine scanning mutation series was constructed across the Nkx2-5 Box and the central VGDL peptide was also deleted (Fig. 1D). Most of these mutations had little or no effect on transcription. Others, notably D293A and ΔVGDL, reduced activity to 44-48% of control levels, although this minor effect may be due to the slightly diminished stability of mutant proteins (Fig. 1F).

We noted that the region essential for transcriptional activity, minimally encompassing amino acids 232-262, was unusually rich in the bulky aromatic amino acid tyrosine (24% over 37 amino acids). To assess whether tyrosines were essential for transcriptional activity, we first mutated each individually to alanine (Fig. 1E). Others, notably D293A and ΔVGDL, reduced activity to 44-48% of control levels, although this minor effect may be due to the slightly diminished stability of mutant proteins (Fig. 1F).
Conservation of the YRD in the cardiac clade of NK2 homeodomain proteins

A YRD was evident C-terminal to the homeodomain and NK2SD in all known chordate members of the ‘cardiac’ subclass of NK2-class homeodomain proteins (Harvey, 1996), including a member from the cephalochordate amphioxus (amphiNk2-tin) (Fig. 2A). These homeodomain proteins form an evolutionary clade based on sequence similarities within their homeodomains and because of common expression in developing cardiac and/or visceral muscles. A tyrosine-rich element is also present in Drosophila bagpipe (bap) (Azpiazu and Frasch, 1993) and its vertebrate homologues [i.e. Nkx2-5 relatives that are expressed in gut mesoderm and other organ and axial systems (Fig. 2A; see Fig. S3 in the supplementary material)]. The YRD was absent from members of a sister clade to the cardiac Nkx2 proteins, including Nkx2-1, Nkx2-2 and Nkx2-4, that are expressed in the nervous system.

Alignment of YRD sequences (Fig. 2A) revealed that the number of tyrosines varied from four to 10 in different NK2 proteins, although there was an overall conservation of spacing, particularly among species orthologues of Nkx2-5 and Nkx2-3. The alignment became more significant if the occasional conservative amino acid change to phenylalanine was allowed, supporting the idea that the tyrosines and phenylalanines are structurally or functionally important. In addition to tyrosines, several other amino acids were strongly, although not absolutely, conserved. The asparagine at position 15 in mouse Nkx2-5, for example, was conserved in all of the Nkx2-5 and Nkx2-3 orthologues shown (Fig. 2A) and valine at position 7 was conserved in 10/11 of these. Asparagine 10, prolines 11, 18 and 37, and cysteine 33 in the mouse sequence were also well conserved in other members.

Cardiac NK2 proteins from cephalopod molluscs also carry the YRD

The YRD was absent from Drosophila Tinman, despite it having a well-established cardiogenic function during Drosophila embryogenesis (Cripps and Olson, 2002). A cluster of tyrosines was present C-terminal to the homeodomain in the C. elegans NK2 homeoprotein, Ceh22, which has a role in specification of the pulsatile (heart-like) pharyngeal muscles of the worm, a function that can be substituted for by Tinman (Haun et al., 1998). However, other signature amino acids of the YRD are not conserved. Furthermore, the NK2SD is lacking in Ceh22. Both insect and nematode phyla are members of the large invertebrate clade Ecdysozoa. Accelerated evolution of gene families has been noted in the genomes of Drosophila and C. elegans (Kortschak et al., 2003), raising the possibility that the absence of C-terminal domains in Tinman and Ceh22 represents a derived rather than ancestral state.

To explore this possibility, we cloned cDNAs encoding Nkx2-5 homologues from the hearts of cephalopod molluscs (octopus Octopus kaurna, cuttlefish Sepia officinalis and squid Loligo pealii). Cephalopod molluscs belong to a separate large invertebrate clade, Lophotrochozoa. They are highly motile invertebrates that possess a sophisticated closed circulatory system with systemic and branchial hearts (Fig. 2B). Remarkably, the systemic hearts of squid produce pressures approaching those of mammalian hearts (Wells, 1992). A full-length cDNA clone was isolated from RNA extracted from the adult systemic heart of the cuttlefish S. officinalis, and shorter clones were isolated from O. kaurna and L. pealii. In situ hybridisation to sectioned L. pealii embryos confirmed expression in the systemic heart and adjacent muscular ink sac (Fig. 2B-D; data not shown).

Fig. 1. Transcriptional activity in the C terminus of Nkx2-5.

(A) Domain structure of the Nkx2-5 C terminus fused to GAL4 DNA-binding domain (GAL4). (B-E) Trans-activation of the GAL4-dependent GST-luciferase reporter in C3H10T1/2 cells by co-transfected GAL-Nkx2-5(232-318) and similar constructs bearing mutations (see text). Relative transcriptional activity compared with vector-only control (bars indicate s.e.m.) is shown on the right of each panel. (F) Western blot showing that GAL-Nkx2-5 proteins are stably expressed in transfected COS cells.
The cuttlefish SoNkx2-5 cDNA was 1.12 kb long and encoded a 326 amino acid protein containing, in addition to an NK2-class homeodomain, four other conserved NK2 protein signature motifs: a TN Domain within the N terminus and (within the C terminus) the NK2SD, YRD and GIRAW motifs (Fig. 2A). The same C-terminal domain structure was evident in proteins predicted from the O. kaurna and L. pealii cDNAs (data not shown). The Nkx2-5 Box, found in only vertebrate and amphioxus Nkx2-5 orthologues (Evans, 1999), was absent.

The cephalopod homeodomain sequences carried a tyrosine at position 54, a defining hallmark of NK2-class homeodomains and essential for their unique DNA-binding site specificity (Tsao et al., 1995).
Homeodomain comparisons clearly demonstrated that the cephalopod proteins were more closely related to their vertebrate Nkx2-5 and Nkx2-3 relatives than to Tinman (Fig. 2A). For example, the SoNkx2-5 homeodomain was 95% identical to that of mouse and human Nkx2-5, 96.6% identical to amphioxus Nk2-tin, but only 66.6% identical to Tinman.

The YRD of the cephalopod proteins contained five or six tyrosines with an additional conservative change to phenylalanine and several non-tyrosine amino acids present in mammalian family members were also conserved (Fig. 2A). The above data suggest that the domain architecture of vertebrate cardiac NK2 homeodomain proteins, as seen in Nkx2-5, was established prior to divergence of the common ancestor of protostomes and deuterostomes, and that Tinman is highly derived.

**Mutation of the YRD alters Nkx2-5 transcriptional activity but not DNA binding in vitro**

Full-length Nkx2-5 is a weak transcriptional activator in vitro and it has been proposed, based on in vitro data, that the C-terminal region of the protein inhibits the activity of its strong N-terminal transactivation domain via an intramolecular mechanism (Sepulveda et al., 1998). An influence of C-terminal amino acids on Nkx2-5 dimerisation on DNA has also been reported (Kasahara et al., 2000). We tested whether the Y-A mutation affected the function of full-length Nkx2-5 in vitro. However, we found no diminishment of DNA binding (Fig. 3A) and there was no change in the transactivation activity of Nkx2-5-Y-A on a synthetic promoter carrying multiple Nkx2-5-binding sites (Fig. 3B), or on the promoter of the Nppa1 gene, a direct Nkx2-5 target, in the absence or presence of cardiac transcription factors Gata4 or Gata5, and Tbx20, with which Nkx2-5 can functionally synergise (Fig. 3C and Fig. S1 in the supplementary material). Furthermore, no effect was seen on the Nppa promoter in the presence of SRF and/or myocardin, and Tbx5 and/or Tbx2 (see Fig. S1 in the supplementary material). However, Nkx2-5-Y-A transcriptional activity was diminished by 50% (P<0.001) relative to wild-type Nkx2-5 on the promoter of the Gja5 gene (encoding connexin 40), another direct target of Nkx2-5; this was most obvious in the presence of Tbx20a and Gata5 (see Stennard et al., 2003) (Fig. 3C).

**Introduction of the Y-A mutation into the native Nkx2-5 locus**

Evolutionary conservation of the YRD in vertebrate, cephalochordate and invertebrate species strongly suggests functional significance that may not be strongly revealed by available in vitro assays. We therefore introduced the Y-A mutant allele into the native Nkx2-5 locus using gene targeting. Four separate targeting experiments were performed to create an allelic series for analysis of YRD function in vitro and in vivo (Fig. 4A-C). In targeting experiment I, we mutated one allele of Nkx2-5 in wild-type ES cells by insertion of a gene expression cassette encoding a nuclear-localising version of E. coli β-galactosidase (lacZ) into the first coding exon creating a new null allele. To ensure that no abnormal DNA-binding protein was produced from this allele, the vector also carried a deletion within the homeodomain region (ΔHD; Fig. 4B), as previously described (Biben et al., 2000). In this and other targeting vectors, drug resistance gene cassettes (hygromycin or neomycin) were flanked by LoxP sequences, the recognition sites of bacteriophage Cre.
recombinase. After validation of correctly targeted ES cell clones using Southern blotting (Fig. 4D), cassettes were removed by transient transfection of ES cells with a Cre recombinase expression vector. Following plating at clonal density, and clone selection and expansion, cassette deletion was validated using polymerase chain reaction (PCR) (alleles ΔH and ΔNH in Fig. 4B,C,E). Strategy I produced ES cell lines with genotypes Nkx2-5lacZ/+ and Nkx2-5lacZ(ΔH), both heterozygous null for Nkx2-5 (Biben et al., 2000) and expressing β-galactosidase under Nkx2-5 control.

In targeting strategy II (Fig. 4A), we used the same lacZ targeting vector to mutate the remaining wild-type allele of Nkx2-5 in a previously established ES cell line (Nkx2-5GFP/+ in which one allele of Nkx2-5 had already been targeted by insertion of a gene cassette encoding an enhanced version of jellyfish green fluorescent protein (eGFP) (Biben et al., 2000). This strategy created ES cell lines with genotypes Nkx2-5GFP/lacZ and Nkx2-5GFP/lacZ(ΔNH), homozygous null for Nkx2-5 and expressing both eGFP and β-galactosidase under Nkx2-5 control.

Fig. 4. Targeted alleles of Nkx2-5. (A) Targeting strategies used to create Nkx2-5 ‘knock-in’ alleles (see text). (B,C) Wild-type Nkx2-5 locus with targeting vectors and targeted alleles shown before and after Cre deletion of drug selection cassettes (H, pgkHygro; N, pgkNeo). Coding region exons shaded black. Arrows show loxP sites. ΔHD indicates the small homeobox deletion (amino acids 141-184). 5’P and 3’P, and p1-p4, respectively, indicate positions of Southern probes and PCR primers for validation of recombinations and deletions. Restriction endonucleases: Nc, Bc, NcoI; Bc, BclI; Bg, BglII; M, MluI; N, Nott; X, XbaI; Xh, Xhol. (D) Southern blot analysis of ES cell DNA of indicated genotype digested with BclI (left) or NcoI (right) using probe 3’P. The 23 kb band is the wild-type allele, while 9 and 6 kb bands represent targeted alleles. (E) PCR validation of Cre-deleted ES cell clones using primers specific for the pgkHygro cassette, as indicated in B and C, and those specific for the GFP and pgkNeo cassettes.
In strategy III, we targeted one Nkx2-5 allele in wild-type ES cells using a vector (Fig. 4C) carrying a mutated YRD domain in which all nine tyrosines were mutated to alanine (Y-A mutation; Fig. 1E), as well as a picornavirus internal ribosome entry site (IRES)-lacZ gene cassette inserted into the 3′ untranslated region (Stanley et al., 2002). This strategy created ES cells with genotypes Nkx2-5Y-A:IRESlacZ/+, and Nkx2-5Y-A:IRESlacZ/+;ΔNh, heterozygous for the Y-A allele and expressing β-galactosidase under Nkx2-5 cis-regulatory control via IRES-mediated translational initiation of a bicistronic mRNA.

Finally, in strategy IV, we targeted the remaining wild-type Nkx2-5 allele in Nkx2-5GFP/+ ES cells with the Y-A vector, creating ES cell lines with genotypes Nkx2-5GFP/Y-A:IRESlacZ and Nkx2-5GFP/Y-A:IRESlacZ;ΔNh, expressing one Y-A allele in the context of the null GFP allele, and both eGFP and β-galactosidase under Nkx2-5 control.

To confirm correct marker expression in targeted clones, ES cells carrying mutant genotypes were differentiated in vitro into embryoid bodies (EBs) until day 5, then allowed to adhere to collagen-coated slides until day 9. Foci of beating cardiomyocytes were evident in both Nkx2-5GFP/lacZ(+/NH) and Nkx2-5GFP/Y-A:IRESlacZ(+/NH) EB colonies, eGFP fluorescence and lacZ staining were coincident with each other, and with foci of beating cardiomyocytes (see Fig. S2A-D in the supplementary material; data not shown). We also confirmed stable expression of the Nkx2-5Y-A allele and expressing β-galactosidase under Nkx2-5 cis-regulatory control via IRES-mediated translational initiation of a bicistronic mRNA.

Cardiomyocyte gene expression is altered in Nkx2-5GFP/Y-A:IRESlacZ embryoid bodies

Cardiomyocytes formed within differentiating EBs represent cells of different states of chamber maturation and conduction phenotypes (Fijnvandraat et al., 2003). To compare gene expression in eGFP-positive cardiomyocytes of different Nkx2-5 genotypes, we developed a protocol for purifying Nkx2-5-GFP-positive cells from EBs using fluorescence-activated cell sorting (FACS) for eGFP fluorescence (Fig. 5A). Contamination with eGFP-negative cells was only 0.1-2% using this protocol. Virtually all surviving cells (>99%) were beating at replicating and culture for 24 hours, suggesting that contamination with other cell types capable of expressing Nkx2-5, including foregut endoderm (Stanley et al., 2002), was minimal. eGFP-positive cells null for Nkx2-5 (Nkx2-5GFP/lacZ(−/NH)) and those expressing only the Y-A mutant allele (Nkx2-5GFP/Y-A:IRESlacZ(ΔNh)) showed similar fluorescence versus cell count profiles, but these profiles were qualitatively different from that of cells heterozygous for the null eGFP allele (Nkx2-5GFP(Y-A-IRESlacZ(ΔNh)) (Fig. 5B).

To explore this difference further, we analysed expression of a subset of Nkx2-5-dependent genes in FACS-purified EB-derived cardiomyocytes of different genotypes, using comparative reverse transcriptase (RT)-PCR and quantitative real-time RT-PCR (Fig. 5C,D). Genes known to be downregulated in the context of Nkx2-5 mutation or dominant-negative inhibition in vivo were analysed, including transcription factors Hand1, Irx4 and Ankrd1 (encoding CARP) as well as Myl2 (encoding myosin light chain 2v), Nppa (encoding atrial natriuretic factor), Tagln (encoding sm22α), Smn (encoding Chisel) and Gja1 (encoding connexin 43). Normalised to levels of gapd expression, all of these targets, with the exception of Hand1, were downregulated significantly and to the same extent in cardiomyocytes of the null (Nkx2-5GFP/lacZ(ΔNh)) and YRD-over-null (Nkx2-5GFP/Y-A:IRESlacZ(ΔNh)) mutant genotypes, relative to levels in FACS-purified heterozygous null Nkx2-5 mutant cells (Nkx2-5GFP/+(ΔNh)), Hand1 was only moderately affected in null and Y-A mutant cells, suggesting that its downregulation in Nkx2-5 mutant hearts (Biben and Harvey, 1997) is indirect.

Analysis of YRD function in chimaeric embryos

To examine the phenotypic effects of the YRD mutation in whole embryos, we created chimaeric embryos by injection of ES cells carrying Nkx2-5lacZ(+/NH), Nkx2-5GFP/lacZ(ΔNh) and Nkx2-5GFP/Y-A:IRESlacZ(ΔNh) genotypes into wild-type blastocysts. Injected
blastoceysts were surgically transferred to pseudo-pregnant mothers for fostering, and embryos were subsequently harvested at different stages of development for lacZ staining and phenotypic analysis. For all genotypes, lacZ was expressed with the correct pattern in the cardiac crescent at ~7.75 dpc and looping heart tube at ~8.0 dpc (Fig. 6A,B) (Stanley et al., 2002). In Nkx2-5lacZ/+ (ΔH)+ wild-type chimaeras in which there was a high contribution of ES cell progeny (judged by the extent of lacZ staining in the heart; Fig. 6D,G), the heart looped normally at 9.0-9.5 dpc and heterozygous cells had contributed to chamber and non-chamber myocardium, trabeculae and extra-cardiac regions. Furthermore, these chimaeras transmitted the mutant allele through the germline when taken to term. By contrast, high level Nkx2-5GFP/lacZ/H9004+/+ wild-type and Nkx2-5GFP/Y-A/IRESlacZ/H9004+/+ wild-type chimaeras arrested development at ~8.5 dpc, showing pericardial oedema, failure of cardiac looping, lack of ventricular chamber discrimination, no trabeculation and a truncated outflow tract (Fig. 6C,E,F,H,I), a close phenocopy of Nkx2-5-null mutant hearts (Lyons et al., 1995).

**Heterozygous Nkx2-5Y-A mutant chimaeras show congenital heart disease features**

We were unable to derive a stable mouse line carrying one Y-A mutant allele using heterozygous Y-A ES cells (Nkx2-5Y-A/IRESlacZ/ΔH), even though high-level chimaeras at 9.5-10.5 dpc with apparently normal general and cardiac morphology could be readily established (Fig. 6J,K). Only low-level chimaeras (<10% contribution) were found at birth and these failed to transmit the mutant allele through the germline after multiple matings. We therefore examined the morphology of Nkx2-5Y-A/IRESlacZ/ΔH+/+ wild-type chimaeras at progressively later gestational stages, comparing them with Nkx2-5lacZ/+ (ΔH)+ wild-type (heterozygous null) chimaeras as controls. We found that all moderate to high-level Y-A chimaeras examined at a gross level (n=25) succumbed just prior to birth from multiple cardiac malformations, while control chimaeras (n=50) showed normal morphology and survived beyond birth. Three independently derived clonal Y-A mutant ES cell lines gave identical results.

As early as 14.5 dpc, high-level Y-A mutant chimaeric hearts were enlarged, had a rounded apex and showed dilated ventricles and grossly dilated right atria (Fig. 7A-D). On their external surface, we observed unusual finger-like protrusions that were positive for lacZ, indicating that they were composed of mutant cells (Fig. 7B,C,G,H). Overall, Y-A mutant chimaeras expressed lower levels of Myl2 (encoding myosin light chain 2v), known to be dependent upon Nkx2-5 during development (Lyons et al., 1995) (Fig. 7E,F). Myl2 downregulation was exaggerated in patches that probably correspond to areas populated predominantly by mutant cells (Fig. 7E,F); indeed, the finger-like projections expressed lower levels of Myl2 compared to surrounding myocardium (Fig. 7J, brackets). A blistering within the epicardium and between epicardium and myocardium was also a common feature (Fig. 7I, brackets). Histological examination showed that the right ventricular wall in Y-A chimaeras was thin and hyper-trabeculated, reminiscent of ventricular non-compaction in humans (Pashmforoush et al., 2004) (Fig. 7K,L,M). The inter-ventricular septum was often fenestrated (Fig. 7L), or showed frank ventricular septal defect (VSD; n=5/8) (Fig. 7F,M). Transmural lesions of ventricular free wall were also occasionally detected (usually plugged with a blood clot) and these were surrounded by mutant cells (Fig. 7N; data not shown). Tricuspid valves were absent or hypoplastic (n=5/8) and, when present, were conical in shape with leaflets sitting below the annulus and partially fused to the interventricular septum or ventricular free wall (Fig. 7O,P). These are classical features of Ebstein’s anomaly, which occurs occasionally in humans with Nkx2.5 mutations (Benson et al., 1999). Mitral valves were relatively normal. In the atria, the trabecular pattern was finer and more florid than in control hearts (Fig. 7E,F,H; data not shown), although this is likely to be secondary to dilation, as atrial trabeculae were not always composed of mutant cells (Fig. 7D).

Nkx2-5 has been suggested to confer resistance to cell death-inducing treatments (Monzen et al., 2002). To examine whether cell death due to compromised myocardium was a feature of the Y-A...
mutant phenotype, we compared the prevalence of apoptosis in atria and ventricular free walls of Nkx2-5Y-A/IRESlacZ/+ (H9004) wild-type (Y-A heterozygous) and control Nkx2-5lacZ/+ (H9004) wild-type (null heterozygous) chimaeras at 14.5 dpc using the TUNEL assay. We chose this stage of analysis to be well before the systemic demise seen in mutant chimaeras. In the atria of Y-A chimaeras, TUNEL-positive cells were 3.34-fold more evident than in controls [4.93±0.59 (mean±s.e.m.) versus 1.48±0.22, P<0.005], while in the ventricular free walls there was a 3.24-fold difference (9.40±0.95 versus 2.90±0.27, P<0.008).

**DISCUSSION**

Nkx2-5 sits high in the cardiac regulatory hierarchy and can act as a transcriptional activator and repressor. As for its *Drosophila* cognate, Tinman, Nkx2-5 probably functions as an organ field-specific ‘selector protein’, defining a cardiac context for the multiple signal-dependent transcriptional processes acting in heart development (Halfon et al., 2000; Mann and Carroll, 2002). In this paper, we have defined a novel and essential tyrosine-rich domain within Nkx2-5 and describe a new model of Nkx2-5 deficiency that displays many phenotypic features of NKX2.5 CHD in humans.

The YRD of mouse Nkx2-5 minimally encompasses a region of 37 amino acids with 24% (9/37) being tyrosine. A similar density of tyrosines, with occasional conservative substitutions to phenylalanine, are present in all known vertebrate and chordate members of the cardiac clade of NK2 homeodomain proteins. Other amino acids within the YRD are also highly conserved. However, the YRD and other conserved domains in the C terminus of Nkx2-5 (Fig. 2A), are lacking in *Drosophila* Tinman. We show here that in cardiac NK2 proteins from cephalopod molluscs, highly active invertebrates that possess a sophisticated closed cardiovascular system, the YRD and three of the conserved Nkx2-5 C-terminal signature domains are present. Thus, the YRD has co-evolved with the homeodomain since before divergence of the vertebrate and invertebrate lines some 550 million years ago. Tyrosine-rich regions, possibly ancestral YRDs, are recognisable C-terminal to the homeodomain in NK2-class proteins from *C. elegans*, mosquito, honeybee, hydra and sea anemone, the last two being members of the diploblastic phylum cnidaria (see Fig. 2A). A YRD-like element is also seen in *Drosophila* bagpipe-related genes. The YRD may therefore have a truly ancient origin in metazoan evolution. We have previously suggested that Tinman and Nkx2-5 have diverged mechanistically, as evidenced by the inability of Nkx2-5 to rescue heart development in Tinman mutant flies (Ranganayakulu et al., 1998). Our data now show that the domain structure of Tinman is in fact highly derived, highlighting a dramatic example of protein evolution within an otherwise conserved pathway. Protein evolution of this sort has been described in other selector gene pathways, for example, those involving *Drosophila* homeotic proteins Ubx and Hox3, and...
segmentation protein fushi tarazu (Mann and Carroll, 2002). In
Timman, loss of C-terminal domains may have coincided with gain
of an alternative cardiogenic mechanism involving an N-terminal
domain (Ranganayakulu et al., 1998).

In mouse Nkx2-5, the YRD is essential for the earliest stages of
cardiac development. Cardiomyocytes purified by FACS from EBs
expressing only the Nkx2-5-Y-A allele possessed the same gene
expression signature defects as fully null cardiomyocytes. Importantly,
chimaeras bearing a high investment of Y-A mutant cells showed a
phenocopy of the genetic null mutant. The strongly compromised
nature of the Y-A allele was also demonstrated by the phenotype of
chimaeras carrying heterozygous Nkx2-5Y-A IRESlacZ/ES cells. These
chimaeras died in the immediate pre-natal period with a
constellation of severe heart malformations, whereas high-level
chimaeras made from heterozygous Nkx2-5Y-A:IRESlacZ/+
ES cells. These
cardiac phenotypes that overlaps with the more severe anomalies
in chimaeric mice, the Nkx2-5Y-A allele produces a spectrum of
NKX2.5 mutations: frank ASD occurs in 1% of
human mutations: frank ASD occurs in 1% of
the YRD should expand our understanding of cardiac
phenotypes that are much less severe than those seen in humans
heterozygous for NKX2.5 mutations: frank ASD occurs in 1% of
mutant pathology. Increased myocyte
dysfunction further highlight the importance of C-terminal domains
for their function and target specificity, and such inter-dependent
relationships may have been necessary for expansion of the
homeobox gene family and diversification of its functional
repertoire. In the case of Pax transcription factors, for example, the
paired domain and paired homeodomain act interdependently as a
bipartite structure, with the paired domain influencing the DNA-
binding properties of the homeodomain (Mann and Carroll, 2002).
The YRD could also act in this way for NKX2-class homeodomains,
or attract accessory proteins that modulate chromatin or
transcriptional activity in other ways.

Haploinsufficiency for Nkx2-5 in mice leads to cardiac
phenotypes that are much less severe than those seen in humans
heterozygous for Nkx2-5. It could also serve to integrate its positive and negative
functions. We note that the ability of Nkx2-5 C-terminal amino acids
to repress the N-terminal trans-activation domain was intact in the
YRD mutant, as was its ability to collaborate with GATA4/5,
Tbx2/5/20, SRF and myocardin on the Nppa promoter (see Fig. S1
in the supplementary material). The activity of the Nkx2-5-Y-A
mutation on the Gja5 promoter in the presence of Tbx20 and Gata5
was compromised, albeit only weakly (~50%). Therefore, the
impact of YRD mutation within the context of Nkx2-5 in vitro is
subtle at best. New assays that more robustly model its in vivo
function await development.

Other homeproteins possess accessory domains that are essential
for their function and target specificity, and such inter-dependent
relationships may have been necessary for expansion of the
homeobox gene family and diversification of its functional
repertoire. In the case of Pax transcription factors, for example, the
paired domain and paired homeodomain act interdependently as a
bipartite structure, with the paired domain influencing the DNA-
binding properties of the homeodomain (Mann and Carroll, 2002).
The YRD could also act in this way for NKX2-class homeodomains,
or attract accessory proteins that modulate chromatin or
transcriptional activity in other ways.

Haploinsufficiency for Nkx2-5 in mice leads to cardiac
phenotypes that are much less severe than those seen in humans
heterozygous for NKX2.5 mutations: frank ASD occurs in 1% of
mutant mice but in more than 70% of humans; conduction system
defects, although evident in mice, are mild and do not progress to
second and third degree conduction block as in humans (Biben et al., 2000). The significantly more severe human phenotypes may be
due to subtle differences in the cardiac genetic program between
species or the dominant-negative nature of some human mutations
(Kasahara and Benson, 2004). Importantly, however, an animal
model that accurately reflects the developmental defects seen in
individuals with NKX2.5 mutations is lacking. We show here that
in chimaeric mice, the Nkx2-5Y-A allele produces a spectrum of
cardiac phenotypes that overlaps with the more severe anomalies
seen in the human disease. ASD, VSD, valvar anomalies, dilated
cardiomyopathy and ventricular non-compaction are all
components of NKX2.5 mutant pathology. Increased myocyte
death, presumably in response to reduced resistance to
biomechanical stress, is also evident in chimaeras, and could be an
unidentified component of the human disease. Indeed, we have
recently also discovered a novel NKX2.5 mutation in a human
family with dilated cardiomyopathy, and ASD and conduction
defects (Diane Fatkin and R.P.H., unpublished). Although
molecular pathways remain to be elucidated, it is likely that the
structural integrity of mutant myocytes and cellular adhesion
between them is compromised in Nkx2-5Y-A chimaeras, as
suggested by phenotypes involving downregulation of myofilament
gene Myl2, transmural lesions, blistering between epicardium and
myocardium, and the possible ‘streaming’ of myocytes into finger-
like protrusions. We have recently developed a hypomorphic
genetic model of Nkx2-5 function in mouse that has phenotypic
manifestations similar to those seen in hearts of Y-A mutant
chimaeras (O. Prall and R.P.H., unpublished). Our new models
should offer valuable opportunities for further understanding of the
complex and varied phenotypic manifestations of NKX2.5
mutations. Furthermore, experiments focused on the specific role
of the YRD should expand our understanding of cardiac
developmental pathways and CHD.
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Supplementary material
Supplementary material for this article is available at http://dev.biologists.org/cgi/content/full/133/7/1311/DC1

References


Benson, D. W., Silberbach, G. M., Kavanaugh-McHugh, A., Cottrill, C., References
http://dev.biologists.org/cgi/content/full/133/7/1311/DC1


