Abstract Submitted
for the MAR14 Meeting of
The American Physical Society

Harmonic force spectroscopy reveals a force-velocity curve from a single human beta cardiac myosin motor JONGMIN SUNG, SUMAN NAG, Stanford University, CHRISTIAN VESTERGAARD, KIM MORTENSEN, HENRIK FLYVBJERG, Technical University of Denmark , JAMES SPUDICH, Stanford University — A muscle contracts rapidly under low load, but slowly under high load. Its molecular mechanisms remain to be elucidated, however. During contraction, myosins in thick filaments interact with actin in thin filaments in the sarcomere, cycling between a strongly bound (force producing) state and a weakly bound (relaxed) state. Huxley et al. have previously proposed that the transition from the strong to the weak interaction can be modulated by a load. We use a new method we call "harmonic force spectroscopy" to extract a load-velocity curve from a single human beta cardiac myosin II motor. With a dual-beam optical trap, we hold an actin dumbbell over a myosin molecule anchored to the microscope stage that oscillates sinusoidally. Upon binding, the motor experiences an oscillatory load with a mean that is directed forward or backward, depending on binding location We find that the bound time at saturating [ATP] is exponentially correlated with the mean load, which is explained by Arrhenius transition theory. With a stroke size measurement, we obtained a load-velocity curve from a single myosin. We compare the curves for wild-type motors with mutants that cause hypertrophic cardiomyopathies, to understand the effects on the contractile cycle

Jongmin Sung
Stanford University

Date submitted: 14 Nov 2013 Electronic form version 1.4