

Force Spectroscopy with a Small Dithering of AFM Tip: A Method of Direct and Continuous Measurement of the Spring Constant of Single Molecules and Molecular Complexes

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ABSTRACT A new method of direct and continuous measurement of the spring constant of single molecule or molecular complex is elaborated. To that end the standard force spectroscopy technique with functionalized tips and samples is combined with a small dithering of the tip. The change of the dithering amplitude as a function of the pulling force is measured to extract the spring constant of the complex. The potentialities of this method are illustrated for the experiments with single bovine serum albumin—its polyclonal antibody (Ab-BSA) and fibrinogen—fibrinogen complexes.

INTRODUCTION

In recent years, single molecule force spectroscopy using the atomic force microscope (AFM) has become an established technique and helped to reveal important characteristics of many proteins, DNA (RNA) molecules, polysaccharides, and other molecular complexes and/or structures of large biological importance (see, for instance, Heinz and Hoh, 1999; Zlatanova et al., 2000; Carrion-Vazquez et al., 2000; Janshoff et al., 2000; Leckband, 2001; Rief and Grubmüller, 2002 for recent reviews). Among numerous interesting results obtained using the force spectroscopy method, one could mention precise determination of the forces acting between complementary strands of DNA (Lee et al., 1994a; Cluzel et al., 1996; Essevaz-Roulet et al., 1997; Noy et al., 1997; and others). These studies seem to have attained such an excellent level that recently DNA-based systems were proposed as a “programmable force sensor” (Albrecht et al., 2003). One could mention also nanomechanical studies of single muscle protein titin molecules (Rief et al., 1997a, 1998; Marszalek et al., 1999) and chromatin fibers (Leuba et al., 2000), observation of force-induced conformational transitions of polysaccharides (Rief et al., 1997b, Marszalek et al., 1998), and so on. Probably the most informative and interesting force spectroscopy studies were the experiments revealing the specific receptor-ligand interactions including antigen-antibody (Ag-Ab) systems (Stuart and Hlady, 1995; Dammer et al., 1996; Hinterdorfer et al., 1996; Allen et al., 1997; Ros et al., 1998; Willemsen et al., 1998, 2000; Merkel et al., 1999; Harada et al., 2000; Schwesinger et al., 2000;

and others), and by this reason below we will discuss the single force spectroscopy approach mainly having in mind exactly Ag-Ab system.

The method consists of functionalizing the AFM tip with the antibody and the substrate with the antigen (or vice versa). After an antibody-functionalized tip enters in contact with an antigen-functionalized sample, a specific bond between the antigen and the antibody can form. This bond will be ruptured (event) when the tip is pulled away from the substrate surface (Fig. 1). The amount by which the pulling cantilever bends before the bond ruptures is measured. From this value the specific interaction (unbinding) force is calculated using the known spring constant, k , of the AFM cantilever. It was shown that the measured unbinding force correlates with the thermal dissociation rate of the antigen-antibody (Ag-Ab) pair (Strunz et al., 2000; Schwesinger et al., 2000) and can be used for molecular recognition.

Very recently it was proposed to slightly modulate the distance between the cantilever and the sample at a driving frequency ω . Measuring the amplitude of the tip vibrations at this frequency leads to an improved molecule recognition fidelity (Schindler et al., 2000). The possibility to measure the dynamical properties of single molecules using this method was also demonstrated for a short polymer molecule of poly(ethylene glycol) (Kienberger et al., 2000). In the present work we report the development of this approach for direct and continuous measurement of the spring constant of a single stretched molecule or molecular complex. Mainly the complex of bovine serum albumin (BSA) with a polyclonal antibody to BSA (Ab-BSA) have been studied, additionally the potentialities of the method are illustrated also for fibrinogen-fibrinogen complex.

MATERIALS AND METHODS

AFM instrumentation

A schematic diagram of the experimental setup is given in Fig. 1. A commercially available AFM (Nanoscope IIIa Multimode Scanning Probe Microscope, Veeco Instruments, Santa Barbara, CA) and standard V-shaped

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RESULTS AND DISCUSSION

Typical experimental results obtained for BSA–Ab–BSA complex are shown in Fig. 3. The recording of the data starts when the tip and sample are far apart (A–B in Fig. 3 A). Then, as the tip approaches, it enters into contact with the substrate (segment B–C). At point C the tip is retracted until point D where it loses contact with the substrate. Between D and E the tip is further retracted from the substrate with the Ag–Ab complex extended. Point E corresponds to the rupture of a BSA–Ab–BSA bond and the unbinding force is measured at this moment. Calibration of the absolute value of the force has been performed based on the linear part of the contact line (B–C and C–D) using the known tip spring constant.

Calculation of spring constant of tip-sample complex

The following procedure was used to extract the value of the spring constant for the tip-sample complex k_{complex} from the recorded data.

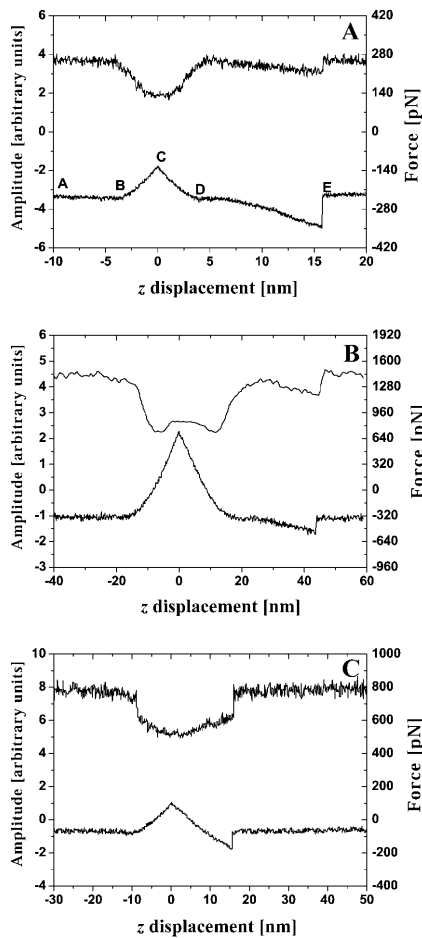


FIGURE 3 Experimental dependencies of the pulling force (lower curves) and lock in output signal used to measure the spring constant (upper curves) on the sample stage z -displacement. Dithering peak to peak amplitude is 2 nm. See text for the classification of the presented events.

The process of excitation of cantilever vibrations in a liquid is very complicated to describe and is not yet fully understood. Nevertheless, for small amplitudes of vibration, it still can be described as forced vibrations of a nonlinear oscillator (Sarid, 1991; Sader, 1998; Schindler et al., 2000; Kienberger et al., 2000). Introducing the variable δz , which describes the deviation of the cantilever from its equilibrium position, z_0 , produced by a (quasi)static pulling force f_{pul} , one can write down:

$$m_{\text{eff}} \frac{\partial^2(\delta z)}{\partial t^2} + \gamma \frac{\partial(\delta z)}{\partial t} + k_{\text{eff}} \delta z = f_{\omega} \cos(\omega \times t). \quad (1)$$

Here, the parameters m_{eff} and γ characterize the vibrations of the cantilever in liquid and k_{eff} is the sum of the spring constant of the cantilever and that of the stretched complex. Note that the differential spring constant of the complex $k_{\text{complex}} = (df/dz)|_{z=z_0}$, rather than its static spring constant f/z_0 , is of importance for this equation, containing δz as a variable. (Here $f(z)$ is the force-extension characteristic of the BSA–Ab–BSA complex; see below.)

Solution of Eq. 1 is well known (Sarid, 1991, or any textbook with an introduction to oscillatory motion); this equation describes the forced vibrations $\delta z = a \cos(\omega \times t + \varphi)$ with an amplitude

$$a = \frac{f_{\omega}}{\sqrt{(k^2 - m_{\text{eff}}\omega^2)^2 + \gamma^2\omega^2}}, \quad (2)$$

and a phase shift

$$\sin \varphi = \frac{\gamma\omega}{\sqrt{(k^2 - m_{\text{eff}}\omega^2)^2 + \gamma^2\omega^2}}. \quad (3)$$

If the driving frequency ω is much smaller than the value of $\omega_0 = \sqrt{k_{\text{eff}}/m_{\text{eff}}}$, which, for the rather small quality factor $Q \geq 2$ is already very close to the resonance frequency of the system $\omega_{\text{res}} = \omega_0 \sqrt{1 - (1/4Q^2)}$, then, evidently, the vibration amplitude can be well approximated by the value of

$$a = f_{\omega}/k_{\text{eff}},$$

because $m_{\text{eff}}\omega^2/k_{\text{eff}} = (\omega/\omega_0)^2 \ll 1$ and $\gamma\omega/k_{\text{eff}} = (1/Q)(\omega/\omega_0) \ll 1$ for this case. The amplitude of the forced oscillation is measured with a lock in amplifier while recording force-distance curves. Three intervals are interesting for the force-distance curve as indicated in Fig. 3 A: 1), A–B where the lever oscillates freely; 2), D–E where the antigen-antibody complex is extended under the action of the pulling force f_{pul} ; 3), after E where the specific bond is ruptured and the cantilever oscillates again freely. From the oscillation amplitude in these three regions one obtains the reciprocal spring constants k^{-1} , $(k + k_{\text{complex}})^{-1}$ and k^{-1} , respectively. The value of k is known, which makes it possible to determine the spring constant k_{complex} of the single Ag–Ab complex as a function of z and f_{pul} .

In principle, the measured value of k_{complex} can be further refined if the parameters of the oscillatory system (m_{eff} and γ) are well known. This is, however, a very difficult problem, especially given the fact that the acting force value f_{ω} in itself depends on the frequency for our excitation method because the piezodriver is a source of displacement (of the cantilever base) rather than directly the force.

For our case, the resonant frequency of the cantilevers in liquid was measured and found to be in the range from 8.5 to 10 kHz. The driving frequency of 3.2 kHz is a trade-off between the necessity to have this value as small as possible for the better interpretation of data as discussed above and the necessity to have a sufficient number of oscillations per averaging time for the proper functioning of a lock in amplifier.

BSA–Ab-BSA complex

We can classify events presented in Fig. 3 as follows: single bond rupture (Fig. 3 A; the value of the unbinding force is 130 pN), double bond rupture (Fig. 3 B; 295 pN), and “no specific event” (Fig. 3 C). The last example is a demonstration of the utility of the measurement of the spring constant for the interpretation of results of pulling-off experiments. Although the standard force-distance curve (*lower*) in Fig. 3 C looks like a single bond rupture event, the upper curve has no peculiarities (that is no decrease of dithering amplitude during the pulling off) and clearly demonstrates that nonspecific interactions take place here. This is a really useful addition to all approaches designed to distinguish between different events in the experiments of this type; see e.g., Kasas et al. (2000) and references cited therein. In some experiments forces larger than 1 nN were observed. These events are believed to be due to the multiple ruptures of glutaraldehyde-amine bonds, and we will not discuss them below.

In Fig. 4 we present typical experimental dependencies $k_{\text{complex}}(z)$ (A) and $f_{\text{pul}}(z)$ (B) for the case of single bond rupture. The linear approximation of the experimental dependence $k_{\text{complex}}(f)$ derived from Fig. 4, A and B is given in Fig. 4 C. Before plotting Fig. 4 C we fitted Fig. 4 A to a straight line in the region from 4.23 nm to 15.72 nm and fitted Fig. 4 B to a second-degree polynomial in the same interval. The spring constant of an individual (and double) BSA–Ab-BSA complex always increases together with the increase of the pulling force and attains the maximal value at a moment of the bond rupture. A good correlation between the value of the specific interaction force, the simultaneously measured spring constant of the complex, and the value of tip-sample distance at this moment is observed. The average value of the complex’s spring constant at the moment of the single antigen-antibody bond rupture was measured to be 0.017 ± 0.003 N/m (average over ~ 50 events). The majority of the events corresponding to the double bond rupture gives k_{complex} values ranging from 0.03 to 0.04 N/m (10 events).

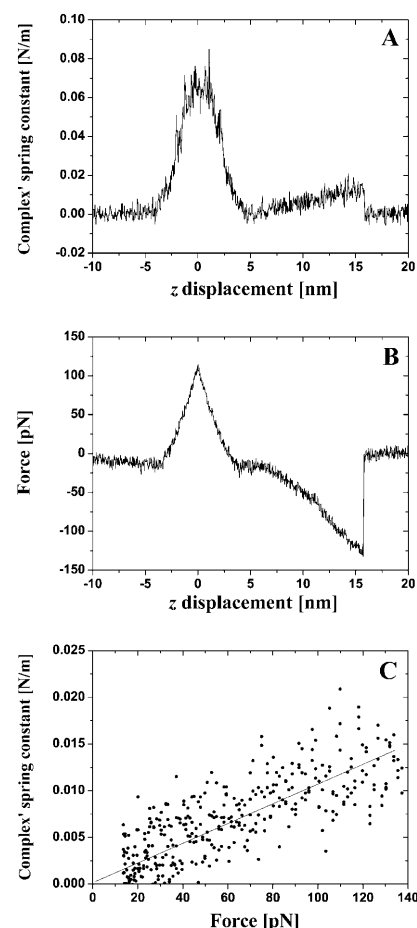


FIGURE 4 Typical dependence of the antigen-antibody complex’s spring constant k_{complex} (A) and pulling force f (B) for a single specific bond rupture event on the sample stage z -displacement. In C we present a dependence $k_{\text{complex}}(f)$ derived from A, B, and its linear approximation.

However, values as large as 0.053 N/m were sometimes observed.

For the interpretation of the experimental results (only the case of single bond rupture is considered here) we should take into account the following. The force f is the derivative of the free energy of the system with respect to the value of the distance between the molecule’s endpoints, i.e., the fragments of a BSA–Ab-BSA complex that are fixed on the tip and sample surface (Doi and Edwards, 1992). The sample stage displacement z is an evident measure of such a distance. It can be argued that the complex’s extension is given by the difference of z and cantilever displacement y . The latter can be determined from the $f_{\text{pul}}(z)$ curve, $y = f_{\text{pul}}/k$, and, thus, the value of z can be corrected, which we did whenever relevant. Note that this correction is of only minor importance for our experiments. For example, for the typical one bond rupture event ($f_{\text{pul}} = 130$ pN) $y = 2.4$ nm and, thus, is essentially smaller than the characteristic (uncorrected) z -value of 16 nm.

Molecular dynamics calculations of the extension curves for antigen-antibody complexes (Grubmüller et al., 1996;

Balsera et al., 1997; Izrailev et al., 1997; Strunz et al., 2000; Heymann and Grubmüller, 1999a,b, 2000, 2001) show that the range of extension during which the details of the antigen-antibody interaction are important is of a few Ångströms very close to the point of rupture. For typical experimental conditions this corresponds to a characteristic timescale of the order of a few milliseconds or less. These values are beyond the reach of our experimental technique, so only the usual “entropy-related” contribution to the antigen-antibody complex’s spring constant (Doi and Edwards, 1992; Marko and Siggia, 1995) was measured.

It is well known that BSA is a globular protein “stiffened” by 17 disulfide bonds, and that this protein has different conformational forms (N, F, B, A, and E) characterized by different contents of helical β -sheets and other structures (Carter and Ho, 1994). Transitions between these forms can be caused either by a stretching (“mechanical denaturation”) or pH change. Earlier it was argued by Pereira et al. (2003) that expanded, E, BSA form (35% helix) corresponds to the “full extent allowed by the disulfide bond structures.” For our experiments, the possibility of BSA–Ab–BSA complex stretching should be limited exactly by attaining this “disulfide bond structures limited” E-form; relatively weak antigen-antibody bond will be ruptured before the rupture of disulfide bonds, which would allow further stretching, will occur. (For different experimental conditions, where essentially larger forces could be applied, the stretching of human serum albumin molecule until “the full contour length” of ~ 200 nm has been observed by Rixman et al. (2003).) Using the data about the sizes of antibody and relevant conformational forms of BSA molecules together with the ≤ 2 -nm thickness of linker layers, one could anticipate the maximal attainable stretching of the BSA–Ab–BSA complex of roughly 15 nm. This value is very close to that which has been indeed observed in our experiments: we have determined an average extension $z = 14 \pm 3$ nm (correction for the cantilever displacement y is taken into account) at the moment of specific bond rupture.

Detailed interpretation of our data using worm-like chain (WLC) or some other more sophisticated statistical polymer model would be somewhat premature at the current stage of experiments, because such a detailed interpretation seems to require a comparison of analogous data for different Ag–Ab complexes and (possibly) careful characterization of the protein binding sites. Nevertheless, we would like to underline the following. For long flexible molecules having numerous conformational degrees of freedom (linear polymers, DNA, etc.) force-extension dependence is given by a quasiuniversal function relatively insensitive to the chemical composition of the molecule. In the frame of WLC model, it was shown that such a force can be expressed by the formula (Marko and Siggia, 1995):

$$f(z) = \frac{k_B T}{p} \left(\frac{1}{4(1 - z/L)^2} - \frac{1}{4} + \frac{z}{L} \right). \quad (4)$$

Here k_B is the Boltzmann constant, T , the temperature, p , the persistence length, and L , the maximal attainable length of a stretched polymer. Of course, a polypeptide chain is not a good linear polymer in the sense that there is not a single monomer unit and, hence, a well-defined persistence length. Moreover, the WLC model does not allow for the secondary and tertiary structure of the complex. Nevertheless, Eq. 4 is often used to approximate experimental data of single protein stretching (Rief et al., 1997a; Mueller et al., 1999; Minajeva et al., 2001; Zhou, 2001; Round et al., 2002; Liu and Pollack, 2002). For our case, where both the force f and the spring constant are simultaneously and independently measured, the following consideration seems to be of interest. The value of the spring constant for the WLC model is given by the derivative of Eq. 4

$$k_{\text{complex}} = df/dz = \frac{k_B T}{2pL} (2 + (1 - z/L)^{-3}). \quad (5)$$

For the case of $z = 0$ in this model one has $k_{\text{complex}} = k_0 = 3k_B T/2pL$. Now it is worthwhile to note that in the frame of the WLC model a simple analytical dependence between the pulling force and spring constant can be given. For this, one needs to solve Eq. 5 for z/L and then to insert the obtained expression in Eq. 4, which results in

$$f = \frac{k_B T}{p} \left(\frac{\xi^{2/3}}{2^{4/3}} + \frac{3}{4} - 2^{-1/3} \xi^{-1/3} \right). \quad (6)$$

Here $\xi \geq 0.5$ is a dimensionless parameter, $\xi = (3k_{\text{complex}}/2k_0) - 1$. The inverse function, i.e., the dependence $k_{\text{complex}}(f)$, can be derived from Eq. 6 but this requires a solution of cubic equation that renders the resulting expression not so practical. The inverse function of Eq. 6 is plotted in Fig. 5.

Thus, the WLC model predicts a monotone increase of the single polymer molecule spring constant with the increase of the pulling force and extension. As it was mentioned before, only such monotone increase has been observed for all single

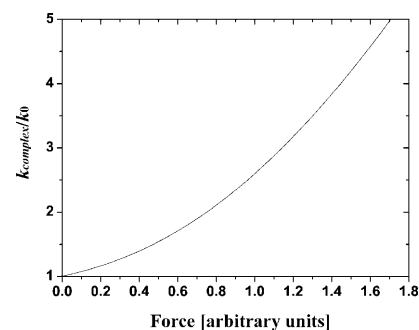


FIGURE 5 Universal dependence of the spring constant k_{complex} of a polymer molecule (measured in units of the spring constant k_0 of this molecule at $z = 0$) on the pulling force for the worm-like chain model of polymer elasticity. Here shown for $k_B T/p = 1$.

bond rupture events in our experiments. (Note that a non-monotone dependence $k_{\text{complex}}(f)$ was observed in our experiments for some multiple glutaraldehyde-amine bonds rupture events; this data is not considered here and will be published elsewhere.) At the current stage of experimental precision and statistics we were not able to approximate the observed dependencies $k_{\text{complex}}(f)$, similar to the one shown in Fig. 4 C by this function; only a linear approximation turns out to be sufficiently reliable and statistically sound. Nevertheless, we are sure that this will be very interesting to do in the near future.

The lack of direct measurements of spring constants of stretching antigen-antibody complexes in the literature makes the comparison of our data with other experiments rather difficult. First, usually it is not possible to determine reliably the relevant differential df/dz from the published results (see the next section for a brief discussion). Surprisingly, even to simply calculate the characteristic force-displacement ratio f/z at the moment of rupture of the antigen-antibody bond turned out to be virtually impossible because the average value of the complex extension at the moment of rupture, z , is rarely accurately reported in the literature. In some cases it also turns out that this is the stretching of linkers rather than of an Ag-Ab complex, which is responsible for observed z and k values. This takes place, for example, for Hinterdorfer et al. (1996) experiments with the complex of a human serum albumin (HSA) and polyclonal antibody to HSA (Ab-HSA), which have been performed using 8-nm poly(ethylene glycol) linkers. No correlation between z and specific interaction value has been reported. This observation is opposite to our data, where, as it was stated above, good correlation between the values of unbinding force, force constant k and extension z has been obtained.

Essentially different values of df/dz have been measured for systems other than antigen-antibody complexes. We can use sufficiently detailed data of Sakai et al. (2002) to estimate the possible effect of the linkers on our k -measurements. Sakai et al. (2002) worked with polystyrene molecules whose stretching data could be a model for the chemicals used to attach the protein molecules onto the tip and sample surface in our experiments. (All our chemicals are simple short molecules for which, as for the polystyrene, ordinary C–C, Si–C, and similar bonds are the only component.) For long polystyrene molecules ($L = 50$ nm, that is ~ 200 styrene monomers and 400 C–C bonds) Sakai et al. (2002) obtained for stretching forces of 100–140 pN (this is exactly the forces that are of interest to us) a value of $k = df/dz$ close to 0.02–0.03 N/m (see Fig. 1 of Sakai et al., 2002). For our linkers, which contain around 10 C–C bonds and have a length $L_1 \sim 1.5$ nm, we have from WLC model the value of k , which is L/L_1 times larger (see Eq. 5), that is ~ 0.8 N/m. This value is much larger than the spring constant of 0.017 N/m measured for Ag-Ab complex, thus we believe that the elasticity of linkers does not contribute significantly to the measured value.

Fibrinogen-fibrinogen complex

For comparison and further illustration of our method of spring constant measurement, in Fig. 6 we present typical experimental dependencies of the spring constant (Fig. 6 A) and pulling force (Fig. 6 B) on the sample stage z -displacement for fibrinogen-fibrinogen complex. The protocol of fixation of fibrinogen molecules on the AFM tip and sample surfaces is briefly discussed above in the Materials and Methods section; all other experimental details are the same as for BSA-Ab-BSA complex. Hence, Fig. 6 contains a data analogous to that of Fig. 4 but obtained for a completely different system.

Fibrinogen-fibrinogen interaction is obviously a nonspecific one, which defines much broader distribution of the value forces at the moment of the bond rupture, f_{rupt} , and corresponding values of z at this moment, z_{rupt} , in comparison with the single BSA-Ab-BSA complex. Indeed, experimentally obtained values of f_{rupt} ranges from 50 to 250 pN whereas the corresponding values of z_{rupt} ranges from 50 to 130 nm for fibrinogen-fibrinogen complex. Accordingly,

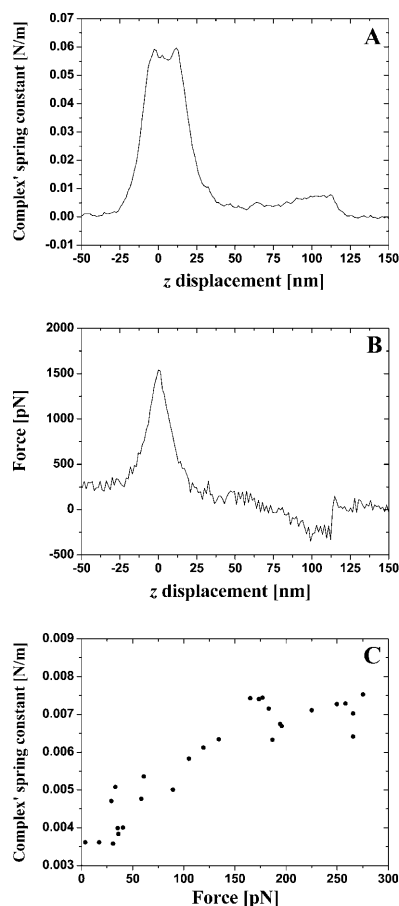


FIGURE 6 Typical experimental dependence of the fibrinogen-fibrinogen complex's spring constant k_{complex} (A) and pulling force f (B) on the sample stage z -displacement. Dithering peak-to-peak amplitude is 2 nm; single bond rupture event is shown. In C we present a dependence $k_{\text{complex}}(f)$ derived from A and B.

much broader distribution of the spring constant at the moment of the bond rupture also has been observed: such a value varies from 0.003 to 0.008 N/m for different events. (Only single fibrinogen-fibrinogen bond rupture events are considered here and below; for rupture events involving multiple bonds as large forces as 2–3 nN and spring constants up to 0.055 N/m have been observed. At the same time the distribution of z_{rupt} does not essentially depend on the number of bonds involved.) Correlation between the values of f_{rupt} and z_{rupt} measured for one concrete event was also rather poor, contrary to the BSA–Ab–BSA case.

Thus, the prominent difference between the experimental data concerning fibrinogen-fibrinogen and BSA–Ab–BSA complexes is evident. Especially we would like to underline an enormous difference between attainable complex extensions. As large z_{rupt} values as 100–130 nm (simply unimaginable for antigen-antibody experiments) have been often observed for fibrinogen-fibrinogen rupture events. These values are consistent with the known long and well-stretchable molecular structure of fibrinogen (Doolittle, 1973, 1981). This circumstance, given all the precautions used by us to eliminate possible effects of linkers for the fibrinogen-fibrinogen case, similar to that of BSA–Ab–BSA (see Material and Methods section), should be considered as an additional proof of utility and reliability of the presented method of direct and continuous measurement of the spring constant for single molecules and molecular complexes. Detailed discussion of fibrinogen-fibrinogen complex stretching experiments will be published elsewhere.

CONCLUSION

In this article the new method of direct and continuous measurement of the spring constant of single molecule or molecular complex is presented and illustrated for the cases of complexes formed by specific BSA–Ab–BSA and non-specific fibrinogen-fibrinogen interactions.

Finally, we would like to underline the following. In principle, one could speculate that similar information can be obtained by analyzing only standard force-distance curves $f(z)$ and calculating the derivative df/dz from them. Albeit this is formally true, in practice such a procedure leads to very poor results due to unavoidable experimental noises: with a closer look, each real experimental curve contains a large number of “noise-induced” local maxima and minima. Hence, its derivative will have the corresponding large number of zeroes and the outcome of the procedure only rarely approaches the “real” values. If, trying to avoid this, one will first process the experimental curve to make it smooth, the derivative will strongly depend on the details of such a processing and hence, again, will be unreliable. Indeed, the necessity and utility to measure the derivative of some function directly (even if it is formally possible to derive it from some other data) is very well known in experimentation. It is sufficient to give here only one

example—tunneling spectroscopy. Based on small modulation of the applied voltage, U , together with the measuring of modulation of a tunneling current, I , such an approach readily enables to observe characteristic vibrations of molecules located in the interelectrode spacing. This is the data practically unobservable when only the dependence $U(I)$ is measured.

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REFERENCES

- Albrecht, C., K. Blank, M. Lalic-Mülthaler, S. Hirler, T. Mai, I. Gilbert, S. Schiffrmann, T. Bayer, H. Clausen-Schaumann, and H. E. Gaub. 2003. DNA: a programmable force sensor. *Science*. 301:367–370.
- Allen, S., X. Y. Chen, J. Davies, M. C. Davies, A. C. Dawkes, J. C. Edwards, C. J. Roberts, J. Sefton, S. J. B. Tendler, and P. M. Williams. 1997. Detection of antigen-antibody binding events with atomic force microscopy. *Biochemistry*. 36:7457–7463.
- Balsera, M., S. Stepananits, S. Izrailev, Y. Oono, and K. Schulten. 1997. Reconstructing potential energy functions from simulated force-induced unbinding processes. *Biophys. J.* 73:1281–1287.
- Carrion-Vazquez, M., A. F. Oberhauser, T. E. Fisher, P. E. Marszalek, H. Li, and J. M. Fernandez. 2000. Mechanical design of proteins studied by single-molecule force spectroscopy and protein engineering. *Prog. Biophys. Mol. Biol.* 74:63–91.
- Carter, D. C., and J. X. Ho. 1994. Structure of serum albumin. *Adv. Protein Chem.* 45:153–203.
- Cleveland, J. P., S. Manne, D. Bocek, and P. K. Hansma. 1993. A nondestructive method for determining the spring constant of cantilevers for scanning force microscopy. *Rev. Sci. Instrum.* 64:403–405.
- Cluzel, Ph., A. Lebrun, C. Heller, R. Lavery, J.-L. Viovy, D. Chatenay, and F. Caron. 1996. DNA: an extensible molecule. *Science*. 271:792–794.
- Dammer, U., M. Hegner, D. Anselmetti, P. Wagner, M. Dreier, W. Huber, and H.-J. Güntherodt. 1996. Specific antigen/antibody interactions measured by force microscopy. *Biophys. J.* 70:2437–2441.
- Doi, M., and S. F. Edwards. 1992. *The Theory of Polymer Dynamics*. Clarendon, Oxford, UK.
- Doolittle, R. F. 1973. Structural aspects of the fibrinogen to fibrin conversion. *Adv. Protein Chem.* 27:1–109.
- Doolittle, R. F. 1981. Fibrinogen and fibrin. *Sci. Am.* 245:92–101.
- Essevaz-Roulet, B., U. Bockelmann, and F. Heslot. 1997. Mechanical separation of the complementary strands of DNA. *Proc. Natl. Acad. Sci. USA*. 94:11935–11940.
- Grubmüller, H., B. Heymann, and P. Tavan. 1996. Ligand binding: molecular mechanics calculation of the streptavidin-biotin rupture force. *Science*. 271:997–999.
- Gunning, A. P., P. J. Wilde, D. C. Clark, V. J. Morris, M. L. Parker, and P. A. Gunning. 1996. Atomic force microscopy of interfacial protein films. *J. Colloid Interface Sci.* 183:600–602.
- Harada, Y., M. Kuroda, and A. Ishida. 2000. Specific and quantized antigen-antibody interaction measured by atomic force microscopy. *Langmuir*. 16:708–715.
- Heinz, W. F., and J. H. Hoh. 1999. Spatially resolved force spectroscopy of biological surfaces using the AFM. *Trends Biotechnol.* 17:143–150.
- Heymann, B., and H. Grubmüller. 1999a. AN02/DNP-hapten unbinding forces studied by molecular dynamics atomic force microscopy simulations. *Chem. Phys. Lett.* 303:1–9.

- Heymann, B., and H. Grubmüller. 1999b. Elastic properties of poly (ethylene)-glycol studied by molecular dynamics stretching simulations. *Chem. Phys. Lett.* 307:425–432.
- Heymann, B., and H. Grubmüller. 2000. Dynamic force spectroscopy of molecular adhesion bonds. *Phys. Rev. Lett.* 84:6126–6129.
- Heymann, B., and H. Grubmüller. 2001. Molecular dynamics force probe simulations of antibody/antigen unbinding: entropic control and non-additivity of unbinding forces. *Biophys. J.* 81:1295–1313.
- Hinterdorfer, P., W. Baumgartner, H. J. Gruber, K. Schilcher, and H. Schindler. 1996. Detection and localization of individual antibody-antigen recognition events by atomic force microscopy. *Proc. Natl. Acad. Sci. USA.* 93:3477–3481.
- Hutter, J. L., and J. Bechhoefer. 1993. Calibration of atomic force microscope tips. *Rev. Sci. Instrum.* 64:1868–1873.
- Izrailev, S., S. Stepanians, M. Balsera, Y. Oono, and K. Schulten. 1997. Molecular dynamics study of unbinding of the avidin-biotin complex. *Biophys. J.* 72:1568–1581.
- Janshoff, A., M. Neitzert, Y. Oberdörfer, and H. Fuchs. 2000. Force spectroscopy of molecular systems—single molecule spectroscopy of polymers and biomolecules. *Angew. Chem. Int. Ed.* 39:3212–3237.
- Jönsson, U., G. Olofsson, M. Malmqvist, and I. Rönnerberg. 1985. Chemical vapor deposition of silanes. *Thin Solid Films.* 124:117–123.
- Kasas, S., B. M. Riederer, S. Catsicas, B. Cappella, and G. Dietler. 2000. Fuzzy logic algorithm to extract specific interaction forces from atomic force microscopy data. *Rev. Sci. Instrum.* 71:2082–2086.
- Kienberger, F., V. P. Pastushenko, G. Kada, H. J. Gruber, C. Riener, H. Schindler, and P. Hinterdorfer. 2000. Static and dynamical properties of single poly(ethylene glycol) molecules investigated by force spectroscopy. *Single Mol.* 1:123–128.
- Leckband, D. 2001. Force as a probe of membrane protein structure and function. *Curr. Opin. Struct. Biol.* 11:433–439.
- Lee, G. U., L. A. Chrisey, and R. J. Colton. 1994a. Direct measurement of the forces between complementary strands of DNA. *Science.* 266:771–773.
- Lee, G. U., D. A. Kidwell, and R. J. Colton. 1994b. Sensing discrete streptavidin-biotin interactions with atomic force microscopy. *Langmuir.* 10:354–357.
- Leuba, S. H., J. Zlatanova, M. A. Karymov, R. Bash, Y.-Z. Liu, D. Lohr, R. E. Harrington, and S. M. Lindsay. 2000. The mechanical properties of single chromatin fibers under tension. *Single Mol.* 1:185–193.
- Liu, X. M., and G. H. Pollack. 2002. Mechanics of F-actin characterized with microfabricated cantilevers. *Biophys. J.* 83:2705–2715.
- Marko, J. F., and E. D. Siggia. 1995. Stretching DNA. *Macromolecules.* 28:8759–8770.
- Marszalek, P. E., A. F. Oberhauser, Y. P. Pang, and J. M. Fernandez. 1998. Polysaccharide elasticity governed by chair-boat transitions of the glucopyranose ring. *Nature.* 396:661–664.
- Marszalek, P. E., H. Lu, H. Li, M. Carrión-Vázquez, A. F. Oberhauser, K. Schulten, and J. M. Fernandez. 1999. Mechanical unfolding intermediates in titin modules. *Nature.* 402:100–103.
- Merkel, R., P. Nassoy, A. Leung, K. Ritchie, and E. Evans. 1999. Energy landscapes of receptor-ligand bonds explored with dynamic force microscopy. *Nature.* 397:50–53.
- Minajeva, A., M. Kulke, J. M. Fernandez, and W. Linke. 2001. Unfolding of titin domains explains the viscoelastic behavior of skeletal myofibrils. *Biophys. J.* 80:1442–1451.
- Mueller, H., H. J. Butt, and E. Bamberg. 1999. Force measurements on myelin basic protein adsorbed to mica and lipid bilayer surfaces done with the atomic force microscope. *Biophys. J.* 76:1072–1079.
- Noy, A., D. V. Vezhenov, J. F. Kayyem, T. J. Meade, and C. M. Lieber. 1997. Stretching and breaking duplex DNA by chemical force microscopy. *Chem. Biol.* 4:519–527.
- Pereira, L. G. C., O. Théodoly, H. W. Blanch, and C. J. Radke. 2003. Dilatational rheology of BSA conformers at the air/water interface. *Langmuir.* 19:2349–2356.
- Rief, M., M. Gautel, F. Oesterhelt, J. M. Fernandez, and H. E. Gaub. 1997a. Reversible unfolding of individual titin immunoglobulin domains by AFM. *Science.* 276:1109–1112.
- Rief, M., F. Oesterhelt, B. Heymann, and H. E. Gaub. 1997b. Single molecule force spectroscopy of polysaccharides by atomic force microscopy. *Science.* 276:1295–1297.
- Rief, M., J. M. Fernandez, and H. E. Gaub. 1998. Elastically coupled two-level systems as a model for biopolymer extensibility. *Phys. Rev. Lett.* 81:4764–4767.
- Rief, M., and H. Grubmüller. 2002. Force spectroscopy of single biomolecules. *Chemphyschem.* 3:255–261.
- Rixman, M. A., D. Dean, C. E. Macias, and C. Ortiz. 2003. Nanoscale intermolecular interactions between human serum albumin and alkane-thiol self-assembled monolayers. *Langmuir.* 19:6202–6218.
- Ros, R., F. Schwesinger, D. Anselmetti, M. Kubon, R. Schäfer, A. Plücktun, and L. Tiefenauer. 1998. Antigen binding forces of individually addressed single-chain Fv antibody molecules. *Proc. Natl. Acad. Sci. USA.* 95:7402–7405.
- Round, A. N., M. Berry, T. J. McMaster, S. Stoll, D. Gowers, A. P. Corfield, and M. J. Miles. 2002. Heterogeneity and persistence length in human ocular mucins. *Biophys. J.* 83:1661–1670.
- Sader, J. E. 1998. Frequency response of cantilever beams immersed in viscous fluids with applications to the atomic force microscope. *J. Appl. Phys.* 84:64–76.
- Sakai, Y., T. Ikehara, T. Nishi, K. Nakajima, and M. Hara. 2002. Nanorheology measurement on a single polymer chain. *Appl. Phys. Lett.* 81:724–726.
- Sarid, D. 1991. Scanning Force Microscopy. Oxford University Press, London, UK.
- Schindler, H., D. Badt, P. Hinterdorfer, F. Kienberger, A. Raab, S. Wielert-Badt, and V. P. Pastushenko. 2000. Optimal sensitivity for molecular recognition MAC-mode AFM. *Ultramicroscopy.* 82:227–235.
- Schwesinger, F., R. Ros, T. Strunz, D. Anselmetti, H.-J. Güntherodt, A. Honegger, L. Jermutus, L. Tiefenauer, and A. Plücktun. 2000. Unbinding forces of single antibody-antigen complexes correlate with their thermal dissociation rates. *Proc. Natl. Acad. Sci. USA.* 97:9972–9977.
- Strunz, T., K. Oroszlán, I. Schumakovitch, H.-J. Güntherodt, and M. Hegner. 2000. Model energy landscapes and the force-induced dissociation of ligand-receptor bonds. *Biophys. J.* 79:1206–1212.
- Stuart, J. K., and V. Hlady. 1995. Effects of discrete protein-surface interactions in scanning force microscopy adhesion force measurements. *Langmuir.* 11:1368–1374.
- Vandenberg, E. T., L. Bertilsson, B. Lieberg, K. Uvdal, R. Erlandsson, H. Elwing, and I. Lundström. 1991. Structure of 3-aminopropyl triethoxy silane on silicon oxide. *J. Colloid Interface Sci.* 147:103–118.
- Willemsen, O. H., M. M. E. Snel, K. O. van der Werf, B. G. de Grooth, J. Greve, P. Hinterdorfer, H. J. Gruber, H. Schindler, Y. van Kooyk, and C. G. Figdor. 1998. Simultaneous height and adhesion imaging of antibody-antigen interactions by atomic force microscopy. *Biophys. J.* 75:2220–2228.
- Willemsen, O. H., M. M. E. Snel, A. Cambi, J. Greve, B. G. De Grooth, and C. G. Figdor. 2000. Biomolecular interactions measured by atomic force microscopy. *Biophys. J.* 79:3267–3281.
- You, H. X., and C. R. Lowe. 1996. AFM studies of protein adsorption. 2. Characterization of immunoglobulin G adsorption by detergent washing. *J. Colloid Interface Sci.* 182:586–601.
- Zhou, H. X. 2001. Loops in proteins can be modeled as worm-like chains. *J. Phys. Chem. B.* 105:6763–6766.
- Zlatanova, J., S. M. Lindsay, and S. H. Leuba. 2000. Single molecule force spectroscopy in biology using the atomic force microscope. *Prog. Biophys. Mol. Biol.* 74:37–61.