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Definite Difference Between In Vitro Actin-Myosin Sliding and Muscle Contraction Revealed by the Effect of Antibody to Myosin Head Converter Domain

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Myofilament sliding in muscle is believed to result from rotation of the myosin head catalytic domain (CAD) around the converter domain (CD). To explore the validity of this mechanism, we compared the effect of antibody to myosin head converter domain (IgG, anti-CD antibody) between in vitro actin-myosin sliding and muscle fiber contraction. In agreement with the expectation that binding of massive antibody to the CD impairs rotation of the CAD around the CD, the ATP-dependent sliding of actin filaments over myosin heads on a glass surface was inhibited by the antibody (0.14mg/ml). Meanwhile, the antibody (up to 1.5mg/ml) showed no appreciable effect on the actin-activated myosin head ATPase activity, indicating that the antibody has no effect on the ATPase activity in the CAD. Unexpectedly, the antibody (up to 3mg/ml) showed no appreciable effect on the maximum Ca²⁺-activated isometric force, the maximum shortening velocity, and the Mg-activated ATPase activity in glycerol-extracted rabbit psoas muscle fibers. The possibility that the antibody does not diffuse into muscle fibers can be excluded by our published results that other antibodies readily inhibit muscle fiber contraction. These findings therefore suggest that the antibody binding to the myosin head CD does not impair performance of myosin heads producing force and motion in muscle fibers.

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Complex *In Vitro* Motility Characteristics Emerge from Mechanical Coupling of Myosin Motors via a Commonly Propelled Actin Filament Lennart Hilbert^{1,2}, Shivaram Cumarasamy², Nedjma B. Zitouni²,

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Background: Collective propulsion of actin by myosin motors is fundamental to most muscle contraction models. Single myosin load-dependent mechanochemistry as well as cooperative action of small numbers of motors are increasingly well-understood. Deducing macroscopic actin propulsion from microscopic actomyosin interaction would help to connect both scales. We developed and tested experimentally a model that explains the emergence of complex features of *in vitro* actin sliding from mechanical coupling of a high but not statistical number of myosins via actin.

Methods: Smooth muscle myosin load-dependent kinetics were modeled based on single molecule experiments [Veigel; NatCellBiol(2003), 5(11):980]; the coupling parameter "I" quantifies the acceleration of the rate-limiting ADP-release/detachment step by the phosphate release-associated main power stroke, as hypothesized by others [Jackson; PhysChemChemPhys(2009), 11:4808]. A simplified two-state model exhibited a saddle-node bifurcation into fast/slow bistable filament motion above a critical number of coupled myosins for I>0, leading to an acceleration relative to the non-coupled I=0 case. Chemical Master Equation and Gillespie-type simulations of the full three state model (Pre Power Stroke, Post Power Stroke, Non-Bound) further predicted a characteristic deviation of velocity fluctuations from the law of large numbers as well as increased sliding velocity autocorrelation times. We developed video analysis software for increased throughput and detail, allowing length-resolved quantification of sliding velocities, velocity fluctuations, and autocorrelation times in in vitro motility assays with myosin purified from phasic smooth muscle.

Results: A previously reported acceleration of *in vitro* actin sliding [Baker; JBiolChem(2003), 278(31):28533] emerges from our model. Qualitative predictions on velocity fluctuations and autocorrelation time were confirmed experimentally.

Conclusions: These results support the hypothesis of actin sliding acceleration by mechanical coupling between different actomyosin kinetic steps.

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In Vitro Motility Assay Studies at Low [MgATP] - Evidence For Inter-Head Cooperativity in Fast Skeletal Myosin II

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The idea that fast skeletal myosin II exhibits processivity with sequential actions of the two myosin heads during muscle contraction has long been a topic of discussion but with appreciable difficulties to obtain conclusive experimental results. The difficulties may be related to a limited processivity (few sequential head actions) that is of greatest importance at low velocity (e.g. high resistive load), difficult to study accurately in vitro. In order to aid the investigations we here make use of recent evidence that the bipyridine drug amrinone inhibits the strain-dependent ADP-release step of myosin II with expected enhancement of processivity (Albet-Torres et al., J Biol Chem., 2009); Månsson, Biophys J., 2010). For accurate velocity measurements, the recombinant expressed capping protein CapZ (Soeno et. al., J Muscle Res Cell Motil., 1998) was fluorescence labeled. Nanometer tracking was achieved by twodimensional Gaussian fits to single molecule fluorescence intensity profiles representing CapZ attached to the trailing actin filament end. Importantly, the heavy meromyosin (HMM) propelled actin filament sliding velocity (1mM MgATP) for CapZ-capped filaments was comparable to that of uncapped filaments at different ionic strengths and HMM surface densities. Studies at low [MgATP] (5-30µM) suggests a non-linearity in the [MgATP]-velocity plot that was enhanced by 1mM amrinone. The result is in contrast to the linearity expected for independent myosin heads and could be interpreted as an apparent velocity dependence of the myosin step length. This is in accordance with the idea of limited processivity of myosin II if it is assumed that a doubled apparent step length corresponds to sequential action of the two heads. Further insight into the mechanism will be obtained using proteolytically prepared oneheaded HMM and e.g. studies with external loads on actin.

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Winding Actin Filament Paths Provide Mechanistic Insights Into Actomyosin Function

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The statistics of heavy meromyosin (HMM) driven actin filament paths in vitro, and thermal fluctuations of actin filaments suspended in a pseudo 2D-space in solution, can be described by the cosine correlation equation (CCE): $\langle \cos(\theta s) \theta$ (0))> = exp(-s/[2*Lp]). Here, θ (0) and θ s) represent tangent angles at distance 0 and s, respectively from one filament end (in solution) or from the starting point of the path. The quantity Lp is the persistence length (proportional to flexural rigidity) of the filament/path. In vitro motility assay (IVMA) studies (27-29°C) were performed along with studies of actin filaments suspended between two cover-slips in solution. Fits to the CCE gave $L_P = 16.5 \pm 1.7 \ \mu m$ (mean \pm 95 % confidence interval) and 11.1 \pm 0.6 μ m for phalloidin stabilized filaments in solution and propelled by HMM, respectively. In contrast, phalloidin free actin filaments (NHS-rhodamine labeled) exhibited similar L_P in solution 10.1 \pm 2.1 μ m and during HMM propulsion (9.8 \pm 0.9 μ m). The filament paths were modeled using a Monte-Carlo approach updating angular changes in sliding direction at short time intervals (dt) assuming 1. lateral displacements due to cross-bridge forces and 2. thermal fluctuations of the leading filament end. The results suggest that > 3nm average lateral displacement during each actomyosin interaction would reduce L_P by >30 % compared to that of filaments without HMM. The findings are consistent with the following ideas: 1. Actin filaments exist in two different flexural rigidity states, one favored by myosin binding and the other by phalloidin stabilization, 2. Changes in actin filament flexural rigidity is not required for motion generation. 3. The myosin crossbridges produce minimal lateral movements (< 3 nm) during the power-stroke.

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Aging's Effect on Physical Performance and Single Muscle Fiber Contractility in a Nonhuman Primate Model

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¹Department of Internal Medicine, Section of Gerontology and Geriatric Medicine, Wake Forest University School of Medicine, Winston-Salem, NC, USA, ²Department of Pathology, Section on Camparative Medicine, Wake Forest University School of Medicine, Winston-Salem, NC, USA. Previous studies on the intrinsic contractile properties of human myofibrils reported increase, decrease, or no change with aging, perhaps due to differences

in physical activity, diet, and other factors. We examined myofilaments' contractile characteristics and physical performance, walking speed and climbing rate, in African green vervet monkeys, housed in social groups in large indooroutdoor enclosures and fed the same diet. Physical performance and skinned vastus lateralis (VL) muscle fiber function were investigated in four young $(11\pm1 \text{ yrs})$ and four old $(23\pm1 \text{ yrs})$ monkeys. Fiber myosin heavy chain (MHC) isoform was determined by gel electrophoresis. The old monkeys walked slower (19%) and climbed less (63%) than young monkeys (p < 0.05). Myofiber cross sectional area (CSA) was 22% and 12% smaller for IIa and hybrid MHC, respectively, in old compared to young monkeys (p<0.001). Specific force (maximal Ca²⁺-activated force normalized to fiber CSA) was 15% and 11% less for type IIa and hybrid fiber, respectively, in old compared to young monkeys (p<0.05). Fiber atrophy does not account for the loss in force with aging; it declined much faster than fiber CSA. Although we observed no difference in shortening velocity, the maximal power output substantially decreased in 21% of type IIa and 22% of hybrid fibers with aging (p<0.05). Regression modeling used to identify factors contributing to lower fiber force revealed that age is the strongest predictor ($r^2=0.31$, p<0.001). The diminished contractile properties measured in vitro correlates strongly with age-dependent decline in physical performance (waking speed: r = 0.41, p < 0.001); climbing rate: r = 0.29, p < 0.001). Our results support a detrimental effect of aging on the innate force and power generation of myofilament lattice and physical performance.

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Slow Myosin ATP Turnover in the Super-Relaxed State in Tarantula Muscle

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We measured the nucleotide turnover activity of myosin in tarantula legmuscle fibers by observing single turnovers of the fluorescent nucleotide analog, mantATP, as monitored by the decrease in fluorescence when mantATP is replaced by ATP in a chase experiment. We find a multi-exponential process, with approximately two-thirds of the myosin showing a very slow nucleotide turnover time constant, ~30 minutes. This slow turnover state is termed the super-relaxed state (SRX) and is a highly novel adaptation for energy conservation in an animal that spends extremely long periods of time in a quiescent state (days) employing a lie-in-wait hunting strategy. If fibers are incubated in mantADP and chased with ADP, the SRX is not seen, indicating that relaxed myosins are responsible for the SRX. Phosphorylation of the myosin regulatory light chain eliminates the fraction of myosin with the very long lifetime. The presence of the SRX measured here correlates well with the binding of myosin to the core of the thick filament in a structure known as the interacting-head motif (or J-motif) observed previously by electron microscopy. Both the structural array and the long-lived SRX require ATP, both are lost upon myosin phosphorylation, and both appear to be more stable in tarantula than in skeletal or cardiac preparations. EPR spectroscopy of a spin-labeled nucleotide bound to the motor domain of myosin in relaxed tarantula fibers likewise shows orientation that is lost when the myosin is phosphorylated. Together, the data support the hypothesis that the SRX myosin and the myosin seen in the EM of the order helical array in tarantula filaments are the same

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The Low Angle X-Ray Diffraction Pattern from Skinned Fibers of Rabbit Psoas Muscle: Effect of Changes in [Ca⁺⁺] and [Orthophosphate] Elisabetta Brunello¹, Marco Caremani¹, Massimo Reconditi¹,

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Bundles of 3-5 fibers were activated isometrically at different pCa by a temperature jump from 1°C to 12°C using a mechanical apparatus (Linari *et al.*, Biophys. J. 92:2476, 2007) modified to collect the X-ray diffraction pattern. The M3 meridional reflection from the axial repeat of the myosin heads was sampled by X-ray interference between half-sarcomeres. In relaxed fibers at 12°C, the M3 reflection had a major peak at 14.56 nm and a minor peak at 14.37 nm. The ratio of peak intensities (R_{M3}) was 0.43 ± 0.06 and the spacing (S_{M3}) was 14.49 ± 0.01 nm. In relaxed fibers the intensity of the main peak reduced with increasing temperature, so that at 36°C (the physiological temperature) the 14.37 nm peak was dominant, with small satellite peaks on either side, as in resting intact fibers from frog muscle. During activation at 12° C at saturating [Ca⁺⁺], pCa 4.5, the intensity of the M3 reflection (I_{M3}) increased to 1.9 ± 0.4 times the relaxed value with major and minor peaks at 14.68 nm and 14.46 nm; $R_{\rm M3}$ was 0.62 ± 0.03 and $S_{\rm M3}$ was 14.59 ± 0.01 nm. Activation at pCa 5.5 or at pCa 4.5 with addition of 10 mM orthophosphate (Pi) had similar effects: force was reduced to 0.34 ± 0.10 the control value and $I_{\rm M3}$ to 0.56 ± 0.03 ; $R_{\rm M3}$ was 0.46 ± 0.07 and $S_{\rm M3}$ was 14.55 ± 0.02 nm. These results give structural support to the conclusion from mechanical experiments (Linari *et al.*, 2007) that both decreasing [Ca⁺⁺] and increasing [Pi] reduce isometric force by a decrease in the number of force generating myosin heads with no change in force per head.

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Structural Changes in Myosin Heads and Filaments during Unloaded Shortening and Force Redevelopment

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X-ray diffraction patterns were recorded with 5-ms time resolution at the ID02 beamline, ESRF, from single intact muscle fibers of the frog during steady shortening at the maximum velocity V_0 , imposed at the plateau of an isometric tetanus (T_0) , and during isometric force redevelopment following such shortening. During the first 20nm/half-sarcomere (hs) of shortening force decreased to near zero and changes in the X-ray pattern were consistent with a working stroke in actin-attached myosin heads followed by net detachment from actin (Piazzesi et al., Cell 131:784, 2007). As V₀ shortening continued the M3 meridional reflection (associated with the conformation of the myosin heads) and its second order M6 (associated with the thick filament structure) became more like those recorded at rest. At 110 nm/hs shortening the M3 spacing and its fine structure were the same as at rest, while the M3 intensity, M6 spacing, and intensity of the first myosin layer line from the helical packing of the myosin heads, had recovered about half-way to their resting values, without sign of saturation. Isometric force redevelopment following 110 nm/hs shortening at V_0 and the associated structural changes were faster than those at the start of electrical stimulation (Reconditi et al., PNAS, 108:7236, 2011). In both cases the initial force generation involves a small fraction of the myosin heads, whilst the majority are in the resting-like helically ordered conformation on the surface of the thick filament. The relationship between force and structural change is the same in the two cases for forces above $40\% T_0$. The rates of the structural changes at the start of stimulation are limited by the rate of thin filament activation.

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Sarcomere-Length Dependence of the Low Angle X-Ray Pattern from Skeletal Muscle Fibers at Rest and during Isometric Contraction

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X-ray patterns were recorded from bundles of 2-3 fibers of R. Esculenta at 4°C at rest and at the plateau of an isometric tetanus (T0) at sarcomere length (SL) 2.0 to 3.6 um at the ID02 beamline at the European Synchrotron Radiation Facility, Grenoble. The patterns were normalized by the intensity of the 1,0 equatorial reflection at rest at each experimental SL to compensate for variation of diffracting mass with SL and between fibers. The axial diffraction pattern from resting fibers was independent of SL in the range 2.0-2.6 µm; in the range 2.6-3.0 µm the intensity and interference fine structure of the meridional M3 reflection from the axial repeat of the myosin heads along the filaments was constant, but its spacing (SM3) increased. The intensity of the first myosin layer line decreased in this SL range, indicating decreased helical ordering of the myosin heads. The intensity of the 44nm merdional reflection associated with myosin binding protein C was constant up to SL 2.7 μ m, but much reduced for SL>2.7 µm. At T0, the M3 reflection intensity was smaller at longer SL, in proportion to the overlap between thick and thin filaments. The interference fine structure of the M3 was independent of SL up to 2.8 µm; at longer SL it varied between preparations and SM3 reduced with increasing SL. The SL-dependence of the M3 reflection at T0 indicates that the detached myosin heads in the non-overlap region of the thick filament are axially disordered compared with actin-attached heads in the overlap region, although the axial center of mass of the detached