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Folding-Unfolding Transitions in Single Titin Molecules Characterized with Laser Tweezers

Miklós S. Z. Kellermayer,*† Steven B. Smith,* Henk L. Granzier,‡ Carlos Bustamante*

Titin, a giant filamentous polypeptide, is believed to play a fundamental role in maintaining sarcomeric structural integrity and developing what is known as passive force in muscle. Measurements of the force required to stretch a single molecule revealed that titin behaves as a highly nonlinear entropic spring. The molecule unfolds in a high-force transition beginning at 20 to 30 piconewtons and refolds in a low-force transition at ~2.5 piconewtons. A fraction of the molecule (5 to 40 percent) remains permanently unfolded, behaving as a wormlike chain with a persistence length (a measure of the chain’s bending rigidity) of 20 angstroms. Force hysteresis arises from a difference between the unfolding and refolding kinetics of the molecule relative to the stretch and release rates in the experiments, respectively. Scaling the molecular data up to sarcomeric dimensions reproduced many features of the passive force versus extension curve of muscle fibers.

Passive force develops when a relaxed muscle is stretched; this force is responsible for restoring muscle length after release, and it is required for maintaining the structural integrity of the sarcomere in actively contracting muscle (1). Titin (2), a giant 3.5 MD protein, spans the half-sarcromere, from the Z line to the M line (3) (Fig. 1A). Because titin is anchored both to the Z line and to the thick filaments of the A band, passive force while the sarcomere is stretched is probably generated by extension of the I-band segments of the molecule (4, 5). It has been suggested (6, 7) that the elasticity of titin derives from the reversible unfolding of the linear array of ~300 immunoglobulin C2 (Ig) and fibronectin type III (FNIII) domains (8) that make up the molecule. In addition, a unique proline (P)-, glutamate (E)-, valine (V)-, and lysine (K)-rich (PEVK) domain recently identified in titin (9) has been hypothesized to form a semistable region that operates as a low-stiffness spring (9).

Here, we stretched titin by attaching each of its ends to a different latex bead (10), one of which was held by a movable micropipette and the other was trapped in force-measuring laser tweezers (11) (Fig. 1B). The micropipette was then moved at a constant rate while the force generated in the molecule was continuously monitored. When a maximum predetermined force (fmax) was reached, the process was reversed to obtain the release half-cycle. The force versus extension (f versus z) curves from these experiments (Fig. 2) illustrate several characteristics of the data. (i) The end-to-end distance (z) at which the common fmax is reached varies considerably, probably as a result of a variation in the location of the bead attachment in titin. (ii) Many molecules were extended far beyond the ~1-μm contour length of native titin (12). (iii) Normalizing the curves to the same length scale reveals that the force generated for a given fractional extension (the ratio of z to the contour length, L) also varies from experiment to experiment, probably reflecting different numbers of titin molecules within the tethers. (iv) All curves show hysteresis.

To identify single-molecule tethers and determine their length, we segregated the data into classes by comparing them with the predictions of two entropic elasticity models: the freely jointed chain [FJC (13)] and the wormlike chain [WLC (14)] models. The FJC model did not describe the data, but the WLC model fit the stretch data at low to moderate forces and the release data at moderate to high forces (15). The WLC model describes the chain as a deformable continuum (rod) of persistence length A, which is a measure of the chain’s bending rigidity. For a WLC, z is related to the external force (f) by $fA/k_BT = z/L +$.
1/4(1 − z/L)² − 1/4, where $k_B$ is the Boltzmann constant and $T$ is absolute temperature (10). The end-to-end length (z) of a WLC approaches its contour length (L) as $f^{-1/2}$. The contour lengths of the tethers were thus estimated by plotting the data as $f^{-1/2}$ versus z and extrapolating to infinite force (16) (Fig. 3A). A histogram of the release contour lengths obtained in this way showed a bimodal distribution with peaks at ~1.5 and ~4 μm (15), reflecting the presence of two titin sizes in our preparations [T1 and the difference fragment (Fig. 1A)]. However, there was a discrepancy between the calculated 10-μm contour length for a fully unfolded titin molecule (17) and the observed contour-length peak at ~4 μm. Possibly the molecules were never fully unfolded and extended under the forces used (18).

In the $f^{-1/2}$ versus z plot, the extrapolated force-axis intercept of a curve at high extension indicates the persistence length of a molecule by the relation $A = k_BT/4F$ [where $F$ is force at the intercept (17)]. When multiple molecules are present in a tether, this intercept (the apparent persistence length of the tether) is divided proportionately. The frequency of apparent persistence lengths for 302 releases of 45 tethers is shown in Fig. 3B. The distribution is multimodal with peaks corresponding to single, double, and triple parallel strands of the molecule. Accordingly, the persistence length of the single, unfolded molecule is ~20 Å. For a given extension, proportionally greater amounts of force were generated when multiple strands of titin were subjected to the stretch-release cycle than when only a single molecule was present (Fig. 3B, inset).

The $f^{-1/2}$ versus z plots revealed that titin does not behave as a WLC throughout the entire stretch-release cycle: Its behavior deviates from that of a WLC at high force during stretch and at low force during release, indicating the onset of structural transitions (Fig. 3A). Because in most experiments the stretch and the release transitions occurred at extensions larger than the contour length of the extended but native titin, these transitions must involve force-induced unfolding and refolding in the molecule. Accordingly, we propose the following model to rationalize these observations: (i) At the beginning of stretch, a variable fraction of the molecule, 5 to 40%, is already unfolded (19). In this early part of the stretch curve (WLC region 1 in Fig. 3A, and from points a to c in Fig. 4A), the molecule behaves as a WLC whose properties are dominated by this pre-unfolded fraction. Consistent with this model, $L_{\text{stretch}}$ (Fig. 3A) is more than twice as long as the contour length of the native molecule, and the persistence length associated with this part of the curve (20 Å) is about one-seventh that estimated for native titin (20). The pre-unfolded fraction may contain the PEVK domain, although in most cases it exceeds the length attributable to this domain (19). (ii) As titin is stretched to high
force (20 to 30 pN), transitions begin to occur in the molecule (onset of stretch transition in Fig. 3A, and point c in Fig. 4A) that convert part of the folded fraction into unfolded protein. As titin is further stretched, mechanical denaturation (unfolding) of additional Ig- and FNIII-type domains in the molecule takes place, a process that may not be completed when the maximum force allowed by the instrument, $f_{\text{max}}$, is reached (stretch transition in Fig. 3A, and points c to d in Fig. 4A). Thus, the contour length of the fully denatured titin molecule was never observed in our experiments. (iii) Upon release of the unfolded titin, the molecule does not refold in the initial ~15 s of the release part of the cycle but behaves instead as a WLC (points d to e in Fig. 4A) with the properties of an unfolded polypeptide (persistence length ~20 Å). (iv) Only when the molecule is allowed to shorten down to about one-half of its release contour length ($L_{\text{release}}$) does refolding begin to take place, which is seen as a transition in both the $f$ versus $z$ curve (from points e to b in Fig. 4A) and in the $f^{-1/2}$ versus $z$ plots (release transition, Fig. 3A). In this region, much of the shortening occurs around 2.5 pN as the data cross various WLC curves corresponding to different persistence lengths. The release transition marks the refolding of the Ig and FNIII domains. (v) As titin shortens below ~40% of its release contour length, the refolding ceases and the force drops (points b to a in Fig. 4), and the molecule again behaves as a WLC with a shortened contour length ($L_{\text{stretch}}$, Fig. 3A).

In this model, the $f$ versus $z$ curves display hysteresis because the rate at which the molecule is stretched or released exceeds the rate of unfolding and refolding of the molecule at equilibrium at that extension. If our stretch-release experiment had been done more slowly, the stretch and release portions of the force curve would have converged toward a single intermediate curve representing the true equilibrium denaturation-renaturation force. The unfolding and refolding rates under force are much lower than those rates in the presence of strong chemical denaturants (21), suggesting that titin’s domains must pass through kinetic folding intermediates with high activation energies ($E_a$), and that pulling a domain does relatively little to lower those energies.

During unfolding, such intermediate states might not increase the axial end-to-end length of a domain significantly and therefore might be accessible only through the generation of force perpendicular to the pulling direction (by thermal fluctuations). Thus, an axial force would do little to speed up the denaturation. Tension in the chain must be increased above its folding-unfolding equilibrium value to access these states at the experimental rate. During renaturation under external force, intermediate states are required that would shorten the unfolded domains axially. Tension in the denatured chain will raise the energy of these states, which now stand as barriers (activation states) to renaturation. Therefore, to access these states at the experimental rate, the tension in the chain must be lowered below its equilibrium value. A simulation based on this model reproduces the hysteresis and other features seen in the $f$ versus $z$ curves of Fig. 4 (22).

In support of our model, stopping short of the transition in either direction abolished hysteresis. Thus, it was possible to stretch and release the molecule reversibly between points b and c, and also between points d and e in Fig. 4 (Fig. 4A, inset). By comparison, hysteresis was reestablished when either transition was allowed to occur, either in part or to completion. As a further test of this model, titin was stretched in the presence of the chemical denaturant guanidinium-HCl (GuCl) at a concentration of 1.6 M (6). Upon addition of GuCl, the molecule exhibited one normal stretch half-cycle but failed to refold on the release half-cycle, so the first stretch-release cycle showed force hysteresis. In the next cycle, hysteresis almost completely disappeared, and the stretch curve approached the release curve, indicating that the release data indeed represents the elastic behavior of an unfolded polypeptide.

Repetitive cycles of stretch and release alone also led to the progressive denaturation of titin. During this process the stretch and release transitions shortened, and the stretch curve moved progressively toward the release curve (Fig. 4B). Thus, it appears that after each stretch-release cycle an increasing fraction of the unfolded titin failed to refold. Such a “wearing out” of titin may be caused by the randomization of proline isomer forms in the Ig and FNIII domains (23).

The force measured for a single titin
molecule can be scaled up by the number of titin molecules in the sarcomere to test the hypothesis that titin is solely responsible for the passive elastic response of muscle. Assuming six titins per thick filament per half-sarcomere (4), the calculated curves of passive force per muscle cross-sectional area as a function of sarcomere length can be obtained. The calculated curve is very similar in shape and magnitude to that obtained experimentally for a single skeletal muscle fiber in which caldesmon had been used to block the weak acto-myosin interaction (24) (Fig. 5). This agreement validates the previous conclusion (24) that titin is the main determinant of the passive force response of muscle. In addition, this analysis indicates that the hysteresis observed in stretch-release experiments in relaxed muscle results from the combined folding-unfolding kinetics of many independent titin molecules (Fig. 5, inset).

It has been argued (6, 7) that domain unfolding-refolding is likely to be involved in all the role of titin as an elastic element in muscle physiology. However, if parts of the molecule unfold and refold each time a muscle physiologically. However, if parts of the molecule unfold and refold each time a muscle is stretched and released, an amount of energy equal to the area inside the hysteresis curve would be wasted as heat. We suggest, rather, that the pre-unfolded fraction of titin functions as an efficient (reversible) entropic spring in muscle. Then the purpose of the slow “wearing out” of titin with recent folding-refolding transitions (Fig. 4B) might be to increase the length of the molecule’s pre-unfolded region; the longer the pre-unfolded region, the longer is also the range of motion over which the force curve is reversible (region 1 in Fig. 4A), thereby minimizing subsequent hysteresis and keeping efficiency high. By pre-unfolding just as much titin as necessary, the maximum of the range of efficient elastic response in muscle may be adjusted. Regulating the range of efficient elastic response in muscle through titin unfolding and refolding may serve as an adaptive mechanism during the repetitive mechanical loading of skeletal or cardiac muscle.

REFERENCES AND NOTES

10. The Z line end of titin (from rabbit back muscle) was attached to a carboxylated polystyrene bead (3-μm diameter, Spinco) using the size of the carboxylated polystyrene bead (3-μm diameter, Spinco) using the size of the pre-unfolded fraction is 0.5 to 2.0 μm, representing 5 to 20% of the entire ~10-μm-long primary structure. If some of these molecules were tethered in their midle, the pre-unfolded fraction could be as high as 10% of the tethered half-molecule. The unfolded PEVK domain of skeletal muscle in 2714 residues, may contribute to only 0.8 μm to the contour length of the whole molecule (4). Early electron micrographs of titin, which showed the molecule as strings of beads connected with thin strands, have already implied the presence of regions that easily unfold or untether under stress (12). J. Trinick et al., J. Mol. Biol. 180, 331 (1984).
12. The relaxation time for the force-denaturation of titin was estimated by rapidly stretching the molecule to high force (~60 pN) and holding its length constant while watching the force decay. This relaxation was best fit with a fast decay time of ~4 s and a slower phase of ~7 s. These two processes are slow compared with the stretch and release rates and very slow compared with the ~1 s required to denature reduced-disulfide Ig domains in 4 M GuC (Y. Goto and K. Hamaguchi, J. Mol. Biol. 156, 911 (1982)).
13. If EF is increased (or reduced by the external force F) because the intermediate state is longer (or shorter) than the native (or denatured) state by an amount Δz, the unfolding (or refolding) rate can then be written as 30/550 ΔF2, where ΔF is an attempt frequency set by Brownian dynamics of the peptide chain. The force dependence in Fig. 4B is well fit by assuming z·ΔF = 28 pNμm and ΔF = 0.3 nm for unfolding, E0 = 0 and ΔF = 8 nm for refolding, and 100 = 1010 s1 for both processes. A refolding intermediate that creates PEVK unfolded in the middle of the FNI domain must shorten the denatured molecule’s extension by ΔF = 8 nm before the proper set of interactions can be made, but an unfolding intermediate with a high (rate-limiting) free energy could be one in which many bonds or hydrophobic interactions are disrupted by a relatively small shift (ΔF = 0.3 nm) away from the ideal shape of the native domain. Source code and simulation results are available at http://alco.uregon.edu/~cblab on the Web.

14. The rate of refolding of the FNI domains could strongly depend on whether or not the unfolding leads to trans-cis isomerization of the ε-oxo prolines at the corners of the β folds of these domains (A. L. Man et al., Cell 71, 671 (1992)). Protein refolding is often limited by the rate of proline isomerization (T. Kielhaber, H. H. Kohler, F. Schmid, J. Mol. Biol. 224, 217 (1992)). Because the state of all eight prolines should randomize in a domain that is unfolded for 10 to 100 s, correct isomerization of all eight prolines might take a thousand years or longer if chosen randomly. On the contrary to this view, K. Páczko et al. (Proc. Natl. Acad. Sci. U.S.A. 93, 10703, (1996)) found that an isolated FNII domain refolded rapidly (~1 s) after chemical denaturation; chemical refolding may be slower than FNII chemical-refolding for several reasons: (i) no residual chemical denaturant helps prevent kinetic traps during refolding, (ii) pulled prolines may be able to adopt the incorrect cis conformation, (iii) a variety of proline-rich FNII and Ig domains
Inhibition of Pathogenicity of the Rice Blast Fungus by Saccharomyces cerevisiae α-Factor

Janna L. Beckerman, Fred Naider, Daniel J. Ebbole*

Magnaporthe grisea is a fungal pathogen with two mating types, MAT1-1 and MAT1-2, that forms a specialized cell necessary for pathogenesis, the appressorium. Saccharomyces cerevisiae α-factor pheromone blocked appressorium formation in a mating type–specific manner and protected plants from infection by M. grisea-2 strains. Experiments with α-factor analogs suggest that the observed activity is due to a specific interaction of α-factor with an M. grisea receptor. Culture filtrates of a MAT1-1 strain contained an activity that inhibited appressorium formation of mating type MAT1-2 strains. These findings provide evidence that a pheromone response pathway exists in M. grisea that can be exploited for plant protection.

The heterothallic ascomycete Magnaporthe grisea is a pathogen of a wide variety of grasses but is best known as the causal agent of rice blast disease. The costs of controlling disease with fungicides and the difficulty in breeding durable and effective resistance have led to intense interest in understanding the mechanisms governing the pathogenicity of this fungus (1). Conidia of M. grisea attach to the plant host with an adhesive that is released from the tip of the conidium upon hydration (2). After germination, the fungus responds to contact with the host surface by producing an appressorium, a specialized cell that uses turgor pressure to aid in penetration of the host cell (3).

The mating behavior of M. grisea is determined by the mating-type locus, which contains either MAT1-1 or MAT1-2 DNA. One parent of each of the two mating types participates in a sexual cross. The mating-type loci of filamentous ascomycetes are thought to encode master regulators that control the expression of mating type–specific genes, such as pheromones and pheromone receptors (4). In Saccharomyces cerevisiae, α-factor and α-factor pheromones are produced by strains with MATα and MATα mating types. Each pheromone is recognized by a corresponding heterotrimeric GTP-binding protein–coupled receptor expressed in the opposite mating type (5).

Appressorium formation of mating type MAT1-2 strains of M. grisea is inhibited when conidia are germinated in the presence of 2% yeast extract. However, 2% peptone and 2% tryptone do not inhibit appressorium formation (6). We found that appressorium formation of MAT1-1 strains was not inhibited by yeast extract to the same degree as MAT1-2 strains (Table 1). Yeast extract contained an unidentified factor that could be partially purified by an organic extraction procedure designed for purification of small peptides (7). This fraction inhibited appressorium formation in MAT1-2 strains, and the active component appears to be a polypeptide. We found 91 ± 7% appressorium formation of strain 4091-5-8 (MAT1-2) with proteinase K–treated extract and 1 ± 1% appressorium formation with untreated extract (8). The mating type–specific effect of yeast extract on appressorium formation suggested that M. grisea might respond to a pheromone by suppressing infection-related development.

The α-factor pheromone of S. cerevisiae has activity in closely related yeast species (9). We tested the effect of synthetic S. cerevisiae α-factor on M. grisea and found that appressorium formation was inhibited in MAT1-2 strains (Table 1 and Fig. 1, A and B) but not in MAT1-1 strains (Table 1 and Fig. 1C). The concentration of α-factor needed to cause >95% inhibition of appressorium formation of all MAT1-2 strains tested was 300 μM. This is 104-fold higher than the concentration of α-factor required

### Table 1. Mating type–specific inhibition of appressorium formation in M. grisea.

<table>
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<tr>
<th>Strain</th>
<th>Mating type</th>
<th>Appressorium formation (%)</th>
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*To whom correspondence should be addressed. E-mail: C.J.0282@zeus.tamu.edu