Stochastic Mechanochemistry for Processive Motor Proteins: Kinesin Crouches before Sprinting. YOUNG C. KIM, MICHAEL E. FISHER, Inst. Phys. Sci. Tech., University of Maryland, MD 20742 — Experiments by Block and coworkers (2003) applied assisting, resisting, and sideways loads $F = (F_x, F_y, F_z)$ to single-molecules of kinesin as they moved along a microtubule (MT) taking steps of size $d \simeq 8.2$ nm. The velocity, $V_x$, and the randomness were observed as functions of $F$ and [ATP]. To uncover substeps and intermediate motions from such data, we have extended a discrete-state stochastic model, previously applied to kinesin$^1$ and myosin V,$^2$ to allow for the vectorial loading of processive motors by invoking a three-dimensional “energy landscape” with a potential $\Phi(F)$.$^3$ The size of the attached bead and the resulting angle of the motor’s tether relative to the track play a crucial role. The analysis for kinesin then indicates that on binding ATP (and, possibly, catalysing hydrolysis, etc.) the motor ‘crouches,’ i.e., the point of attachment of the tether moves downwards (toward the MT) by 0.5-0.8 nm but forwards by only 0.1-0.2 nm, before completing a rapid swing of close to 8 nm. Unlike the scalar, $F_x$-only, analysis,$^1$ this is consistent with the observations of Higuchi and coworkers. Furthermore, assisting (i.e., forward) loads are opposed since the ‘upwards’ component, $F_z$, is enhanced by $\sim 2$ pN which reduces the velocity.


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