The RNA-binding protein ELAV regulates Hox RNA processing, expression and function within the Drosophila nervous system

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ABSTRACT
The regulated head-to-tail expression of Hox genes provides a coordinate system for the activation of specific programmes of cell differentiation according to axial level. Recent work indicates that Hox expression can be regulated via RNA processing but the underlying mechanisms and biological significance of this form of regulation remain poorly understood. Here we explore these issues within the developing Drosophila central nervous system (CNS). We show that the pan-neural RNA-binding protein (RBP) ELAV (Hu antigen) regulates the RNA processing patterns of the Hox gene Ultrabithorax (Ubx) within the embryonic CNS. Using a combination of biochemical, genetic and imaging approaches we demonstrate that ELAV binds to discrete elements within Ubx RNAs and that its genetic removal reduces Ubx protein expression in the CNS leading to the respecification of cellular subroutines under Ubx control, thus defining for the first time a specific cellular role of ELAV within the developing CNS. Artificial provision of ELAV in glial cells (a cell type that lacks ELAV) promotes Ubx expression, suggesting that ELAV-dependent regulation might contribute to cell type-specific Hox expression patterns within the CNS. Finally, we note that expression of abdominal A and Abdominal B is reduced in elav mutant embryos, whereas other Hox genes (Antennapedia) are not affected. Based on these results and the evolutionary conservation of ELAV and Hox genes we propose that the modulation of Hox RNA processing by ELAV serves to adapt the morphogenesis of the CNS to axial level by regulating Hox expression and consequently activating local programmes of neural differentiation.

KEY WORDS: Central nervous system, Drosophila, ELAV/Hu, Hox, RNA-binding protein, RNA processing, Alternative polyadenylation (APA), Alternative splicing, Segment-specific apoptosis

INTRODUCTION
The nervous system of vertebrates and invertebrates shows a remarkable level of regionalisation along the anteroposterior (AP) axis, so that the identity, arrangement and connectivity of nerve cells change according to axial level (Arendt and Nubler-Jung, 1999; Lumsden and Keynes, 1989; Lumsden and Krumlauf, 1996; Arendt and Nubler-Jung, 1999; Lumsden and Keynes, 1989; Lumsden and Krumlauf, 1996; Reichert, 2002; Thor, 1995). At the molecular level, axial neural specification relies centrally on the regulated expression of the Hox genes, a group of evolutionarily conserved genes that encode a family of homeodomain-containing transcription factors that activate specific cell differentiation programmes in different parts of the nervous system (McGinnis and Krumlauf, 1992; Alonso, 2002; Mallo and Alonso, 2013). An understanding of the molecular mechanisms underlying Hox gene expression and function within the CNS is thus crucial to decipher the ability of these genes to direct pluripotent neural populations along different developmental routes.

Hox gene expression can be regulated at multiple levels through a variety of transcriptional and post-transcriptional mechanisms (Simon et al., 1990; Shimell et al., 1994; Alonso and Wilkins, 2005; Alonso, 2012; Mallo and Alonso, 2013). Previous work in our laboratory and elsewhere has demonstrated that, in Drosophila, several Hox transcripts undergo mRNA processing by alternative splicing and alternative polyadenylation (Akam and Martinez-Arias, 1985; Kornfeld et al., 1989; Lopez and Hogness, 1991; O’Connor et al., 1988; Reed et al., 2010; Thomsen et al., 2010), that these processes affect Hox gene expression and function in a range of developmental contexts (Mann and Hogness, 1990; Subramaniam et al., 1994; Thomsen et al., 2010; Reed et al., 2010; de Navas et al., 2011) and are evolutionarily conserved over large phylogenetic distances (Bomze and Lopez, 1994; Patraquim et al., 2011). Notably, within the Drosophila embryonic CNS several Hox genes express specific splicing and 3’UTR isoforms (Thomsen et al., 2010), suggesting that RNA processing might represent a control system involved in fine-grain regulation of Hox expression within the CNS. Nonetheless, the underlying mechanisms and biological relevance of Hox RNA processing within neural tissues remain largely unknown.

Here we apply a reverse genetics approach designed to detect factors involved in Hox RNA processing, focusing on genes expressed within the Drosophila embryonic CNS. As a gene model we use the Hox gene Ultrabithorax (Ubx), as this is the system in which RNA processing is understood in greatest detail (Hatton et al., 1998; Alonso and Akam, 2003; de la Mata et al., 2003; Reed et al., 2010; Alonso, 2012; Mallo and Alonso, 2013). Our approach led us to identify the pan-neural RNA-binding protein (RBP) ELAV (also known as Hu antigen) (Robinow et al., 1988; Robinow and White, 1988; Good, 1995) as a key regulator of Ubx RNA processing, expression and function within the Drosophila embryonic CNS and to define what is, to our knowledge, the first specific cellular role of ELAV during neural development. We discuss the implications of our findings for the understanding of the molecular programmes controlling neural differentiation along the head-to-tail axis of animals.

RESULTS
ELAV regulates Ubx RNA processing in the embryonic CNS
Embryos carrying a null mutation in the elav gene [elav null] produced patterns of Ubx alternative splicing (AS) and alternative polyadenylation (APA) that were significantly different from those found in wild-type embryos (Fig. 1A-H),


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indicating that Drosophila ELAV is necessary for normal Ubx RNA processing within the embryonic CNS. During normal embryonic development, alternatively spliced forms of Ubx are produced in a specific spatiotemporal pattern of expression: isoforms containing both M1 and M2 exons (Ubx I, Fig. 1A,B) account for most of the Ubx mRNAs expressed in epidermis and mesoderm, whereas isoforms lacking M1 and/or M2 (Ubx II and IV, Fig. 1A,B) are most abundant in neural cells (Artero et al., 1992). With regards to APA, Ubx mRNA forms bearing short 3'UTRs are dominant during early and mid-embryogenesis, but later on in development (late embryogenesis) the formation of long 3'UTR forms becomes predominant, especially in neural tissue (Akam and Martinez-Arias, 1985; Kornfeld et al., 1989; O’Connor et al., 1988; Lopez and Hogness, 1991; Thomsen et al., 2010).

We examined Ubx RNA processing profiles using two independent experimental approaches: RT-PCR and RNA in situ hybridisations in dissected ventral nerve cords (i.e. oligo in situ hybridisations) or in whole embryos (Fig. 1C-H). Remarkably, both approaches were consistent in showing that, in elav mutants at stage 16, Ubx splicing isoforms Ia and IVa were over- and under-represented, respectively (Fig. 1C-E) (whereas isoform Ubx IIa showed comparatively little change across genotypes). This analysis also revealed an overall reduction in Ubx long 3'UTR mRNAs within the CNS of embryos (H). Notably, ectopic expression of ELAV at the germband extension stage (I) shows a clear increase in the Ubx mRNA forms bearing short 3'UTRs as it possibly can (supplementary material Fig. S2).

ELAV interacts with discrete elements within Ubx RNA

To determine the mechanisms that link ELAV expression level with Ubx RNA processing events we explored the model that ELAV exerts its effects via direct interaction with Ubx RNA. ELAV/Hu proteins possess an RNA-binding unit bearing three RNA recognition motifs that show high affinity for AU-rich elements (Wang and Tanaka, 2001). Given that elav encodes an RBP we
Fig. 2. See next page for caption.
Fig. 2. ELAV binds to discrete elements within Ubx RNAs. (A) Based on the computational detection of RNA sequence elements with high similarity to those present in other ELAV targets (Neuroglian, Nrg; erect wing, ewg) and AU-rich elements (AREs) we determined that the Ubx locus contains at least 16 putative binding sites for the neural protein ELAV. Phylogenetic analysis of Ubx sequences within distantly related Drosophilids reveals that a subset of ELAV putative binding sites (EBSSs) (sites 3, 8, 13 and 16) have been conserved for more than 60 million years of independent evolution (i.e. ultraconserved), suggesting that they might be functionally relevant. (B) UV cross-linking experiments reveal that Drosophila ELAV is able to bind to discrete elements in Ubx mRNAs. A panel of radioactively labelled (32P) RNA probes (top, see Input RNA gel), including elements from the ewg mRNA (a previously described experimentally validated ELAV target) and the four ultraconserved Ubx ELAV binding sites detected bioinformatically (sites 3, 8, 13 and 16), were incubated with ELAV protein and treated with RNase A, with or without prior UV crosslinking (UV-CL; – or +) and the products of these reactions were resolved by PAGE-SDS. These experiments revealed that ELAV has high affinity for sites 3 and 8, but very low affinity for sites 13 and 16 (bottom left shows quantification of ELAV-bound RNA per Ubx mRNA site). Furthermore, site-specific mutagenesis affecting the core binding sequences of ELAV in sites 3 and 8 led to a significant reduction in interaction between ELAV and Ubx mRNAs (bottom right shows quantification of ELAV-bound RNA per wild-type or mutated Ubx mRNA site). These experiments show that ELAV is able to strongly interact with specific sites within Ubx mRNAs. AS, antisense. (C-E) EMSAs using 32P-labelled Ubx and ewg RNAs further confirms that ELAV has high affinity for Ubx sites 3 and 8 and that mutation of these sites leads to a change in ELAV-RNA interaction. (C) RNA probes were radioactively labelled and quantified so that equal molar units of each type of RNA were included. ELAV forms a range of complexes as a result of multimerisation on ewg probes (asterisks). Multimerisation is also observed on Ubx probes (asterisks). Note that the amount of probe is not saturating, therefore allowing us to estimate the affinity of ELAV protein for each RNA probe by following the disappearance of free RNA signal as a function of the increase in ELAV protein concentration (IELAV) in the experiment. If free RNA probe signal disappears at lower concentrations of ELAV then this is an indication of higher affinity of ELAV for such RNA sequences as compared with those for which ELAV concentration has to reach maximum levels to generate shifted complexes. (D) Quantification of the binding profiles of ELAV protein to ewg and Ubx RNA probes as shown in C. (E) EMSA using mutated versions of probes 3 and 8 shows reduced binding activity (dashed rectangles) and a change in the range of protein-RNA complexes formed. (F) RNA cross-linking and immunoprecipitation (RNA-CLIP) assay using embryonic nuclear extracts shows that anti-ELAV antibodies are able to precipitate RNAs from ewg and Ubx sites 3, 8 and 13 (above). These experiments also reveal the formation of protein-RNA complexes, including multimerised forms of ELAV on RNA (Fig. 2C,D). This has been observed previously in the interaction of ELAV with ewg RNAs (Soller and White, 2005).

To determine the extent to which ELAV-Ubx RNA interactions take place within the physiological environment of the developing embryo we developed a series of RNA cross-linking and immunoprecipitation (RNA-CLIP) assays using embryonic nuclear extracts (Fig. 2F). These experiments confirmed that ELAV interacts with Ubx RNAs at EBS3 and EBS8 in normal tissue, while a negative control antibody (anti-Tubulin) rendered a significantly lower level of Ubx RNA precipitation (Fig. 2F). We conclude that our biochemical analysis supports the model that ELAV interacts with Ubx RNAs directly via sites in Ubx introns 1 and 3 (EBS3 and EBS8, respectively; see Fig. 2A).

ELAV regulates Ubx expression levels within the CNS

To investigate the biological consequences of ELAV interactions with Ubx during development we first sought to explore whether these had an impact on Ubx expression. First, we examined the extent to which the effects observed at the level of RNA processing (Fig. 1C-H) were reflected at the protein level. Western blot analysis of whole-embryo protein extracts produced from wild type and elav5 mutants (stage 16) revealed that elav5 mutant embryos produce a larger amount of Ubx 1a and reduced levels of Ubx 1a compared with wild-type embryos, closely matching the ELAV-dependent changes observed in Ubx mRNA isoforms (Fig. 1C-H and Fig. 3B). Interestingly, our western blot experiments also showed that elav5 mutants produced reduced levels of Ubx protein. Given that at this point in development Ubx is also expressed in other tissues (e.g. epidermis) we carried out a series of immunostainings to detect Ubx protein expression exclusively in dissected ventral nerve cords (Fig. 3A). These experiments showed that elav5 embryos produce significantly less Ubx protein than their wild-type counterparts at stage 16 (Fig. 3A,C). Heterozygous elav5 mutant embryos showed an intermediate level of expression between homozygous mutants and wild-type embryos (not shown). These data confirmed that ELAV removal leads to a significant reduction in Ubx protein expression.

In principle, ELAV could exert its effects on protein expression at multiple points, including Ubx mRNA synthesis, stability and/or the extent to which the effects observed at the level of RNA processing (i.e. AS and APA, both of which occur co-transcriptionally (Di Giannmartino et al., 2011; Licatalosi and Darnell, 2010; Proudfoot, 2011). Second, our protein-RNA binding experiments (Fig. 2) indicate that ELAV binds Ubx RNAs via interactions with elements present in Ubx introns (see above), making it somewhat unlikely that ELAV would remain physically associated to the fully processed Ubx mRNA and act directly on the translational process. Based on these considerations, we decided to test the hypothesis that ELAV exerts its effects on Ubx protein expression by affecting Ubx transcriptional...
ELAV removal leads to reduced expression of *Ubx* mRNA and protein and promotes accumulation of nascent *Ubx* RNA transcripts within the *Drosophila* CNS. (A) Immunostaining of dissected embryonic ventral nerve cords (anterior is to the left) showing the expression of Ubx protein in wild-type and homozygous elav (elav5) mutant embryos at stage 16; elav5 mutant embryos express significantly lower levels of Ubx protein within their CNS. (B) Western blot analysis of late wild-type and elav5 embryos shows that the spectrum of Ubx protein isoforms produced in wild-type and mutant embryos closely matches the changes observed at the level of mRNA (Fig. 1) and reveals that elav5 embryos express overall lower levels of Ubx protein than their wild-type counterparts. \( n = 9 \) per genotype; error bars indicate s.e.m.; \(* P < 0.01 \) [Wilcoxon matched-pairs signed rank test (non-parametric \( t \)-test)]. (C) Profile quantification of Ubx protein expression along the AP axis (axial expression) as shown in A (standard error is indicated by grey shading). (D) Total Ubx mRNA levels as detected by amplification of the constant Ubx5' exon region are significantly reduced in elav5 embryos compared with wild type. \( n = 6 \) per genotype; error bars indicate s.e.m.; \(* P < 0.05 \) [Wilcoxon matched-pairs signed rank test (non-parametric \( t \)-test)]. (E) Analysis of Ubx transcriptional inputs in elav mutants and wild-type embryos using the 35UZ Ubx-lacZ promoter fusion. No appreciable difference in Ubx-lacZ expression is detected between wild-type and elav5 embryos. (F) Ubx nascent transcript expression detected by FISH using Ubx intronic probes (intron 3) indicates that elav mutant embryos show an overall higher signal in Ubx nascent transcript foci. Inset shows Ubx signal detected in two discrete nuclear foci (orange arrowheads) per nucleus (blue, DAPI). (G) Quantification of Ubx nascent transcript expression in wild type and elav5 mutants shows that the distributions of Ubx nascent transcript foci \([\log(10)]\) versus voxel signal intensity are substantially different among genotypes. Best fit curves are shown. Plotting either the relative number of Ubx foci (middle) or relative intensity of Ubx foci (right) detected in wild-type and elav5 mutant embryos further confirms that elav5 mutants show an overall higher level of expression of Ubx nascent transcripts. \( n = 7 \) per genotype; error bars indicate s.e.m.; \(* P < 0.05 \) [Wilcoxon matched-pairs signed rank test (non-parametric \( t \)-test)].
rates, as this is a regulatory process known to affect the kinetics and outcome of both AS and APA reactions (de la Mata et al., 2003; Licatalosi and Darnell, 2010; Proudfoot, 2011).

To explore this possibility we first tested the total levels of Ubx mRNAs produced in wild type and elav5 mutants and observed that, indeed, elav mutant embryos show reduced levels of Ubx mRNA (Fig. 3D). This finding led us to look more closely at the levels of Ubx transcription in elav mutants. We first explored the transcriptional activity of Ubx cis-regulatory regions using the Ubx transcriptional reporter 35UZ (Irvine et al., 1991). This reporter construct includes 35 kb of Ubx regulatory DNA linked to the lacZ reporter and drives Ubx-like lacZ expression during embryogenesis (Irvine et al., 1991). Contrary to our expectations, these experiments showed no significant differences in Ubx transcriptional activity in the presence and absence of ELAV (Fig. 3E), indicating that ELAV effects on Ubx expression were likely to occur after transcriptional initiation. Bearing this in mind, we then looked at the levels of Ubx nascent transcripts in wild-type and elav5 embryos, developing a series of fluorescence in situ hybridisation (FISH) experiments using intronic probes so as to detect precursor RNAs rather than mature mRNAs as visualised by standard RNA in situ hybridisation (Fig. 3F). Remarkably, we found that in ≥70% of elav5 embryos the abundance of Ubx nascent transcripts was significantly higher than in their wild-type counterparts at an identical developmental stage (Fig. 3F, G). Furthermore, applying an image segmentation and quantification pipeline based on the Fiji imaging platform (Schindelin et al., 2012) to nascent Ubx transcript signals detected in elav5 and wild-type samples, we observed that elav5 embryos show both a higher number of transcriptional foci (Fig. 3G, middle) and an overall higher signal intensity level per focus (Fig. 3G, right).

Based on these experiments, we propose that the absence of ELAV leads to inefficient Ubx RNA processing and retention of RNA at the site of transcription, with a consequential reduction in Ubx mRNA release from DNA and lower Ubx protein formation, suggesting that ELAV-dependent Ubx RNA processing could ‘fine-tune’ the levels of expression of Ubx within the nervous system. This model is consistent with a series of fluorescence in situ hybridisation (FISH) experiments using intronic probes so as to detect precursor RNAs rather than mature mRNAs as visualised by standard RNA in situ hybridisation (Fig. 3F). Remarkably, we found that in ≥70% of elav5 embryos the abundance of Ubx nascent transcripts was significantly higher than in their wild-type counterparts at an identical developmental stage (Fig. 3F, G). Furthermore, applying an image segmentation and quantification pipeline based on the Fiji imaging platform (Schindelin et al., 2012) to nascent Ubx transcript signals detected in elav5 and wild-type samples, we observed that elav5 embryos show both a higher number of transcriptional foci (Fig. 3G, middle) and an overall higher signal intensity level per focus (Fig. 3G, right).
with our data and with previous reports on other systems (including human beta-globin, glyceraldehyde 3-phosphate dehydrogenase, ribosomal protein L3, DNA damage-inducible transcript 3) indicating that non-canonical RNA processing reactions usually prevent mRNA flow to the cytoplasm by tethering processed mRNAs to DNA around transcription sites (Custodio et al., 1999, 2007; Schwartz et al., 2012).

**ELAV removal leads to respecification of neural differentiation programmes under Ubx control**

Having established the roles of ELAV in Ubx expression within the CNS, we then explored further the biological consequences of ELAV-regulated Hox expression during nervous system development, focusing on the functions of Ubx during the establishment of specific cellular programmes within the developing CNS. We reasoned that if ELAV regulation of Ubx RNA processing and protein expression were relevant to the biological functions of Ubx during neural development then we should be able to find specific cellular processes affected in elav mutants and these should be reverted by artificial provision of Ubx protein. To test these predictions we used a cellular system that had been shown to be sensitive to Ubx dosage (the lineage NB7-3 (Fig. 4A)). Here, variations in Ubx expression lead to a notable respecification of the apoptosis patterns of the NB7-3– derived GW neuron (Rogulja-Ortmann et al., 2008). In particular, reductions in Ubx expression, such as those observed in Ubx1 heterozygotes, lead to a decrease in the proportion of GW neurons undergoing apoptosis in the posterior thorax and abdomen (Rogulja-Ortmann et al., 2008). We examined to what extent the apoptosis patterns in GW neurons were affected in elav mutants (Fig. 4B-E). Remarkably, when we restored expression of Ubx mRNAs within the NB7-3 lineage in elav embryos we observed normal apoptosis levels of GW (Fig. 4D,E), demonstrating that the effects of ELAV on the cellular behaviour of GW are mediated by Ubx. Interestingly, selective expression of distinct Ubx splicing isoforms (i.e. Ubx la versus Ubx IVa) in the elav mutant background revealed isoform-specific roles of Ubx proteins in the rescue of GW apoptosis patterns: Ubx la was significantly less efficient than Ubx IVa in rescuing GW apoptosis. These observations suggest that individual Ubx isoforms might play differential roles in neural differentiation along the AP axis. In addition, the fact that Ubx isoform Ia is less efficient than IVa in rescuing normal GW apoptosis patterns provides another explanation for why GW apoptosis is diminished in elav mutants: in the absence of ELAV the system produces overall reduced levels of Ubx protein (Fig. 3A,C) and, in addition, much of the protein formed is of the ‘wrong’ kind (i.e. high

**Fig. 5. Artificial expression of ELAV promotes Ubx protein expression in glial cells.** (A,C,E) Expression of Ubx nascent RNAs (nRNA, red) can be detected (white arrows) in ∼30% of all glial cells (Repo, blue) across dorsal (top), medial (middle) and ventral (bottom) planes within T3 and abdominal segments (not shown). Taking into account that Ubx protein expression is not seen in the glia (Miguel-Aliaga and Thor, 2004), these observations suggest that Ubx protein expression is somehow inhibited in glial cells in which Ubx transcription is active. Grey arrows indicate Ubx transcribing cells in posterior or anterior segments to T3. Approximate midline positions are indicated by a dashed line; please note that symmetry may not be apparent in these images due to the thinness of confocal imaging. (B,D,F) Artificial expression of ELAV within the glial domain by means of repo-gal4 leads to an increase in Ubx protein expression in Ubx transcribing cells (circled with dashed white lines) in the dorsal (B), medial (D) and ventral (F) glia suggesting that ELAV is sufficient to stabilise Ubx protein expression in those glial cells in which Ubx transcription is normally active.

**Quantification under confocal microscopy of the apoptosis patterns of GW: genetic removal of ELAV leads to a significant reduction in the levels of apoptosis of GW in both thoracic and abdominal segments (Fig. 4E), indicating that changes in the ELAV supply can respecify cellular subroutines under Hox gene control within the developing CNS. Similar effects on GW apoptosis were observed in elav mutants (in which expression of ELAV is reduced but not entirely abolished), which show a clear reduction in GW apoptosis when compared with wild-type embryos (supplementary material Fig. S1). In addition, elav mutants display reduced levels of Ubx protein expression in the CNS, confirming by means of an independent genetic context to the elav mutation that reduction in ELAV supply determines a reduction in Ubx protein expression (supplementary material Fig. S5).

Furthermore, the observed reduction in Ubx protein expression level in elav mutants (Fig. 3) is fully consistent with the apoptotic effects observed in NB7-3 in that a reduction of Ubx expression is expected to reduce the level of GW apoptosis, exactly as observed (Fig. 4B-E). Remarkably, when we restored expression of Ubx mRNAs within the NB7-3 lineage in elav embryos we observed normal apoptosis levels of GW (Fig. 4D,E), demonstrating that the effects of ELAV on the cellular behaviour of GW are mediated by Ubx. Interestingly, selective expression of distinct Ubx splicing isoforms (i.e. Ubx Ia versus Ubx IVa) in the elav mutant background revealed isoform-specific roles of Ubx proteins in the rescue of GW apoptosis patterns: Ubx Ia was significantly less efficient than Ubx IVa in rescuing GW apoptosis. These observations suggest that individual Ubx isoforms might play differential roles in neural differentiation along the AP axis. In addition, the fact that Ubx isoform Ia is less efficient than IVa in rescuing normal GW apoptosis patterns provides another explanation for why GW apoptosis is diminished in elav mutants: in the absence of ELAV the system produces overall reduced levels of Ubx protein (Fig. 3A,C) and, in addition, much of the protein formed is of the ‘wrong’ kind (i.e. high...
Ubx Ia low Ubx Iva to efficiently activate GW apoptosis. Interestingly, similar effects on apoptosis were observed when studying the role of ELAV in the apoptotic behaviour of MNa neurons in the posterior thoracic segment (T3) (supplementary material Fig. S4), which showed a clear reduction in apoptosis compared with wild-type embryos. These cells are derived from the NB2-4 lineage and their apoptosis profiles were previously shown to rely on Ubx protein level (Rogulja-Ortmann et al., 2008). All in all, our analysis here reveals that ELAV modifies the outcome of specific cellular subroutines under Hox control within the Drosophila developing embryonic CNS.

Artificial expression of ELAV promotes Ubx protein expression in glial cells

To further explore the biological roles of ELAV in Hox expression within neural tissue we considered the possibility that the absence of ELAV from specific neural cell types (e.g. glial cells) could be related or even contribute to the known lack of Hox protein expression in such cells (Miguel-Aliaga and Thor, 2004). Indeed, the fact that both ELAV and Hox genes are not expressed in the glia could form the basis for an experimental approach to test this idea. Based on the molecular functions of ELAV as an RBP primarily involved in RNA processing and stability, and the fact that its genetic removal does not affect the effects of ELAV removal on the other Hox genes within the CNS vary from gene to gene. (I) Quantification of Antp protein expression in wild-type and elav5 embryos. (C,F,I) Grey shading represents standard error. (A,B,D,E,G,H) DAPI, blue.

Effects of ELAV on the expression of other Hox proteins

Finally, we decided to investigate the generality of our observations by testing whether ELAV was capable of exerting any effects on the expression of other Hox genes within the nervous system. We looked at the effects of ELAV removal on the other Hox genes within the Drosophila Bithorax complex (BX-C), namely abdominal A (abdominal A) and Abdominal B (Abdominal B) (Sánchez-Herrero et al., 1985), given that these genes also display neural-specific patterns of RNA processing (Thomsen et al., 2010). Immunostaining of late embryos (late stage 16) using anti-Abd-A and anti-Abd-B antibodies (Fig. 6A,B,D,E) established that expression of both Abd-A and Abd-B proteins was markedly reduced when ELAV was genetically removed, demonstrating that our observations concerning the effects of ELAV on Ubx expression reflected a more general case concerning all Hox proteins encoded within the BX-C. Nonetheless, the reduction in Ubx, Abd-A and Abd-B protein expression in the absence of ELAV could also be explained by a potentially pleiotropic effect of ELAV on neural gene expression: if ELAV were required for the normal expression and function of cellular components involved in gene expression (e.g. ribosomal proteins) then its removal would be expected to impact the expression of a large
number of genes, including the Hox genes. Further experiments made this possibility very unlikely, as the expression of another Hox gene, Antennapedia (Antp), is unaffected by ELAV removal (Fig. 6G-I), demonstrating that the effects of ELAV on BX-C genes are specific and not the consequence of a general shutdown of protein synthesis in neural tissue caused by the absence of ELAV.

**DISCUSSION**

Our work shows that the pan-neural RBP ELAV regulates Ubx RNA processing, expression and function within the *Drosophila* embryonic CNS, demonstrating that changes in ELAV level specifically alter cellular subroutines under Ubx control. Based on these findings we propose a model whereby the regulation of Hox gene expression by RNA processing factors adapts the morphogenesis of the nervous system according to axial level by specifically activating local programmes of cell differentiation.

Our study also adds to the understanding of the biological roles of ELAV/Hu by revealing that ELAV is part of the molecular machinery underlying an intrinsic and highly specific programme of cell death within the developing *Drosophila* CNS. This is, to our knowledge, the first demonstration of a specific cellular role for this neural protein. Based on the recent finding that ELAV controls the formation of 3′ UTR extensions of several other *Drosophila* mRNAs (Hilgers et al., 2012), we envisage that our present findings are likely to have revealed the first of a wider set of cellular functions played by ELAV through the regulation of its targets in neural tissue.

The notion that the activation of particular patterns of Hox RNA processing via RBPs such as ELAV/Hu can lead to significant fluctuations in Hox protein expression in selected cellular environments suggests the existence of a novel regulatory framework whereby cellular decision making within neural tissue could be adapted to axial level via specific RNA processing programmes triggered and controlled by RNA regulatory factors.

At the molecular level, we interpret the changes observed in *Ubx* RNA processing patterns in the absence of ELAV to represent the outcome of those transcription-processing rounds that were completed despite the absence of this crucial regulator of the process. According to this view, the unavailability of ELAV, with the consequential effects on normal *Ubx* RNA processing, leads to the retention and accumulation of *Ubx* RNAs close to the site of transcription. This interpretation is in line with previous work suggesting that disruption of normal RNA processing reactions can prevent mRNA flow to the cytoplasm by tethering of incompletely processed RNAs to DNA around sites of transcription (Custodio et al., 1999, 2007; Schwartz et al., 2012). We speculate that the cell must have ways to determine, via a series of molecular devices, whether a certain RNA processing pathway has been completed successfully and, should this be not apparent, to trigger an appropriate course of action that seeks to prevent potentially deleterious RNAs from proceeding to export and translation.

Finally, taking into consideration that: (1) Hox genes are evolutionarily conserved between insects and mammals; (2) mammalian Hox genes are key developmental regulators of neural differentiation and undergo substantial levels of RNA processing (P.P. and C.R.A., unpublished); (3) ELAV/Hu RBPs are also evolutionarily conserved between insects and mammals (Yao et al., 1993); and (4) mutations in ELAV-like Hu proteins lead to various forms of neural pathology in humans, we envisage that our findings in *Drosophila* might be of general relevance for understanding the molecular and cellular specification of Hox gene function during the development of the mammalian nervous system. We are currently testing this possibility in the mouse, in which the role of Hox genes during neural specification, differentiation and connectivity has been studied in great detail (Phillippidou and Dassen, 2013).

**MATERIALS AND METHODS**

**Fly strains**

Flies were cultured following standard procedures at 25°C on a 12 h light/dark cycle. Oregon Red was used as a wild-type strain. The following mutant fly strains were used: *elav* null mutant (Robinow and White, 1991) and *UAS-Elav*22, *UAS-Elav*21 (both kindly provided by Matthias Soller, University of Birmingham, UK), *UAS-Apolinaire* (Bardet et al., 2008), *elav* (Bloomingtom Stock Center). Act5c–GAL4 (a gift from Rob Ray, University of Sussex, UK), Ubx–35ULZ (Irvinne et al., 1991), eagle–Gal4 (MZ260) (Dittrich et al., 1997), *UAS-UbxA* and *UAS-UbxAv* (Reed et al., 2010).

**Embryo collection, RNA isolation and RT-PCR**

Embryos were collected using standard procedures and antibody stainings, embryos were fixed following standard procedures. For RT-PCR, total RNA was extracted from staged embryo collections using TRI Reagent (Sigma), followed by RNase-free DNasel treatment (New England BioLabs). Total RNA (1-2 μg) was used for cDNA synthesis using random hexamer or oligo(dT) primers and MuLV reverse transcriptase (Invitrogen). Expression values were normalised using *RpL32* (Rp49). At least three independent biological replicates were performed.

**RNA in situ hybridisations**

Embryos were fixed using standard protocols. Templates of RNA probes for *RNA in situ* hybridisation were obtained from PCR-amplified genomic fragments cloned into pGEM-T (Promega). RNA probes were labelled using a digoxigenin (DIG) RNA Labelling Kit (SP6/T7; Roche) according to the manufacturer’s instructions. Embryos were treated as described (Beckvordersandforth et al., 2008) and hybridised with riboprobes according to standard protocols. RNA probes were detected using anti-DIG-AP (Roche; 1:2000) and a chromogenic reaction using NBT/BCIP substrate (Roche). Enzymatic detection reactions with NBT/BCIP (Roche) were carried out in parallel and stopped at exactly the same time for probes targeting universal and distal 3′UTR sequences to ensure comparability of results. Fluorescent detection of RNA probes was performed using anti-DIG-POD (Roche; 1:300) followed by FITC or Cy3 TSA Plus Amplification Kit (PerkinElmer; 1:50). Subsequent imaging was performed on a Zeiss Axiohot confocal microscope and the images were processed using ImageJ and Adobe Photoshop.

**Immunocytochemistry**

Antibody stains were performed following standard procedures. Primary antibodies were monoclonal mouse anti-Ubx (FP3.38, a gift from Robert White, University of Cambridge; 1:20), mouse anti-Antp (4C3; 1:20), mouse anti-Abd-B (1A2E9; 1:20), rat anti-ELAV (7E8410; 1:300) and mouse anti-ELAV (9F8A9; 1:300) (all from Developmental Studies Hybridoma Bank); goat anti-Abd-A (dH-17, Santa Cruz Biotechnology; 1:20); rabbit anti-Eg (Dittrich et al., 1997; 1:500); mouse anti-Eg (a gift from Chris Doe, University of Oregon, USA; 1:100); rabbit cleaved Drosophila Dcp-1 (Asp216, Cell Signalling; 1:50); guinea pig anti-Ah (J. Urban, University of Mainz, Germany; 1:500), rabbit anti-jugal (A11132, Molecular Probes; 1:300), rabbit anti-GFP (A11055, Molecular Probes; 1:300) and rabbit anti-Repo (as described by Halter et al., 1995; 1:500). Secondary antibodies used were anti-mouse-A488 (A21202; 1:500), anti-rat-A488 (A21202; 1:500) and anti-rabbit-Alexa568 (A10042; 1:500) (all from Molecular Probes); anti-rabbit-Rhodamine (711-025-152; 1:500), anti-rat-Rhodamine (712-026-153; 1:500), anti-guinea pig-Cy5 (706-175-148; 1:500), anti-rat-DyLight 405 (712-475-153; 1:500), anti-goat-Cy3 (705-160-003; 1:500) (all from Jackson ImmunoResearch Laboratories).

**Oligo in situ hybridisation**

Embryos were fixed in 4% paraformaldehyde (PFA; freshly dissolved in PBS):heptane (1:4) solution for 20 min. Following devitellinisation and methanol washes, embryos were refixed in 4% PFA for 20 min.
Permeabilisation was performed in 3 µg/ml Proteinase K solution for 13 min at 22°C, followed by incubation on ice for 1 h. Proteinase K was inactivated by washes in 2 mg/ml glycine in PBTrween (PBS with 0.1% Tween 20) and embryos refixed for 20 min in 4% PFA. Prehybridisation was carried out overnight at 37°C. DIG-labelled oligo probes were hybridised for 1 day at 37°C, washed in hybridisation buffer at 40°C and in PBTrween at room temperature. For detection of oligo probes, embryos were incubated with sheep anti-DIG-AP antibody (Roche) and stained for 20 h at 4°C using the ABC Kit (Vectorstain). After a series of washes, embryos were fixed in 4% formaldehyde. For identification of elav\(^*\) mutant embryos, a rabbit anti-fibrin-gal antibody was used (55976, MP Biomedicals; 1:1000). Embryos were mounted and stored in 70% glycerol.

Bioinformatic search of ultraconserved ELAV targets

We scanned the Ubx sequence of Drosophila melanogaster for elements with high similarity to experimentally validated EBSSs present in the previously reported ELAV target genes Neuroglian (Nrg, Nrg-like) (TTTTTGTGT, TTGTGTTTTT, TTITTTAT, TTTTTTTT) (Lisbin et al., 2001) and erect wing (ewg, ewg-like) (AAUUUUUU, CAUUUUUU) (Soller and White, 2003). To explore the evolutionary conservation of these elements across related Drosophila species we retrieved the sequences corresponding to the full Ubx transcription unit from the 12 fully sequenced drosophilids from the UCSC Genome Browser (D. melanogaster, D. simulans, D. sechellia, D. yakuba, D. erecta, D. ananassae, D. pseudoobscura, D. persimilis, D. willistoni, D. mojavensis, D. virilis, D. grimshawi) and confirmed their identity as Ubx-encoding sequences using BLAST. Ubx sequences derived from different Drosophila species were then aligned using the mVISTA LAGAN algorithm (Brudno et al., 2003). We defined as putative ELAV binding sites (pEBSSs) all those elements that: (1) presented an exact match to those present in Nrg and ewg and (2) were evolutionarily conserved in a homologous position across eight or more of the 12 drosophilid species (i.e. ultraconserved). In addition to sequence elements similar to those present in Nrg and ewg RNAs, we also included in our list of Ubx pEBSSs a previously described AU-rich element (ARE) present in the 3\'UTR of D. melanogaster Ubx (Cairroz et al., 2009) given that AREs were shown to be crucial regulators of RNA metabolism through binding of Hu proteins (López de Silanes et al., 2004). All 16 pEBSSs are presented in supplementary material Fig. S3.

Site-specific mutation of the putative ELAV binding sequences contained within EBSS3 and EBSS8 (site 3 WT, ATTTTTT; site 3 Mut, AGTGTGT; site 12 WT, TTTTTTTT) (Lisbin et al., 2004) presented an exact match to those present in Ubx-encoding sequences using bioinformatic analysis, A.R.-O., J.P.-O., C.V., J.A., G.M.T. and C.R.A. analysed data; and C.R.A. designed research, supervised the study and wrote the paper.

EMSA experiments

Recombinant GST-ELAV protein was produced in E. coli using an expression vector kindly provided by Matthias Soller (described in Soller and White, 2003) following the manufacturer’s instructions (Amersham). GST tag was cleaved with PreScission Protease (Amersham). EMSA experiments were performed as described by Soller and White (Soller and White, 2003). In brief, gel purified ‘body’ labelled RNA was incubated with tRNA (50 µg/ml) at 65°C for 5 min, renatured at room temperature for 10 min and then mixed with binding buffer (50 µM Tris-HCl pH 7.5, 40 mM KCl, 35 mM NaCl, 25 µg/ml tRNA, 0.5 mM DTT, 50 µg/ml BSA) in a total of 10 µl and incubated at room temperature for 20 min with either 0, 200, 400 or 600 mM ELAV protein. Ten microlitres reaction with 3 µl 50% glycerol were loaded on 4% (80:1 acrylamide/bisacrylamide) gel purified multimeric site-directed mutagenesis.

UV cross-linking experiments

Uniformly labelled RNA (typically 700 pM) was incubated in 5\(^{\circ}\) binding buffer (400 mM KCl, 100 mM HEPES pH 7.6, 20 mM MgCl\(_2\), 25% glycerol and 5 mM DTT). 1 µl tRNA (1 mg/ml) and 38 µg/µl ELAV protein or 40% nuclear extract in 10 µl total volume. The mix was incubated at room temperature for 10 min and then divided into two samples, one of which was subsequently UV cross-linked (Stratalinker) for 12 min on ice whereas the other (negative control) was kept on ice in the absence of UV. Samples were then treated with RNase A at 37°C for 15 min. Reaction products were resolved by SDS-PAGE and dried gels were exposed to phosphorimagery plates.

Cross-linking and immunoprecipitation (CLIP) experiments

Immunoprecipitation of nuclear extracts from an overnight collection of embryos was performed following the RNA immunoprecipitation protocol of Hilgers et al. (Hilgers et al., 2012), except that the nuclear extracts were incubated overnight with 2 µg mouse anti-ELAV 9F8A9 or mouse anti-Tub7 E7 antibodies (Developmental Studies Hybridoma Bank).

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Competing interests

The authors declare no competing financial interests.

Author contributions

A.R.-O., J.P.-O., C.V., E.L. and S.T. performed experiments; P.P. carried out the bioinformatic analysis, A.R.-O., J.P.-O., C.V., J.A., G.M.T. and C.R.A. analysed data; J.P.-O., A.R.-O. and G.M.T. made comments on the manuscript; G.M.T. supervised the study; and C.R.A. designed research, supervised the study and wrote the paper.

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Supplementary material

Supplementary material available online at http://dev.biologists.org/lookup/suppl/doi:10.1242/dev.101519/-/DC1

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**Effects of the elav<sup>ts</sup> allele on the apoptotic behaviour of GW neurons.** Analysis of apoptotic behaviour of GW cells in the thoracic/abdominal segments of control elav<sup>ts/ma</sup> (purple) and elav<sup>ts/ts</sup> mutants (red) further confirms that genetic removal of ELAV expression leads to a significant change in the incidence of apoptosis on GW neurons.
Ectopic expression of ELAV during late embryogenesis does not cause any detectable increase in the expression of long 3′UTR Ubx mRNA forms. RNA in situ hybridisation of stage 16 embryos with Ubx distal 3′UTR probes (symbolised by a red line) shows that the artificial increase of ELAV expression from a UAS-elav construct driven by the actin-gal4 driver (act>Elav, (B)) shows no appreciable change in the pattern of long Ubx 3′UTR expression when compared to wild type embryos (A) suggesting that endogenous expression of ELAV at this late embryonic stage is likely saturating and/or that a maximal production of long-3′UTR Ubx RNA forms had been achieved.
Computational prediction of putative ELAV binding sites (pEBSs) on Ubx RNAs detects sixteen candidate elements. In order to determine putative ELAV binding sites within Ubx RNA we combined the scanning of *Drosophila melanogaster* Ubx sequences for elements with high similarity to experimentally validated ELAV-binding sites present in the genes *neuroglian* (*nrg*, Nrg-like) (tttttgtt, ttgttttt, ttgttatt, ttatttt) (Lisbin et al., 2001) and *erect-wing* (*ewg*, ewg-like) (aaauuuuu, caauuuuu) (Soller, M., and K. White, 2003) with an analysis of the evolutionary conservation of these elements across twelve related Drosophila species (*D. melanogaster*, *D. simulans*, *D. sechellia*, *D. yakuba*, *D. erecta*, *D. ananassae*, *D. pseudoobscura*, *D. persimilis*, *D. willistoni*, *D. mojavensis*, *D. virilis*, *D. grimshawi*). This approach defined fifteen putative Elav binding sites (pEBSs) which (i) presented an exact match to those in *nrg* and *ewg* and (ii) were evolutionarily conserved in a homologous position across eight or more Drosophila species (i.e. ultraconserved) out of the twelve Drosophilid species investigated. In addition to sequence elements similar to those present in *nrg* and *ewg* RNAs we also included in our list of Ubx pEBSs a previously described A-U rich element (ARE) present in the 3' UTR of *D. melanogaster* Ubx (Site 16) (Cairrao et al., 2009) given that ARE elements were shown to be critical regulators of RNA metabolism through binding of Hu proteins (Lopez de Silanes et al., 2004).
**Effects of ELAV on the apoptotic behaviour of MNa neurons.** Analysis of apoptotic behaviour of MNa cells in the posterior thoracic segment (T3) in wild type (purple) and elav^5 mutants (red) by means of: (A) the fluorescent genetically-encoded caspase sensor *Apollinaire* (Bardet et al. (2008) PNAS 105(37): 13901-13905) and (B) the number of Dcp-1^+ cells demonstrates that MNa apoptotic rates are markedly reduced (30-50% reduction depending on method) when Elav is absent from the system confirming the same trend observed in the GW motorneuron system.
**Effects of the **elav<sup>ts1</sup>** allele on expression of Ubx protein.** (A,B) Comparison of ELAV protein (magenta) expression levels in dissected ventral nerve cords of wild type (A) and elav<sup>ts1</sup> mutant (B) embryos at stage 16 shows that ELAV protein levels are reduced in the elav<sup>ts1</sup> mutant. (C,D) Expression levels of Ubx protein (cyan) are clearly higher in wild type (C) than in elav<sup>ts1</sup> mutant embryos (D) further confirming that reducing expression of ELAV protein results in lower levels of Ubx protein within the CNS. (E) Average profile quantification of Ubx protein along the A-P axis of wild type (purple) and elav<sup>ts1</sup> mutant embryos (red) (standard error is indicated in light purple and pink shading, respectively)