The Dorsocross T-box genes are key components of the regulatory network controlling early cardiogenesis in Drosophila

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Summary

Cardiac induction in Drosophila relies on combinatorial Dpp and Wg signaling activities that are derived from the ectoderm. Although some of the actions of Dpp during this process have been clarified, the exact roles of Wg, particularly with respect to myocardial cell specification, have not been well defined. Our present study identifies the Dorsocross T-box genes as key mediators of combined Dpp and Wg signals during this process. The Dorsocross genes are induced within the segmental areas of the dorsal mesoderm that receive intersecting Dpp and Wg inputs. Dorsocross activity is required for the formation of all myocardial and pericardial cell types, with the exception of the Eve-positive pericardial cells. In an early step, the Dorsocross genes act in parallel with tinman to activate the expression of pannier, a cardiogenic gene encoding a Gata factor. Our loss- and gain-of-function studies, as well as the observed genetic interactions among Dorsocross, tinman and pannier, suggest that co-expression of these three genes in the cardiac mesoderm, which also involves cross-regulation, plays a major role in the specification of cardiac progenitors. After cardioblast specification, the Dorsocross genes are re-expressed in a segmental subset of cardioblasts, which in the heart region develop into inflow valves (ostia). The integration of this new information with previous findings has allowed us to draw a more complete pathway of regulatory events during cardiac induction and differentiation in Drosophila.

Key words: Mesoderm patterning, Heart development, T-box genes, Drosophila

Introduction

Studies in several vertebrate models and Drosophila have uncovered a surprising degree of evolutionary conservation of regulatory mechanisms and genes that control early cardiogenesis. In all these organisms, cardiac induction in the lateral mesoderm involves the concerted action of signals mediated by Bmp, Wnt and Fgf family members, which act upon cardiogenic genes encoding NK homeodomain, Gata and T-box transcription factors (reviewed by Zaffran and Frasch, 2002). Together, these signaling and transcriptional pathways set up complex and only partially defined regulatory networks that result in the progressive delineation and specification of heart progenitors.

In Drosophila, the primordial cells generating myocardial cells (cardioblasts) and pericardial cells are induced within mesodermal areas receiving a combination of Dpp (i.e. BMP) and Wg (i.e. Wnt) signals (Zaffran and Frasch, 2002). Dpp is secreted from a dorsal domain of the ectoderm on either side of the embryo, whereas Wg derives from transversely striped segmental domains; hence, the cardiac progenitors are generated in bilateral, segmentally repeated areas of the dorsal mesoderm of the early embryo. The NK homeobox gene tinman (tin), which is crucial for the generation of all types of cardiac progenitors and all other dorsal mesodermal derivatives, is a direct downstream target of the Dpp signaling cascade and, as such, is induced in the entire dorsal mesoderm (Azpiazu and Frasch, 1993; Bodmer, 1993; Frasch, 1995; Xu et al., 1998). In addition, Tinman protein is required to provide mesodermal cells with the competence to respond to Dpp and other signals during additional events in cardiac induction (Halfon et al., 2000; Knirr and Frasch, 2001; Han et al., 2002). tin, potentially in combination with Dpp, is required for the transcriptional activation of the Gata factor-encoding gene pannier (pannier) in the cardiogenic mesoderm (Gajewski et al., 2001). pnr is crucial for the specification of both cardioblasts and pericardial cells (Gajewski et al., 1999; Alvarez et al., 2003; Klinedinst and Bodmer, 2003). One of the earliest regulatory genes turned on specifically in all cardioblasts downstream of pnr is the Tbx20 ortholog midline (mid) (Miskolczi-McCallum et al., 2005; Qian et al., 2005; Reim et al., 2005). Together with its paralog H15, mid serves to activate late-stage expression of tin specifically within cardioblasts, which in turn is required for the normal patterning of the heart tube and the differentiation of myocardial cells (Reim et al., 2005).

When compared with Dpp, the exact role of Wg during cardiac induction is less well understood. For example, the lack of spatial correlation between pnr and wg expression suggests that pnr is not a direct target of Wg signals. Whereas ectodermal wg is striped, pnr expression initiates almost uniformly along the anteroposterior axis near the dorsal margin of the mesoderm (Gajewski et al., 1999; Klinedinst and...
Development is the induction of Wg signals is the induction of sloppy paired (slp1 and slp2) in striped domains in the early mesoderm (Riechmann et al., 1997; Lee and Frasch, 2000). The slp genes encode forkhead domain repressor factors, which prevent the induction of visceral mesoderm regulators by Dpp that would otherwise interfere with cardiac induction in the presumptive cardiogenic areas (Zaffran et al., 2001).

In addition to excluding these inappropriate regulators from the cardiogenic areas, wg is thought to promote the formation of both pericardial and myocardial progenitors also in a direct fashion. Indeed, such a mechanism operates during the specification of one specific subset of pericardial cells, termed Eve-PCs, and the induction of the even-skipped (eve) gene in progenitors of these cells requires binding sites for the Wg effector Pangolin (Pan, also known as dTCF) in combination with binding sites for Tinman and the Dpp-effectors Mad and Medea (Halfon et al., 2000; Knirr and Frasch, 2001; Han et al., 2002). Hence, the combinatorial inputs from Wg, Dpp and the cardiogenic competence factor Tinman are directly integrated at the level of the enhancer of a pericardial regulatory gene. Based upon the available genetic data on cardioblast specification, it is likely that an analogous integration of Wg and Dpp signals also occurs during the induction of certain early-acting myocardial regulatory genes. However, clear candidates for common targets of Wg and Dpp in myocardial development have not been described.

Our current study identifies the Dorsocross T-box genes as crucial new components that mediate the combinatorial activities of Wg and Dpp during early steps of myocardial induction. The Dorsocross (Doc) locus encodes a cluster of three genes, Doc1, Doc2 and Doc3, that are closely related in terms of their T-box sequences and embryonic expression patterns (Reim et al., 2003). Our previous work has identified important roles of these genes during amnioserosa development and epidermal patterning of the embryo (Reim et al., 2003). We now show that, within the mesoderm, the Doc genes have an essential role for the formation of cardioblasts and a subset of pericardial cells. The induction of Doc gene expression occurs in dorsal mesodermal quadrants of cells at the intersections of the Dpp and Wg domains, and requires the activities of both Dpp and Wg, but not tin. We demonstrate that, in the absence of all three Doc genes, only very few cardioblasts become specified and no dorsal vessel is formed. In addition, the subpopulations of odd-skipped (odd)-expressing pericardial cells (Odd-PCs), odd-positive lymph gland cells and tin-only-expressing pericardial cells (Tin-PCs) require Doc gene activity. However, eve + tin-positive pericardial cells (Eve-PCs) and dorsal somatic muscle founders develop independently of Doc. We observe genetic interactions among Doc, tin and pnr, which suggests that these three cardiogenic regulators synergize during the specification of myocardial and certain pericardial cells. Accordingly, simultaneous ectopic expression of Doc2 with tin, pnr or both generates large numbers of ectopic cardioblasts in the mesoderm. We demonstrate that one of the key functions of the Doc genes during cardiogenesis, which they exert in combination with tin, is the activation of pnr expression in the cardiogenic mesoderm. Altogether, the incorporation of the Doc genes into the cardiogenic network has allowed us to close important gaps in our understanding of the regulatory circuits operating during the induction of myocardial and pericardial cells.

Materials and methods

Drosophila strains and crosses

Df(3L)DocA, which contains EP(3)3556 at its breakpoint, and the Doc1-deleting deficiency Df(3L)29A6 have been described by Reim et al. (Reim et al., 2003). Df(3L)29A6 and the null allele pnrVX6 were obtained from the Bloomington Stock Center. The null allele tinD-lacZ was described in Azpiazu and Frasch (Azpiazu and Frasch, 1993). Stocks with the following genotypes in a w- background were generated via recombination: Df(3L)DocA pnrVX6, Df(3L)DocA tinD-lacZ and Df(3L)DocA pnrVX6 tinD-lacZ. Mutant stocks were balanced with TM3, eve-lacZ for the identification of homozygous mutant embryos. Alternatively, genotypes causing protein nulls were confirmed by appropriate antibody staining. Oregon R was used as wild-type control unless indicated otherwise. The following enhancer-lacZ reporter lines were used: Mef2-Htr1D-lacZ #2 and #6 (2nd and 3rd chromosome insertions, respectively, unpublished; a gift from H. Nguyen, Albert Einstein College, New York), tin–D-lacZ #23b (3rd chromosome) (Lo and Frasch, 2001), tin–D-lacZ #25 (X chromosome) (Yin et al., 1997), 1010 B2-lacZ (Yin and Frasch, 1998), AE127 (svp-lacZ enhancer trap; gift from Yasushi Hiromi, National Institute of Genetics, Mishima, Japan). The following GAL4 and UAS lines were used: c381-GAL4 (2nd chromosome) (Manseau et al., 1997), tinD-GAL4 (TM66-GAL4 #52D1; 2nd chromosome) (Baker and Schubiger, 1996), UAS-dpp #4 and UAS-wg (X and 3rd chromosomes, respectively) (Frasch, 1995), UAS-Doc1 #2, UAS-Doc2 #2; #3 and #22, and UAS-Doc3 #2 (Reim et al., 2003), UAS-pnr (2nd and 3rd chromosome insertions; obtained through R. A. Schulz, University of Texas, M. D. Anderson Cancer Center, Houston), UAS-tin #1 (Yin and Frasch, 1998) and UAS-tin #2 (Nellen et al., 1994). For expression of multiple UAS constructs, UAS-Doc2 #2 (2nd chromosome) was combined with UAS-tin or UAS-pnr on chromosome 3 or with a recombinant UAS-tin, UAS-pnr 3rd chromosome. Except for embryos carrying c381-GAL4, which were kept at 25°C, embryos for UAS/GAL4 experiments were left to develop at 28°C.

Staining of embryos

Immunostaining of embryos using DAB, fluorescent immunostaining and in situ hybridization were carried out essentially as described by Knirr et al. (Knirr et al., 1999). Primary antibodies were detected with FITC-, Cy3- or Cy5-conjugated AffiniPure goat anti-rabbit IgG (H+L) (1:200; Jackson ImmunoResearch Laboratories). If necessary, Tyramide Signal Amplification (TSA) was performed using biotinylated secondary antibodies (1:500) in combination with the Vectastain ABC Kit (Vector Laboratories) and fluorescent Tyramide Reagent (PerkinElmer). Primary antibodies included rabbit anti-Bap (1:500 with TSA) (Zaffran et al., 2001), rabbit anti-Doc2 (1:2000), guinea pig anti-Doc2+3 (1:400), guinea pig anti-Doc3+2 (1:600) (Reim et al., 2003), rabbit anti-Eve (Frasch et al., 1987), guinea pig anti-Eve (1:400), rat anti-Odd (1:500), guinea pig anti-Runt (1:300) (Kosman et al., 1997), rabbit anti–β-Galactosidase (1:1500; Promega), mouse polyclonal anti–β-Galactosidase (1:200; Sigma), rabbit anti–Mef2 (1:750; a gift from H. Nguyen, Albert Einstein College, Bronx, NY) (Bour et al., 1995), rabbit anti–Phospho-Smad1/5/9 (1:2000 with TSA; gift from C.-H. Heldin, Ludwig Inst., Upsala), rabbit anti–Pmr (1:3000 with TSA) (Herranz and Morata, 2001), rabbit anti–Srp (1:800) (gift from D. Hoshizaki), rabbit anti–Tin (1:750) (Yin et al., 1997) and rabbit anti–Zifh-1 (1:2000) (Brower et al., 1998). Monoclonal anti–Wg 4D4 (1:40 with TSA) and anti–β-Galactosidase.
Dorsocross genes control early cardiogenesis

40-1a (1:60 with TSA) were obtained from the Developmental Studies Hybridoma Bank at the University of Iowa. Digoxigenin-labeled RNA in situ probes for Doc (Reim et al., 2003), bkh, hand (S. Zaffran and M.F., unpublished) and H15 were prepared from cloned genomic fragments, and the mid in situ probe from the BDGP EST RE27439 (Reim et al., 2005). Images of DAB-stained embryos were taken using Nomarski optics and images from fluorescent staining using confocal laser scanning microscopy with Leica TCS-SP and Zeiss LSM 510 META microscope systems.

Results
Dynamic expression and regulation of Dorsocross in the early dorsal and cardiogenic mesoderm

The three Dorsocross (Doc) genes Doc1, Doc2 and Doc3 are co-expressed in a number of embryonic tissues, including the amnioserosa, the dorsolateral ectoderm and the dorsal mesoderm (Reim et al., 2003). Our present study focuses on the role of the Doc genes in the development of the dorsal vessel, which derives from the Doc-expressing areas of the early dorsal mesoderm.

In the trunk mesoderm, Doc expression emerges first at stage 10 within segmentally repeated patches of cells located in dorsal areas (Reim et al., 2003). As shown in Fig. 1A for Doc3 mRNA, the ventral borders of Doc expression coincide with the ventral border of nuclear phosphorylated Mad (pMad).
from the dorsal ectoderm. The fully developed clusters of Doc expression at mid stage 10 are reciprocal to the clusters of cells expressing the homeobox gene bagpipe (bap), which mark the precursors of the trunk visceral mesoderm (Fig. 1B). Ectopic activation of the Dpp signaling pathway throughout the mesoderm via a constitutively active Dpp receptor, Thickveins, TkvQ253D (Nellen et al., 1994), leads to ventral expansion of bap expression (Yin and Frasch, 1998), and Doc expression expands in a similar fashion upon pan-mesodermal Tkv Q253D or Dpp expression (Fig. 1C, compare with 1B, and data not shown). TkvQ253D, or Dpp-induced ectopic Doc and bap occur only within their appropriate segmental domains that are defined by positive and negative Wg inputs, respectively (Azpiazu et al., 1996; Lee and Frasch, 2000; Reim et al., 2003).

In the case of Doc, Wg is essential for the segmental induction in both mesoderm and ectoderm (Reim et al., 2003). Accordingly, triple immunostaining with antibodies recognizing the Doc proteins Doc2/Doc3, the dorsal mesoderm marker Tin and Wingless (Wg) protein demonstrates that Doc co-localizes with Tin in the dorsal mesoderm, but unlike Tin is restricted to the areas that are close to the Wg-secreting cells of the ectoderm (Fig. 1D). In addition, forced pan-mesodermal Wg expression causes the induction of Doc in a largely continuous fashion along the anteroposterior axis of the dorsal mesoderm, in a pattern that closely resembles that of continuous fashion along the anteroposterior axis of the dorsal wg expression causes the induction of Doc in a largely continuous fashion along the anteroposterior axis of the dorsal mesoderm (Fig. 1D). Additionally, these data confirm that early mesodermal Doc is induced by intersecting Dpp and Wg signaling pathways. As a consequence, Doc becomes expressed in the entire anterior dorsal quadrant of each mesodermal parasegment (i.e. the dorsal region of each mesodermal A domain) (Azpiazu et al., 1996). These areas will eventually generate the dorsal vessel as well as dorsal somatic muscles, as opposed to the bap-positive areas of the P domains that contain most of the primordial cells of the visceral musculature.

During stage 11, the trunk visceral mesoderm primordia separate from the A domains by moving inwards, while the Doc-positive cells of the dorsal A domains maintain contact with the ectoderm and spread out along the anteroposterior axis. Doc expression undergoes dynamic changes during this period. The highest levels of expression are retained along the dorsal margin of the mesoderm, except in the areas that express the homeobox gene even-skipped (eve), which remain directly underneath each Wg stripe (Fig. 1F and data not shown). Eventually, Doc expression becomes completely excluded from the eve- and runt-expressing dorsal muscle progenitors that derive from this cluster (Fig. 1G; data not shown). At the same time, new clusters of high-level Doc expression appear at more lateral positions, which are not considered part of the dorsal mesoderm as they lack tin expression and later contribute to lateral somatic muscles (Fig. 1F; arrows; I.R. and M.F., unpublished).

For additional clarification of the developmental events in the early cardiogenic mesoderm, we examined Doc expression relative to other cardiogenic regulators, including the Gata factor-encoding gene pannier (pnr). In addition to its expression in the cardiogenic mesoderm, pnr is expressed in a broad band of cells along the adjacent dorsal ectoderm (Winick et al., 1993; Herranz and Morata, 2001). We first detect Pnr protein in the mesoderm at early stage 11, which is notably later than the earliest Doc expression but coincides with the time when Doc expression starts to refine along the dorsal margin. Doc and Pnr protein colocalize within the most dorsal areas of the tin-positive portion of the mesoderm (Fig. 1H; tin expression is monitored with tinD-lacZ, a reporter driven by the Dpp-responsive enhancer of tin) (Yin et al., 1997). Like Doc, Pnr does not overlap with Eve (data not shown). Hence, the cardiac mesoderm in the Drosophila embryo (in a more stringent definition excluding the Eve-positive cells, which also produce dorsal muscles) is characterized by the co-expression of tin, pnr and Doc.

During stage 12, Doc maintains its co-expression with pnr and tin, although the expression of all three genes becomes further restricted to the dorsal margin (Fig. 1I) (Bodmer and Frasch, 1999). For a brief period, Doc is expressed in all cardioblasts that form during this time and are marked by expression of the Tbx20 ortholog midline (mid) or the COUP-TFI-related gene seven-up (svp) (Fig. 1J) (Reim et al., 2005). Doc and Pnr gradually disappear during stage 12-13, except for two out of six cardioblasts per hemisegment that maintain Doc expression until the end of embryogenesis (Lo and Frasch, 2001; Reim et al., 2003). tin expression is maintained in a complementary set of cardioblasts, as well as in certain pericardial cells (Yin and Frasch, 1998; Ward and Skeath, 2000; Lo and Frasch, 2001).

Next we asked whether tin and pnr regulate Doc expression in the dorsal and cardiogenic mesoderm. Despite the importance of tin for the specification of all dorsal mesodermal derivatives, Doc expression initiates normally in the dorsal mesoderm of tin null mutants (Fig. 2B, compare with 2A). Likewise, early Doc expression is also unaffected in pnr-null mutants (Fig. 2F; compare with 2E), which is consistent with the observed onset of pnr expression after that of Doc. Therefore, Doc induction at stage 10 seems to be a direct result of Dpp and Wg signaling and, unlike bap (Lee and Frasch, 2005), does not require Tin as a mesodermal competence factor. We presume that Dpp and Wg induce Doc expression in a similar fashion in both the dorsal mesoderm and the dorsal ectoderm.

In contrast to stage 10, Doc expression is affected in both tin and pnr mutants at later stages, and fades prematurely from the dorsal mesoderm. In stage 11 tin mutants, we see only few irregularly arranged cells that still express Doc in the dorsal mesoderm (Fig. 2D; compare with 2C), and by mid stage 12 Doc expression is absent in this area. We also find that pnr is never activated in the mesoderm of tin mutants (Fig. 2D′; compare with 2C′), which is consistent with previous findings that a pnr-lacZ reporter construct requires tin and essential Tin-binding sites in order to be activated in the mesoderm (Gajewski et al., 2001). Indeed, loss of Doc expression in tin mutants might be caused indirectly by the absence of pnr products, as high-level Doc expression also fails to emerge in the dorsal mesoderm of stage 11 pnr mutants and is virtually absent from stage 12 onwards (Fig. 2H; compare with 2G). The loss of Doc expression in stage 11-12 pnr mutants is accompanied by decreased tin expression (Fig. 2H) (Alvarez et al., 2003; Klinedinst and Bodmer, 2003), with the strongest reduction in the dorsal-most cells that would normally show high levels of Pnr and Doc.

As pnr is also required for dpp expression in the dorsal ectoderm at this stage (Herranz and Morata, 2001), it is conceivable that the loss of Doc expression is caused indirectly by the lack of the ectodermal Dpp inputs. To address this...
possibility, we restored either *pnr* expression or Dpp signaling exclusively in the mesoderm of *pnr* mutant embryos. We found that forced mesodermal *pnr* expression can significantly rescue high-level Doc expression in stage 11 *pnr*–embryos (Fig. 2I, arrowheads; compare with 2H). There is also a significant rescue of cardioblast specification, as indicated by the activation of cardioblast-specific *midline* in this background (Reim et al., 2005) and by late stage Doc and Tin expression in a complementary pattern (as in wild-type cardioblasts, albeit in fewer cells; data not shown). By contrast, activating Dpp signaling in the mesoderm of *pnr* mutants with UAS-*tkv*Q253D or UAS-*dpp* does not result in a significant rescue of Doc expression in the dorsal mesoderm (Fig. 2J and data not shown; compare with 2H,I). These data suggest that *pnr* is required, perhaps directly, to regulate Doc expression in the dorsal mesoderm during stages 11-12, although it is not involved in the initial activation of Doc during stage 10.

Unexpectedly, forced mesodermal *pnr* expression can activate Doc ectopically at stage 10, when endogenous *pnr* is not yet expressed in the mesoderm (Fig. 2L; compare 2K). The
observed restriction of ectopic Doc expression to the mesodermal A domains indicates that the activation of Doc by Pnr in this situation additionally requires Wg signals, as it does normally. We also considered the possibility that pnr can activate dpp in the mesoderm, which in turn would induce Doc. Indeed we observe ectopic activation of phospho-Mad in embryos with pan-mesodermal Pnr, which correlates with expanded Doc expression (Fig. 2L; compare 2K). This effect may reflect the normal activity of pnr in activating dpp expression in the dorsal ectoderm, although it is possible that pnr normally also activates low levels of dpp expression in the dorsal mesoderm, which may have escaped detection so far.

**Dorsocross is required for the specification of cardioblasts**

We used a recently generated small deficiency, Df(3L)DocA, that deletes all three Doc genes, Doc1, Doc2 and Doc3 (Reim et al., 2003), to investigate the role of the Doc genes in dorsal vessel development. As described previously, DocA mutants (i.e. embryos homozygous for Df(3L)DocA) do not undergo germ band retraction owing to the requirement of Doc in the amnioserosa. To avoid this complication and rule out indirect influences of morphogenetic defects on cardiogenesis, we performed our analysis predominantly with DocA mutants in which germ band retraction has been rescued by amnioserosa-specific expression of Doc2 via c381-GAL4 (Reim et al., 2003). Dorsal vessel development in these embryos was analyzed through expression of genes that normally mark all or subsets of cardioblasts.

**Fig. 3.** Cardiac phenotype of Dorsocross loss-of-function mutants. (A,B) Stage 16 embryos carrying Mef2-HtΔD-lacZ, stained with anti-β-Galactosidase (dorsal view). β-Galactosidase signals mark all cardioblasts of the dorsal vessel of wild-type embryos (A), but are absent in homozygous Df(3L)DocA embryos (B). (C-H) Lateral views of stage 14 embryos fluorescently labeled for markers, as indicated by the color code. Control embryos (left column) and homozygous Df(3L)DocA mutant embryos (right column) carry c381-GAL4 and UAS-Doc2 used for amnioserosa rescue. (C,D) Detection of mid RNA and Tin protein as markers for cardioblasts (CB; mid-positive and Tin+) and Tin+ pericardial cells (PC; mid-negative). The number of Tin+ cells is severely reduced and mid-expressing cardioblasts are almost absent in mutants. mid RNA is still detectable in ectodermally derived tissues. (E,F) Detection of Tin and Eve proteins. Tin+ cardioblasts (Tin-CB, red) and pericardial cells (Tin-PC, red) are largely lost in the DocA mutant. Most of the remaining Tin+ cells are Eve-negative pericardial cells that express both markers (Eve-PC, yellow). Eve+ dorsal muscles (DA1, green) are also present in DocA mutants. (G,H) Embryos carrying one copy of AE127 (svp-lacZ) stained for β-Galactosidase and Mef2 to identify Svp-cardioblasts (Svp-CB), which are absent in the DocA mutant (asterisk). (I,J) Dorsal vessel of Df(3L)DocA svp-lacZ heterozygous embryo at stage 16 stained as in G showing normal number of cardioblasts. (J) Defective dorsal vessel of Df(3L)DocA svp-lacZDf(3L)29A6 transheterozygous embryo stained as in G and I. The reduced Doc gene copy number has caused the loss of numerous cardioblasts, especially of the Svp-CB type. Asterisks indicate positions of Tin-CB loss. (K-M) Dorsal trunk mesoderm of early to mid stage 12 embryos stained for Mef2 protein (red) and mid RNA (green). (K) mid expression initiates in small clusters along the dorsal edge of the mesoderm (arrowhead) in the wild-type (K) but not in the DocA mutant embryo (L). (M) Mesodermal expression of Doc2 via tinD-GAL4 rescues cardiac mid expression in a homozygous Df(3L)DocA mutant background.
transcription factor Mef2 in cardioblasts (Nguyen, 1998) (H. Duan and H. T. Nguyen, unpublished). In *Doc* mutants, almost no β-Galactosidase is detected from this reporter (Fig. 3B; except for the distortions, the results were essentially the same in both amnioserosa-rescued and non-rescued embryos for this and all other markers tested). Likewise, examination of *tin* expression at stage 14 or later reveals that *Doc* mutants have a greatly reduced number of Tin-positive cells (Fig. 3D, compare with 3C). Consistent with our findings with the *Me2f-HtΔD-lacZ* marker, no or very few Tin-positive cells express the cardioblast marker *mid* (Fig. 3D, compare with 3C) or *H15* (data not shown) in *Doc* mutants. Double staining for the pericardial cell marker *even-skipped* (*eve*) shows that most of the residual Tin-positive cells co-express *tin* and *eve*, and, hence, correspond to Eve-pericardial cells (Eve-PCs) (Fig. 3F). Like the Eve-PCs, the *eve*-expressing somatic muscles #1 (also known as DA1) are also not affected by the loss of Doc activity (Fig. 3F).

Two distinct types of cardioblasts can be discriminated by their mutually exclusive expression of either *tin* or *svp*. We performed anti-β-Galactosidase/anti-Mef2 double staining of embryos carrying one copy of the *svp-lacZ* enhancer trap insertion AE127 to confirm that not only the Tin-cardioblasts (Tin-CBs) but also the Svp-cardioblasts (Svp-CBs) are affected by the loss of Doc genes. As shown in Fig. 3H, Svp-CBs are absent in *Doc* mutants, as is the Mef2-stained row of cardioblasts above the somatic mesoderm (compare with Fig. 3G). Heterozygous *Doc* embryos usually have normal numbers of cardioblasts (Fig. 3I), although a small fraction of embryos do have reduced numbers, which indicates less robust development of cardioblasts with decreased Doc activity. Indeed if Doc dose is further reduced by combining *Df(3L)DocA* with *Df(3L)29A6*, a deletion that removes *Doc1*, there is a significant reduction from normally 104 cardioblasts in wild-type embryos to 80±6 cells (*n*=10) (Fig. 3J). Although all types of cardioblasts are affected by the reduction of Doc levels, Svp-CBs appear to be more sensitive than Tin-CBs. This suggests that Doc has an early function required for all cardioblasts as well as a more specific function for Svp-CBs, in which it is expressed at later stages.

To distinguish whether Doc genes are required for the specification versus survival of cardioblasts, we examined the expression of a number of markers for newly specified cardioblasts at early stages of cardiogenesis. Cardioblast expression of *mid* (Fig. 3L; compare with 3K), *svp-lacZ* (Lo and Frasch, 2001), the *G0 α-subunit gene brokenhearted* (*bkh*) (Fremion et al., 1999) and *hand* (Kölsch and Paululat, 2002) (data not shown) never initiates during early stage 12 in *Doc* mutants, although *bkh* and *hand* are still expressed in Eve-PC progenitors as in wild-type embryos. Cardiac expression of several markers, including *mid*, *H15*, *Me2f-HtΔD-lacZ*, *svp-lacZ*, *hand* and *bkh*, is partially rescued by forced expression of either *Doc1*, *Doc2* or *Doc3* via *tinD-Gal4* in the dorsal mesoderm in the background of *Df(3L)DocA* (Fig. 3M; see also Fig. 7; other data not shown; *Doc1* and *Doc3* rescuing activity was only tested with *mid* and *Me2f-HtΔD-lacZ*). As observed previously for the amnioserosa (Reim et al., 2003), the best rescue was consistently obtained with *Doc2*. These data demonstrate that mesodermal expression of Doc is sufficient to rescue cardioblast specification and that it is the Doc genes and not any of the other genes uncovered by *Df(3L)DocA* that are responsible for the observed cardiac phenotypes. We conclude that Doc genes have an essential role and act in a dose-dependent manner in specifying cardioblasts.

**Doc is required for Odd-positive pericardial and lymph gland cells but not for Eve-positive pericardial cells and dorsal somatic muscles**

The dorsal quadrants of Doc-expressing mesodermal cells from stage 10 embryos not only give rise to cardioblasts, but also to pericardial cells and dorsal somatic muscle founders. The observed reduction of Tin-positive cells already indicates that the pericardial cells expressing *tin* but not *eve*, called Tin-PCs, are also drastically reduced in number in Doc loss-of-function mutants (Fig. 3D,F). To complete the analysis of dorsal mesodermal cell types, we analyzed *Doc* mutants for the presence of Tin-pericardial cells that express *odd-skipped* (*odd*). Two out of the four Odd-positive pericardial cells (Odd-PCs) in each hemisegment are Svp-CB siblings, while the other cells derive from a different lineage (Ward and Skeath, 2000). All Odd-PCs are missing in the mutants, as are Odd-positive cells that originate from the thoracic dorsal mesoderm and normally form the lymph glands (Fig. 4B; compare with 4A). This result is consistent with an early defect in the specification of a common pool of precursors of pericardial/lymph gland cells and cardioblasts (see Mandal et al., 2004). By contrast, and as described above, progenitors that produce Eve-pericardial cells and Eve-expressing founders of muscle 1 (DA1) from a distinct pool of cells are specified normally in the absence of Doc (Fig. 4B; compare with 4A). Runt marks another somatic muscle founder and the corresponding muscle #10 (DO2) that are derived from the early Doc-expressing domains. As for Eve, the Runt pattern in *Doc* mutants with rescued germ band retraction is very similar to wild type, even at later stages (Fig. 4D, compare with 4C). Likewise, staining for *1010 B2-lacZ*, a reporter gene fortuitously expressed in all dorsal muscles (Yin and Frasch, 1998), shows that the dorsal muscles are present in *Doc* mutants, although they are distorted because of the defects in embryo morphology without the amnioserosa (Fig. 4F, compare with 4E). Therefore Doc genes, although present in the entire dorsal quadrants of the early mesodermal A domains, are specifically required for pure cardiac cell lineages, but not for those that generate in addition or solely somatic muscles. This function correlates with the restricted Doc expression at stage 11-12, where Doc expression is excluded from the Eve-positive clusters.

**Genetic interactions between Doc, *pnr* and *tin***

The observed co-expression of Doc, *tin* and *pnr* during stages 11 and 12, and defective cardioblast specification upon loss of function of these genes suggest that these three genes act in a common pathway during early cardiogenesis. The occurrence of genetic interactions among these genes would be further indicative of this possibility. Because we observe mild defects in cardioblast specification in embryos with a reduced Doc dose (*Df(3L)29A6/Df(3L)DocA*, Fig. 3I), we asked whether reduction of *tin* and *pnr* gene dose would have any further impact on cardiogenesis. In order to test this possibility, the null alleles *pnr*^VX6^ and *tin*^346^ were individually recombined onto the *Df(3L)DocA* chromosome. In addition, triple mutants carrying *Df(3L)DocA*, *pnr*^VX6^ and *tin*^346^; as well as *pnr*^VX6^ *tin*^346^ double mutants, were generated. Heterozygous individuals of
all combinations are viable, although heterozygous triple mutants have a slightly reduced viability (63%) when compared with tin^{466} heterozygotes. If Df(3L)DocA/TM3 heterozygous flies are crossed to Df(3L)29A6/Df(3L)DocA tin^{466}, but not with Df(3L)29A6/Df(3L)DocA tin^{466} among about 200 progeny, indicating more severe defects with the latter combination.

Fig. 5 shows representative phenotypes of transheterozygous embryos. As described above, Df(3L)29A6/Df(3L)DocA embryos, with one copy each of Doc2 and Doc3 and no Doc1, have a reduced number of cardioblasts (Fig. 5B; compare with 5A). Although all types of cardioblasts are affected, the number of Doc-positive cardioblasts is most strongly reduced, and not all of the residual svp-lacZ-positive cells retain Doc expression (Fig. 5B and data not shown, compare also with Fig. 3J). If one copy of tin or pnr is removed in Df(3L)29A6/Df(3L)DocA background, even fewer cardioblasts are specified, which frequently causes gaps in the dorsal vessel (Fig. 5C,D). This synergistic effect becomes very strong in Df(3L)29A6/Df(3L)DocA pnr^{VX6} tin^{466} embryos, in which less than half the normal number of cardioblasts are formed (Fig. 5E). However, if only one Doc gene copy (Doc1) is removed, the reduction of one copy of pnr and tin has only mild effects (Df(3L)29A6/pnr^{VX6} tin^{466}; Fig. 5F). Odd-pericardial cells and the lymph glands are also strongly reduced in Df(3L)29A6/Df(3L)DocA pnr^{VX6} tin^{466} embryos, suggesting that Doc interacts with pnr and tin already early during the specification of the cardiac mesoderm (Fig. 5H; compare with 5G). The impact on Eve-pericardial cells is much weaker (data not shown), which is consistent with the observation that these cells are not affected upon complete loss of the Doc genes in DocA mutants. These observations indicate that Doc genes, tin and pnr cooperate or depend on each other during the specification of cardiac progenitors.

**Activation of pnr and maintenance of tin expression are major functions of Dorsocross during early cardiogenesis**

The above-described expression patterns, phenotypes and genetic interactions among Doc, pnr and tin raise the possibility that Doc functions by activating or maintaining the expression of pnr and tin. tin and pnr expression in the cardiac mesoderm are also interdependent (Gajewski et al., 2001; Alvarez et al., 2003; Klinedinst and Bodmer, 2003), hence the reduced expression of either tin or pnr would reduce the products of both genes. In DocA mutants, Tin protein distribution appears normal until mid-stage 11, during which tin expression is activated from the dpp- and tin-dependent tinD enhancer (Fig. 6B; compare with 6A) (Xu et al., 1998). Accordingly, reporter gene expression driven by the tinD enhancer also appears to be normal (Fig. 6F), and tinD-GAL4 can be used to rescue cardioblast specification via UAS-Doc transgenes (see Fig. 3M). By contrast, cardioblast-specific expression of tin driven by the tinC enhancer version tinC\Delta7 (active in all cardioblasts) (Lo and Frasch, 2001) is never detected (data not shown). This is consistent with the observation that progressively fewer Tin-positive cells are present in Doc mutants after mid-stage 11, in which tin expression is maintained at high levels only in cells that express eve (Fig. 6D; compare with 6C). Of note, the number of the Eve-positive cells is increased from 3-4 to 6-10 cells per cluster at mid-stage 11 (Fig. 6B; compare

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**Fig. 4. Effects of Dorsocross mutation on pericardial cell and dorsal somatic muscle formation.** (A) Lateral view of stage 14 control embryo that carries the amnioserosa rescue constructs c381-GAL4/UAS-Doc2, but is otherwise wild type. Staining for Zfh-1, Odd and Eve allows discrimination of lymph gland (LG) and Odd-pericardial cells (Odd-PC) (yellow, Odd^+ + Zfh-1^+) from Eve-pericardial cells (Eve-PC, purple, Eve^+ + Zfh-1^+) and from pericardial cells that express only Zfh-1 (Tin-PC and other tissues, red). Odd is also expressed in ectodermal stripes (green), and Eve in DA1 (#1) muscles (blue). (B) *DocA* mutant embryo with amnioserosa rescue constructs stained as in A. Odd^+ pericardial and lymph gland cells as well as the great majority of Tin-PCs are absent, while Eve-PCs and DA1 muscles are present. (C,D) Expression of the dorsal muscle marker proteins Eve (red) and Runt (green) in stage 14 embryos carrying amnioserosa rescue constructs. In control embryos (C), Eve is present in the nuclei of DA1 muscles and pericardial cells (Eve-PC, red) and Runt in DO2 (#10) muscles. In amnioserosa-rescued homozygous DocA mutants (D) muscles DA1 and DO2 are largely unaffected. Ectodermal cut (ect) is dorsally expanded owing to the function of Doc in the dorsolateral ectoderm. (E,F) Anti-β-Galactosidase staining of stage 16 embryos carrying the 1010 B2-lacZ-reporter gene to visualize nuclei of dorsal muscles. (E) Wild-type embryo (dorsal view) with multinucleated dorsal muscles. (F) Homozygous DocA mutant embryo showing the presence of dorsal muscles, albeit distorted owing to the morphogenetic defects of these embryos.
Dorsocross genes control early cardiogenesis

with 6A). The broadened eve expression is only transient; it persists until stage 12 (Fig. 6D; compare with 6C) but at later stages nearly normal numbers of Eve-pericardial cells and lineage-related muscles (muscles #1/DA1 and #10/DO2) are present (see Fig. 4B,D).

In the wild type, mesodermal pnr expression starts later and in a more restricted domain when compared with tinD-driven tin expression. In DocA mutants we found that pnr is
not activated at all in the dorsal mesoderm, whereas its expression in the dorsal ectoderm is normal (Fig. 6F). We conclude that the Doc genes act upstream of pnr during a very early step in the specification of the cardiac mesoderm. As pnr is crucial for downstream events of cardiac specification, including the cardioblast-specific expression of mid, H15, tin and Doc, it is conceivable that many of the functions of Doc in cardioblast specification are mediated through pnr. We addressed this possibility by expressing pnr in the DocA mutant background. Restoring Pnr in the dorsal mesoderm of Doc-null mutants via tinD-GAL4 and UAS-pnr is sufficient to rescue cardioblasts, which are identified as mid mRNA/Tin double-positive cells (Fig. 7C; compare with Fig. 7A,B) and with Mef2-HtΔD-lacZ (data not shown). The degree of rescue is not as high as with UAS-Doc2 (Fig. 7E), but at least as efficient as that with UAS-Doc3 (Fig. 7F). In an analogous experiment with UAS-tin, only very few mid-positive cells are detected (Fig. 7D), although their number appears still slightly higher as compared with DocA mutant controls (Fig. 7B). The observation of rescued cardioblasts and Odd-PCs (data not shown) in DocA mutants with ectopic Pnr in the mesoderm supports the notion that one of the major functions of Doc is the activation of pnr in the presumptive cardiac mesoderm. However, the failure of pnr to rescue Doc phenotypes fully indicates that Doc also functions in parallel with Pnr, for example, by synergizing with Pnr at common target enhancers, or that Doc activates additional targets that contribute to normal cardioblast development.

**Ectopic Doc2 promotes cardioblast cell fates in conjunction with tin and pnr**

Given the observed requirement of Doc genes for cardioblast specification, we also asked whether misexpression of Doc can produce ectopic cardioblasts. Ectopic expression of Doc2 with tinD-GAL4, a driver that is active in the dorsal mesoderm at stage 11-12 when Doc also functions in normal embryos, leads to formation of some additional cardioblasts (as monitored by co-expressed Mef2 protein and mid RNA; Fig. 8B, compare with 8A). Conversely, the number of Odd/Zfh1-positive pericardial cells is reduced, whereas the Eve-positive pericardial cells and dorsal muscles are less affected (Fig. 8J, compare with 8I). The number of extra cardioblasts is lower than the number of missing pericardial cells. In addition, the nuclei of the somatic mesoderm in dorsolateral areas are arranged irregularly. Together, these observations indicate that ectopic Doc2 can transform some pericardial and/or dorsal muscle progenitors into cardioblasts, although more frequently it disrupts the development of these progenitors without transforming them.

As the observed genetic interactions suggest a synergistic action of Doc with tin and pnr, we asked whether combined expression of Doc2 with tin and pnr would increase the efficiency of generating ectopic cardioblasts. Ectopic expression of pnr alone in the entire mesoderm has been reported to increase cardioblast numbers (Gajewski et al., 1999), but with the more restricted and slightly weaker driver tinD-GAL4, we find only few extra cardioblasts (data not shown). No increase in cardioblast number was seen in embryos in which only tin is overexpressed (data not shown), but co-expression of tin and pnr produces more cardioblasts than pnr alone (Fig. 8C). Although this increase in cardioblasts is similar to that of Doc2 expression, the numbers of pericardial cells are only slightly reduced (Fig. 8K). If Doc2 is expressed together with tin or pnr, or with both, large numbers of extra cardioblasts are formed (Fig. 8D,E,F). Combined expression of Doc2 and pnr consistently produces more cardioblasts than expression of Doc2 and tin, and nearly as many as the triple co-expression of Doc2, pnr and tin, under which conditions cardioblast numbers are roughly doubled.

Broader ectopic expression of Doc2, via the early pan-mesodermal driver 2xPE-twi-GAL4, causes even stronger expansion of early cardioblast markers such as mid, H15, Toll305-clacZ and tinCΔ7-lacZ in the mesoderm of stage 12-13 embryos (data not shown) (Wang et al., 2005). However, even under these conditions, the effects tend to be stronger in dorsal areas of the mesoderm, suggesting that Doc cooperates with other dorsally localized activities to promote cardioblast fates. Likely candidates include tin and pnr, because the combined ectopic expression of Doc2, tin and pnr causes widespread ectopic cardioblast formation (Fig. 8H; compare with 8G) to a much greater extent than compared with Doc2 alone or the combination of tin plus pnr (data not shown).
Dorsocross genes control early cardiogenesis

(Klinedinst and Bodmer, 2003). However, twi-driven Doc2 by itself is sufficient to repress the visceral mesoderm markers bagpipe (bap) and biniou (bin) (data not shown).

Altogether, the ectopic expression data suggest that Doc genes synergize with pnr, and to some degree tin, in promoting cardioblast formation. Although the loss-of-function data show that Doc activity is required for the formation of both cardioblasts and Eve-negative pericardial cells, ectopic expression of Doc, especially in combination with pnr and tin, appears to transform these types of pericardial cells into cardioblasts. This may indicate that, after their initial role in generating progenitors of both cardioblasts and Eve-negative pericardial cells, Doc genes exert a second role in promoting cardioblast versus pericardial cell identities.

Discussion

In vertebrate species, genetic studies with loss-of-function alleles have implicated Tbx1, Tbx2, Tbx5 and Tbx20 in the control of heart morphogenesis and the regulation of cardiac differentiation markers (Basson et al., 1997; Li et al., 1997; Bruneau et al., 2001; Jerome and Papaioannou, 2001; Lindsay et al., 2001; Merscher et al., 2001; Garrity et al., 2002; Harrelson et al., 2004; Brown et al., 2005; Cai et al., 2005; Singh et al., 2005; Stennard et al., 2005). In the case of Tbx5, a small number of cardiac differentiation genes have been identified as direct downstream targets (reviewed by Plageman and Yutzey, 2005). However, owing to the complexity of the system, the respective positions of these genes within a regulatory network during early cardiogenesis are still poorly understood.
Drosophila offers a simpler system to study regulatory networks in cardiogenesis. Recently, the Tbx20-related T-box genes mid and H15 were shown to play a role in cardiac development downstream of the early function of the NK homeobox gene tin and the Gata gene pannier (pnr) (Miskolczi-McCallum et al., 2005; Qian et al., 2005; Reim et al., 2005). Whereas the role of these genes in the morphogenesis of the cardiac tube is minor, they are involved in processes of cardiac patterning and differentiation during the second half of cardiogenesis, which includes the activation of tin expression in myocardial cells (Reim et al., 2005). In our present report, we have characterized the roles of the Tbx6-related Dorsocross T-box genes (which may actually have arisen from a common ancestor of the vertebrate Tbx4, Tbx5 and Tbx6 genes) (Reim et al., 2003), in Drosophila cardiogenesis. We have shown that the Doc genes have a fundamental early role that is required for the specification of all cardiac progenitors that generate pure myocardial and pericardial lineages. They are not required for generating dorsal somatic muscle progenitors and lineages with mixed pericardial/somatic muscle, even though their early expression domains also include cells giving rise to these lineages.

The new information on the regulation and function of Doc fills a major gap in our understanding of early Drosophila cardiogenesis. Previous data have shown that the combinatorial activities of Wg and Dpp are required for the formation of both myocardial and pericardial cells (Frash, 1995; Wu et al., 1995; Carmena et al., 1998). In addition, the homeobox gene even-skipped (eve) is a direct target of the combined Wg and Dpp signaling inputs in specific pericardial cell/dorsal somatic muscle progenitors (Halfon et al., 2000; Knirr and Frasch, 2001; Han et al., 2002). Our current data identify the Doc genes as downstream mediators and potential direct targets of combined Wg and Dpp signals during the induction of myocardial and Eve-negative pericardial cell progenitors. The induction of Doc expression by Wg and Dpp occurs concurrently with the induction of tin by Dpp alone, at a time when the mesoderm still consists of a single layer of cells (Fig. 9). As a result, tin and Doc are co-expressed in a segmental subset of dorsal mesodermal cells that include the presumptive cardiogenic mesoderm. Conversely, in the intervening subset of dorsal mesodermal cells (the presumptive visceral mesoderm precursors) tin is co-expressed with bagpipe (bap) and binio (bin), which are negatively regulated by Wg via the Wg target sloppy paired (slp) (Lee and Frasch, 2000; Zaffran et al., 2001). Ultimately, these shared responses to Dpp, differential responses to Wg and the specific genetic activities of Doc versus bap and bin lead to the reciprocal arrangement of cardiac versus visceral mesoderm precursors in the dorsal mesoderm (Zaffran et al., 2002; Lee et al., 2004).

Although the Dpp signaling pathway (and likewise, the Wg pathway) is activated in both ectodermal and mesodermal germ layers, tin and bap respond to it only in the mesoderm. We have recently shown that the germ layer-specific response of these genes to Dpp relies on two probably interconnected mechanisms. The first of these involves the additional requirement for Tin protein as a mesodermal competence factor for Dpp signals, which is initially produced in the mesoderm downstream of twist. The second involves the specific repression of the responses of tin and bap to Dpp in the ectoderm by yet unidentified factors that bind to the Dpp-responsive enhancers of these two genes (Xu et al., 1998; Lee and Frasch, 2005). By contrast, the Doc genes are induced by Dpp and Wg with the same spatial and temporal expression patterns in both germ layers. This implies that the (yet unknown) Dpp and Wg-responsive enhancer(s) of the Doc genes are not subject to the ectodermal repressor activities acting on the tin and bap enhancers, and fits with the
observation that induction of Doc in the mesoderm does not require Tin as a mesodermal competence factor. However, because of the distinct roles of Doc in the ectoderm and mesoderm (Reim et al., 2003) (present study), this situation also implies that Doc must act in combination with germ layerspecific co-factors to exert its respective functions. Our data suggest that, in the early mesoderm, Doc acts in combination with tin.

A key gene requiring combinatorial Doc and Tin activities for its activation in the cardiac mesoderm is the Gata factor-encoding gene pannier (pnr) (Fig. 9). pnr expression is activated in the cardiac mesoderm shortly after the induction of Doc and tin, at a time when Doc expression has narrowed to the mesodermal precursors giving rise to pure cardiac lineages. The mechanisms restricting Doc expression to the cardiac mesoderm are currently not known, but as a consequence, pnr expression is also limited to the cardiac mesoderm. It is conceivable that Doc receives continued inputs during this period from the ectoderm through Dpp, whose expression domain narrows towards the dorsal leading edge by then (as was proposed for pnr) (Klinedinst and Bodmer, 2003). Together with the observed feedback regulation of pnr on tin and Doc, this situation leads to a prolonged co-expression of Tin, Doc and Pnr in the cardiac mesoderm of stage 11 to stage 12 embryos. Based upon the onset of the expression of early markers such as mid and svp, this is precisely the period when cardiac progenitors become specified.

We anticipate that the activation of some downstream targets in presumptive cardiac progenitors requires the combination of two, or perhaps all three, of these cardiogenic factors. Potential target genes include mid, svp and hand. However, none of these candidates is essential for generating cardiac progenitors, although mid and svp are known to be required for the normal diversification of cardioblasts within each segment.

Our observation that forced expression of Pnr in the absence of any Doc partially rescues cardiogenesis could indicate that the early, combinatorial functions of tin and Doc are primarily mediated by pnr. Alternatively, or in addition, this observation and the fact that a few cardioblasts can be generated without Doc could point to the existence of some degree of functional redundancy among these three factors. In the context of the latter possibility, it is tempting to speculate that the functional redundancy among T-box, Nkx and Gata factors during early cardiogenesis has further increased during the evolution of the vertebrate lineages. This would explain the less dramatic effects of the functional ablation of Tbx5, Nkx2-5 and Gata4/5/6 on vertebrate heart development (reviewed by Harvey, 1996; Peterkin et al., 2005; Plageman and Yutzey, 2005) as compared to the severe effects of Doc, tin or pnr mutations on dorsal vessel formation in Drosophila. Like the related Drosophila genes, these vertebrate genes are co-expressed in the cardiogenic region and developing heart of vertebrate embryos, which at least for Nkx2.5 and Gata6 also involves cross-regulatory interactions that reinforce their mutual expression (Molkentin et al., 2000) (reviewed by Bruneau, 2002).

The observed co-expression of Doc, Tin and Pnr allows for the possibility that, in addition to combinatorial binding to target enhancers, protein interactions among these factors play a role in providing synergistic activities during cardiac specification. Physical interactions of Tbx5 with Gata4 and Nkx2-5, as well between Nkx2-5 and Gata4 in vitro as well as synergistic activities cell culture assays have been demonstrated in mammalian systems and may be relevant to human heart disease (Durocher et al., 1997; Bruneau et al., 2001; Hiroi et al., 2001; Garg et al., 2003) (reviewed by Bruneau, 2002). In Drosophila, the genetic interactions between Doc, tin and pnr observed both in loss- and gain-of-function experiments reveal similar synergistic activities of the encoded factors during early cardiogenesis. Altogether, our observations make it likely that these Drosophila factors also act through combinatorial DNA binding and mutual protein interactions to turn on target genes required for the specification of cardiac progenitors.

Whereas pnr is expressed only transiently during early cardiogenesis, tin and Doc continue to be expressed in developing myocardial cells, suggesting that they act both in specification and differentiation events. We recently showed that the T-box gene mid is required for re-activating tin in cardioblasts (Fig. 9) (Reim et al., 2005). Of note, owing to the action of svp, Doc and tin are expressed in complementary subsets of cardioblasts within each segment (Lo and Frasch, 2001). This mutually exclusive expression of tin and Doc implies that they are not acting combinatorially but, instead, act differentially during later stages of myocardial development. Hence, their activities could result in the differential activation of some differentiation genes such as Sulfonylurea receptor (Sur), which is specifically expressed in the four Tin-positive cardioblasts in each hemisegment (Nasonkin et al., 1999; Lo and Frasch, 2001), and wingless (wg), which is only turned on in the two Doc-positive cells in each hemisegment of the heart that generate the ostia (Lo et al., 2002). Surprisingly, even the activation of some genes that are expressed uniformly in all cardioblasts has turned out to result from differential regulation within the Tin-positive versus Doc-positive cardioblasts. For example, regulatory sequences from the Mef2 gene for the two types of cardioblasts are separable and those active within the four Tin-positive cells are directly targeted by Tin (Gajewski et al., 1997; Cripps et al., 1998; Nguyen, 1998; Gajewski et al., 2000). Likewise, regulatory sequences from a cardioblast-specific enhancer of Toll have been shown to receive differential inputs from Doc and Tin, respectively, in the two types of cardioblasts (Wang et al., 2005). In parallel with this differential regulation, we anticipate that yet unknown differentiation genes are activated uniformly in all cardioblasts downstream of mid/H15 and hand. The integration of the new information on the roles of Doc in cardiogenesis has now provided a basic framework of signaling and gene interactions through all stages of embryonic heart development, which in the future can be further refined upon the identification of new components and additional molecular interactions.

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