**The Dichaeate gene of Drosophila melanogaster encodes a SOX-domain protein required for embryonic segmentation**

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**SUMMARY**

We have cloned and characterised a member of the High Mobility Group superfamily of genes from Drosophila, Sox70D, which is closely related to the mammalian testis determining gene SRY. Sox70D corresponds to the dominant wing mutation Dichaeate. Homozygous deletions of the Sox70D gene and recessive lethal Dichaeate alleles have a variable embryonic segmentation phenotype. Dichaeate is expressed in early embryos in a dynamic pattern reminiscent of gap and pair-rule genes and is required for the appropriate expression of the primary pair-rule genes even skipped, hairy and runt. The molecular nature of Dichaeate and its expression pattern during early embryogenesis suggest that the gene plays a key role in early development; the variability in both the segmentation phenotype and the effects on pair-rule gene expression suggests that this role is to support the transcriptional regulation of key developmental genes rather than directly regulate any one of them.

Key words: Sox70D, Dichaeate, pair-rule, gene regulation, segmentation, Drosophila

**INTRODUCTION**

The transcriptional regulation of eukaryotic genes during development is a dynamic process which requires the regulated assembly of multiprotein complexes at promoter and enhancer elements (Tjian and Maniatis, 1994). For example, early zygotic gene expression in the Drosophila embryo occurs in a syncytial environment and the enhancer elements that regulate the transcription of segmentation genes respond to gradients of transcription factors (Driever and Nüsslein-Volhard, 1988), resulting in the expression of segmentation genes in very precise temporal and spatial domains (Pankratz and Jackle, 1993 for review). Thus the regulation of segmentation gene expression provides an attractive system for the study of enhancer protein/DNA complexes and the elucidation of a molecular description of developmental gene regulation.

In Drosophila the genetic and subsequent molecular analysis of embryonic segmentation has identified a number of key transcriptional regulators that function in segmentation (Akam, 1987). The success of this approach relied upon the identification of mutations with unambiguous phenotypes which delete specific subsets of the body plan. These studies led to a model in which the embryo is progressively subdivided along the anterior-posterior axis by a hierarchy of regulatory genes (Nüsslein-Volhard and Wieschaus, 1980). Briefly, the products of maternal coordinate genes generate broad domains of zygotic gap gene expression. The products of the gap genes, along with the maternal coordinate genes, regulate the expression of the primary pair-rule genes in a characteristic seven-stripe pattern. The primary pair-rule and gap genes control the expression of secondary pair-rule genes and a combination of these factors generate the single segment expression of the segment polarity genes.

In the case of the primary pair-rule genes even skipped (eve) and hairy (h), it has been shown that the seven-stripe expression of these genes is generated by transcriptional regulators which act at enhancer elements specific for each stripe (Goto et al., 1989; Riddihough and Ish-Horowicz, 1991). The regulatory elements for each of these genes are large and extend for several kb upstream of the transcriptional start sites. Here we describe a Drosophila gene, Sox70D, which encodes a member of the recently characterised family of SOX domain proteins, that is implicated in the regulation of pair-rule genes. The SOX domain is a sequence-specific DNA-binding domain found in those proteins of the High Mobility Group (HMG) superfamily, which are closely related to the mammalian sex determining factor SRY (Sinclair et al., 1990). Several genes containing this motif have been implicated in a variety of developmental processes from organisms as diverse as man and yeast (Laude et al., 1993). One striking feature of HMG domain proteins is their ability to bend DNA upon binding (Ferrari et al., 1992; Giese et al., 1992). Moreover, two SOX domain proteins from mouse, SOX2 and LEF-1, have been shown to be unable to activate transcription on their own; they must act in concert with other enhancer binding proteins (Travis et al., 1991; Yuan et al., 1995). This has led to the suggestion that SOX domain proteins have an architectural role (Grosschedl et al., 1994). We show that Sox70D corresponds to the Dichaeate (D) gene and that the striking features of null mutations in D are...
the variability of their phenotypes and their variable effects on the expression of other segmentation genes. This suggests that the gene has a supporting role in regulating the expression of key developmental genes during segmentation.

**MATERIALS AND METHODS**

**Drosophila stocks**

*Drosophila* stocks and crosses were maintained on standard yeasted cornmeal-agar food at 25°C. Mutant nomenclature is as described (Lindsley and Zimm, 1992, FlyBase, 1996). In line with FlyBase nomenclature gene symbols are designated with lower case italics and their mRNA by upper case italics. D1, D2, D4 and Df(3L)fz-GS1a are described in Lindsley and Zimm (1992). The remaining chromosomes have been generated in this laboratory and will be described elsewhere (S. R. H. Russell and others, unpublished data). Df(3L)fz-GS1a all delete the Sox70D gene and two other complementation groups, l(3)70Da and deviner; neither of these other loci have segmentation defects and both fully complement all lethal D alleles.

**Molecular biology**

Genomic clones were isolated from a λGem11 library and cDNA clones from a λZapII prepupal cDNA library (a gift of P. Hurban). Northern blots were generated from poly(A)+ mRNA separated on agarose-formaldehyde gels and probed with random primed Sox70D cDNA. All were carried out with minor modifications to standard techniques (Sambrook et al., 1989). A 4 kb HindIII genomic fragment encompassing the gene and a 1.8 kb cDNA clone corresponding to the Sox70D transcription unit were sequenced on both strands using a Sequenase-2 kit according to the manufacturer’s instructions. In situ hybridisation to embryos was carried out using minor modifications to standard techniques (Tautz and Pfeifle, 1989). DNA probes for ftz, h and run were a gift from D. Ish-Horowicz and for eve a gift from A. Brandt. Grasshopper anti-EVE was a gift from N. Patel (Patel et al., 1992) and was used with minor modifications to the procedure of Kushiton et al. (1995).

**Transgenic flies**

To construct transgenic flies containing the Sox70D gene, a full-length cDNA was cloned into the EcoRI site of the pCaSpeR-HS vector under the control of the Hsp70 promoter. The construct was injected into y w embryos using standard techniques (Karess, 1985). In the experiments described, flies carrying three or four copies of the transgene, homozygous for inserts on both the X and second chromosomes, were used. For heat-shock experiments, embryos were collected from rapidly laying population cages for 30 minutes or 60 minutes and allowed to age for 2½ hours or 2 hours, respectively. The embryos were collected onto Niteau gauze and placed in a water bath at 36.5°C for 5 minutes or 30 minutes; they were then placed in a 25°C water bath for 15 minutes to recover. Embryos were dechorionated in 50% commercial bleach for 2 minutes and fixed for in situ hybridisation as before. Wild-type embryos were processed in parallel. The material from six consecutive collections was pooled and processed for in situ hybridisation, then divided and hybridised with appropriate probes.

**Developmental biology**

Embryonic staging was according to Campos-Ortega and Hartenstein (1985). For cuticle preparations, embryos were dechorionated in 50% commercial bleach, devitellinised in 1:1 heptane:methanol, washed with methanol and then 0.1% Triton X-100 and mounted in 3:1 Hoyer’s:lactic acid medium. Embryos were cleared overnight at 65°C and viewed with dark-field optics.

**RESULTS**

**Isolation of a Drosophila SOX box gene**

We identified a *Drosophila* SOX box gene using a PCR product amplified from *Drosophila* genomic DNA with SRY specific primers (a gift of P. Koopman and R. Lovell-Badge). The PCR product was used to isolate clones from *Drosophila* genomic and cDNA libraries which correspond to a single copy gene that maps to 70D1-2 on the left arm of chromosome 3. Sequence analysis of cDNA and genomic clones reveals a single transcription unit of 1800 nucleotides without introns (a feature of some mammalian SOX genes (Colligon et al., 1996)) that would encode a protein of 382 amino acids. Within the predicted protein sequence, there is a 76 amino acid stretch with 88% identity (92% similarity) to the DNA-binding domain of SOX2 proteins from human, mouse and chicken (Colligon et al., 1996; Kamachi et al., 1995; Stevanovic et al., 1994) (Fig. 1). This extraordinary degree of sequence conservation suggests that the *Drosophila* protein may bind the same, or very similar, DNA sequences as SOX2. Outside of the DNA-binding domain there is no similarity to other proteins in the database, although there is a 30 amino acid stretch at the C-terminal end with limited similarity to a potential SOX2 activation domain (Kamachi et al., 1995).

**SOX70D expression in the embryo is dynamic**

The expression of the SOX70D transcript was characterised by northern blotting and whole-mount in situ hybridisation to embryos. A single 1800 nucleotide transcript, consistent with the length of the cDNA clone, is expressed at high levels during early embryogenesis and thereafter at very low levels through the remainder of the life cycle (Fig. 2). The temporal and spatial profile of expression in the early embryo is dynamic (Fig. 3). Zygotic expression is initiated late in stage 4 as a broad central domain which is rapidly followed by the appearance of an anterior domain. We do not detect transcripts prior to nuclear cycle 10, suggesting little or no maternal contribution of transcript. As cellularisation proceeds, the central domain splits and is resolved ventrally into seven stripes while dorsally it remains continuous. By the end of stage 5, the six anterior stripes and the dorsal expression have faded but the most posterior stripe remains strong. During stage 6, the posterior stripe follows the pole cells as the germ band extends and eventually fades as the pole cells are internalised at the amnioproctodeal invagination. Concomitantly, expression is initiated in a region of the neuroectoderm which will give rise to the CNS. The neuromere based expression is transiently observed as fourteen discrete stripes, which rapidly expand to become a continuum along the length of the germ band. Later in development expression is prominent in the nervous system (N. S., S. R. H. R., M. A. and Susana Romani, unpublished data). The early pattern of expression is reminiscent of many of the genes involved in segmentation, from an initial gap-like domain, through seven and then fourteen stripes; this suggests that the gene plays a role in segmentation.

**Sox70D corresponds to the Dichaete gene**

The dominant wing mutation *Dichaete* (*D*) maps to the 70D1-2 region (Bridges and Morgan, 1923) and was used as the starting point for our analysis. The dominant *D* phenotype corresponds to misexpression of *SOX70D* since it is ectopically
expressed in the wing imaginal discs of all dominant D alleles; moreover, dominant wing mutations, with phenotypes similar to those of D alleles, can result from ectopic expression of SOX70D induced in enhancer trapping experiments (S. R. H. R., Adelaide T. C. Carpenter and M. A., unpublished data). Three D alleles were available at the outset of this work; we have generated six new alleles by X-ray mutagenesis. Seven of the nine D alleles have associated recessive lethal phenotype that maps to 7D1-2; the two that do not are the spontaneous In(3L)D2 and the X-ray-induced Df(3L)D3. One allele, D9, is recessive but has no dominant phenotype. In five of the seven lethal alleles, early embryonic SOX70D expression is severely reduced (D5, D9) or altered (D3, D6, D10) (Fig. 4). In D6, D3 and D10, the anterior domain never forms and the central domain into seven stripes is abnormal and does not reach wild-type levels. Moreover, wild-type levels of expression are never observed. Later in development, SOX70D expression in the nervous system is also disrupted in D alleles (not shown). We have not detected disruptions of the early expression of SOX70D in the remaining two lethal alleles (D4, D7); however, both are chromosome translocations and half of the embryos are grossly aneuploid, which makes whole-mount preparations very difficult to analyse. All D alleles are chromosome aberrations and their relationship to the Sox70D gene has been determined by in situ hybridisation to polytene chromosomes and by Southern blotting. We have localised breakpoints in three D alleles close to the gene (Fig. 5); the remainder map more than 10 kb distal to the 3’ end of Sox70D. All lethal D alleles have breakpoints 3’ to the Sox70D transcription unit whereas the two viable alleles (D4, D7) have breakpoints 5’ (Fig. 5). D7, a spontaneous partial revertant of D1 (Plunkett, 1926), shares the D1 breakpoint as well as an additional DNA lesion close to the 3’ end of Sox70D. In this allele over a deficiency for the region, SOX70D expression prior to embryonic stage 6 is barely detectable (Fig. 4B,C). Taken together, these data suggest that D corresponds to the Sox70D gene and that the recessive lethality associated with D alleles is a result of regulatory mutations that reduce SOX70D expression in the embryo. Here we focus on the lethal phenotype of D and show that the gene has a role in segmentation.

Dichaete mutations have a segmentation phenotype

The embryonic phenotype of lethal alleles was examined in cuticle preparations. In In(3L)D/Df(3L)D-5rv6 (D3/Df) and also in D’ embryos generated from the overlapping deficiencies Df(3L)D-1rv16/Df(3L)JFz-GS1a (not shown), we observe variable segmentation defects, which include deletions removing half of the segments as well as weaker partial deletions and also segment fusions; in all cases, even numbered metameres are more often affected (Fig. 6B-D). There are also variable defects in head development. In D' embryos, 56% of mutants have a strong segmentation phenotype and 44% have intermediate or weak phenotypes (135/350 embryos examined from crosses between balanced deficiency stocks have a mutant phenotype). In D3/Df, 51% of mutant embryos show strong segmentation phenotypes, the remainder being intermediate or weak (n=412 embryos, 111 with a mutant phenotype). D3/Df is therefore close to the null condition for the gene as far as the segmentation defects are concerned and has been used in subsequent experiments as such. Other alleles, in which SOX70D expression is reduced but not absent, show weak segmentation defects in approximately half of the expected mutant embryos and most often these are segment fusions; here again even numbered metameres are most frequently affected (Fig. 6E,F). It is important to emphasise the variability in the phenotype; in both D3/Df and the overlapping deletions, a range of phenotypes is observed, indicating that the gene may be acting as a supporting rather than a specific factor in segmentation.

Pair-rule gene expression is disrupted in Dichaete mutants

The effects of lethal D mutations on segmentation was further characterised by analysing the expression of a number of key genes in the segmentation pathway. Expression of the gap genes, Krippel, knirps and giant, was normal in D3/Df, indicating that D acts downstream or in parallel with these gap genes. With the pair-rule genes, however, we find strong, but
variable, effects on expression. We have focused on the so-called primary pair-rule genes even-skipped (eve), hairy (h) and runt (run) since these are thought to be the earliest acting of this class (Howard and Ingham, 1986). In all three cases, we observe reductions in the levels of expression at syncytial blastoderm, a time when these genes are strongly expressed in seven-stripe domains in wild-type embryos (Fig. 7).

In the case of EVE, the weakest effects are reduced expression of stripe 5 while the strongest effects abolish most of the dorsal expression in stripes 2 through 6 and slightly disrupt the spacing of ventral stripes. Stripes 1 and 7 appear not to be affected. In the case of HAIRY, stripes 4, 5 and 6 are most affected with stripes 3 and 7 less so; again dorsal effects are more pronounced than ventral. With RUN, stripes 2, 5 and 6 are most frequently affected, 4 and 7 less so with 1 and 3 rarely affected. These patterns of pair-rule gene expression are never observed in wild-type embryos and do not resemble the temporal evolution of the stripe patterns. Again, we emphasise the variability of the effects of these genes; there is no single stripe in any of these phenotypes that is always affected. We also examined the expression of the fushi tarazu (ftz) gene in the same genotype. In this case, the defects appear more general; we find a reduction in the intensity of all seven stripes with some stripes more severely affected. Since the stripes of pair-rule gene expression generally occur in the correct anterior-posterior position in D- embryos, the gene is unlikely to provide key positional information; it is more likely to be required in the maintenance or establishment of appropriate levels of pair-rule gene expression in the central region of the embryo.

**Ectopic expression of SOX70D disrupts pair-rule gene expression**

To support the hypothesis that loss or reduction of SOX70D expression is responsible for both the alterations in pair-rule gene expression and the segmentation defects observed in lethal D combinations, we constructed transgenic flies containing a full-length copy of the Sox70D cDNA regulated by the Hsp70 promoter. None of the lines generated rescue the lethality of D alleles. We have used these transgenes to study the effects of ectopic SOX70D early in embryonic development in a wild-type background. These experiments assay direct effects of SOX70D on target genes, since the time between the heat shock and fixation is short and would not permit the action of a secondary factor induced by SOX70D (Manoukian and Krause, 1992). The heat-shock-induced SOX70D transcripts are very unstable; ectopic transcripts disappear within 15 minutes of a five minute heat shock (not shown). Two heat-shock regimes were used to assess the effects of ectopic SOX70D early in embryonic development in a wild-type background. These experiments assay direct effects of SOX70D on target genes, since the time between the heat shock and fixation is short and would not permit the action of a secondary factor induced by SOX70D (Manoukian and Krause, 1992). The heat-shock-induced SOX70D transcripts are very unstable; ectopic transcripts disappear within 15 minutes of a five minute heat shock (not shown). Two heat-shock regimes were used to assess the effects of ectopic SOX70D. In the first, a 5 minute heat shock of 2 to 3 hour old embryos was followed by 15 minutes recovery and then fixation. There is no consistent effect on the expression of EVE or FTZ. With RUN and HAIRY probes, however, there are reproducible alterations in expression (Fig. 8A-D). In both cases, there is precocious expression of normal wild-type
3673 Dichaete gene of Drosophila encodes a SOX-domain protein

features. In the case of RUN, the transition from seven to fourteen stripes occurs earlier than in wild-type controls. The appearance of fourteen RUN stripes normally occurs during stage 6 (Klingler and Gergen, 1993); in the Hs-Sox70D embryos, this occurs during late stage 5. 65% of late stage 5/early stage 6 heat-shocked Hs-Sox70D embryos have initiated expression of RUN between the seven primary stripes (n=129) compared with 25% of heat-shocked wild type (n=83). With HAIRY almost all embryos have a patch of dorsal expression posterior to the seventh stripe and show a posterior expansion of the HAIRY anterior domain; 93% (n=112) of late stage 5/early stage 6 heat-shocked Hs-Sox70D embryos compared to 10% (n=71) of wild-type controls. These patches of expression normally appear during stage 7 (Hooper et al., 1989, Ingham et al., 1985). Thus short pulses of ectopic SOX70D early in development result in subtle, but reproducible, effects on the expression of a subset of pair-rule genes.

Since the effects of short heat shocks were subtle, the level of SOX70D was increased by giving a 30 minute heat shock to embryos 2 to 3 hours old. In these experiments, the longer egg collection allowed an analysis of the effects of ectopic SOX70D both before and after gastrulation. Here over 90% of embryos heat shocked before gastrulation exhibit severe disruptions in the expression patterns of all three primary pair-rule genes (n>100 in all cases; Fig. 8E-G). Specifically, we observe posterior expansion of the seventh stripe and repression of the central fourth stripe with EVE, HAIRY and RUN. In addition, there is a high level of ectopic expression of both HAIRY and RUN between the second and third stripes as well as other, more variable, patches of expression between stripes. These effects are never observed in heat-shocked wild-type controls and do not reflect any wild-type pattern of expression. In heat-shocked wild-type embryos, there are no obvious effects on EVE; with HAIRY 50% of embryos fail to resolve stripes 3 and 4 and with RUN 40% of embryos show a reduction in stripe 2.

We have also examined FTZ expression in Hs-Sox70D embryos. All of the stripes appear to be equal in size and intensity; however, the most posterior stripe is shifted posteriorly by 3-4 cells in over 90% of embryos. There are no obvious effects on wild-type embryos (Fig. 8H). This observation confirms that we are examining a direct effect of SOX70D since the effects on FTZ are subtle and are not those that would be expected if the aberrantly expressed primary pair-rule genes had time to affect FTZ expression.

In those embryos that had begun gastrulation before the heat shock, the expression of the pair-rule genes is more or less normal, indicating that SOX70D can only influence transcription of the pair-rule genes early in development (not shown). A proportion of embryos from the heat-shock experiments
were allowed to develop and their cuticle phenotypes examined. After a 5 minute heat shock, there is a low level of weak segmentation defects. After a 30 minute heat shock, 65% of embryos show strong segmentation defects very similar to those of strong D alleles; this frequency approximates the proportion of embryos in the sample that had not initiated gastrulation at the time of the heat shock. Almost all of these have defects in the 6th abdominal segment as well as severe head defects \((n=524)\) (Fig. 8I,J). In heat-shocked wild-type embryos processed in parallel, 35% have segmentation defects; however, these are more general than in Hs-Sox70D embryos and only 7% have head defects.

**DISCUSSION**

**Sox70D corresponds to the Dichaete gene and is required for normal embryonic segmentation**

We have cloned and characterised a gene encoding a SOX domain protein from *Drosophila* which is dynamically expressed in early embryos in a pattern resembling that of segmentation genes. By two criteria Sox70D corresponds to the *Dichaete* gene. (1) Its misexpression appears to cause the dominant wing phenotype since it is ectopically expressed in the wing discs of all eight dominant D alleles and dominant wing phenotypes can result from ectopic expression generated by mobilising a Sox70D cDNA containing P element in a wild-type background (S. R. H. R., Adelaide T. C. Carpenter and M. A., unpublished data). (2) Seven D alleles have an associated recessive lethal phenotype and, in at least five of these alleles, the early embryonic expression of SOX70D is aberrant. The data presented in this paper and discussed below support the hypothesis that the lethality of D alleles is due to regulatory mutations that disrupt SOX70D expression.

Lethal D alleles that eliminate or severely reduce SOX70D expression in the early embryo have severe segmentation defects. In alleles in which SOX70D expression is reduced but not eliminated segmentation defects are milder. Thus the severity of the segmentation defect correlates with the expression of SOX70D. Our data shows that the segmentation phenotype is due, in part, to repression of the primary pair-rule genes *eve*, *h* and *run* since the characteristic seven-stripe expression of these genes is altered in strong lethal D mutations. The expression pattern of SOX70D fits well with a factor required for the expression of pair-rule genes since it is strongly expressed at the same time, or shortly before, they are established in their seven-stripe domains. Furthermore, the stronger dorsal expression of SOX70D in wild type is consistent with the more pronounced dorsal effects on pair-rule gene expression observed in lethal D genotypes. The experiments do not allow us to ascertain whether alterations in the expression of a particular pair-rule gene are directly due to loss of D function or...
due to secondary effects. For example, the general reduction in 
FTZ expression that we observe may be due to the prior dis-
ruption in primary pair-rule gene expression.

**Dichaete directly regulates pair-rule genes**

To address the possibility of direct effects of *D* on pair-rule gene 
development, we have ectopically expressed the gene early in 
embryonic development and monitored changes in the 
expression of *EVE, FTZ, HAIRY* and *RUN*. High levels of *D* 
expression administered prior to gastrulation severely disrupt 
*EVE, HAIRY* and *RUN* expression in three ways. Firstly, there 
is an expansion of the most posterior stripe, sometimes reaching 
the posterior end of the embryo. Secondly there is expansion of 
stripe domains so that stripes are fused or patches of ectopic 
expression are visible between the normal stripes. These effects 
are the reciprocal of those observed in *D* embryos where pair-
rule gene expression is reduced. The third effect of ectopic *D* 
expression is a repression of each of the primary pair-rule genes 
in the central domain of the embryo which encompasses stripe 
four. This is particularly apparent with *EVE*, where stripe four 
is eliminated in a high proportion of *Hs-Sox70D* embryos. Sig-
nificantly, this corresponds to the region of the embryo that first 
loses wild-type *D* expression prior to its resolution into stripes 
(Fig. 3C). Double labelling of embryos with *SOX70D* and *EVE* 
confirm that *EVE* stripe four lies within this initial gap in *D* 
expression (N. S. S. and S. R. H. R., unpublished observations).

We interpret the effects observed in the heat-shock experiments 
as reflecting the direct action of *D* for two reasons. Firstly, the 
time between the heat shocks and fixation is short and would 
not be expected to permit a secondary factor to be translated 
and then to modulate the expression of the pair-rule genes 
(Manoukian and Krause, 1992). Secondly, the effects of ectopic 
*D* on the expression of *FTZ* are not what would be expected 
if other regulators are being induced by *D*. If, for example, the 
aberrantly expressed *EVE* protein had time to affect the 
expression of *FTZ*, we would expect more dramatic effects on 
*FTZ* RNA (Manoukian and Krause, 1992; Yu and Pick, 1995). 
Taken together, the ectopic expression experiments and the 
loss-of-function studies indicate that *D* can act to both activate 
and repress a particular stripe domain and suggests that 
changing levels of *D* protein may be important in modulating 
pair-rule gene expression early in development.

We have also examined the effects of extremely short pulses 
of *D*. In this case, the effects are more subtle and appear to 
represent precocious expression of normal wild-type features. 
Thus there is expression of *RUN* in between the seven primary 
stripes and the appearance of anterior and posterior domains of 
*HAIRY*. It is possible that these effects are a reflection of wild-
type *D* function slightly later in development since *D* is tran-
siently expressed in fourteen stripes at the onset of gastrulation 
and at stage 7 in the areas that correspond to the patches of 
*HAIRY* expression induced by ectopic *D* (Fig. 3F). This 
supports the view that the level of *D* protein is important for 
regulating gene expression.

**Dichaete may act as modulator of chromatin structure**

A striking feature of the loss of *D* function is the variability 
obscerved at both the phenotypic and molecular levels; in over-
lapping deficiencies that remove *D* approximately half of the 
mutant embryos have strong segmentation defects and the 
remainder have weaker defects. Three possible explanations 
could account for the variable phenotype. Firstly, zygotic *D* 
function could be augmented by a maternal contribution; we do 
not detect maternal *D* transcripts but we cannot exclude maternal 
contribution of protein to the embryo. However, given that levels 
of *D* expression in the adult female are low, we do not expect a 
substantial maternal contribution. Secondly, the variability might 
be due to partial complementation by the normal activity of 
another SOX gene. Although we cannot eliminate this possibil-
ity, we have cloned and partially characterised a further four 
members of the SOX family in *Drosophila* and these genes are 
not expressed as early in embryonic development as is *D* 
(S.R.H.R. unpublished observations). Thirdly, the variability 
may be intrinsic to the wild-type activity of *D*. This view implies 
that *D* is not absolutely required for pair-rule gene regulation 
and suggests that it has an accessory role in transcription.

The data that we have presented do not support models in 
which *D* acts as a general transcription factor at basal promoters. 
If the protein did act in this way we would expect more constant 
and dramatic effects on pair-rule gene expression in its absence. 
It is also unlikely that *D* provides key positional information, 
so that effects of *D* gene expression are generated in 
approximately the correct anterior-posterior position in the 
absence of the gene. At present, we favour a model in which *D*
modulates chromatin structure to assist in generating appropriate levels of pair-rule gene expression in the domains established by both the gap genes and interactions between primary pair-rule genes. In this view, transcription factors act less efficiently at stripe-specific enhancers in the absence of D; conversely, ectopic expression of D allows transcriptional activation or repression of target genes by concentrations of transcription factors below those normally active. In the early syncytial embryo, where complex patterns of gene expression are rapidly generated by gradients of transcription factors, there may be a requirement for architectural components that regulate the formation of particular chromatin configurations. It is expected that favourable chromatin conformations would promote the interaction of regulatory molecules, bound to sequences distant from the promoter, with the basal transcription complex. The D protein is a candidate for such an activity. Since SOX box containing genes are known to bend DNA upon binding (Ferrari et al., 1992; Giese et al., 1992), the role of the gene may be mediated by this function. The primary pair-rule genes are distinguished by their very long 5' regulatory sequences spanning several kb upstream of the transcription start site. We have examined the available regulatory sequences upstream of primary pair-rule genes for the presence of mouse SOX2 DNA-binding motifs (our preliminary data indicates that D binds to a similar sequence, Stefan Oehler and S. R. H. R, unpublished observations). We find a cluster of these elements located between the promoter and the stripe-specific enhancers in the h gene, a location consistent with a bending model.

The Sox70D gene has been independently isolated by P. A. Nambu and J. R. Nambu (1996, this issue of Development) as the fish-hook gene. These authors reach very similar conclusions to those described in this paper. We thank John Nambu for providing his manuscript prior to publication. This work was supported by an MRC programme Grant to M. A., a Winston Churchill fellowship and Wellcome Trust studentship to C. R. W and a BBSRC fellowship to N. S. S. This work would not have been possible without the generous assistance of Adelaide Carpenter, whose genetic analysis of the region provided a basis for the characterisation of Sox70D. We are indebted to A. Brandt, J. F. de Celis, P. Goodfellow, D. Ish-Horowicz, R. Lovell-Badge, N. Patel, S. Romani and R. Rivera-Pomar for probes and helpful discussions.

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