Supplementary Material (ESI) for PCCP

Supplementary material S1: Energy of myosin bound to actin with a flexible S2 domain

Sam Walcott,[a] Sean X. Sun[a,b]

[a] Department of Mechanical Engineering.
E-mail: samwalcott@gmail.com

[b] Whitaker Institute of Biomedical Engineering,
Johns Hopkins University, Baltimore MD, USA.
E-mail: ssun@jhu.edu

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The actin filament consists of 2 helical strands of actin monomers[1;2;3]. Each monomer can bind myosin. For each x-position, there are roughly 2 possible binding sites. To bind to a site that is not directly in the plane of the thick and thin filament, the coiled-coil stalk domain has to bend and twist to accommodate the binding geometry. Given the 2 possible binding sites, the myosin will bind preferentially to the site that costs the least amount of elastic energy. For instance, myosin will bind more frequently underneath the filament than on top of it. The configuration where both sites have the same elastic energy cost is docking to the side at $\pm\pi/2$ positions. (See Fig.). Here the end of the stalk domain has to bend by roughly 17nm, and twist by $\pi/2$. We use linear elastic theory to estimate this energy.

The stalk domain protruding from the thick filament is roughly 50nm in length. The persistence length of the stalk is estimated to be 100-150nm[4;5;6]. Within the linear elastic theory of rods, bending and twist are independent. Therefore we can estimate these contributions separately.

1 Bend

From Fig. , we see that the largest possible bend of the stalk is: $\Delta\ell = 2\ell\cos\pi/4 \approx 17$nm, where ℓ is roughly 12nm. Compared to the overall length of the stalk, this deflection is relatively small. In Lan and Sun (2005)[7], the small deflection energy of the stalk was found to be

$$E_{\mathrm{bend}} = \frac{3\ell_p k_{\mathrm{B}}T}{2L^3\cos^3\alpha}(\Delta\ell)^2 \tag{1}$$

where L is the overall length and α is the angle between the stalk and the thick filament. Using this estimate, the bending energy is $\approx 0.29k_{\mathrm{B}}T$, quite small compared to thermal energy.

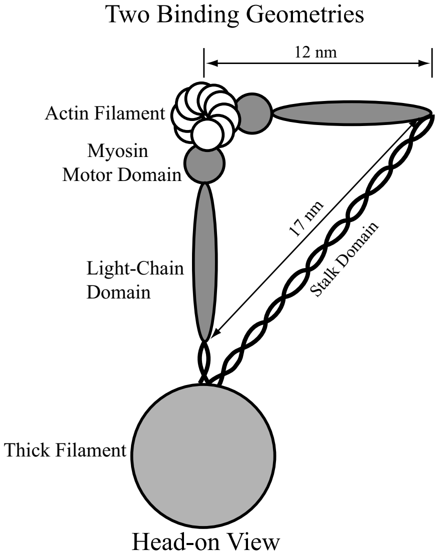

Figure 1: Two extreme configurations of the actin-bound motor. Configuration 1 is where the motor binds directly in between the thick and thin filament. This is the energetically most favorable configuration. There are 25 other possible actin binding sites. Configuration 2 is where the motor domain binds to the side of the filament. In this configuration the stalk domain must bend and twist to allow binding. The elastic energy cost in this configuration is $\approx 1.5 k_{\mathrm{B}}T$.

2 Twist

The twist elastic energy is given by:

$$E_{\text{twist}} = \frac{k_{\mathrm{B}}T}{2} \int_0^L ds A \left[\frac{\partial \phi(s)}{\partial s}\right]^2 \tag{2}$$

where A is the twist modulus of the stalk and $\phi(s)$ is the twist angle as a function of the arc-length, s. In a separate study, it was found that the twist modulus of α-helices is roughly half of the bending modulus[5]. Since the stalk domain is a coiled-coil whose bending modulus corresponds to $\ell_p = 100$nm, we therefore use $A = 50$nm. $\phi(s)$ is the twist angle along the stalk which is a function of s.

At mechanical equilibrium, the twist angle obeys a linear function along the stalk:

$$\phi(s) = \frac{\phi(L) - \phi(0)}{L} s + \phi(0) \tag{3}$$

Since $\phi(0) = 0$, we have

$$\frac{\partial \phi}{\partial s} = \frac{\phi(L)}{L} \tag{4}$$

Finally, there are 2 α-helices in the coiled-coil S2 domain, the total twist energy is then

$$E_{\text{twist}} = \frac{A \phi(L)^2}{L} \tag{5}$$

Examining Fig. , we see that $\phi(L) = \pi/2$ and the twist energy is $\approx 2.4 k_{\mathrm{B}}T$.
The total elastic energy, $E_{\mathrm{tot}} = E_{\mathrm{bend}} + E_{\mathrm{twist}}$, is about $2.8 k_{\mathrm{B}}T$ and is quite close to the thermal energy $k_{\mathrm{B}}T$. In addition, there are 2 available binding sites with the same elastic energy. Therefore, the probability of binding to actin is essentially uniform along x. The geometrical mismatch energy cannot be a dominant effect. Furthermore, if myosin is bound to actin in the geometry shown in Fig. 7, to relieve the elastic strain after a power-stroke, the actin filament must twist by $\pi/2$. This is highly unlikely since the actin filament is elastically rigid and there are other bound myosin heads that resist this additional strain. Therefore, mostly likely, the motor will complete its power-stroke without releasing the elastic strain in the stalk. The elastic strain in the stalk is unavailable as an energy source in the usual ratchet sense.
An interesting conclusion from this estimate is that the stalk is quite flexible and the myosin heads can bind to an adjacent thin filament. Thus, the net probability of binding of an actin site is in fact roughly equal. Thus, we have used an identical actin binding constant for the cross-bridges. The elastic strain will, however, affect the geometry between the LCD and the motor domain, even though only slightly. The slight strain in joint C can change the kinetics of the motor, including the crucial step of ADP release. This additional complication is not considered in the present model.

References

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