Biochemical and Biophysical Research Communications 391 (2010) 193–197

Contents lists available at ScienceDirect

Biochemical and Biophysical Research Communications

journal homepage: www.elsevier.com/locate/ybbrc

Electron microscopy and three-dimensional reconstruction of native thin filaments reveal species-specific differences in regulatory strand densities

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ARTICLE INFO

Article history:
Received 27 October 2009
Available online 10 November 2009

Keywords:
Actin
Troponin
Tropomyosin
Electron microscopy
Indirect flight muscle
Contraction

ABSTRACT

Throughout the animal kingdom striated muscle contraction is regulated by the thin filament troponin–tropomyosin complex. Homologous regulatory components are shared among vertebrate and arthropod muscles; however, unique protein extensions and/or components characterize the latter. The Troponin T (TnT) isoforms of *Drosophila* indirect flight and tarantula femur muscle for example contain distinct C-terminal extensions and are ~20% larger overall than their vertebrate counterpart. Using electron microscopy and three-dimensional helical reconstruction of native *Drosophila*, tarantula and frog muscle thin filaments we have identified species-specific differences in tropomyosin regulatory strand densities. The strands on the arthropod thin filaments were significantly larger in diameter than those from vertebrates, although not significantly different from each other. These findings reflect differences in the regulatory troponin–tropomyosin complex, which are likely due to the larger TnT molecules aligning and extending along much of the tropomyosin strands' length. Such an arrangement potentially alters the physical properties of the regulatory strands and may help establish contractile characteristics unique to certain arthropod muscles.

Introduction

ATP-dependent cyclical interactions between myosin-containing thick filaments and actin-containing thin filaments drive muscle contraction in all animals. In resting striated muscle of vertebrates and higher invertebrates, the thin filament troponin–tropomyosin regulatory complex inhibits contraction by blocking high affinity myosin binding sites on actin [1–3]. Upon activation, tropomyosin moves azimuthally over the filament away from these sites in a stepwise manner as a result of Ca^{2+} binding to troponin followed by myosin crossbridge binding to actin [4–6]. Biochemical and structural data suggest that initial crossbridge binding evokes allosteric effects on thin filaments involving a propagated opening of myosin binding sites along the filaments leading to cooperative activation of contraction [1,3–5]. Thus, both elevated Ca^{2+} levels and crossbridge binding are required for complete activation of muscle contraction.

Tropomyosin is an elongated 42 nm coiled-coil protein that assembles end-to-end to form continuous strands which run along the entire length of the F-actin helices [7–9]. Each tropomyosin molecule possesses seven successive quasi-repeating motifs and is designed to bind to and span seven neighboring actin monomers along the filaments [10,11]. In vertebrate striated muscles, the C-terminal two-thirds of tropomyosin associates with specific domains of troponin, an asymmetric protein complex comprised of TnT (37 kDa), TnI (24 kDa), and TnC subunits (18 kDa) [9,12–15]. Thus, a single thin filament "regulatory unit" consists of seven actin subunits controlled by a single troponin–tropomyosin complex. TnC serves as the Ca^{2+} sensor of the troponin complex. Ca^{2+} binding to TnC relieves the inhibition of actomyosin interactions imposed by TnI. Elongated TnT (19 nm in vertebrates) binds the entire complex to tropomyosin [9,12,13,16]. The N-terminal "tail" of vertebrate TnT, predicted to be alpha helical, extends along the C-terminal half of tropomyosin as well as the end-to-end contacts between neighboring tropomyosin molecules [1,9]. The C-terminal portion of TnT forms part of the structural scaffold that supports TnC and TnI in the globular core domain of troponin [17,18]. TnT may also contribute to regulating actomyosin ATPase activity and to establishing the cooperative activation of the thin filament [1] by increasing the inhibition of actomyosin ATPase activity in the absence of Ca^{2+} and increasing activation in the presence of Ca^{2+} [19,20].

The components of thin filaments in invertebrates and vertebrates are highly homologous. For example, well-studied *Drosophila melanogaster* indirect flight muscle (IFM) and tarantula leg muscle thin filaments contain actin, tropomyosin, TnC, TnT and

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0006-291X/$ - see front matter © 2009 Elsevier Inc. All rights reserved.
doi:10.1016/j.bbrc.2009.11.030

TnI homologues [21,22]. However, arthropod muscles often express troponin subunits with discrete extensions. For example, the TnT homologues in *Drosophila* IFM (46 kDa) and in tarantula muscle (major isoform 43 kDa) share 51% identity with each other and are ~20% larger than their vertebrate counterparts [22–24]. In IFM, the TnT subunit contains a ~136 amino acid long C-terminal extension that is highly acidic [23,24] and may account for the observed Ca^{2+}-binding properties of this species of TnT [24]. The major tarantula TnT isoform also possesses an acidic C-terminal extension, though shorter than that expressed in *Drosophila* IFM [22]. Furthermore, *Drosophila* IFM expresses a TnI isoform (30 kDa) larger than that found in vertebrate or in tarantula (major isoform 24 kDa) skeletal muscle [22,25,26]. The ~6 kDa difference is predominately attributed to expression of an IFM specific exon that encodes an N-terminal proline- and alanine-rich extension. Additionally, two different "heavy" tropomyosin molecules (TmH), which contain a ~250 amino acid proline-rich carboxy-terminal domain beyond the normal tropomyosin sequence, are expressed in the IFM (but not in insect synchronous muscles or in other arthropod muscles) [27]. Stoichiometric measurements and protein–protein interaction studies of the TmH isoforms with standard IFM tropomyosin suggested that the TmH N-termini are integrated into the thin filament structural unit as tropomyosin homo- or heterodimers [27]. Immuno-electron microscopy indicated that TmH is homogeneously distributed along with normal tropomyosin on IFM thin filaments [28,29]. The proline-rich, C-terminal portion of TmH was modeled as an extended globular "spring" projecting out from the thin filament in a region close to the globular domain of the troponin complex [29].

EM and three-dimensional (3D) helical reconstruction are powerful imaging techniques for high resolution analysis of native and reconstituted thin filaments. They have played a key role in revealing the reorganization of the troponin–tropomyosin regulatory components that occurs in response to Ca^{2+} [30–32]. However, helical reconstruction treats all densities associated with F-actin as if they are identical on each monomer along the filament, and the average density contribution of discretely distributed structures, such as troponin complexes, can potentially merge into continuous structures (like tropomyosin), and not be easily delineated [33]. In particular, extended proteins such as TnT that run parallel to tropomyosin along much of their length, may not be discretely detected or resolved separately from the tropomyosin regulatory strands [33]. Therefore, tissue and phylogenetic differences in tropomyosin and/or TnT molecules could make different contributions to the apparently well-defined actin monomers or the tropomyosin strands. Thus, in addition to comparing differences in thin filament structure under defined chemical conditions that correspond to different physiological states from the same organism, EM and helical reconstruction can be used to compare thin filaments under a single defined state from different organisms. This allows direct comparison and statistical evaluation of potential differences that exist in thin filaments possibly due to unique or distinct arrangements of regulatory components.

Previous imaging of *Drosophila* IFM thin filaments suggested the occurrence of larger tropomyosin regulatory strands when compared to those present in other organisms [31]. However, these inferences were not quantified, nor were the sources of these differences identified. In the present study, we have compared the structures of *Drosophila*, tarantula and frog thin filaments and find that the extra density associated with arthropod tropomyosin strands is due to the larger TnT isoform. We conclude that the arthropods' negatively charged C-terminal TnT extensions align and extend along tropomyosin and do not project outward or away from the thin filament. Such an orientation could alter the regulatory strands' physical properties and likely contributes to the muscles' contractile characteristics.

Materials and methods

Thin filament isolation. IFM thin filaments were isolated from the thoraces of *Mhc*^{7} *Drosophila* according to [31]. Tarantula thin filaments were purified from femur muscles as in [34]. Vertebrate thin filaments were extracted from Sartorius muscles of *Rana pipiens* according to [35] with minor modifications. Frogs were decapitated and the sartorius muscles were isolated. During the dissection the tissue was continually rinsed with cold rigor buffer (100 mM NaCl, 3 mM $MgCl_2{\cdot}6H_2O$, 0.2 mM EGTA, 5 mM PIPES, 5 mM $NaH_2PO_4{\cdot}H_2O$, 1 mM NaN_3, 0.5 mM PMSF, pH 7.0). Both muscles from individual frogs were placed in 45 ml of skinning solution and slowly agitated overnight on ice. Superficial muscle layers were dissected, rinsed in 10 ml of rigor buffer and homogenized in 5 ml of rigor buffer with an omnimixer for 15 s and cooled for 15 s on ice. The blending and cool down steps were repeated three times. The homogenate was filtered through cheesecloth and was spun at 13,000*g* for 15 min to pellet myofibrils. The myofibrils were washed and centrifuged at 13,000*g* for 15 min three times. The final "washed" myofibrils were resuspended in 200 μl of relaxing solution (rigor buffer supplemented with 5 mM EGTA) and gently homogenized to dissociate thick and thin filaments. The sample was spun at 15,000*g* for 20 min to pellet thick filaments and the supernatant containing thin filaments was diluted 10–20-fold with relaxing solution immediately prior to grid preparation. All thin filaments preparations were maintained in EGTA to ensure low Ca^{2+} conditions.

Electron microscopy and 3D reconstruction of thin filaments. In this work, only low Ca^{2+} thin filament images were analyzed. This is because the variance associated with the relative positions of F-actin and tropomyosin densities in maps of 3D reconstructions of low Ca^{2+} data is less than those in high Ca^{2+}.

Five microliters of Ca^{2+}-free filament suspension was applied to thin carbon films that were layered over holey carbon films supported on 400 mesh copper electron microscope grids. The thin filaments were negatively stained with 1% (w/v) uranyl acetate and the grids were dried as previously [5,36,37]. Images of filaments lying on thin carbon over the holes were recorded under low dose conditions at a magnification of 60,000× with a Philips CM 120 electron microscope operated at 80 kV. Images were digitized on a Zeiss SCAI scanner. Helical reconstruction of negatively stained thin filaments, which resolves actin monomer structure and tropomyosin strands, was carried out according to standard methods [5,36,38]. Helical projections were calculated from the 3D reconstructions of the thin filaments by projecting the component densities in the reconstructions down the long-pitch actin helical paths onto a plane perpendicular to the thin filament axis [30,38]. The resulting maps thus show axially averaged positions of actin and tropomyosin densities, appearing symmetrically on both sides of the filament. These projections are well suited for aligning and comparing the averaged densities from different species. A Student's *t*-test was performed for every component density of the averaged 3D maps [36,39]. Only regions whose average density was greater than baseline density in each map at better than the 99.95% confidence level are shown. Difference density analysis [30] between aligned maps from different organisms can reveal phylogenetic differences among their tropomyosin strand densities. The difference maps were evaluated by a Student's *t*-test [40].

Results and discussion

Electron microscopy and 3D reconstruction of low Ca^{2+}-treated thin filaments

Thin filaments were isolated from *Drosophila* indirect flight, tarantula leg and frog Sartorius muscles and maintained in low