RESEARCH ARTICLE

*Drosophila* small heat shock protein CryAB ensures structural integrity of developing muscles, and proper muscle and heart performance

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ABSTRACT

Molecular chaperones, such as the small heat shock proteins (sHsps), maintain normal cellular function by controlling protein homeostasis in stress conditions. However, sHsps are not only activated in response to environmental insults, but also exert developmental and tissue-specific functions that are much less known. Here, we show that during normal development the *Drosophila* sHsp CryAB [L(2)ef] is specifically expressed in larval body wall muscles and accumulates at the level of Z-bands and around myonuclei. CryAB features a conserved actin-binding domain and, when attenuated, leads to clustering of myonuclei and an altered pattern of sarcomeric actin and the Z-band-associated actin crosslinker Cheerio (filamin). Our data suggest that CryAB and Cheerio form a complex essential for muscle integrity: CryAB colocalizes with Cheerio and, as revealed by mass spectrometry and co-immunoprecipitation experiments, binds to Cheerio, and the muscle-specific attenuation of cheerio leads to CryAB-like sarcomeric phenotypes. Furthermore, muscle-targeted expression of CryAB<sup>R120G</sup>, which carries a mutation associated with desmin-related myopathy (DRM), results in an altered sarcomeric actin pattern, in affected myofibrillar integrity and in Z-band breaks, leading to reduced muscle performance and to marked cardiac arrhythmia. Taken together, we demonstrate that CryAB ensures myofibrillar integrity in *Drosophila* muscles during development and propose that it does so by interacting with the actin crosslinker Cheerio. The evidence that a DRM-causing mutation affects CryAB muscle function and leads to DRM-like phenotypes in the fly reveals a conserved stress-independent role of CryAB in maintaining muscle cell cytoarchitecture.

KEY WORDS: *Drosophila*, Cheerio, CryAB, Heart, Muscle, sHsp

INTRODUCTION

Most heat shock proteins operate as molecular chaperones in stress conditions and play a central role in the maintenance of normal cellular function by preventing the aggregation of misfolded proteins into large deleterious complexes (Morimoto, 1998). However, some heat shock proteins are also activated in a stress-independent way to control the transport, folding, assembly and degradation of various proteins (Colinet et al., 2010; Lindquist and Craig, 1988; Mymrikov et al., 2010; Sorensen et al., 2003). The cell-specific expression of small heat shock proteins (sHsps) during development, cell differentiation or after activation by growth factors and oncogenes has been reported in a wide range of organisms, including *Drosophila* and mammals (Michaud and Tanguay, 2003; Morimoto, 1998). For example, the *Drosophila* sHsp Hsp22, in spite of its heat-induced expression and nonspecific chaperone activity, is regulated during normal development and plays a role in protection against apoptosis (Colinet et al., 2010; Morrow and Tanguay, 2003).

In human, seven sHsps are expressed in cardiac and skeletal muscles, including αB-crystallin (CRYAB), HSPB2 and HSPB3, which are induced during the initial phase of skeletal muscle differentiation, controlled by MYOD1, suggesting a muscle-specific function in development. Also, Hspb2 and CryAB proteins display sarcomeric localizations; they are localized on Z-bands or I-bands of the skeletal and cardiac muscle myofibrils, maintaining and protecting contractile cytoskeletal structures (Mymrikov et al., 2010; Sugiyama, 2000).

CryAB displays particularly intriguing cell-specific functions, acting as a chaperone for intermediate filament (IF) proteins such as desmin in muscle cells and vimentin in eye lenses. IFs are known to overlie Z-discs and M-lines, stabilizing myofibrils and protecting them from mechanical insult (Goldfarb and Dalakas, 2009). IFs also link membranous organelles, such as nuclei and mitochondria, and play an important role in maintaining their correct morphology and positioning.

CryAB stabilizes IFs and prevents them from aggregating under stress conditions, and also assists IFs during developmental reorganizations (Nicholl and Quinlan, 1994). Importantly, mutations in CryAB, such as replacement of arginine by glycine at conserved position 120 (R120G), lead to altered CryAB-IF interactions responsible for desmin-related myofibrillar myopathy (DRM) (Dalakas et al., 2000; Goldfarb and Dalakas, 2009; Goldfarb et al., 2004). The R120G missense mutation alters the spatial organization of CryAB, leading to the loss of its chaperone activity and the formation of desmin aggregates in muscle fibers (Vicart et al., 1998; Perng et al., 2004). As a result, the desmin IF network is severely affected, leading to altered myofibril alignment, irregular sarcomere architecture and abnormal mitochondrial organization (Goldfarb and Dalakas, 2009). In DRM patients this leads to progressive muscle weakness, including the limb, neck and respiratory muscles, for which no appropriate treatments have yet been developed.

To further characterize muscle-specific roles of CryAB and better understand DRM-associated muscle defects we took advantage of its evolutionary conservation to analyze the function of the *Drosophila* CryAB ortholog. The fruit fly *Cryab* ortholog, CryAB, which is also known as lethal (2) essential for life (*l(2)efl*), has been shown to...
be involved in the modulation of insulin signaling and the regulation of lifespan (Flatt et al., 2008) but its expression and function in differentiated muscle have not been analyzed.

Here we show that, like its vertebrate counterpart, the Drosophila CryAB protein displays stress-independent muscle-specific expression. In larval muscles it accumulates around the myonuclei and at the level of Z-bands and is required for correct nuclei localization, myofibril integrity and muscle performance. CryAB features a conserved actin-binding domain and is required for the correct sarcomeric pattern of actin filaments and also of the Z-band-associated actin crosslinker Cheerio. CryAB binds to Cheerio in muscles, indicating that this interaction might help to maintain myofibrillar integrity in Drosophila muscle. We also report that muscle-targeted expression of CryAB carrying the DRM-associated R120G mutation leads to severe alterations in the striated actin pattern, reduced muscle performance and marked cardiac arrhythmia. These observations point to a conserved stress-independent role of CryAB in the maintenance of muscle cell cytoarchitecture. Thus, our findings provide evidence that the Drosophila sHsp CryAB shares not only sequence but also functional similarities with its human counterpart, suggesting that Drosophila can serve as a model system for dissecting molecular determinants of myofibrillar myopathies.

RESULTS
Drosophila CryAB is a conserved sHsp with stress-independent expression in larval body wall muscles

The Drosophila sHsp genes are clustered within the 67B region on the left arm of the third chromosome (Corces et al., 1980), except for CryAB [l(2)efl], which is located on the right arm of the second chromosome (Kurzik-Dumke and Lohmann, 1995). Drosophila CryAB shows significant homology to human CRYAB (Fig. 1A) and to other sHsp members, in particular the Hspb1 and Hspb8 subfamilies (Fink et al., 2009; McWilliam et al., 2013) (Fig. 1C). CryAB encodes a protein of ~22 kDa (Fig. 1B) that has a highly conserved α-crystallin domain located in the C-terminal portion of the protein (Fig. 1A), similar to other sHsps (Ingolia and Craig, 1982). Within this domain, CryAB features several conserved motifs, including an actin-binding domain, a capping box and the residues R120 and D109 involved in desminopathies (Fig. 1A).

In addition to coordinately induced expression in response to a heat stress, several members of the sHsp family show a specific pattern of expression in diverse tissues and cells (Marin and Tanguay, 1996; Michaud and Tanguay, 2003). To determine whether CryAB also displays stress-independent expression during development we first analyzed its expression pattern in third instar larvae. Using a polyclonal antibody raised against the whole CryAB protein, we found that CryAB is abundantly expressed in the larval body wall muscles (Fig. 2). Within an individual larval muscle, CryAB accumulated in the perinuclear area (Fig. 2A) and displayed a striated sarcomeric pattern at the level of Z-lines and M-lines (Fig. 2A-D). We confirmed this observation by the immunogold detection of CryAB on the ultrathin sections visualized in electron microscopy (EM) (supplementary material Fig. S1). When analyzing CryAB distribution on longitudinal optical sections through the muscle fibers, we also found that it accumulated around the nuclei and enveloped the external surface of myonuclei (Fig. 2E). We observed a granular pattern of CryAB both around

Fig. 1. Drosophila CryAB is a highly conserved member of the CryAB sHsp family that is phylogenetically related to the Hspb1 and Hspb8 sHsp families. (A) Protein sequence alignment of Drosophila and human CryAB proteins. Conserved amino acid residues are in red and conserved functional domains are highlighted by boxes or underlining. (B) Western blot of third instar larvae protein extract showing the 22 kDa band of the expected size of CryAB protein. (C) Phylogenetic tree of the related CryAB, Hspb1 and Hspb8 families.
CryAB displays Z-band-associated and perinuclear expression in larval muscles. (A,C) CryAB expression at the superficial level of external myofibrils. Note the accumulation of CryAB at the level of Z-bands (arrowhead) and around the nuclei (arrow). (B,D) CryAB expression within the myofiber. CryAB protein is detected at the Z-bands (white arrowhead) but also in M-lines (yellow arrowhead). (E) A portion of larval segment border muscle at the level of the nuclei. Note high CryAB accumulation in a perinuclear area (arrow) and at the external surface of the nucleus. (F) Imaris-rendered 3D reconstruction of confocal scans through ventral VL3 larval muscle stained for CryAB and with phalloidin (F-actin). Note the external localization of CryAB on the top of phalloidin-stained Z-bands (arrowhead). Asterisks indicate nuclei. Scale bars: 10 µm.

Fig. 3. Muscle-specific attenuation of CryAB leads to morphological muscle defects and disrupted sarcomeric Z-band pattern. (A) Lateral view of wild-type third instar larval muscles stained with phalloidin. (B,C) Effects of muscle-targeted RNAi attenuation of CryAB. Arrows in B indicate splitting of myofibers. Arrow in C denotes fuzzy Z-band pattern; compare with wild-type muscles (asterisks in A). (D) A portion of wild-type VL3 muscle showing a regular pattern of Msp300 co-stained with phalloidin. (E) Representative view of a portion of VL3 and VL4 muscles from Mef2>CryAB-RNAi animals. Arrows point to muscle areas with a fuzzy actin pattern in which Msp300 labeling is reduced or missing. (F) EM view of wild-type VL4 sarcomeres. (G) Similar view from Mef2>CryAB-RNAi larvae showing interrupted Z-bands. Yellow arrowheads point to Z-bands, which are also traced by the red line. Asterisks indicate electron-dense accumulations of glycogen. Double-ended arrows indicate the extension of sarcomeres. (H) Statistical representation of muscle defects observed in Mef2>CryAB-RNAi larvae. (I) RT-PCR analysis of CryAB attenuation in Mef2>CryAB-RNAi versus wild-type (Wt) larvae. Gapdh provides a loading control. Scale bars: 20 µm in A-E; 2 µm in F-G.

CryAB is required for Z-band patterning and muscle integrity

To assess the role of CryAB in larval muscles we applied RNAi-mediated muscle-specific gene attenuation (Fig. 3I) using two different UAS-CryAB-RNAi lines (VDRC 40532 and 107305) crossed to the Mef2-Gal4 driver (Fig. 3; supplementary material Fig. S2). We observed that most Mef2>CryAB-RNAi larvae (from both RNAi lines examined) exhibited defects in sarcomeric organization, characterized by an irregular, fuzzy pattern of phalloidin staining in the large muscle segments (Fig. 3C,H; supplementary material Fig. S2). This aberrant organization of sarcomeric actin is consistent with the fact that CryAB has an actin-binding domain (ABD) (see Fig. 1), which appears to play an important role in actin filament organization assuming that muscle-targeted expression of CryAB carrying a mutated ABD leads to RNAi-like phenotypes (supplementary material Fig. S3). Moreover, CryAB attenuation also leads to muscle splitting (Fig. 3B; supplementary material Fig. S4A), which in some cases is associated with altered muscle attachments (Fig. 3B) or even with the loss of affected muscle (supplementary material Fig. S4B). The observed muscle defects are not due to apoptotic events, as we do not detect Caspase 3 activation associated with muscles in the CryAB-RNAi context (supplementary material Fig. S2I). Altogether, these
findings demonstrate a role of CryAB in the maintenance of muscle fiber integrity.

To better characterize the influence of CryAB attenuation on the sarcomeric pattern we used Msp300 antibody to reveal the Z-bands (Fig. 3D,E). We found that, in the muscle segments displaying fuzzy phalloidin staining, the Z-band-associated signal of Msp300 was weak or lacking (Fig. 3E). We also noted that Msp300 was irregularly distributed around the myonuclei (Fig. 3D,E), suggesting that it might potentially interact with CryAB. We tested this possibility by co-immunoprecipitation (co-IP) (supplementary material Fig. S5) and found that there is no physical interaction between these two Z-disk-associated proteins. Gaps in Z-bands were also detected when examining EM sections of CryAB attenuated muscles (Fig. 3F,G), supporting the view that CryAB acts to stabilize Z-band-associated sarcomeric components.

Assuming that each of the larval muscles displays a specific number of sarcomeres (Bate, 1990), we also tested whether muscle-targeted CryAB knockdown impacted on sarcomere number. We focused on three distinct muscles (VL3, VL4 and SBM) and found that, in all cases, the number of sarcomeres was significantly reduced (supplementary material Fig. S4A), whereas, except for the fuzzy pattern areas, the size of sarcomeres was unaffected (supplementary material Fig. S4B). Thus, CryAB also appears to play a role in larval muscle growth, which occurs by the addition of sarcomere units.

**CryAB is required for correct myonuclei localization, mitochondrial organization and muscle performance**

Next we investigated whether the cellular organization and the performance of muscles are affected by the reduction of CryAB function. Previous studies demonstrated that the localization of nuclei is crucial for proper muscle performance (Metzger et al., 2012) and that mitochondria are highly organized in muscles (Picard et al., 2012). The accumulation of CryAB around the nuclei (Fig. 2) prompted us to test whether it was involved in the correct distribution of myonuclei within the muscle fibers. We found that in the CryAB-RNAi context they were irregularly distributed along the muscle fibers (Fig. 4A,B). Nuclei are also misarranged in muscles overexpressing CryAB with a mutated ABD (supplementary material Fig. S3), providing evidence that the actin binding function of CryAB is essential for nuclei localization.

Cheerio, which makes a link between perinuclear actin and cytoplasmic actin cables, is involved in nuclei positioning in Drosophila nurse cells (Huelsmann et al., 2013). It is also well known that in vertebrate muscles the Cheerio ortholog Filamin C is associated with Z-bands and when mutated leads to myofibrillar myopathies (Goldfarb and Dalakas, 2009). We tested whether Cheerio is expressed in larval muscles and whether CryAB influences its localization. Cheerio was detected aligned with Z-bands (Fig. 4C), but its pattern was more expansive than the sharp Z-line revealed by phalloidin. As in nurse cells, it also accumulated in the perinuclear area. However, in muscles attenuated for CryAB the sarcomeric localization of Cheerio was severely affected, with pronounced accumulation around the mislocalized nuclei (Fig. 4D), strongly suggesting that CryAB is required for Cheerio localization. In addition, the mitochondrial signal appeared significantly reduced in CryAB-RNAi muscles compared with the wild type (Fig. 4E,F), indicating impaired respiratory functions. This possibility was supported by EM analysis revealing mitochondrial swelling, broken cristae and glycogen deposits (Fig. 4G,H).

To test whether the described morphological alterations affected the locomotive abilities of larvae, we carried out three behavioral tests. We measured the speed of crawling and found that **CryAB-RNAi** larvae needed ~20% more time to travel the appointed distance (Fig. 4I). We also measured the time needed for each larva to right itself from the dorsal to ventral position. In this test, **CryAB-RNAi**-attenuated individuals took twice as long (Fig. 4J).

Fig. 4. CryAB is required for muscle integrity and performance. (A) Distribution of nuclei in wild-type VL3 and VL4 muscles. VL3 muscle diameter is indicated by the yellow line. A slightly reduced number of nuclei is observed in muscles with attenuated CryAB, which could be due to destabilization of myofibrillar architecture and subsequent loss of some of mislocalized nuclei. (B) Mef2>CryAB-RNAi VL3 muscles displayed reduced diameter (yellow line) and mislocalized nuclei (arrows). (C) Wild-type pattern of Z-band-associated Cheerio. Asterisks indicate nuclei. (D) Disrupted Cheerio pattern in Mef2>CryAB-RNAi context. (E) Wild-type pattern of mitochondria revealed by MitoTracker Red. (F) Attenuation of CryAB leads to a reduced MitoTracker signal. (G) EM view of wild-type third instar muscle with functional mitochondria. (H) EM view of a Mef2>CryAB-RNAi muscle with morphologically abnormal mitochondria. Arrowheads indicate mitochondria and asterisks indicate the Z-band. (I-L) Muscle performance tests showing reduced motility and affected contractility of Mef2>CryAB-RNAi larvae. Error bars indicate s.e.m.; n=30 flies per genotype. *P<0.05 (one-way ANOVA). Scale bars: 20 µm in A,B; 10 µm in C,D; 5 µm in E,F; 1 µm in G,H.
least 20% fewer peristaltic movements than controls (Fig. 4L). To confirm the contraction disturbance, we also compared the length of muscle fibers relaxed by EDTA with that of contracted muscle fibers. This showed that the analyzed muscles from CryAB-RNAi individuals had a significantly lower contractility index (Fig. 4K). Thus, these data show that CryAB is required for proper muscle contraction and efficient motility. Finally, we found that these functions of CryAB in muscles also influence the survival of flies (supplementary material Fig. S3C).

The R120G mutation of DRM patients leads to a dominant-negative CryAB protein and affects sarcomeric pattern and muscle performance

DRM is caused by the missense R120G mutation within the α-crystallin domain of CRYAB. It is due to intracellular aggregations of desmin and Vimentin IFs, which abnormally interact with the mutated CRYAB (Simon et al., 2007; Zobel et al., 2003). Comparison of amino acid sequences of human and Drosophila CryAB proteins showed conservation of arginine at position 120 (Fig. 1A) and prompted us to test whether the R120G mutation in Drosophila CryAB could mimic muscle defects observed in DRM patients. We generated transgenic lines carrying either the wild-type or mutated form of CryAB fused to GFP (Fig. 5A-D').

Compared with endogenous CryAB (Fig. 2), both CryAB-GFP and CryABR120G-GFP displayed irregular accumulations along the muscle fibers in addition to their localization in sarcomeres (Fig. 5A'−D'). We therefore tested whether these accumulations affected sarcomeric organization. In the area where the wild-type CryAB-GFP accumulated, the sarcomeric pattern marked with phalloidin
appeared normal, although the intensity of actin bands was attenuated (Fig. 5A–A″, asterisk). Occasionally, we observed misalignments of myofibrils (Fig. 5A, arrowheads), suggesting that the overexpression of CryAB leads to a local destabilization of myofibrillar organization. In contrast to these mild phenotypes, the accumulations of CryABR120G resulted in severely altered sarcomeric patterns (Fig. 5B–D″), with virtually all muscles affected. We observed a striking complementary distribution of CryABR120G with respect to sarcomeric actin along the muscles. Large segments of muscle fibers with high levels of CryABR120G displayed reduced phalloidin staining with abnormally interspaced and irregular Z-bands (Fig. 5B, arrowheads), whereas the neighboring CryABR120G-free regions were characterized by a high-intensity phalloidin signal probably resulting from the disorganization and local compaction of sarcomeres (Fig. 5B, arrows). In addition to localizing to the Z-bands, CryABR120G accumulated in either a fuzzy pattern (Fig. 5B′, B″) or a punctate pattern suggesting the formation of aggregates (Fig. 5C′, C″). We also observed small patches of accumulated CryABR120G (Fig. 5D–D″) in which the sarcomeric pattern was not particularly affected. However, we noted that within each sarcomere CryABR120G was not only present in the Z-bands but also in two additional stripes between the Z-bands (Fig. 5D″), and that myofibrils were misaligned (Fig. 5D, arrowheads).

These alterations prompted us to test whether the mutated form of CryAB also affected larval muscle function. We tested muscle performance using the righting, motility and journey tests. In all these tests (Fig. 5E–G), Mef2>CryABR120G larvae showed markedly reduced muscle performance than those expressing wild-type CryAB in muscles. We also found that muscle-targeted expression of CryABR120G affected muscle contractility (Fig. 5H). The fact that several phenotypes of CryABR120G overexpression are similar to those observed after knocking down CryAB suggests that CryABR120G acts as a dominant negative.

**Cardiac-specific attenuation of CryAB and expression of CryABR120G impair heart performance**

A recent study demonstrated that when the mutated human CRYAB is expressed in adult *Drosophila* heart it mimics DRM-related cardiac defects such as arrhythmia and an increase in systolic heart diameter (Xie et al., 2013). However, it remained unclear whether these defects were due to reduced functions of the endogenous *Drosophila* CryAB gene. We therefore tested whether CryAB is expressed in the adult *Drosophila* heart and if it is required for normal heart function.

We found that CryAB protein is present in a striated pattern in both the transverse myofibrils of the myocardium and in the layer of the longitudinal muscle fibers that is associated with the heart (Fig. 6A). This CryAB expression plays an important role in the adult heart because the heart-specific attenuation of CryAB resulted in an accelerated cardiac rhythm (Fig. 6B,E). The video-captured M-modes of hearts expressing CryAB RNAi illustrate the increased heart rate and the rhythmic beating patterns. M-modes from hearts expressing CryABR120G reveal arrhythmic beating patterns. Diastolic (red) and systolic (black) intervals are indicated in each M-mode trace. Scale bars: 200 μm in A, left; 25 μm in A, middle and right.
control flies (Fig. 6E). The heart period was strongly reduced in young flies (Fig. 6B,E) and continued to be significantly shortened in aged Hand>CryAB-RNAi animals (data not shown). The shortened heart periods in CryAB-attenuated flies were mainly due to decreased diastolic and systolic intervals (Fig. 6E; supplementary material Fig. S6). Conversely, the heart periods of flies overexpressing the wild-type or R120G form of CryAB were unaffected or only slightly (non-significantly) decreased (Fig. 6B). However, heart-specific expression of CryABR120G led to a significant increase of arrhythmia in 1-week-old flies (Fig. 6C), a phenotype similar to that observed in transgenic Drosophila lines expressing the mutated form of human CRYAB in the heart (Xie et al., 2013). Additionally, altering the expression of CryAB or introducing CryABR120G in the heart resulted in enlarged heart diameter (Fig. 6D; supplementary material Fig. S6) and significantly reduced the fractional shortening in CryABR120G flies, impairing systolic function (supplementary material Fig. S6). Thus, this analysis reveals a novel role of CryAB in the regulation of heartbeat and demonstrates that introducing the R120G mutation into Drosophila CryAB leads to pathological cardiac arrhythmia and mimics cardiac defects observed in DRM patients.

CryAB interacts with Cheerio in larval muscles

The altered Cheerio pattern in larval muscles with attenuated CryAB prompted us to test whether these two proteins physically interact. We first performed a co-IP experiment with anti-CryAB antibody followed by proteomics analyses. Peptide sequencing of co-immunoprecipitated proteins ranging from 30 to 170 kDa revealed that not only actin but also Tropomyosin 1 and 2 and a few other sarcomeric components, including α-Actinin, Myosin heavy chain and Paramyosin, were strongly represented in CryAB-containing protein complexes (supplementary material Table S1). Importantly, mass spectrometry data also revealed nine matches in Cheerio, corresponding to six different peptides all located in the C-terminal...
involves high-molecular-mass Hsps such as Hsp70 (McArdle et al., 2010). We tested whether knocking down Drosophila Hsc70, the mammalian co-chaperone Starvin/BAG3, which plays an important role in the maintenance of Z-band components (Amrdt et al., 2010). We tested whether knocking down starvin in muscles influences CryAB sarcomeric localization. The attenuation of starvin led to Z-band breaks and an irregular sarcomeric actin pattern associated with clustering of myonuclei (supplementary material Fig. S8). However, the CryAB sarcomeric pattern and perinuclear localization appeared unaffected (supplementary material Fig. S8), supporting a view that CryAB-Cheerio and Starvin-Cheerio interact independently. Since the CRYAB-filamin interaction contributes to the muscle defects and affected muscle performance observed in CryAB-RNAi larvae.

It has been demonstrated that unfolded filamin interacts with Drosophila/mammalian co-chaperone Starvin/BAG3, which plays an important role in the maintenance of Z-band components (Amrdt et al., 2010). We tested whether knocking down starvin in muscles influences CryAB sarcomeric localization. The attenuation of starvin led to Z-band breaks and an irregular sarcomeric actin pattern associated with clustering of myonuclei (supplementary material Fig. S8). However, the CryAB sarcomeric pattern and perinuclear localization appeared unaffected (supplementary material Fig. S8), supporting a view that CryAB-Cheerio and Starvin-Cheerio interact independently. Since the CRYAB-filamin interaction has not as yet been tested in vertebrate skeletal muscles, whether this interaction is a conserved feature of CryAB proteins remains to be elucidated.

**DISCUSSION**

The physiological response to stressful conditions in muscle tissue involves high-molecular-mass Hsps such as Hsp70 (McArde et al., 2004), together with a set of sHsps (Koh and Escobedo, 2004; Haslebeck et al., 2005). However, besides this classical role, in recent years stress-independent and tissue-specific expression and function have been reported for several members of the Hsp gene family (Michaud and Tanguay, 2003; Rupik et al., 2011).

Here, we provide evidence that in Drosophila, the sHsp subfamily member CryAB [which is also known as l(2)efl (Kurzik-Dumke and Lohmann, 1995)], which encodes the fruit fly ortholog of mammalian CRYAB, is specifically expressed in developing larval somatic muscles and is required for myofibrillar integrity and muscle performance.

**The tissue-specific expression and subcellular localization of CryAB are reminiscent of its vertebrate counterpart**

In the developing mammalian heart and skeletal muscles, CRYAB and six other sHsps (HSPB1, HSPB2, HSPB3, HSPB6, HSPB7 and HSPB8) are expressed at a relatively high levels (Davidson et al., 2002). It is not known whether all these genes diverged from a common ancestor with developmental functions, but our phylogenetic analysis indicates that two sHsps involved in muscle development, Hspb8 and CryAB, do have a common ancestor. We also showed that, like its vertebrate counterpart (Doran et al., 2007), the fruit fly CryAB displays muscle- and heart-specific expression and accumulates at the level of the Z-bands and around the nuclei. Interestingly, *Drosophila* CryAB is also localized in between the Z-bands and muscle cell membranes and displays a punctate expression pattern that suggests that it might be a component of Z-band-associated protein complexes. It is well known that vertebrate CRYAB is also expressed at the level of Z-bands and, by acting as a chaperone of the type III IF protein desmin, helps to maintain cytoskeletal integrity in skeletal and cardiac muscle cells (Golenhofen et al., 1999). Desmin IFs are mainly associated with Z-bands and interact with other sarcomeric proteins to form a continuous cytoskeletal network that maintains the spatial organization of contractile apparatus (Goldfarb and Dalakas, 2009). However, neither desmin nor vimentin (another type III IF protein) orthologs exist in *Drosophila* (Sparrow and Schöck, 2009), suggesting that other cytoskeletal components of muscle cells replace them functionally to ensure myofibrillar integrity. The subcellular localization of *Drosophila* CryAB strongly suggests that it interacts with sarcomeric components and, in particular, with Z-band-associated proteins, thereby helping to maintain myofibrillar architecture.

**Muscle-specific knockdown of CryAB reveals its stress-independent role in sarcomeric organization, muscle performance and heart rhythm**

Point mutations in human sHsps lead to several aggregation diseases (Clark and Muchowski, 2000). For example, mutations in α-A-crystallin (*CRYA*) lead to cataract (Litt et al., 1998), missense mutations in *HSPB1* (HSPB1) are associated with Charcot-Marie-Tooth disease (Evgrafov et al., 2004), and point mutations in *CRYAB* cause DRM (Vicart et al., 1998; Sacconi et al., 2012). Yet, the stress-independent functions of individual members of the sHsp gene family have not been systematically assessed in animal models because of functional redundancies and compensation effects. In the case of *Cryab*, mice knocked out for this gene also lack the adjacent Hspb2 gene and display no obvious developmental defects (Brady et al., 2001). However, as they become older, *Cryab* Hspb2 homozygous knockout mice show postural defects and other health problems that appear to stem from progressive myopathy (Brady et al., 2001). For *Drosophila* CryAB, the impact of its loss of function and its lethality have not yet been confirmed.
Here, we analyzed the effects of muscle- and heart-targeted knockdown of *Drosophila* CryAB to better evaluate its stress-independent functions. We focused on larval musculature and on the adult heart, and found that attenuation of CryAB led to a number of morphological and ultrastructural defects in body wall muscles, impaired muscle performance and accelerated heartbeat. Importantly, muscle alterations lead to local Z-band misalignment, which could be responsible for the observed muscle fiber splitting. Affected myofibrillar integrity results in a markedly altered contractility index in *Mef2>CryAB-RNAi* larvae, which also display lower motility compared with age-matched wild-type individuals. The sarcomeric alterations are also associated with the clustering/mislocalization of nuclei in muscle fibers and with abnormal swelling of mitochondria, together revealing the important developmental role of CryAB in *Drosophila* in the maintenance of correct muscle function and structural integrity. Some of the phenotypes resulting from the muscle-specific attenuation of *Drosophila* CryAB, including disruption of myofibrillar organization and muscle weakness, are reminiscent of those observed in myofibrillar myopathies in human (Goldfarb and Dalakas, 2009).

**Body wall and cardiac muscle alterations in larvae expressing CryAB with the R120G mutation**

In human pathological cases, when the IF network does not assemble correctly and creates aggregates, CRYAB can reorganize the malfolded IF proteins into a normal filamentous network (Koyama and Goldman, 1999). Some mutations in *CRYAB*, such as R120G (Vicart et al., 1998) or D109H, are claimed to affect dimerization of the protein (Sacconi et al., 2012) leading to loss of its chaperone activity and ultimately to pathological muscle defects. Interestingly, protein sequence alignment revealed that both these residues (R120 and D109) are conserved in *Drosophila* CryAB. When we generated a *Drosophila* strain carrying a mutation in one of these residues, CryAB(R120G), we found that in larval muscle cells with accumulations of CryAB(R120G) the sarcomeric architecture and, in particular, the actin filament pattern were severely affected. We also observed a misalignment of myofibrils and the appearance of protein aggregates containing CryAB(R120G), symptoms also seen in DRM patients (Goldfarb and Dalakas, 2009). The affected myofibrillar integrity and irregular sarcomeric pattern correlated with reduced muscle performance as measured by motility assays in *Mef2>CryAB(R120G)* third instar larvae. Taken together, these observations suggest that the R120G mutation in *Drosophila* CryAB has an impact on larval body wall muscles similar to that which the analogous mutation in CRYAB has on human skeletal muscles leading to disruption of myofibrillar integrity and muscle weakness. In DRM patients carrying the *CRYAB(R120G)* mutation, muscle defects appear in mid-age adults, whereas in our *Drosophila* model, following forced expression of CryAB(R120G) in muscles, they are apparent in third instar larva. At this late stage of larval development muscles are fully functional and differentiated, like those in adult humans.

Another important phenotype observed in patients carrying the R120G mutation in CRYAB is increased systolic heart diameter, dilated cardiomyopathy and arrhythmia. Here again, targeted cardiac expression of CryAB(R120G) resulted in arrhythmic heart beating in the adult fly, reminiscent of that observed in the DRM mouse model and in DRM patients (Wang et al., 2001).

Thus, expressing the R120G-mutated form of CryAB in body wall or in cardiac muscles in *Drosophila* leads to pathological defects similar to those observed in patients harboring the *CRYAB(R120G)* mutation. This suggests that this mutation, which potentially impairs CryAB dimerization (Sacconi et al., 2012), might have a more general impact on the chaperone function of CryAB and not only on interactions with desmin IFs.

**Cheerio and other potential CryAB-interacting proteins in Drosophila muscles**

As reported above, muscle-specific expression of *Drosophila* CryAB(R120G) leads to DRM-like phenotypes with Z-band disruption and adversely affected muscle performance. However, as revealed by sequencing of the *Drosophila* genome (Adams et al., 2000), no gene orthologous to desmin has been identified in the fruit fly, suggesting that CryAB interacts with other sarcomeric components to stabilize the contractile apparatus. To identify potential CryAB-interacting proteins we performed co-IP experiments using dissected third instar larvae. Highly enriched sarcomeric proteins bound by CryAB include actins, Tropomyosin 1 and 2, α-Actinin, Paramyosin, Myosin heavy chain and Cheerio.

*Drosophila* CryAB accumulates in Z-bands and to a lesser extent in M-lines, and thus can potentially interact with all these sarcomeric components. Identifying actin in the IP material is consistent with the fact that CryAB has an ABD and that the actin pattern is affected in muscle fibers with attenuated CryAB as it is in muscles expressing CryAB carrying a mutation in the ABD. However, the finding that CryAB can potentially interact with Z-band-associated Cheerio was of particular interest, as in humans mutations in filamin C lead to myofibrillar myopathy with dissolution of myofilaments similar to that observed in DRM (Kley et al., 2007; Luan et al., 2010). Filamins are actin-crosslinking proteins consisting of an N-terminal ABD followed by 24 immunoglobulin-like repeats (Stossel et al., 2001) and are involved in a number of cellular processes including cell-matrix adhesion, mechanoprotection and actin remodeling (Feng and Walsh, 2004). In vertebrates, filamin C is muscle specific and localizes at myotendinous junctions and also at Z-bands and costameres (Ohashi et al., 2005; van der Ven et al., 2000a,b). It has been shown that filamin C interacts with two major protein complexes at the sarcolemma, namely the dystrophin-associated glycoprotein complex (DGC) (Thompson et al., 2000) and the integrin complex (Gontier et al., 2005; Loo et al., 1998), both of which are known to have important roles in affording mechanical integrity to striated muscle. However, through its C-terminal region, filamin C also binds the Z-band proteins myotilin (van der Ven et al., 2000b) and myopodin (synaptopodin 2) (Linnemann et al., 2010), suggesting that it ensures a link between Z-bands and sarcolemmal DGC and integrin complexes, thus maintaining the mechanical integrity of muscle cells. This possibility is supported by the detachment of myofilaments from sarcolemma and intercalated Z-bands in muscles of *zacro* (filamin C) medaka mutants (Fujita et al., 2012). In *Drosophila*, overall filamin protein structure its actin-crosslinking function are conserved in Cheerio. It plays a key role in ring canal formation during oogenesis (Sokol and Cooley, 1999) and is involved in the positioning of nuclei in ovarian nurse cells (Huelsmann et al., 2013), but the role of Cheerio in muscles had remained elusive.

Here, we show that in third instar larval muscles Cheerio protein accumulates between myofilaments and the muscle cell membrane at the level of Z-bands and around the nuclei, a subcellular localization reminiscent of that of filamin C. We also found that the sarcomeric Cheerio pattern was disrupted in larvae with attenuated CryAB, suggesting that the identified interactions between CryAB and Cheerio might help to maintain myofibrillar integrity. Thus, we hypothesize that CryAB exerts a chaperone function on Cheerio in...
Drosophila muscles, which are devoid of desmin IFs, and that this interaction helps to stabilize the contractile apparatus.

Recently, it was reported that the conserved BAG3/Starvin complex detects mechanical unfolding of filamins caused by cell stretching (Arndt et al., 2010; Ulbricht et al., 2013). This complex binds unfolded filamins and targets them to autophagosomes for degradation. It is unclear whether Drosophila CryAB is part of the same complex or of another sHsp complex that regulates filamin and muscle cell function. The fact that Drosophila CryAB can interact with cher-90, the Cheirio isoform that does not contain an ABD and thus might not be stretched and mechanically opened up, suggests that the CryAB complex might bind the folded C-terminus of Cheirio and thus not be part of the BAG3/Starvin complex. Future experiments are required to determine whether the CryAB and BAG3/Starvin complexes bound to filamins have overlapping or specific roles during the development and function of skeletal and cardiac muscle cells.

These findings raise the question as to the extent to which Cheirio is able to replace the IF network in Drosophila muscles. Human CRYAB is known to interact with desmin (Goldfarb and Dalakas, 2009), with sarcomeric actin (Bennardini et al., 1992) and with titin (Golenhofen et al., 2002); however, whether the identified interaction between Drosophila CryAB and Cheirio is conserved in human muscles and, if so, whether it helps to stabilize myofibrillar architecture remains to be elucidated.

MATERIALS AND METHODS

Drosophila stocks

The following Drosophila stocks were used: w1118 strain as wild type; MeF2-Gal4 [Bloomington Stock Center (BSC) BL27390]; Hand-Gal4 (kindly provided by L. Perrin, TAGC, Marseille, France); Gal4 [Bloomington Stock Center (BSC) BL27390]; and heart physiology are described in the supplementary Materials and Methods. Analyses of RT-PCR analysis of transcript levels after RNAi-based attenuation are described in the supplementary Materials and Methods. The heart physiology assay was performed as described previously (Fink et al., 2009).

Immunofluorescence staining of larval muscles and adult fly heart

Third instar larvae were dissected as described previously (Budnik et al., 2006) in ice-cold Ca2+-free saline buffer containing 128 mM NaCl, 2 mM KCl, 4 mM MgCl2, 1 mM EGTA, 35 mM sucrose and 5 mM HEPES pH 7.2 (Demonis and Perrimon, 2009). Buffer without EGTA was used for measurements of contracted muscles. Body wall muscles were fixed with 4% formaldehyde in PBS for 15 min and then rinsed three times for 5 min each in PBS with 0.5% Tween 20 (PBT). Muscles were blocked for 30 min in 20% horse serum in PBT at room temperature. Dissection and staining of adult flies were performed as described previously (Taghil-Lamalle et al., 2008). Primary antibodies were applied overnight at 4°C. After three washes in PBT, secondary antibodies were applied for 2 h at room temperature with or without phalloidin-TRITC as appropriate. MitoTracker Red CMXRos (Invitrogen) was used at 1.5 µM in ice-cold Ca2+-free saline buffer; it was incubated for 15 min at 37°C with dissected larvae. Subsequently, larvae were fixed in 4% formaldehyde for 15 min and washed in PBS three times for 10 min each. Muscle and heart preparations were mounted in Fluoromount-G anti-fade reagent (Southern Biotech) and analyzed using SP5 or SP8 (Leica) confocal microscopes. 3D models of labeled muscles were generated using Imaris software (Bitplane).

Transmission electron microscopy (TEM)

TEM of dissected larvae and immunogold detection of CryAB in TEM sections are described in the supplementary Materials and Methods.

CryAB interactions by co-IP and mass spectrometry

For the co-IP assay, 300 dissected and frozen MeF2>cher90-GFP (for CryAB-Cheirio) or w1118 (for CryAB-Mef2) larvae were homogenized at 4°C in 500 µl HEB extraction buffer [containing 50 mM Tris (pH 7.6), 140 mM NaCl, 5 mM EDTA, 1% (V/V) NP40 and 0.5% (W/V) sodium deoxycholate] as described previously (Perng et al., 2006) and supplemented with a protease inhibitor cocktail (Roche). After 30 min incubation on ice, lysate was centrifuged at 17,000 g for 10 min at 4°C. Supernatant was pre-absorbed 1 h at 4°C with 50 µl protein G-Sepharose (Amersham) to eliminate non-specific binding of the proteins to the beads. The protein G-Sepharose beads were separated from the lysate by centrifugation 1 min at 13,000 g at 4°C. The supernatant was incubated 4 h at 4°C with 5 µl rat anti-CryAB antibody or with 5 µl rat non-immune serum as a negative control. The protein G-Sepharose was subsequently added to each lysate/antibody mixture and incubated overnight at 4°C with gentle agitation. The complexes were then washed three times with washing buffer [50 mM Tris-HCl pH 7.5, 500 mM NaCl, 0.1% (NP40) and proteins eluted by boiling the beads in 2× SDS-PAGE buffer for 10 min. Eluted proteins were separated on a 4-10% SDS-PAGE gradient gel and blotted to PDF membrane (Whatman), blocked with 5% non-fat milk. The membrane was incubated with anti-GFP antibody (1:5000; for CryAB-Cheirio) or with anti-Mef2 (1:100; for CryAB-Mef2) followed by anti-mouse or anti-guinea pig HRP-conjugated secondary antibody (1:10,000) at 25°C for 1 h, and subsequently washed three times with TBST (TBS containing 0.5% Tween-20). Protein bands were visualized using the ECL detection kit (Amersham) and analyzed with the Chemi Doc imaging system (Bio-Rad).

Mass spectrometry to identify CryAB-interacting proteins is described in the supplementary Materials and Methods.

Antibodies and fluorescent markers

Primary antibodies: goat anti-GFP (1:500; Abcam, ab5450); rabbit anti-CryAB (1:500; generated in the K.J. lab); anti-Kettin (1:25; Abcam, ab50585); mouse anti-LamC28.26 [1:1000; Developmental Studies Hybridoma Bank (DSHB)]; rabbit anti-β-tubulin (1:10,000; gift from R. Renkawitz-Pohl, Marburg University, Germany); mouse anti-β-actin (1:10; Invitrogen, AC-15); guinea pig anti-Msp300 (1:300; gift from T. Volk, Weizmann Institute, Israel); rat anti-Cheirio (1:200; Sokol and Cooley, 1999); and rabbit anti-active Caspase 3 (1:1000; Abcam, ab13847). We also used different secondary fluorescent antibodies as well as 18 nm colloidal gold-AffiniPure goat anti-rat IgG (whole molecule) (Jackson ImmunoResearch; 1:20) and 10 nm goat anti-rat IgG (whole molecule)-gold (Sigma-Aldrich; 1:100) conjugated to Alexa Fluor 488, CY3 or CY5 (1:300; Jackson ImmunoResearch). Phalloidin-TRITC (1:1000; Sigma) was used for revealing sarcomeric actin.

RT-PCR analysis of CryAB gene attenuation

Analyses of CryAB transcript levels after RNAi-based attenuation are described in the supplementary Materials and Methods. Methods. The heart physiology assay was performed as described previously (Fink et al., 2009).

Bioinformatic analysis of phylogenetic relationships among sHsps is described in the supplementary Materials and Methods.

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Competing interests
The authors declare no competing or financial interests.

Author contributions
I.W. and T.J. designed the study; I.W., J.J., M.Z., O.T.-L., Y.R., M.D. and G.J. performed the research and analyzed the data; Y.R. performed bioinformatics analyses; I.W. and M.D. analyzed EM muscle preparations; S.H. provided cheroio alleles; I.W., S.H., K.J. and T.J. wrote the paper.

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Supplementary material

Supplementary material available online at http://dev.biologists.orglookup/suppl?doi=10.1242/dev.115352/-/DC1

References


Supplemental materials and methods

Viability and behavioral tests
In the viability test, 200 embryos were plated on a Petri dish containing 3% agarose supplemented with grape juice and with yeast paste. Subsequently, 1st instar larvae were moved to vials with a standard medium. Individuals, achieving each stage of development (3rd larval instar, pupae, imago) were quantified. Behavioral assays were carried out on fifteen 3rd instar larvae per genotype and repeated 3 times for each individual. For all locomotor assays larvae were placed for at least 120s on a Petri dish filled with solidified 3% agarose for adaptation before being tested. In the righting assay, individuals were placed on a Petri dish with 3% agarose on a dorsal position and the time needed to reverse to a ventral position was measured. For the journey test a 2 mm wide, 5 mm deep and 60 mm long track was created on a Petri dish containing 3% agarose. Fresh yeast paste was placed behind the end line as a stimulus. Larvae were placed on the test track and the time taken to crawl 50 mm distance was recorded. In motility test larvae were crawling on a Petri dish with 3% agarose and the number of peristaltic movements were counted during 30 s.

Muscle morphology measurements
VL3, VL4 and SBM muscles of abdominal segments 3 or 4 were analysed in 15-22 dissected and fixed 3rd instar larvae, as described above. Observations of muscle morphology, as well as measurements of muscle length, diameter, number and size of sarcomeres were carried out on muscles stained with phalloidin. Muscle nuclei were visualized by anti-Mef2 antibody. The fibre contractility index (CI) was calculated from following formula: CI = (size of relaxed fibres – size of contracted fibres)/size of relaxed fibres. FV300 (Olympus) confocal microscope was used for imaging and Fluoview software (Olympus) for muscle measurements. Statistical analyses were carried out using the GraphPad Prism5 software. T-test non-parametric or one-way ANOVA were used for phenotypes comparison. The results are reported on the graphs as a standard error of a mean and $P<0.05$ is considered as statistically significant.

RT-PCR
To obtain Drosophila cDNA, total RNA was extracted from 50 3rd instar larvae (WT and Mef> CryAB-RNAi, using a TRIzol reagent (Invitrogen). The remaining DNA was removed by RQ1 DNase (Promega). 2 μl of each RNA were used for reverse transcription, performed with the Superscript III First strand Synthesis System (Invitrogen) according to manufacturer’s instructions. To compare the level of cryAB expression in selected fly strains, 2 μl of reverse transcription products (described above) were amplified via PCR, by using following pairs of primers: forward, 5’-TCCGTAGTGCCACTGATGTT-3’ and reverse, 5’-CTAGGCGGTGGAGGTCTCC-3’. As a control gapdh1 was used, whose expression remains at a constant level. All the DNA amplifications were obtained with a Taq DNA polymerase (Invitrogen) according to manufacturer’s instructions.

Heart physiological analysis
Anesthetized flies with fly nap (Carolina Biol., Corp.) were dissected to expose the heart for filming according to previously described protocols (Fink et al., 2009). These beating heart movies were taken at rate of about 130 frames per second using Simple PCI software (Compix, Sewickley, PA). We use MatLab-based image analysis program to quantify and generate cardiac parameters measurements (Fink et al., 2009). M-modes illustrate movements
of the heart tube edges in Y-axis over time in X-axis, generated by excising and aligning a single pixel-wide from successive movie frames. Heart periods are defined as the time between the ends of two consecutive diastolic intervals. We used Prism software—one way ANOVA analysis and Tukey test to perform the statistics on 20 flies for each genotype.

**Generation of UASp-Cher90_GFP line**

To generate pUASP-Cher90 we cloned a NotI-EcoRI cheerio fragment with an EcoRI-XbaI mGFP6 fragment into the attB-UASP vector (kindly provided by Beat Suter) cut NotI-XbaI. We used the following primers to generate the cheerio fragment from the EST RE60544 (DGRC):

ATATATCGGCGCATGCTAGCGGTAAAGTAGACAAACCCGTGAT and ATATATTCTAGGAATTCACATCGATCTGGAATGGGGAGGCGGGTTATATGC;

We used the following primers to generate the mGFP6 fragment:

ATATATGAATCCCTCGAGCTACTGATGAGTAAAGGAGAAGAA and TATATATCTAGATCGAGCTACTGATGAGTAAAGGAGAAGAA.

The construct was sequenced and integrated into the attP landing site 51D (Bischof et al., 2007).

**Generation of UASp-Venus-dCryAB, UASp-Venus-dCryABR120G and UASp-Venus-dCryAB ABDmut lines**

For plasmid construction dCryAB coding sequences were amplified on cDNA obtained by reverse transcription of total RNA from 3rd instar larvae. PCR reaction using a high-fidelity DNA polymerase (Phusion, Biolabs) was performed with the following pair of primers, containing XbaI and BamHI restriction sites (underlined):

Forward 5’-ATATCTAGATCCGTAGTGCCACTGATGTTC-3’;

Reverse 5’- TATGGATCCCTAGGCGGTGGAGGTCTCC-3’.

Amplified dCryAB PCR product was digested with BamH1 and XbaI and cloned into pUASp-PL-Venus vector which was then injected into a w1118 embryos to produce transgenic flies, a step performed by the Fly Facility platform (www.fly-facility.com Clermont-Ferrand, France).

To introduce R120G and ABDmut point mutation into dCryAB we applied PCR-based mutagenesis. Two overlapping PCR products carrying point mutation were first generated with following pairs of primers (mutated nucleotides are underlined and in bold):

Forward 5’-ATATCTAGATCCGTAGTGCCACTGATGTTC-3’
Reverse R120Gmut 5’-AGCTTGAGCTGCGTGGACGCTCCGGGAGAAGACTGGCAGG-3’

Reverse ABDmut 5’-GTCAATCATCAGCAGCTCCTGCTTGAGGCATCGACATCGACACATTAAGG-3’
Forward ABDmut 5’-GCCTTTGATGCGATCAGAGCCATGGAGAGGGGACGTGAC-3’
Forward R120Gmut 5’- CCCGCCACGCTCCTCCTCGGACGCTACAGCT-3’
Reverse 5’- TATGGATCCCTAGGCGGTGGAGGTCTCC-3’.

2 µl of each PCR product carrying point mutation were mixed in 16 µl of water, heated to 99°C and annealed by cooling down to 37°C during 25 min. 2 µl of annealed PCR products were then used for final PCR amplification with Forward and Reverse primers. Cloning of mutated dCryABR120G and dCryAB ABDmut and generation of transgenics were as for the wild type UASp-Venus-dCryAB.

**Mass spectrometry**

We applied Mass Spectrometry (MS) to identify the dCryAB interacting proteins. Immunoprecipitation was performed as described below using dCryAB antibody on cytoplasmic protein extract from the dissected wild type larvae. The immunoprecipitated protein complexes were subjected to SDS-PAGE separation and Coomassie staining to
visualize bands of interest. Proteins ranging from 30 to 170 kDa were excised from the gel and analyzed by a specialized Mass Spectrometry and Proteomics Platform (MSPP, SupAgro INRA, Montpellier).

**TEM**

Dissected larvae (as described above) were fixed in 2.5% glutaraldehyde in 0.1M phosphate buffer, 3 times washed in phosphate buffer for 15 min, incubated over night and again washed 3 times. Material was post-fixated for 90min in the mixture of osmium tetroxide and potassium ferricyanide in the ratio 1:1. After dehydration in alcohol series (50%, 70%, 90%, 100%, 100%), material was embedded in a mixture acetone-epoxy resin in the ratio 1:1 and incubated for 24h in a very tight dish. The dish was opened for at least 7h for acetone to evaporate. Polymerization of material embedded in epoxy resin was performed during 24h at 45°C and subsequently for 3 days at 60°C. Ultrathin sections were observed in electron microscope Zeiss EM 900.

**Immunogold**

Dissected larvae (as described above) were fixed in 1:1 mixture of 0.5% glutaraldehyde and 4% paraformaldehyde in a PBS, at RT for 1.5h. Than the material was postfixed in 2% paraformaldehyde, at 4°C overnight, washed in PBS with 0.5% TritonX100 (PBT) and dehydrated with graded ethanol series. After dehydration specimens were infiltrated in mixtures of 85% ethanol and LR White (London Resin Company Ltd) (2:1), (1:1), (1:2) 1h for each series. Then the material was infiltrated in two times with pure LR White for 12h at RT and once overnight at 4°C and embedded in LR White and polymerized at 59°C for 24h. Ultrathin sections were cut using an ultramicrotome (ReichertUltracut E). Ultrathin sections were preincubated for 2 h in 1% BSA in PBS. Then sections were incubated with primary antibodies: mouse anti-β-actin 1:10 and rat anti-dCryAB 1:500 at 4°C overnight. After rinsing several times in PBT the material were incubated with secondary antibodies conjugated with gold particles. After washing in PBT, sections were contrasted with lead citrate for 2 min and analyzed using transmission electron microscope Zeiss EM 900.

**Bioinformatics search for homologues**

To compare amino acid sequences associated to dCryAB and CryAB, we used MUCLE (Multiple Sequence Comparison by Log-Expected) with default settings (McWilliam et al., 2013). We visualized the result with Jalview2 (Waterhouse et al., 2009) highlighting equivalences in red. Phylogenetic tree was built considering amino acid sequences of dCryAB, CryAB, Hspb1 and Hspb8 and those of some of their different homologues in various vertebrate and non-vertebrate species. We used phylogenetic analysis « One Click » pipeline available on (http://www.phylogeny.fr) to manage the different building steps and generate the final tree.
Supplemental figure legends

**Figure S1.** Double EM immunogold staining for dCryAB and actin showing that immunogold dots for dCryAB (18 nm of diameter) localize mainly to the Z-band but are also detected within the M-band. Note that small immunogold dots of 10 nm of diameter detecting actin are found at the Z-band. Scale bar 300 nm.

**Figure S2.** Effects of muscle targeted RNAi attenuation of dCryAB using VDRC 107305 line. (A) Lateral view of wild type dissected 3rd instar larval muscles from one hemisegment stained with phalloidin. Note altered pattern of sarcomeric actin suggesting disruption of Z-bands (arrowheads). (B) Statistical representation of muscle defects observed in examined Mef>dCryAB-RNAi larvae. (C) No significant changes in sarcomere size have been observed. (D) Significantly reduced number of sarcomeres observed in 3 different muscles (VL3, VL4 and SBM) in 3rd instar larvae with muscle-specific attenuation of dCryAB. (E-H) Affected contractility and muscle performance tests showing reduced motility of Mef>dCryAB-RNAi larvae. (I) No apoptotic events can be detected in Mef>dCryABRNAi muscles as judged by the activated Caspase 3 staining. Arrow points to cells that undergo apoptosis in the analyzed 3rd instar larvae preparation. Significant differences were determined by t-Student test. Asterisks indicate statistical level of significance of observed differences: *p<0.1, **p<0.5, ***p<0.001. Scale bar 40 μm.

**Figure S3.** Muscle targeted expression of dCryAB carrying mutated actin binding domain (ABD) affects sarcomeric actin pattern and nuclei positioning. The alignment of wild type and mutated amino acid sequence of dCryAB actin binding domain are shown. Mutated residue is in red and highly conserved residues are in bold (refer to Mounier and Arrigo, 2002). Arrows in (A) point to irregular actin pattern. Arrowheads in (A’) indicated abnormally located dCryAB with mutated ABD whereas asterisk point to the area in which dCryAB-ABDmut displays a diffused pattern and is not detected in sarcomeres. Arrowheads in (A”) denote clustered nuclei. Scale bar 50 μm.

**Figure S4.** Additional muscle defects observed after attenuation of dCryAB. (A) Muscle splitting (yellow arrowhead) with partial loss of splitted myofibrils. (B) Complete loss of a muscle. Arrowheads indicate position of extremities of lacking segment border muscle. Scale bar 40 μm. (C) Slightly but significantly reduced number of sarcomeres observed in 3
different muscles (VL3, VL4 and SBM) in 3rd instar larvae with muscle-specific attenuation of dCryAB. (D) No significant changes in sarcomere size have been observed. (E) Mef>dCryAB-RNAi animals display increased lethality at all developmental stages tested. Significant differences were determined by t-Student test. Asterisks indicate statistical level of significance of observed differences: *p<0.1, **p<0.5, ***p<0.001. Error bars indicate SEM.

**Figure S5.** dCryAB does not physically interact with Msp300. Western blot from IP experiment with anti-dCryAB on protein extract from 3rd instar larvae. Anti-Msp300 antibody was used to reveal immunoprecipitation reaction. Notice high molecular weight Msp-300 detected in the protein extract (Input) but not in the IP sample.

**Figure S6.** Bar graph representations of changes in heart parameters upon cardiac-restricted expression and knockdown of dCryAB. (A, B) Plot of mean systolic (A) and diastolic (B) intervals indicates shortening in contraction and relaxation phases for dCryAB lines. (C) Heart diastolic diameters for 1 week-old flies. Note the dilated diameters across the heart tube in dCryAB^{R120G} flies. (D) Percent fractional shortening shows significant decrease when driving R120G dCryAB at 1 week old, in comparison to controls. Movies were taken from 20 flies for each genotype. Significant differences were determined by one-way ANOVA ([*] P<0.05; [**] P<0.005; [***] P<0.0005). Error bars indicate SEM.

**Figure S7.** Genetic interactions of dCryAB and cheerio and their impact on sarcomeric pattern. (A-A”) Simultaneous RNAi knockdown of dCryAB and cheerio leads to misalignment of myofibrils (arrows in A) associated with severely affected sarcomeric actin and kettin patterns. High kettin level (asterisk in A’) is detected in the sarcomeres displaying reduced/fuzzy actin (asterisk in A), a phenotype that has not been observed in muscles in which only dCryAB has been attenuated (see Fig. 4B). (B-B”) Overexpression of dCryAB in cherRNAi context partially rescues irregular/fuzzy actin patterns observed in muscle with attenuated cheerio (Fig. 7E). Notice that some myofibrils misalignment can still be observed but sarcomeric kettin distribution appears regular in this context (B’). Scale bar 40 µm.

**Figure S8.** Muscle targeted RNAi knockdown of Starvin leads to misalignment of myofibrils and affected nuclei position but has no influence on sarcomeric and perinuclear localization of dCryAB. Arrows point to misaligned myofibrils and accumulation of dCryAB. Arrowheads indicate clustered nuclei. Scale bar 40 µm.
References:

Table S1. Proteins identified by Co-IP with CryAB

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Supplementary figures

Figure S1
Figure S2

A

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Development 142: doi:10.1242/dev.115352: Supplementary Material

Development | Supplementary Material
Figure S3

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Figure S4

Figure S5
Figure S6

A  Systolic intervals  

B  Diastolic intervals  

C  Diastolic Diameters  

D  Fractional Shortening  

Figure S7
Figure S8