Specimen Description

Full Sample Name (no acronyms)

Description of Sample (buffer concentrations, additives, etc.): 5 mM MgAcetate, 5 mM NaATP, 5 mM EGTA, 20 mM MOPS, 100 mM NaCl, 5 mM DTT, and 10 mM Na·PO4 (pH 7.0

Total Mass (kDa)

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(32,000 Å - 1,600 Å)/145Å = 210 crowns

210*4 = 840 myosin molecules
840 * 520,000 = 436,800,000

210*4 = 840 flightin molecules
840 * 20,000 = 16,800,000

210*4 = 840 myofilin molecules
840 * 20,000 = 16,800,000

210/5*2 = 84 paramyosin molecules
84 * 214,000 = 17,976,000

210/5*4 = 168 stretchin-klp molecules
168 * 231,000 = 38,808,000
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Total mass = 527,184 kDa

Estimated Dimensions: Diameters up to 420 Å, Lengths from 1.6 micrometers to 3.2 micrometers.

Particle Symmetry: C-3 (vertebrate), C-4 (invertebrate), or C-7 (molluscan) depending on filament type

Final Sample BSL: No containment needed. Completely non-pathological.

Figures/Preliminary Data

Our preliminary results are largely from the flight muscles insects that utilize asynchronous flight muscle. These include the Hemipteran *Lethocerus indicus*, and the Dipteran *Drosophila melanogaster*. We plan to investigate vertebrate striated muscle thick filaments as well.

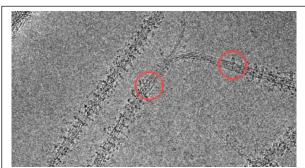


Figure 1. cryoEM of a frozen-hydrated *Lethoce-rus* thick filament recorded in integration mode on the DE-64. Red circles outline the first crown (crown-0). At the bare zone ends heads become ordered into shelves called "crowns". Although all parts of the thick filament showing ordered myosin heads are useful for a helical reconstruction, only those for which crown-0 can be identified are useful for the asymmetric reconstruction. If asymmetric reconstruction shows sufficient variability along the filament, potentially multireference alignment can place filament segments in their correct location.



Figure 3. Portion from the 2.8Å reconstruction of flight muscle thick filaments from *Drosophila melanogaster* showing well-resolved side chains. This region from the myosin α -helical coiled coil tail but not the same region shown in Figure 2.

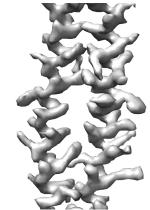


Figure 2. Portion of the 2.7 Å reconstruction (FSC) from *Lethocerus indicus* showing well resolved side chains. This region from the myosin α -helical coiled coil tail.

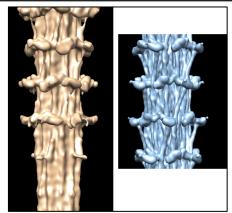


Figure 4. Comparison of *Lethocerus* thick filaments reconstructions. (left) The crown-0 reconstruction which imposed only rotational symmetry on 542 motifs (2,168 asymmetric units), reaching 16Å resolution by FSC criteria. Images were recorded in integration mode on a DE-64 detector. (right) Previously published 6Å helical reconstruction from ~24,000 segments, low pass filtered to 16Å. Images recorded on a DE-20 direct electron detector operated in integration mode. The DE-20 detector is inferior to both the DE-64 and K3. Both reconstructions show myosin heads projecting from the backbone and their S2 linkage, though not as well as in the crown-0 reconstruction.

Bibliography

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