Functional analysis of the chicken δ1-crystallin enhancer activity in Drosophila reveals remarkable evolutionary conservation between chicken and fly

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Summary

Functional conservation of enhancers among evolutionarily diverged organisms is a powerful way to identify basic regulatory circuits and key developmental regulators. This is especially applicable to Crystallin genes. Despite unexpected heterogeneity and diversity in their DNA sequences, many studies have revealed that most of the Crystallin genes are regulated by a relatively small set of developmentally important transcription factors. The chicken δ1-crystallin is one of the best-characterized Crystallin genes. Its lens-specific regulation is governed by a 30 bp long DC5 fragment present in the third intron of the gene. DC5 contains PAX6 and SOX2 binding sites, and its activity depends on the cooperative binding of these two transcription factors. To test the idea that Pax6 and Sox2, together with the DC5 enhancer, could form a basic regulatory circuit functional in distantly related animals, we introduced the DC5 fragment into Drosophila and studied its activation pattern and regulation. The results show that the DC5 enhancer is not only active in the compound eye but, remarkably, is specifically active in those cells responsible for Crystallin secretion in Drosophila, i.e. the cone cells. However, regulation of the DC5 enhancer is carried out not by Pax6, but by Pax2 (D-Pax2; shaven – FlyBase) in combination with the Sox2 homologue SoxN. Both proteins (D-PAX2 and SOXN) bind cooperatively to the DC5 fragment and activate the enhancer synergistically. As PAX6 and PAX2 proteins derive from the same ancestor, we propose that during evolution Pax6 function in vertebrate lens development was retained by Pax2 in Drosophila.

Key words: Crystallin, Enhancer conservation, Pax6, Pax2, Sox2, SoxN, Drosophila

Introduction

Many transcription factors that play key developmental roles are functionally conserved among distantly related organisms. Several examples have been reported in which one transcription factor can substitute for an orthologous counterpart in an evolutionarily diverged organism and rescue the defects associated with loss-of-function mutations. In other cases, transcription factors that control appendages or organ identity induce homologous organ development when expressed ectopically in an evolutionarily unrelated organism (e.g. Acampora et al., 2000; Halder et al., 1995 and Onuma et al., 2002). As these transcription factors are supposed to interact with different regulatory sequences to control the expression of multiple genes, the principle that arises from these results is that, to some extent, the regulatory sequences to which they bind should be also conserved in different phyla. Hence, the study of functional conservation of enhancers in a wide range of organisms is a reliable way to identify basic regulatory circuits.

Lens development has long been used as a model system for the study of tissue differentiation. Complex eyes with lenses exist in a wide range of animals, from vertebrates to invertebrates (Tomarev and Piatigorsky, 1996; Piatigorsky, 2003). In all cases, the lenses are transparent structures, the primary function of which is to refract light on to the retina. Lens differentiation is accompanied by the expression of several lens-specific genes, such as Crystallins, which encode structural proteins responsible for the transparent and refractive properties of the lens. The Crystallin proteins accumulate in the lenses and can account for 80-90% of the water-soluble protein content of the lens (Piatigorsky, 2003). Although all Crystallin proteins fulfil a similar function, comparative analysis has revealed an unexpected heterogeneity and diversity among the members of this family (Piatigorsky, 1993). The vertebrate Crystallins can be divided into two groups: ubiquitous Crystallins and taxon-specific Crystallins. The former are present in all major vertebrate lenses and show sequence similarity to stress proteins. The latter are restricted to certain taxonomic groups or species, and are related or identical to metabolic enzymes (Wistow and Piatigorsky, 1998; Piatigorsky, 2003). The invertebrate Crystallins have not been studied so extensively. Nevertheless, some of them have been
molecularly characterized and also show sequence similarity to metabolic enzymes (Piatiogorsky, 2003). In *Drosophila*, one of the Crystallin proteins from the corneal lens was isolated and showed to be related to insect cuticle proteins (Komori et al., 1992; Janssens and Gehring, 1999).

Despite Crystallin heterogeneity, many studies have shown that most Crystallin genes are regulated by a small set of evolutionarily conserved transcription factors (Cvekl and Piatiogorsky, 1996). The chicken δI-crystallin is one of the best-characterized Crystallin genes. It is a taxon-specific Crystallin present in birds and reptiles (Wistow and Piatiogorsky, 1987). Its lens-specific regulation is under the control of the DC5 fragment located within the 1 kb-long intronic enhancer. The DC5 fragment is just 30 bp long and contains both a PAX6 and a SOX2 binding site. Extensive in-vitro and in-vivo analyses have demonstrated that DC5 activity depends on the synergistic action and cooperative binding of PAX6 and SOX2 to the DC5 fragment (Kamachi et al., 2001). PAX6 is a member of the Pax protein family and contains two DNA-binding domains: a paired domain and a homeodomain. It is considered a master regulator of eye development (Gehring and Ikeo, 1999) and a key transcription factor in vertebrate lens development (Cvekl et al., 1999; Wilson and Koopman, 2002). It has been proposed that partnering with co-DNA-binding factors is the mechanism SOX proteins use to distinguish their regulatory targets and act in a cell-type-specific fashion (Kamachi et al., 2000).

To test the idea that Pax6 and Sox2, together with the DC5 enhancer, could form a basic regulatory circuit functional in distantly related animals, we introduced the DC5 enhancer into *Drosophila* and studied its activation pattern and regulation in the eye field. The *Drosophila* compound eye is made up of compound eye, basic genetic regulatory circuits involving in the development of these two evolutionarily diverged eyes have been largely conserved.

### Materials and methods

#### Fly strains and clonal analysis

Flies were reared on standard medium at 25°C. The following lines were used alone or in combinations: *dppblun*Gal4 (Stuehling-Hampton and Hoffmann, 1994), UAS-ey (Halder et al., 1995), UAS-shaven (Czerny et al., 1999), UAS-SoxN (this study), UAS-D (Sanchez-Soriano and Russell, 2000), UAS-DSred1 (this study), spdc1GFP, SoxNΔ9(35) (Overton et al., 2002), w; P[w+mC]36F FRT40A (Bloomington Stock Center), ey-flp (Newsome et al., 2000).

SoxN loss-of-function clones were generated by Flp-mediated mitotic recombination using the null allele SoxNΔ9,35 and the FLP/FRT system (Xu and Rubin, 1993). Flies with the genotype w; SoxNΔ9,35 FRT40A/Cyo were crossed to w; Bac[P3-DSr]-DC5(8x)wt; P[w+mC]36F FRT40A/P[w+mC]36F FRT40A; ey-flp/Cyo and the offspring analysed to detect mutant clones in the compound eye.

#### DNA constructs and transgenic flies

Wild-type (wt) and mutant forms (M4 and M7) of the octamerized DC5 enhancer were cloned as EcoRI fragments into the vector pSLfaGFPfa upstream of a *Drosophila* basal promoter (hsp27 heat-shock promoter) and the EGFP reporter gene. The vector pSLfaGFPfa was constructed by cloning the fragment EcoRI-hsp27-EGFP-SV40polyA-HindIII into the plasmid pSLfa1180fa (Horn and Wimmer, 2000). The ‘cassettes’ containing DC5(8x)-hsp27-EGFP-SV40polyA were then isolated as AscI fragments and cloned into the piggyBac transposon derived vector pBac[3xP3-DsRedaf]. This vector contains the DsRed1 gene, under the control of the artificial 3xP3 eye promoter, as a transgenesis marker (Horn et al., 2002). The resulting plasmids pBac[P3-DSr]-DC5(8x)wt, pBac[P3-DSr]-DC5(8x)M4 and pBac[P3-DSr]-DC5(8x)M7 were used to generate *Drosophila* transgenic lines by germline transformation in *yw*11. The EGFP modified version, containing the Drosocrystralxin signal peptide in its N-terminus (SP+EGFP), was obtained by standard PCR techniques. The wild-type EGFP was then substituted by its modified version in the plasmid pBac[P3-DSr]-DC5(8x)wt, and the resulting plasmid pBac[P3-DSr]-DC5(8x)wt-SP+EGFP used for germline transformation in *Drosophila*. The SME enhancer (a minimal D-Pax2 eye-specific enhancer) (Flores et al., 2000) was amplified by PCR and cloned as an EcoRI fragment into the vector pSLfaGFPfa. This vector is similar to pSLfaGFPfa but contains mRFP (Campbell et al., 2002) instead of EGFP. The ‘cassette’ SME-hsp27-mRFP-SV40polyA was isolated as an EcoRI (partial digestion)-AscI fragment and used to substitute the 3xP3-basal promoter-EGFP-SV40polyA ‘cassette’ present in the Hermes transposon derived vector pHer[3xP3-EGFPaf] (Horn et al., 2000), giving rise to the plasmid pHer[SME-mRFPaf]. Then, the ‘cassette’ DC5(8x)wt-hsp27-EGFP-SV40polyA was cloned as an AscI fragment into the vector pHer[SME-mRFPaf], and the resulting plasmid pHer[SME-mRFPaf]-DC5(8x)wt used for germline transformation. The transgenic flies harbouring this construct express mRFP under the control of the SME enhancer and EGFP under the control of the DC5(8x) enhancer. A DNA fragment containing the promoter and the 5’ untranslated region of SoxN (from −2939 to +869, P*SoxN*) was amplified by PCR and cloned as an EcoRI-NcoI fragment into the vector pSLfaGFPfa. The use of the NcoI site eliminates the hsp27 basal promoter present in pSLfaGFPfa. Then the ‘cassette’ containing P*SoxN*-EGFP-SV40polyA was isolated as an AscI fragment and cloned into the vector pHer[SME-mRFPaf]. The resulting plasmid pHer[SME-mRFPaf]-P*SoxN* was used for germline transformation in *Drosophila*. The transgenic flies containing this construct express mRFP under the control of the SME enhancer and EGFP under the control of the P*SoxN* promoter. Detailed descriptions of the primers used for the cloning procedure described above are available upon request.

The UAS-SoxN construct was made as follows: a genomic P1 clone containing the complete SoxN gene was digested with *Nhel*, filled in with *Klenow* and digested with *Nof*, and introduced into pCasper cut
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Activity in living adult flies without histological dissection.

These vectors contain fluorescence markers (RFP and EGFP) transposons (Horn and Wimmer, 2000; Horn et al., 2002).

A constitutively active actin5c vector pAc5.1B/V5His (Invitrogen) under the control of the stomach SOX2 site and PAX6 site mutations (M4 and M7, Fig. 1B). DsRed1 under the control of the synthetic promoter 3xP3 (Horn et al., 2000) was used as a marker for transgenesis. Two mutant forms of the enhancer representing the most specific enhancer action in its multimeric form in chicken cells (Kamachi and Kondoh, 1993). Accordingly, an octamerized version of the DC5 enhancer was introduced into Drosophila upstream of the reporter gene EGFP and a minimal promoter (Fig. 1B). DsRed1 under the control of the synthetic promoter 3xP3 (Horn et al., 2000) was used as a marker for transgenesis. Two mutant forms of the enhancer representing the most stringent SOX2 site and PAX6 site mutations (M4 and M7, respectively) (Fig. 1A) (Kamachi and Kondoh, 1993) were also octamerized and introduced in the same way. In these transgenic flies, the wild-type DC5 enhancer was active in the adult compound eye, but not in the ocelli (Fig. 1C). Furthermore, the two mutant forms of DC5 showed no enhancer activity (Fig. 1D,E), suggesting that the integrity of both binding sites is also important for the enhancer action in Drosophila.

Fig. 1. Functional analysis of the chicken DC5(8x) enhancer in Drosophila. (A) Wild-type and mutant sequences of the DC5 enhancer used in this study. SOX and PAX6 binding sites are indicated. Altered nucleotides are shown in red. (B) Scheme of the construct used to test the functionality of the DC5 enhancer in Drosophila. The octamerized DC5 enhancer was cloned upstream of a minimal promoter (MP) and the EGFP reporter gene. (C-I) Activity pattern of the DC5(8x) enhancer in the adult Drosophila head. Enhancer activity was detected in the compound eye when the wild-type sequence was used (C). The mutant M4 and M7 enhancers failed to drive EGFP expression (D,E), although the transgenesis marker used (3xP3-DsRed1) was equally expressed in the three cases (F,G,H), indicating that the chromosomal insertion point of the different constructs did not affect enhancer functionality. (I) Enhancer activity is also detected in the adult antenna (red arrow), the maxillary palps (blue arrow) and the labial palps (yellow arrow). (J-L) During larval development, the DC5(8x) enhancer is active in the eye imaginal disc (J) and in Bolwig’s organ (K,L).

Results

In order to test the activity of the chicken DC5 enhancer in Drosophila, we made use of recently described new transformation vectors based on the piggyBac and Hermes transposons (Horn and Wimmer, 2000; Horn et al., 2002). These vectors contain RFP and EGFP that allow detection of transgenic flies and analysis of enhancer activity in living adult flies without histological dissection.

**DC5 is active in the cone cells of the adult Drosophila compound eye and its precursors in the larval eye imaginal disc**

The DC5 fragment contains elements sufficient to elicit lens-specific enhancer action in its multimeric form in chicken cells (Kamachi and Kondoh, 1993). Accordingly, an octamerized version of the DC5 enhancer was introduced into Drosophila upstream of the reporter gene EGFP and a minimal promoter (Fig. 1B). DsRed1 under the control of the synthetic promoter 3xP3 (Horn et al., 2000) was used as a marker for transgenesis. Two mutant forms of the enhancer representing the most stringent SOX2 site and PAX6 site mutations (M4 and M7, respectively) (Fig. 1A) (Kamachi and Kondoh, 1993) were also octamerized and introduced in the same way. In these transgenic flies, the wild-type DC5 enhancer was active in the adult compound eye, but not in the ocelli (Fig. 1C). Furthermore, the two mutant forms of DC5 showed no enhancer activity (Fig. 1D,E), suggesting that the integrity of both binding sites is also important for the enhancer action in Drosophila. Additional EGFP expression was also detected in the antennae of young flies and in the adult mouthparts (the labial and maxillary palps) (Fig. 1I). The activity of the DC5 enhancer was traced back during Drosophila development. Enhancer action was first detected in the eye imaginal disc during the third instar larva, in cells posterior to the
Development factors could also be involved in DC5 regulation in chicken was shown to be due to the cooperative molecular mechanism conserved in both organisms. DC5 chicken, raises the question of whether there is an underlying Drosophila Pax6/2 and Sox2 homologues can cooperatively bind to the DC5 sequence.

The exactly functional conservation of DC5 activity in evolutionarily highly diverged animals such as Drosophila and chicken, raises the question of whether there is an underlying molecular mechanism conserved in both organisms. DC5 activity in chicken was shown to be due to the cooperative binding and synergistic action of PAX6 and SOX2. Therefore, we started our analysis checking whether these transcription factors could also be involved in DC5 regulation in Drosophila.

Drosophila contains two Pax6 homologues, eyeless (ey) and twin of eyeless (toy) (Quiring et al., 1994; Czerny et al., 1999), and two Sox2 homologues, Dichaete (D) and SoxNeuro (SoxN) (Nambu and Nambu, 1996; Russell et al., 1996; Crémazy et al., 2000). Two additional Pax6-like genes are also present in Drosophila: eyegone and twin of eyegone (twin of eyg – FlyBase) (Jang et al., 2003). However, their paired domains are truncated, and hence were not considered in our analysis. By contrast, we did analyse Drosophila Pax2 homologue (D-Pax2) (Fu and Noll, 1997), because it contains a complete paired domain and its expression pattern overlaps with the activity profile displayed by the DC5 enhancer (Fig. 2E-J). We expressed and purified from E. coli chimeric proteins containing the paired domain of EY, TOY and D-PAX2 (tagged with a Histidine tail) and the HMG DNA-binding domain of D and SOXN [fused to glutathione transferase (GST)] (Fig. 3A). The ability of these recombinant proteins to bind to the monomeric DC5 sequence was tested using gel mobility shift assays. The results (Fig. 3B,C) show that the five proteins can bind to DC5. Binding was prevented when the mutant forms of DC5 were used (data not shown). In the presence of DC5-M4 (SOX2 site mutant) binding of GST-D and GST-SOXN was abolished, whereas His-EY, His-TOY and His-D-PAX2 considerably reduced their binding capabilities in the presence of DC5-M7 (PAX6 site mutant). These results are in agreement with the in-vivo data presented above, concerning the lack of functionality of the mutant forms of the enhancer in Drosophila. We also compared the binding affinity displayed by His-EY, His-TOY and His-D-PAX2 paired domains in their binding to the monomeric DC5 enhancer (Fig. 3C). The results showed that His-D-PAX2 bound efficiently to the DC5 sequence, and that its binding affinity was at least ten times higher than the one displayed by His-EY and His-TOY under the same conditions. Indeed, a retardation band was detected in the presence of 0.5 ng of His-D-PAX2, whereas 5 ng of His-TOY were required to detect a band with approximately the same intensity. In the case of His-EY, even a higher amount of

Fig. 2. The cells responsive to DC5 activity in Drosophila are the cone cells. The activity pattern of DC5(8x) in the adult compound eye (A) and in the larval eye imaginal disc (B) was compared with the activity pattern of the cone-cell-specific enhancer SME (C,D). SME is the minimal eye-specific enhancer of D-Pax2 (Flores et al., 2000). Fluorescence microscopy indicates that both activity patterns are identical, as shown in preparations of the larval eye imaginal disc (E,F,G) and in cryosections of the adult compound eye (H,I,J). When a signal–peptide-tagged EGFP was used as a reporter for the enhancer activity, the fluorescence signal was detected in the lenses of the compound eye (K). This experiment was done in a w+ genetic background to keep the ommatidium structure unaltered (L).
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A protein would have been needed to match this result. Therefore, we can consider the PAX6 binding site present in the DC5 sequence as a putative PAX2 binding site, and from now on it will be called a PAX6/2 binding site.

We then addressed the question of whether the proteins could bind to the enhancer in a cooperative way, as it was described for the chicken counterparts (Fig. 3D,E,F). When PAX6/2 and SOX2 homologues – i.e. EY, TOY, D-PAX2, D and SOXN – were included in binding reactions, a slowly migrating band was detected, which probably represents the ternary complex DC5-PAX6/2-SOX2. This band appeared even at low concentrations of PAX6/2 and SOX2 homologues, concentrations at which either of them alone failed to form a retardation band with DC5. For instance, 2.5 ng of GST-D were needed to form a clear retardation band with DC5, whereas at least 5 ng of His-EY were necessary to do the same thing (Fig. 3D). However, the triple complex band was detected when 0.5 ng of GST-D were combined with 1 ng of His-EY. Furthermore, in the presence of 2.5 ng of GST-D a clear retardation band was formed with DC5 (red asterisk in Fig. 3D). Upon addition of increasing concentrations of His-EY, the band migrated more slowly (triple complex) and became more intense (blue asterisk in Fig. 3D). All these data indicate that GST-D and His-EY cooperate in their binding to DC5. The same can be applied to the rest of combinations of PAX6/2 and SOX2 homologues (Fig. 3D,E,F).

In summary, we can conclude that in vitro *Drosophila* PAX6/2 and SOX2 homologues can bind cooperatively to the DC5 enhancer.

*Fig. 3.* Cooperative binding of the *Drosophila* PAX6/2 and SOX2 homologues to the DC5 sequence in vitro. (A) Schemes of the *Drosophila* PAX6, PAX2 and SOX2 homologues and their variants with different molecular tags. DNA-binding domains are indicated: paired domain (PD), homeodomain (HD), N-terminal portion of the homeodomain (H) and high mobility group domain (HMG). The octapeptide sequence (O) present in D-PAX2 is also shown. (B) Binding of the *Drosophila* PAX6 and SOX2 homologues to the wild-type monomeric DC5 sequence. Five nanograms of the tagged variants of the different proteins were used in gel mobility shift assays. (C) Comparison of the binding affinities of D-PAX2-PD, EY-PD and TOY-PD for the monomeric DC5 sequence. (D,E,F) Cooperative binding of *Drosophila* PAX6/2 and SOX2 homologues to the wild-type monomeric DC5 sequence. Combinations of the different tagged variants were included in the binding reaction, and their ability to cooperatively bind to the DC5 sequence was analysed by gel mobility shift assays. In all the cases, the results were similar. The duplex complex SOX2 homologue-DC5 (red asterisks) migrated more slowly and became more intense upon addition of increasing amounts of the PAX6/2 homologues, giving rise to the triple complex SOX2 homologue-PAX6/2 homologue-DC5 (blue asterisks).
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Fig. 4. Synergistic activation of the DC5(8x) enhancer in vivo. (A) Cell culture co-transfection assays in Schneider 2 cells. Wild-type and mutant DC5 enhancers were tested for activation by exogenous Drosophila Pax6, Pax2 and Sox2 homologues. The structure of the reporter and effector plasmids is shown (A1). β-gal activity of the reporter vector co-transfected with the empty effector vector was taken as 1 (column C). (B) Ectopic activation in Drosophila tissue. Wild-type DC5(8x) enhancer was tested for activation in the wing imaginal disc by ectopic expression of Drosophila Pax6, Pax2 and Sox2 homologues.

activation of the enhancer ex vivo. To test this possibility, we carried out cell culture co-transfection assays using Drosophila Schneider 2 (S2) cells. A reporter plasmid containing the DC5 enhancer upstream of the β-galactosidase gene was co-transfected with effector vectors expressing Drosophila Pax6, Pax2 and Sox2 homologues (Fig. 4A1). When these genes were separately expressed, the enhancer was only very modestly activated (Fig. 4A2). High-level activation was detected only when combinations of Pax6/2 and Sox2 homologues were co-transfected at the same time, and activation of the DC5 enhancer reached the highest level when ey, toy or D-Pax2 were co-expressed with SoxN (Fig. 4A2). When the mutant forms of the enhancer were used, the activation levels remained almost basal, even when combinations of Pax6/2 and Sox2 homologues were co-expressed (Fig. 4A3,A4).

The results shown above support the model proposed for the regulation of DC5 in chicken, and indicate that the synergistic action of Drosophila Pax6/2 and Sox2 homologues is also able to efficiently activate the DC5 enhancer. Nevertheless, these results do not determine to what extent the five Drosophila genes are really involved in this process, and if the activation levels detected in S2 cells ex vivo are sufficient to achieve activation of the DC5 enhancer in Drosophila tissue in vivo. In order to corroborate our previous findings, we carried out ectopic expression of the candidate genes in Drosophila imaginal discs and checked for activation of the DC5 enhancer (Fig. 4B). We used the UAS/Gal4 system (Brand and Perrimon, 1993) to ectopically express the five genes under the control of the dpp\textsuperscript{blank}.Gal4 driver. The dpp\textsuperscript{blank} enhancer specifically drives expression of the yeast Gal4 transcription factor in the anterior-posterior compartment boundary of the imaginal discs at the third larval stage (Fig. 4B3). When each gene was separately expressed, no DC5 enhancer activation was detected (Fig. 4B2). Combinations of ey and D, or toy and D, also failed to activate the DC5 enhancer. However, when SoxN was co-expressed with ey, toy or D-Pax2 a clear GFP expression band appeared in the anterior-posterior border of the wing imaginal disc (Fig. 4B4,B5,B7). Interestingly, D-Pax2 could synergistically activate the enhancer in the presence of D (Fig. 4B6), whereas both ey and toy failed to do so. Probably, this is a consequence of the different binding affinities to the DC5 sequence displayed by the paired domains of the proteins encoded by those genes, and suggests that in vivo the triple complex D-PAX2-D-DC5 can form due to the higher affinity of the D-PAX2 paired domain for the PAX2/6 binding site present in the DC5 enhancer.
DC5 activation in the Drosophila compound eye is attained by synergism of D-Pax2 and SoxN

The data presented above indicate that several combinations of transcription factors can be responsible for activating the DC5 enhancer in vivo in the Drosophila compound eye, e.g. ey/SoxN, toy/SoxN, D-Pax2/D and D-Pax2/SoxN (Fig. 4B,5,6B,7). However, a major constraint to their effective involvement in this process is their expression pattern. The expression of Drosophila Pax6 homologues in the adult compound eye is controversial and has not been firmly demonstrated. Furthermore, their expression in the third instar eye imaginal disc during larval development is restricted to undifferentiated cells anterior to the MF, whereas the DC5 enhancer is active posterior to the MF in cone cell precursors (Fig. 2). By contrast, D-Pax2 expression in cone cell precursors of the eye imaginal disc during the 3rd instar larval stage has been well documented (Fu and Noll, 1997). As revealed by the activity of its minimal eye-specific enhancer SME, D-Pax2 is expressed not only in those cone cells precursors (Fig. 2F), but also in the cone cells of the adult compound eye (Fig. 2C). This expression pattern overlaps with the activity profile displayed by the DC5 enhancer (Fig. 2E,H).

D and SoxN expression in the eye imaginal disc has also been described. D is expressed anterior to the MF, along the ventro-lateral region of the eye-antennal disc (Mukherjee et al., 2000), in a domain where the DC5 enhancer is not active. However, immunostaining reveals expression of SoxN in cells posterior to the MF (Crémazy et al., 2001), in the same domain in which the DC5 enhancer is active. Expression of D and SoxN in the adult compound eye has not been described. However, we have found that a 3.4 kb DNA fragment containing the promoter and the 5′ untranslated region of SoxN (PSoxN) (Fig. 5A) harbours regulatory sequences that recapitulate SoxN expression in the eye imaginal disc during larval development (Fig. 5C). These sequences drive expression of a reporter gene in cells posterior to the MF, which, by comparison to the SME enhancer activity pattern, were identified as cone cells (Fig. 5D,G,H). The PSoxN fragment also drove expression of a reporter gene in the adult compound eye (Fig. 5B).

In conclusion, only D-Pax2 and SoxN show an expression profile coincident with the activity pattern of the DC5 enhancer, we favour the combination of these two transcription factors as the tandem responsible for the activity of the enhancer in the Drosophila compound eye. To unambiguously demonstrate this hypothesis, we analysed the activity of the DC5 enhancer in D-Pax2 and SoxN loss-of-function situations. spd01 is a Drosophila mutant characterized by the lack of D-Pax2 expression in cone cells and primary pigment cells of developing larval and pupal eye discs (Fu and Noll, 1997). The mutant fly is homozygous viable, but the compound eye shows a severe disruption of the ommatidia structure that gives rise to a rough eye phenotype. When the construct containing the DC5 enhancer was introduced into the Drosophila spd01 mutant, no expression of the reporter gene (EGFP) was detected in the adult compound eye (Fig. 6A), although the cone cells were still present, as revealed by the action of the cone-cell specific enhancer SME (Fig. 6B) (see also Fig. 6 in Fu and Noll, 1997). In the case of SoxN, all the available mutants were embryonic lethal. In order to analyse the effect of SoxN depletion on the activity of the DC5 enhancer, we generated loss-of-function clones in the adult compound eye using the yeast FLP/FRT system (Xu and Rubin, 1993). As displayed in Fig. 6E, we induced site-specific mitotic recombination between the mutant chromosome arm (blue line) and the wild-type chromosome arm (red line), using the eyeless enhancer to drive flip recombinase expression. As this enhancer is specifically active in the developing eye (Hauck et al., 1999; Newsome et al., 2000), the homozygous mutant clones are only induced in the compound eye, allowing the mosaic fly to survive. Under white light, the clonal mutant tissue was identified by a white coloration (red arrow in Fig. 6C), whereas the homozygous or heterozygous wild-type tissue displayed a red or orange coloration, respectively (black arrows in Fig. 6C). The mutant clones were more readily identified with the use of UV light (red arrow in Fig. 6D). The red and orange of the wild-type tissue did not completely mask the

![Fig. 5. D-Pax2 and SoxN are expressed in the Drosophila compound eye and in the eye imaginal disc. (A) Genomic map of the SoxN locus and structure of the construct used to trace SoxN expression. The intronless SoxN gene consists of a translated region (TR) flanked by extensive 5′ and 3′ untranslated regions (5′ UTR and 3′ UTR, respectively). Regulatory sequences important for SoxN expression in the adult compound eye (B) and in the eye imaginal disc (C) are present in the promoter and the 5′ untranslated region of SoxN (from –2939 to +869. PSoxN). D-Pax2 expression was monitored using its minimal eye-specific enhancer SME. This enhancer is active in the cone cells of the adult compound eye (E) and their precursors in the eye imaginal disc (F). Comparison of both expression patterns in the eye imaginal disc shows that they are coincident (D,G,H).](image-url)
EGFP signal induced by the activity of the DC5 enhancer, and clear EGFP spots were visible at the top of every illuminated ommatidium when the objective was focused at the proper level (Fig. 6F). However, no EGFP signal was detected in the colourless mutant tissue, indicating that SoxN depletion in the compound eye abolishes the activity of the DC5 enhancer (Fig. 6F). In summary, the results obtained with the loss-of-function experiments corroborate our previous conclusions and indicate that, in wild type, DC5 enhancer activity in the Drosophila compound eye is due to the cooperative action of the transcription factors D-PAX2 and SOXN.

Discussion

A conserved regulatory circuit involved in lens development

The δ1-crystallin gene is an early marker for differentiating lens cells in chicken. The extensive work carried out by Kondoh and collaborators have led to the finding that this gene is regulated by a 1 kb-long enhancer located in the third intron. Within this enhancer, a small DNA fragment of only 30 bp (DC5 fragment) confers lens-specificity. The DC5 fragment contains two binding sites, a PAX6 binding site and a SOX1/2/3 (Group B1 SOX proteins, SOX2 being the major player) binding site, and the cooperative binding of these transcription factors to the DC5 sequence activates the enhancer in a synergistic fashion (Kamachi and Kondoh, 1993; Kamachi et al., 1995, 2000, 2001; Kondoh et al., 2004). The simplicity of the DC5 fragment, the well-characterized nature of its transcription factor binding sites, and the fact that Pax6 and Sox2 are important developmental regulators conserved in evolution, prompted us to consider these three elements (DC5 sequence, Pax6 and Sox2) as part of a conserved regulatory circuit involved in lens development. To test this idea, we performed a functional enhancer test and introduced the DC5 fragment into a distantly related organism, D. melanogaster. Functional conservation of enhancer elements has been previously reported. Exchanges of Hox and eyeless enhancer elements between flies, worms and vertebrates gave rise to expression patterns that were characterized as homologous (Streit et al., 2002; Frasch et al., 1995; Xu et al., 1999). In other cases, enhancer elements from a variety of D. melanogaster neuronal and muscular genes failed to activate the expression of a reporter gene in the homologous cell types in Caenorhabditis elegans (Ruvinsky and Ruvkun, 2003). These various outcomes are probably due to differences in the evolutionary pressure exerted on different enhancers according to their developmental roles. However, these results emphasize the importance of this test when the result is positive, meaning that the functional conservation of an enhancer is a reliable way to identify basic regulatory circuits.

The fruit fly and the chicken are separated by hundreds of millions of years of evolution, and their visual organs reflect this evolutionary distance at the anatomical, developmental and physiological level. Even the eye lenses, although fulfilling a similar function, are formed differently. In chicken the lenses are cellular structures, whereas in Drosophila they are secreted into an acellular space by the cone cells and the primary pigment cells. The introduction of the chicken DC5 enhancer into Drosophila had a remarkable effect. Not only was the DC5 enhancer active in the Drosophila compound eye, but also it was specifically active in the cells that are in part responsible for lens secretion in Drosophila, i.e. the cone cells. The experiment was done with an octamerized version of the DC5 enhancer to augment the sensitivity of the system. Actually, when a single copy of the DC5 enhancer was used, no activity was detected in the Drosophila compound eye (data not shown). This suggests that although lens-specificity is retained by DC5 in Drosophila, additional sequences have to be present to provide full activity to the enhancer.
Development conserved, i.e. whether DC5 activity in the other two elements of the regulatory circuit were also, we focused our attention on finding out whether DC5 regulation is under the control of D-Pax2 and synergistically activated upon co-expression of with D and SOXN. Cell culture co-transfection assays and paired domain was sufficient for DNA binding and cooperation cooperatively to the DC5 sequence. Interestingly, the PAX6 homologues, and thus activate the enhancer in a (indeed it showed a higher affinity for DC5 than could cooperate with SOXN in binding to the DC5 sequence. In-vitro and in-vivo studies showed that D-Pax2 is able to induce ectopic eyes (Pax6 function) and ey and toy can rescue speol mutation (Pax2 function) (Kozmik et al., 2003). In agreement with this, a recently characterized cnidarian PaxB gene was tentatively identified as the descendant of the last common ancestor of the Pax6 and Pax2 genes (Kozmik et al., 2003; Gehring, 2004; Patigosky and Kozmik, 2004). Like Pax2, PaxB protein contains a Pax2/5/8-type paired domain and octapeptide; and, like Pax6, a complete paired-type homeodomain. As a consequence, PaxB is able to rescue the Drosophila sped mutation (Pax2 function) and to induce small ectopic eyes in Drosophila (Pax6 function). Interestingly, PaxB is also able to activate the jellyfish J3-crystallin promoter in cell culture co-transfection assays (Kozmik et al., 2003). It is tempting to speculate that after duplication and diversification of the ancestor PaxB-like gene, Crystallin regulation was retained by Pax6 in the vertebrate lineage, whereas this function was taken over by Pax2 in Drosophila. We can speculate further and suggest that this functional diversification was probably due to changes in the regulatory elements of these two genes and not in their coding sequences. At present, Pax6 and Pax2 genes show structural differences that reflect the changes that occurred in their coding sequences during evolution. As well as the paired domain, Pax6 contains a homeodomain; Pax2, however, has only part of the homeodomain and, in addition, an octapeptide sequence accompanying the paired domain. Nevertheless, as mentioned above, Drosophila Pax6 and Pax2 genes are functionally exchangeable and can largely substitute for some of each other's functions. The same seems to apply to the regulation of the DC5 enhancer in Drosophila. Both Pax6 (ey and toy) and D-Pax2 can activate this enhancer in vivo when they are co-expressed with SoxN, but the main limitation to their real involvement in DC5 regulation is their expression pattern, meaning differences in their regulatory elements.

In summary, we propose that after duplication of the PaxB-like ancestor, changes in the regulatory sequences determined which paralogous gene took over Crystallin regulation. Once the expression pattern of the duplicated genes diverged, changes in their coding sequences brought about the structural differences detected today, to better adjust each of the paralogous genes to its developmental role. According to our analysis, it seems that Crystallin regulation was taken over by Pax6 in vertebrates, whereas this function was retained by Pax2 in Drosophila.
**Drosophila Crystallin genes under the control of the same regulatory circuit**

The fact that lens-specificity of the DC5 fragment is retained in *Drosophila* suggests that a similar mechanism could be responsible for Crystallin regulation in the fruit fly. This is supported by the phenotype of the *Drosophila* spa^\text{dol} mutant. In this mutant, as previously mentioned, *D-Pax2* expression is abolished in both the cone cells and the primary pigment cells (Fu and Noll, 1997). As a consequence, the hexagonal lattice of ommatidia is severely disrupted, giving rise to a rough eye phenotype. In spa^\text{dol} most of the cone cells and many primary pigment cells are still present (Fu and Noll, 1997) and retain the ability to secrete corneal lenses and crystalline cones. However, these lens structures are frequently defective and fused or display the blueberry-eye phenotype (Fu and Noll, 1997). Consequently, these results support the idea that a similar mechanism could be involved in the regulation of crystallin genes in both *Drosophila* and mammals. Current studies are focusing on the promoter regions of the murine cdc5 gene and are aimed at identifying the regulatory elements involved in the expression of this gene.

As mentioned above, *Drosophila* Crystallin proteins are secreted by cone cells and primary pigment cells, and accumulate on the top of the ommatidium forming the corneal lens and the crystalline cone. Two-dimensional gel electrophoresis has identified 14 different proteins in the crystalline cone (Tomarev and Piatigorsky, 1996) and only three proteins in the corneal lens (Komori et al., 1992). The most abundant protein in the corneal lens is Drosocrystallin, a 52 kDa protein that contributes to lens development by providing the appropriate refractive index to the corneal lens (Komori et al., 1992). Sequencing of the N-terminus end of Drosocrystallin allowed the cloning of the *drosocrystallin* (*dcy*) gene and its characterization as a member of the insect cuticular protein gene family (Janssens and Gehring, 1999). Interestingly, *dcy* expression was detected in the primary pigment cells, but not in the cone cells (Komori et al., 1992) (data not shown). As *D-Pax2* is expressed in both cell types, other regulatory differences between *dcy* and *DC5* must exist to account for their distinct expression patterns. A 441 bp DNA fragment, including the promoter region of *dcy*, was shown to be sufficient to drive expression of a reporter gene into the primary pigment cells (Janssens and Gehring, 1999). We are currently dissecting this DNA fragment and investigating its regulation to find similarities and differences with DC5 regulation.

The isolation and characterization of new *Drosophila* Crystallin genes has been impaired by the heterogeneous nature of these genes. During evolution, proteins with different enzymatic activities have been recruited (co-opted) to fulfill a Crystallin role, both in vertebrates and in invertebrates. An event common to all these Crystallin co-options has been the acquisition of highly lens-specific expression of the recruited proteins, through changes in the regulatory regions of their genes (Piatigorsky, 2003). The results presented in this report suggest that the chicken DC5 enhancer might be one of the genetic elements used throughout evolution to recruit new genes into lens development. We are currently using this information to identify new *Drosophila* Crystallin genes, and to find out whether their lens-specific expression is achieved by regulatory elements similar to the chicken DC5 enhancer.

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**References**


