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Familial Hypertrophic Cardiomyopathy can be Characterized by a Specific Pattern of Orientation Fluctuations of Actin Molecules

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Abstract

A single-point mutation in the gene encoding the ventricular myosin regulatory light chain (RLC) is sufficient to cause familial hypertrophic cardiomyopathy (FHC). Most likely, the underlying cause of this disease is an inefficient energy utilization by the mutated cardiac muscle. We set out to devise a simple method to characterize two FHC phenotypes caused by the R58Q and D166V mutations in RLC. The method is based on the ability to observe a few molecules of actin in working *ex-vivo* heart myofibril. Actin is labeled with extremely diluted fluorescent dye and a small volume within the I-band ($\sim 10^{-16}$L), containing on average 3 actin molecules, is observed by confocal microscopy. During muscle contraction myosin cross-bridges deliver cyclic impulses to actin. As a result, actin molecules undergo periodic fluctuations of orientation. We measured these fluctuations by recording the parallel and perpendicular components of fluorescent light emitted by an actin-bound fluorophore. The histograms of fluctuations of fluorescent actin molecules in wild-type (WT) hearts in rigor were represented by perfect Gaussian curves. In contrast, histograms of contracting heart muscle were peaked and asymmetric, suggesting that contraction occurred in at least two steps. Furthermore, the differences between histograms of contracting FHC R58Q and D166V hearts *versus* corresponding contracting WT hearts were statistically significant. Based on our results we suggest a simple new method of distinguishing between healthy and FHC R58Q and D166V hearts by analyzing the probability distribution of polarized fluorescence intensity fluctuations of sparsely labeled actin molecules.

Familial Hypertrophic Cardiomyopathy (FHC) is an autosomal dominant disease characterized by ventricular hypertrophy, myofibrillar disarray and sudden cardiac death (SCD) [1]. It is believed to be caused by single-point mutations in sarcomeric proteins of the heart. In this report we have focused on the two FHC mutations in the ventricular regulatory light chain (RLC) of myosin [2–8], R58Q (Arginine 58 replaced by Glutamine) and D166V (Aspartate 166 replaced by Valine). Even though mutations in RLC are less common than mutations in the myosin heavy chain, they are often associated with malignant outcomes. Both RLC mutations, R58Q and D166V have been shown to cause SCD [2–8].

Using transgenic (Tg) animal models expressing R58Q and D166V mutations of RLC we have determined the effect of these FHC mutations on the ability of the myocardium to develop isometric tension, Ca^{2+} sensitivity of force and ATPase activity [9–11]. However,

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∞dedicated to the memory of Prof. M.F. Morales

such characterization is only possible in a transgenic mouse model, because it usually expresses more than 95% of the mutant protein that replaces the endogenous mouse cardiac RLC. Humans are heterozygous for FHC, so in muscles of affected individuals 50% of myosin-containing thick filaments are composed of the non-mutant myosin heads interspersed with the FHC mutant heads. If the distribution of the healthy and diseased molecules is random, any collection containing more than a few molecules carries a high probability of containing a mixture of healthy and diseased moieties. It is likely that the gross properties of such muscles will not show any differences compared to tissue from healthy individuals. That is why it is important to take measurements from as few molecules as possible. In this paper we propose a method of characterization of FHC hearts in which histograms of fluctuations of polarized fluorescence of ~3 sarcomeric actin molecules are compared in the mutated *versus* WT heart muscles.

The method is based on the ability to observe a few molecules of actin in an *ex-vivo* heart muscle, as illustrated in Fig. 1 (top). Muscle is labeled with an extremely diluted dye so that only one in ~ 100,000 actin monomers is probed. A small volume within labeled heart muscle (~10^{-16} L) containing only a few actin molecules is observed by confocal microscopy. In rigor muscle (left panel), the thin filaments are immobile. There are no fluctuations in orientation of the transition dipole (red arrow). During isometric contraction (right panel) the situation is quite different. Now, myosin cross-bridges deliver impulses to actin [12]. The force impulses deform actin filament, changing the orientation of a transition dipole of rhodamine. The orientation of this rhodamine dipole fluctuates in time. In addition, fluctuations arise because rhodamine may leave and re-enter the observational volume, as cross-bridges pull filaments to the left, and filaments recoil during isometric contraction to the right. We measure fluctuations by recording parallel (∥) and perpendicular (⊥) components of fluorescent light emitted by an actin-bound fluorophore. The ratio of these components, called Polarized Fluorescence, is a sensitive indicator of the orientation of the transition dipole of the fluorophore [13–20]. It is worth pointing out that that the current method does not rely on computing the correlation function of fluctuations. Although sophisticated and elegant [21,22], the correlation analysis is complex and depends on a number of assumptions, which are avoided here. The current method involves only the elementary statistical analysis.

It is advantageous to observe actin rather than myosin, because labeling of actin with fluorescent phalloidin was shown not to alter the enzymatic properties of skeletal muscle [23,24], labeling is stoichiometric and thus allows for a strict control of the degree of labeling and actin is labeled non-covalently and therefore rigidly. Rigid binding is a must when orientation of the dipole moment of a probe is measured.

The fluctuations of WT rigor heart muscles were distributed according to a perfect Gaussian curve in which both the skewness and kurtosis of distribution approach zero. In contrast, the histograms of contracting heart muscles were peaked and asymmetric (i.e. they had high skewness and kurtosis), suggesting that contraction occurred in at least two steps. Moreover, the differences between histograms of contracting FHC mutated *versus* WT heart muscles were statistically significant. These results suggest that a simple way to distinguish between FHC hearts carrying R58Q and/or D166V mutations from WT hearts is to analyze the probability distribution of polarized intensity fluctuations.

MATERIALS AND METHODS

Chemicals and solutions

Rhodamine-phalloidin (RP) and Alexa-488-phalloidin were purchased from Molecular Probes (Eugene, OR). All other chemicals were from Sigma-Aldrich (St Louis, MO). The composition of solutions were as in [25].

Transgenic muscle

The hearts from Tg-WT and Tg-R58Q male mice of various ages were used for the preparation of glycerinated muscle strips. Skinned fiber measurements were performed as described previously [25]. Myofibrils, prepared as described in [25] were labeled with 0.1 nM rhodamine-phalloidin (RP) + 10 μM unlabeled-phalloidin (UP) in Ca^{2+}-rigor solution as described in [26]. Since the ratio of fluorescent to non-fluorescent phalloidin was 1:100,000, only 1 in ~10^5 actin monomers carried a fluorophore. Myofibrils were prevented from shortening during contraction by cross-linking with the water-soluble cross-linker EDC [27]. Myofibrils (1 mg/ml) were incubated with 20 mM EDC for 20 min at room temperature. The reaction was stopped by adding 20 mM DTT. The lack of shortening was checked under differential contrast [28].

Coverslips

Cardiac myofibrils attached weakly to glass. To help them attach, the coverslips were thoroughly cleaned with 100% ethanol, and spin coated with Poly-L-lysine solution (Sigma-Aldrich 0.1%) at 3,000 rpm for 120s using a spincoater P6700 (Specialty Coating Systems, Indianapolis, Indiana).

Probability distribution measurements

Alba-FCS (ISS Co, Urbana, IL) confocal systems coupled to an Olympus IX 71 microscope was used to obtain fluorescence data. Fluorescence was collected every 10 μs for 20 s (2M data points). The signal was smoothed by binning 1000 data points (final frequency response = 100 Hz). Before each experiment the instrument was calibrated and optimized with 50 nM solution of rhodamine G. The excitation was by a 532 nm CW laser. The linearly polarized laser beam was delivered by single mode fiber, but to ensure that the exciting light was polarized a sheet analyzer was inserted before the entrance to the microscope. The laser polarization was vertical on the microscope stage. The confocal pinhole was 50 μm. The fluorescent light was split by a prism and each component was detected by a separate Avalanche PhotoDiode (APD). Orthogonally polarized linear analyzers were placed before APD's. The myofibrils were always placed with the axis pointing vertically on the microscope stage. Channel 1 and 2 measured the polarized intensities oriented perpendicular and parallel to the myofibrillar axis, respectively.

Anisotropy decay

To ascertain whether the phalloidin probe is immobilized by the protein so that the transition dipole of the fluorophore reflects the orientation of the protein, we measured the decay of anisotropy, defined as $r=(I_{\parallel}-I_{\perp})/(I_{\parallel}+2I_{\perp})$. It was best fitted by the exponential function $r(t)=R_{\infty}+a \cdot \exp(-t/\theta)$ where $R_{\infty} = 0.29$ is the value of anisotropy at infinite time, a = 0.07, the amplitude of the anisotropy change, and $\theta = 1.3$ ns is the rotational correlation time. The short correlation time was due to the rotation of phalloidin, consistent with rotation of a molecule with M_w=1,250. The maximum value of anisotropy was 0.35. It decayed to an asymptotic value of R_{∞} (0.29). Thus the mobile fraction was contributed by (0.35−0.29)/0.35 = 17% of fluorophores. 100−17=83% of fluorescent phalloidin was immobilized by F-actin. This is consistent with the fact that phalloidin attaches to F-actin through long-range

interactions that impart on a probe the rigidity necessary for quantitative polarization measurements.

Steady-State Force Measurements

Skinned papillary muscle fibers from Tg-R58Q and Tg-D166V mice were used to assess the effect of the mutation on maximal force compared to Tg-WT. A bundle of fibers of an approximate diameter of 100 μm was isolated from a batch of glycerinated mouse papillary muscle fibers and attached by tweezer clips to a force transducer [29]. The fibers were relaxed in 1 ml of pCa 8 solution and then tested for maximal steady state force in pCa.

RESULTS

Imaging

A typical fluorescence lifetime image of a rigor Tg-WT myofibril from the right ventricle of mouse heart is shown in Fig. 1 (bottom). **A** is the lifetime image (the lifetime image is shown because it is of better quality than the intensity image). The entire I-bands are labeled because heart muscle does not contain nebulin. In skeletal muscle nebulin prevents phalloidin from labeling all-but the pointed ends of actin filaments [30,31]. As expected, the intensity of fluorescence in Z-lines is ~ double of that in the I-band [32]. The dark areas are the H-bands that do not contain actin. The red circle is a 2D projection of the confocal aperture on the image plane. Its diameter is equal to the diameter of the confocal aperture (50 μm) divided by the magnification of the objective (40×). The parallel ($I_{\parallel}$) and perpendicular ($I_{\perp}$) polarization images are shown in Fig. 1 (bottom) **B** and **C**, respectively. They show that fluorescence is highly anisotropic as is expected from the aligned array of polar actin filaments [32].

Intensity fluctuations during rigor and contraction of healthy hearts

We first measured the time course of polarized intensities of rhodamine-phalloidin (RP) bound to an actin filament in a cardiac half-sarcomere (HS). Since rhodamine is rigidly immobilized on the surface of actin [25], the polarized intensity reflects the orientation of actin. A myofibril is placed on the stage of a confocal microscope. Its axis is always vertical on a microscope stage. The linear polarization of the illuminating laser light is also vertical on a stage (i.e. it is parallel to muscle axis). The fluorescence emanating from the Detection Volume (DV) is split 50-50 by a beam splitter and projected through the confocal apertures and orthogonal analyzers on the photosensistive surface of two APD's. The signal in the first (channel 1) and the second (channel 2) of APD corresponds to the intensity of fluorescence polarized perpendicular (⊥) and parallel (∥) to the muscle axis. Fig. 2 shows a typical time course of ⊥ polarized intensity of a rigor (**A**) and contracting (**B**) myofibril from the left ventricle of transgenic WT heart. The original data was collected every 10 μsec, but to keep the data files to the manageable size 1000 points were binned together to give time resolution of 10 msec. The vertical scale is the number of counts during 10 msec. Individual impulses resulting from the myosin cross-bridge imparting force impulses on actin can be clearly seen. The impulses can be even better visualized on the expanded time scale (inset).

Number of observed molecules

For the meaningful interpretation of histograms, it is important that the data originate from only a few molecules. If it were not, asynchrony between cross-bridges would have averaged out the fluctuations, and no asymmetry would have been visible. To be able to assess how many molecules contribute to the observed fluorescence, it is necessary to know the photon rate associated with a single molecule. To this end, we measured the intensity of a signal at increasing concentrations of rhodamine B in solution. To estimate the number of

molecules contributing to the signal, we measured the associated autocorrelation function. The value of the autocorrelation function at delay time 0 [G(0)] is equal to the inverse of the number of molecules N contributing to the signal, N=1/G(0) [33,34]. Correlation functions were obtained for the solution of rhodamine B in the range 0.5–50 nM. For example, when the dye concentration was 5 nM, the signal measured in channels 1 and 2 averaged to 99 and 115 counts/10 ms. The autocorrelation function of the signal is shown in Fig. 3B. The G(0) was 0.127, giving the number of molecules ~8. The amplitude of the signal was plotted against the average number of molecules in the DV (Fig. 4A). The straight line curve was extrapolated as shown by the red line in Fig. 3A; and from this the number of photons per one fluorophore was estimated to be ~800 counts/sec per channel.

We can now estimate the number of molecules contributing to the signal. In Fig. 2, the average intensities in contracting myofibrils in channels 1 and 2 were 19 and 29 counts/10 ms for rigor and 43 and 60 counts/10 ms,, respectively (note that Fig. 2 is a bar plot). The excess counts for contacting muscle, which takes into account the contribution of the background, was on average 27 counts/10 ms=2700 counts/s. This corresponds to ~3 actin molecules.

Histograms of fluctuations

A histogram is a plot of the size of fluctuation (x-axis) *versus* the number of times that a given fluctuation occurs (y-axis). We compared the histogram distributions of rigor and contracting myofibrils. Fig. 4 shows examples of six histograms obtained from the left ventricles of rigor WT hearts, randomly selected from a pool of 262 histograms. It is clear that a 3-parameter Gaussian relationship, $y=a\exp[-0.5(x-x_o/b)^2]$ fits the data well. As mentioned previously, Gaussian distribution is characterized by a skewness and kurtosis of zero. Rigor histograms (from left to right and top and bottom) had skewness of 0.234, 0.249, 0.208, 0.252, 0.369 and 0.278 with an average of 0.265±0.055 (SD). Kurtosis values were 0.018, 0.170, 0.048, 0.153, 0.144 and 0.247 with an average of 0.130±0.084 (SD). These values are reported in Table 1. The fact that both kurtosis and skewness were close to 0 suggests that fluctuations in rigor muscle reflected a stationary process whose magnitude was controlled solely by random fluctuations in an APD current.

In contrast, corresponding histograms of $I_{\perp}$ fluctuations obtained from contracting left ventricles from Tg-WT hearts were heavily right-shifted (Fig. 5). The histograms had high positive skewness of 1.701, 1.767, 1.916, 1.372, 1,129 and 1.543 (left to right and top and bottom) with an average of 1.571±0.286 (SD). Kurtosis values were 4.240, 5.897, 5.946, 2.859, 2.492 and 5.939 with an average of 4.562±1.605 (SD) reflecting a substantial number of large fluctuations. The differences between the rigor and contraction data were statistically highly significant ($p<0.001$, $t=9.503$, paired t test for skewness; $p=0.001$, $t=6.790$, paired t-test for kurtosis). The results are summarized in Table 1.

The marked skewness and kurtosis of polarized intensity during contraction is probably due to the fact that a cross-bridge power-stroke affects orientation of actin in two or more steps, as originally proposed by Huxley & Simmons [35]. Our results suggest that unwinding of the “kink” in the relay helix of the converter domain of myosin head, which then leads to a rotation of the converter domain through 60° [36] and a consequent rotation of actin may occur in steps.

The asymmetric contracting data could be fitted by a mixture of two Gaussian curves with the dominant curve containing most of the power, centered significantly to the left of the secondary Gaussian. Fig. 6 represents a pair of Gaussian curves with the experimental curve, labeled in blue (data from experiment in Fig. 5, top left) fitted with the dominant Gausssian

curve $f_1(x)=\frac{1}{\sqrt{2\pi}}\left(\frac{0.7377}{7.906}\exp(-\frac{(x-37.092)^2}{2*7.906^2})\right)$ (mean=37.1, SD=7.9), 74% contribution, red), and the secondary Gaussian curve (labeled in green) fitted with:

$f_2(x)=\frac{1}{\sqrt{2\pi}}\left(\frac{0.2623}{19.161}\exp(-\frac{(x-60.510)^2}{2*19.161^2})\right)$ (mean=60.5, SD=19.2, 26% contribution). The overall fitted curve is given by the sum of these two equations. The relative contribution of both Gaussian curves was 74% (red) and 26% (green).

Intensity fluctuations of contracting myofibrils from Tg-R58Q and Tg-D166V mutated hearts

From the previous section it appears that the analysis of histograms can distinguish between the resting and active myofibrils from Tg-WT hearts. The question arises whether the same analysis of contracting heart muscles is capable of predicting whether the heart muscle carries an FHC-causing mutation. Fig. 7 shows 6 randomly picked histograms obtained from fluctuations of R58Q mutated Tg myofibrils. The histograms are also right-shifted. A careful comparison of 98 perpendicular and 120 parallel histograms of fluctuations in the intensity of fluorescence originating from contracting Tg-WT and Tg-R58Q myofibrils reveals a statistically significant difference. The comparisons were performed on myofibrils from left and right ventricles or papillary muscles from age matched Tg-WT and Tg-R58Q male mice. The absolute values were (mean±SE) 5.2±0.5 and 3.9±0.4 for kurtosis, and 1.5±0.07 & 1.2±0.06 for skewness for Tg-WT and Tg-R58Q mutated hearts, respectively. The differences in kurtosis and skewness were statistically significant at <10% level for kurtosis (t=1.860, P=0.064), and at <5% for skewness (t=2.955, P=0.003). The results are summarized in Fig. 8 and Table 2. We also analyzed 20 and 16 histograms of fluctuations in ⊥ and ∥ polarized intensity, respectively from myofibrils of left ventricles carrying the D166V FHC mutation. The absolute values were 1.2±0.4 and 2.2±0.4 for kurtosis and 0.6±0.09 and 1.0±0.1 for skewness for Tg-WT and Tg-D166V mutated hearts, respectively. The differences were statistically significant at ~10% level for kurtosis (t=−1.639, P=0.110) and at <5% for skewness (skewness t=−3.267,P=0.002). In this case, in contrast to R58Q result, the values of kurtosis and skewness were greater for the mutated myofibrils compared to WT muscle. The results are summarized in Fig. 9 and Table 2.

Functional studies

Maximal Level of Steady-state Force—Fig. 10 demonstrates the effect of both mutations, D166V and R58Q on the maximal force per cross-sectional area of muscle developed in mouse skinned papillary muscle fibers from female mutant mice compared to control, age matched Tg-WT mice. The value of maximal force determined at high Ca^{2+} concentrations (pCa 4) in Tg-D166V fibers was decreased by 28% compared to Tg-WT fibers, P=0.037 . Interestingly, Tg-R58Q fibers demonstrated a 3.3-fold decrease in force compared to Tg-WT (P=0.001) and a 2.3-fold decrease compared to Tg-D166V fibers (P<0.001). Therefore, both mutations, D166V and R58Q led to the compromised development of force in these mutated hearts ultimately resulting in compensatory hypertrophy.

DISCUSSION

Skewness and kurtosis during rigor and contraction

A histogram can be quantitatively characterized by the values of kurtosis and skewness. A positive skewness means that the tail of the curve directs towards positive values of the histogram, while in the negative skewness the tail goes towards the negative values. A positive kurtosis is expressed by long tails compared to the Gaussian curves and the negative

kurtosis means that the tails are smaller than those of Gaussian curves. The skewness and kurtosis are defined by the Equations (1) and (2).

$$\text{skewness}=\frac{\mu_3}{\sigma^3} \tag{1}$$

$$\text{kurtosis}=\frac{\mu_4}{\sigma^4}-3 \tag{2}$$

where $\sigma=\sqrt{\frac{1}{N}\sum_{n=1}^{N}(x_n-\bar{x})^2}$ is the standard deviation of the N values x_n with mean $\bar{x}$, and the moments μ_m are defined by $\mu_m=\frac{1}{N}\sum_{n=1}^{N}(x_n-\bar{x})^m$. This is illustrated in Fig. 11.

Skewness and kurtosis of FHC heart myofibrils

We observed significant differences in the histogram shape of rigor and contracting myofibrils from transgenic mouse hearts containing WT RLC (Figs 5 & 6, Table 1). The difference in histograms was not limited to rigor and contracting muscles. We observed a statistically significant difference between skewness and kurtosis of fluctuations during contraction of Tg-WT (healthy) and Tg-mutant (diseased) hearts (Figs 9, 10, Table 2). While the difference was not as obvious as between the rigor and contracting myofibrils, it was statistically significant.

Implications for heart studies

In our transgenic mouse myocardium, the mutated human ventricular RLC-WT replaces the endogenous mouse ventricular RLC in ~ 95%. Likewise, Tg-D166V and Tg-R58Q mice express ~95% transgene and the transgenic mutant myocardium contains ~95% mutated RLC incorporated in their myofilaments. In such hearts it is possible to detect differences between Tg and WT muscles by the simple measurement of tension as presented in Fig. 11. In agreement with our previous studies [9,11], maximal steady state force development was significantly impaired in Tg-mutant hearts, with the R58Q mutation causing the most dramatic effect (Fig. 10). Similarly, it was possible to show differences between the WT and mutated hearts using Surface Plasmon Effect in a population containing many labeled molecules [37]. However, human patients harboring these FHC RLC mutations are usually heterozygous and their myosin-containing thick filaments contain ~ 50% of the mutant myosin heads interspersed with ~50% of non-mutated myosin cross-bridges. Because of this heterozygous assembly of molecules the information of the differences in functional characterization of their muscles might be lost unless the diseased muscle manifests a poison-peptide effect [38]. The necessity of studying the FHC-linked disease by observing a single, or at the most, a few molecules becomes apparent. Even if our data originates from more than one molecule, they all reside in the same HS and are likely subjected to an FHC mutation.

Compared with WT hearts, skewness and kurtosis were decreased in both R58Q and D166V hearts. We want to emphasize that no correlation analysis of the kinetic data was used here. This is a significant advantage of the present method, because the correlation analysis requires that a specific model of cross-bridge-actin interaction be assumed. For example, the decay of autocorrelation function can be fitted with a single parameter κ. Using a single

exponential fit of the autocorrelation function, we found an increase in κ from κ=69 s^{-1} for WT hearts to κ=169 s^{-1} for R58Q mutated hearts. The same analysis applied to the D166V mutation revealed that the median rate increased from κ=58 s^{-1} for WT hearts to κ=102 s^{-1} for D166V mutated hearts. The similar behavior of these two mutations is consistent with the fact that both mutations demonstrated similar effect on the maximal steady-state force measured in skinned papillary muscle fibers (Fig. 10). The results obtained with the R58Q mutation are consistent with studies by Greenberg et al., where myosin purified from R58Q hearts showed higher actin-activated ATPase rates compared to controls (0.63 s^{-1} vs. 0.43 s^{-1}) [39]. In addition, Tg-R58Q myosin showed an increase in actin filament sliding velocity in an *in vitro* motility assay compared to Tg-WT (2.17 μm · s^{-1} vs. 1.57μm · s^{-1}) [39]. Our recent Surface Plasmon Microscopy study using Reverse Kretschmann excitation confirmed faster cross-bridge kinetics associated with the R58Q mutation [37].

However, the single exponential fit of the correlation function for the D166V mutated myofibrils results in a larger value of kinetic constant κ compared to the fit for WT (58 s^{-1} for WT hearts increased to 102 s^{-1} for D166V mutated hearts). These findings appear to be in conflict with the results of our earlier work [25], wherethe autocorrelation function was fitted with a train of triangles model, giving the times when the cross-bridges were accessible (t_A) or unaccessible (t_U) to bind to actin. In work by Muthu et. al., we found that (t_A) was profoundly increased in D166V compared to WT and that the cycle times, t_{ON} and t_{OFF} were increased or not changed, respectively in D166V muscle compared to WT. This suggests that the value of kinetic constant κ as well as the times t_A, t_U, t_{ON} & t_{OFF} are all model-specific.

Interestingly, the similar effect of both mutations was found in functional studies as they both decreased maximal steady-state force in skinned papillary muscle fibers (Fig. 10). In conclusion, the increase in the κ value, decrease in force development (Fig. 10), small increase in ATPase activity (data not shown) and retardation of relaxation, all argue for the fact that mutations may have caused changes in cross-bridge kinetics by shifting the rate-limiting step of the cross-bridge cycle from the release of ADP/Pi to release of cross-bridges from actin.

It is speculated that when placed *in vivo* both mutations would lead to compensatory hypertrophy and inefficient workings of the heart. It seems that a larger change in myosin cross-bridge kinetics leads to a more severe force phenotype since the difference in maximal force between WT and R58Q muscle fibers was much larger than between WT and D166V mutant fibers (Fig. 10). Both mutations were reported to cause malignancy in humans but the R58Q mutation was associated with multiple cases of sudden cardiac death in a few ethnically different families [3,5–7]. The strength of the few- molecule method presented here includes the ability to clearly determine the kinetic properties of the myosin cross-bridges from healthy and FHC individuals.

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Abbreviations

FHC	Familial Hypertrophic Cardiomyopathy
RLC	Regulatory Light Chain of Myosin

R58Q	Arginine 58 replaced by Glutamine
D166V	Aspartate 166 replaced by Valine
LV	Left Ventricle
Tg	Transgenic
DV	Detection Volume
RP	Rhodamine-Phalloidin
HS	Half Sarcomere
APD	Avalanche PhotoDiode

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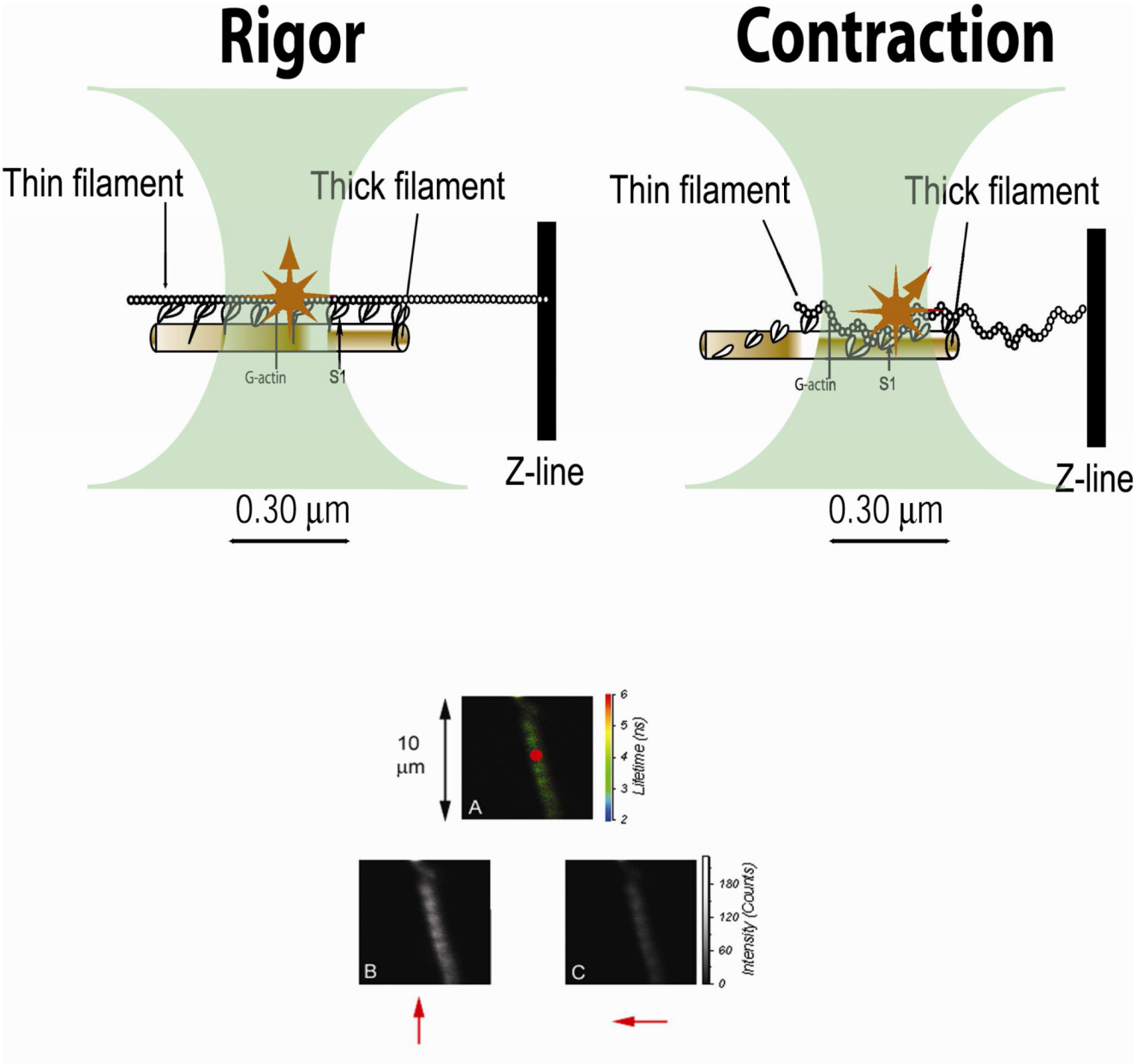

Fig. 1.

Top: Origin of fluctuations. Actin is labeled with extremely diluted fluorescent dye (red star) and is placed in the center of confocal volume of a confocal microscope. The diameter of this detection volume (DV) is (1.2 µm) is equal to the diameter of the confocal pinhole ($2\omega_o$=50 µm) divided by the magnification of the objective (40×). The DV is assumed to be an ellipsoid of revolution with a waist ω_o and height, z_o, equal to the thickness of a typical myofibril. Taking this thickness as 1 µm, DV=$4/3\pi\omega_o^2 z_o$ is ~1 μm^3. This is approximately equal to the volume of a half-sarcomere of typical length, width and height of 1, 1, and 1 µm, respectively. Therefore the signal detected by the instrument is contributed by the fluorescent molecules in one half-sarcomere. In rigor muscle (left panel) the thin filaments are stationary. There are no fluctuations in orientation of the transition dipole (red arrow). During isometric contraction (right panel) myosin cross-bridges deliver impulses to actin

which deform actin filament, changing the orientation of a transition dipole of rhodamine. The orientation of the rhodamine dipole fluctuates in time. In addition, fluctuations arise because rhodamine may leave and re-enter observational volume, as cross-bridges pull filaments to the left, and filaments recoil during isometric contraction to the right. We measure fluctuations by recording parallel (∥) and perpendicular (⊥) components of fluorescent light emitted by an actin-bound fluorophore. **Bottom**: Lifetime (**A**) and polarization (**B**, **C**,) images of rigor Tg-WT myofibril from the mouse right ventricular muscle. The color bar at right of lifetime image is the lifetime scale, with red corresponding to 6 nsec and blue to 2 nsec. The red circle is the projection of the confocal aperture on the sample plane. Its diameter (1.2 μm) is equal to the diameter of the confocal aperture (50 μm) divided by the magnification of the objective (40). The B/W intensity scale is 0–255, with 255 corresponding to white and 0 to black. Red arrows indicate the direction of polarization of fluorescent light. The exciting light is polarized vertically. Myofibrils were labeled with 1 μM Alexa488-phalloidin. Sarcomere length=2.2 μm. Images acquired with the PicoQuant Micro Time 200 confocal lifetime microscope. Excitation with a 470 nm pulse of light, emission through LP500 filter.

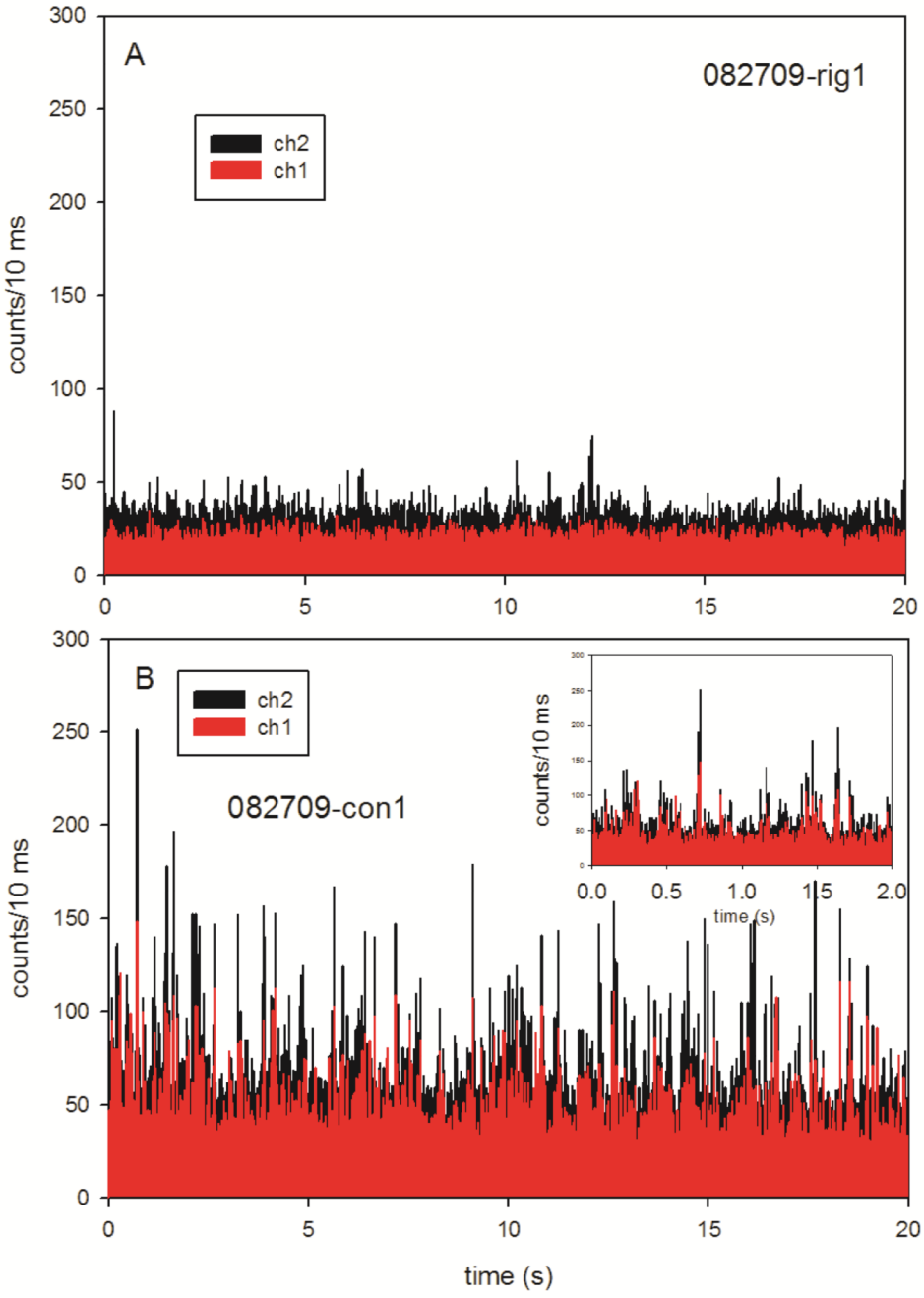

Fig. 2.

The time course of polarized intensity of rigor WT (**A**) and contracting (**B**) myofibril from left ventricle of transgenic WT heart. The original data was collected every 10 μsec, 1000 points are binned together to give time resolution of 10 msec. This is a bar plot, where the vertical scale is the number of counts during 10 msec. Ch1 (red) and Ch 2 (black) are the fluorescence intensities polarized perpendicular ($I_{\perp}$) and parallel ($I_{\parallel}$) to the myofibrillar axis, respectively Myofibrillar axis is vertical on the microscope stage. Inset to B: the time course on 0–2 s time scale.

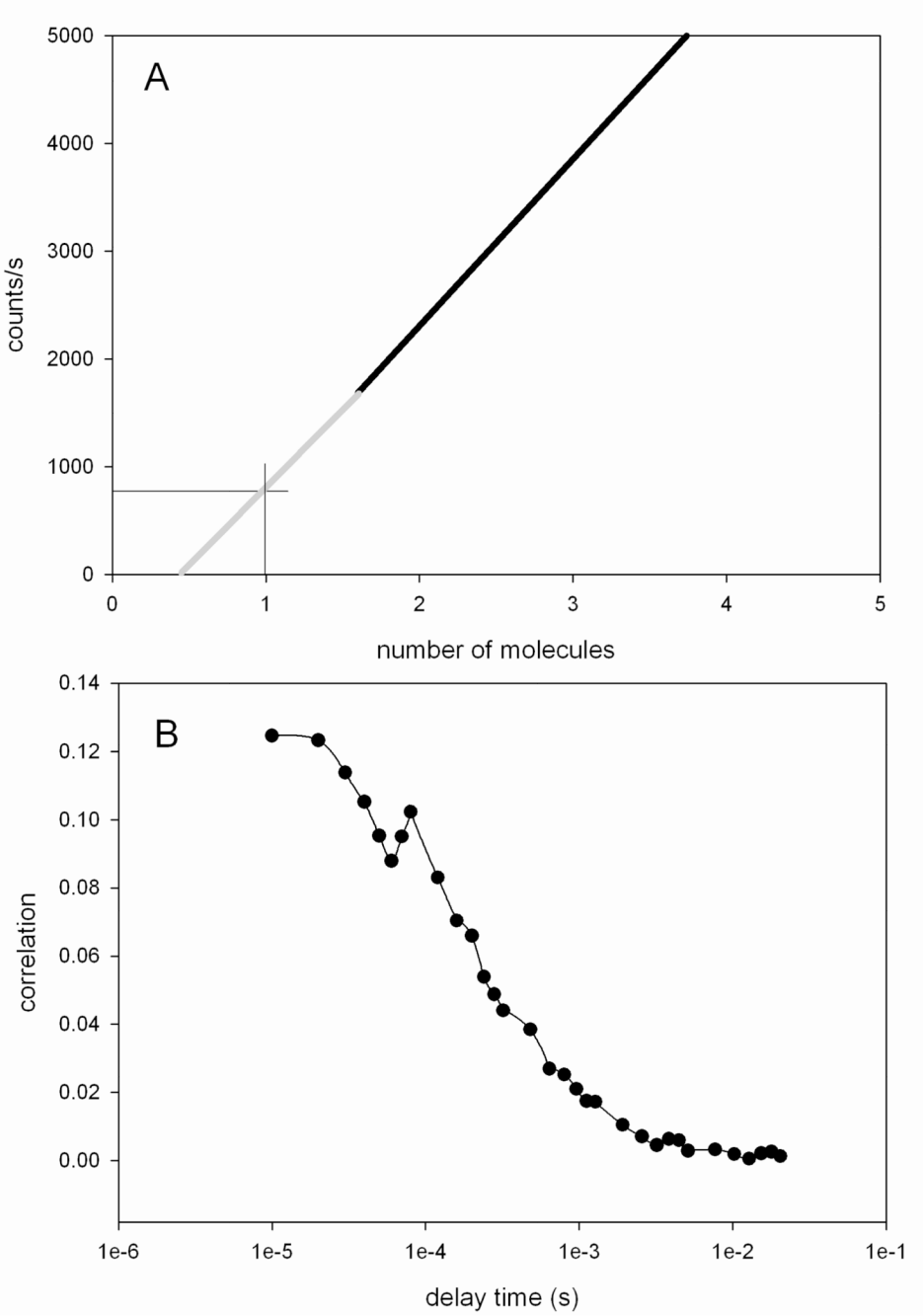

Fig. 3.

Estimation of the number of observed molecules: **A** - relation between measured intensity of the signal at increasing concentrations of rhodamine B in solution. The signal intensity of 0.5–50 nM solution of rhodamine B was plotted against number of molecules in the DV. For example, when the dye concentration was 5 nM, the signal measured in channel 1 and 2 was averaged to 99 and 115 counts/10 ms. The curve was extrapolated as shown by the gray line, from which the number of photons per one fluorophore was estimated as ~800 counts/sec per channel. The number of molecules contributing to signal was measured by recording the autocorrelation function associated with each signal. The value of the autocorrelation function at delay time 0 [G(0)] is equal to an inverse of the number of molecules N

contributing to the signal, N=1/G(0). The autocorrelation function of the signal of 5 nM rhodamine B is shown in **B**. The G(0) was 0.127 giving the number of molecules as ~8.

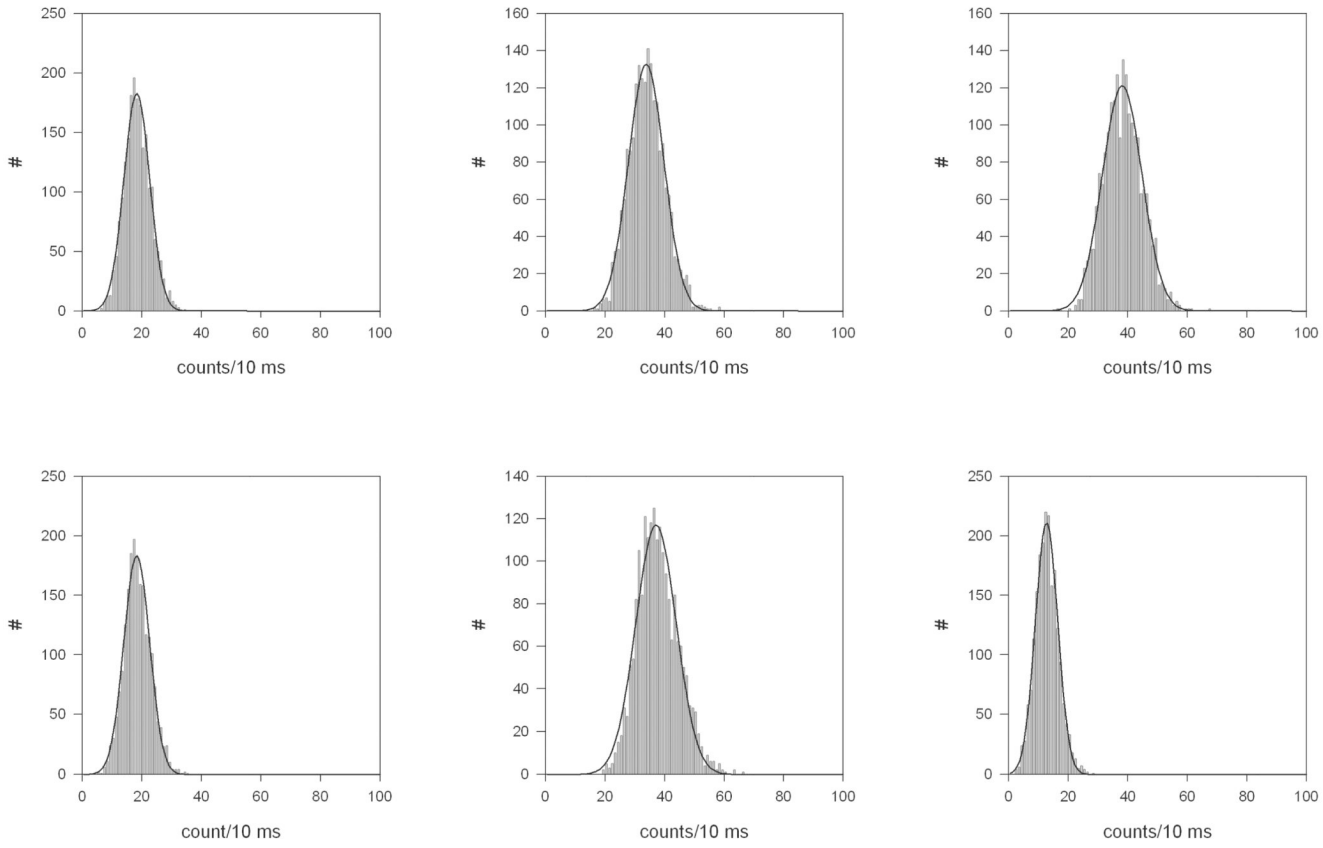

Fig. 4.

Examples of histograms of $I_{\perp}$ of rigor WT myofibrils. The solid line shows the fit to the 3 parameter Gaussian $y=a\ \exp[-0.5(x-x_o/b)^2]$. LV muscle.

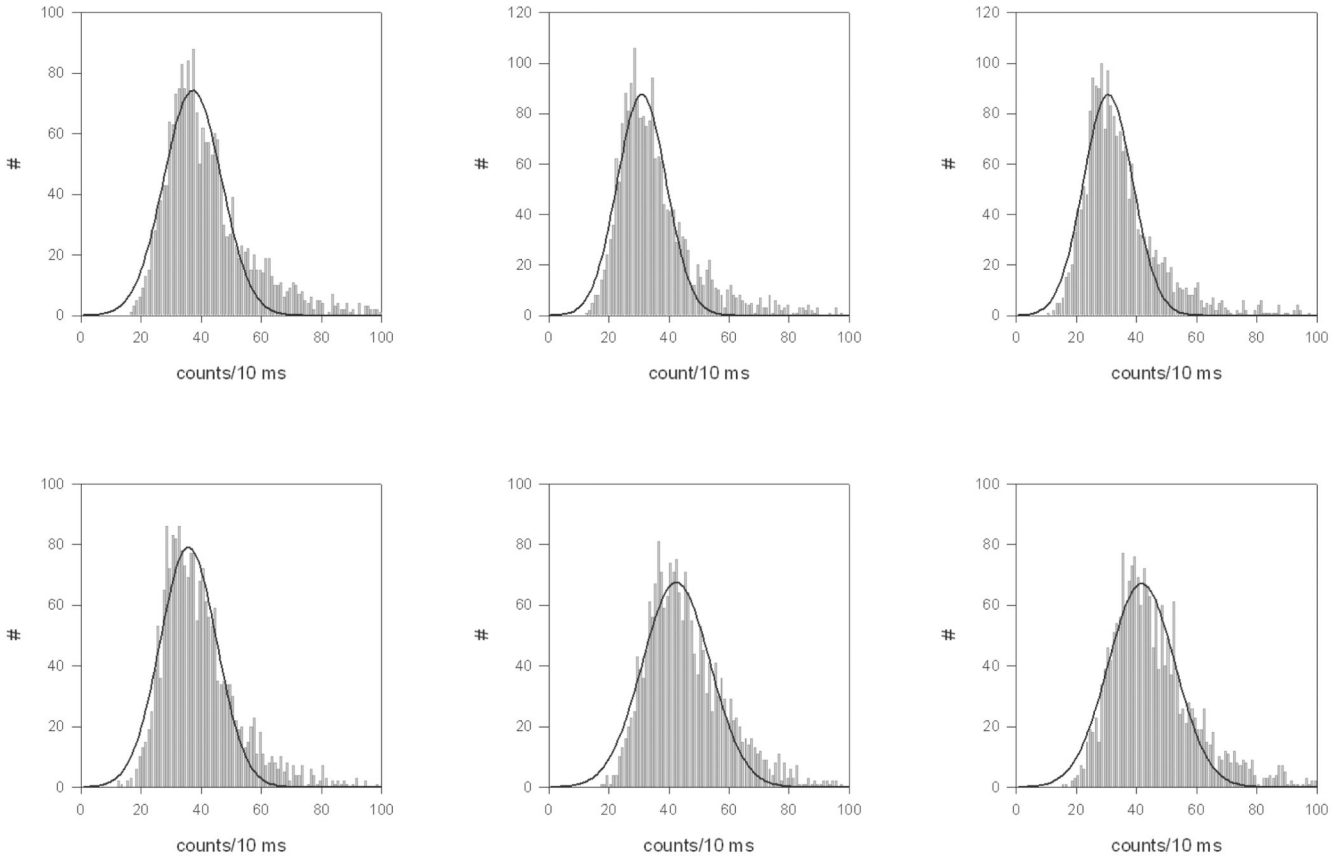

Fig. 5.

Examples of histograms of $I_{\perp}$ of contracting WT myofibrils. The solid line shows the fit to the 3 parameter Gaussian $y=aexp[-0.5(x-x_o/b)^2]$. LV muscle.

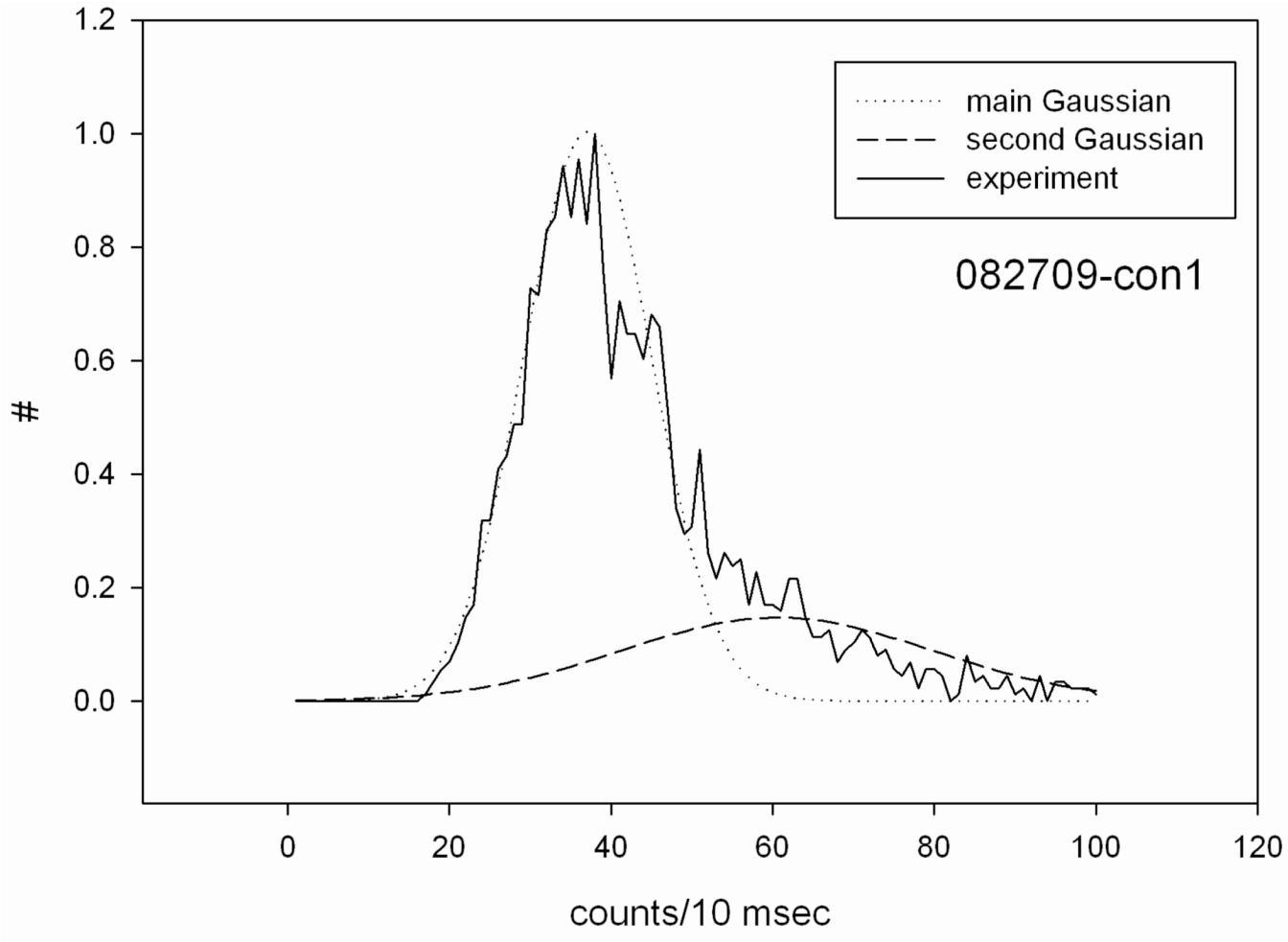

Fig. 6.

Top: Fit of the experimental curve (solid line) (data from the experiment of **Fig. 6**, top left) with the main Gaussian curve (dotted line) (mean=37.1, SD=7.9, red) and a secondary one (dashed line) (mean=60.5, SD=19.2, green). The relative contributions are 74% (main) and 26% (secondary).

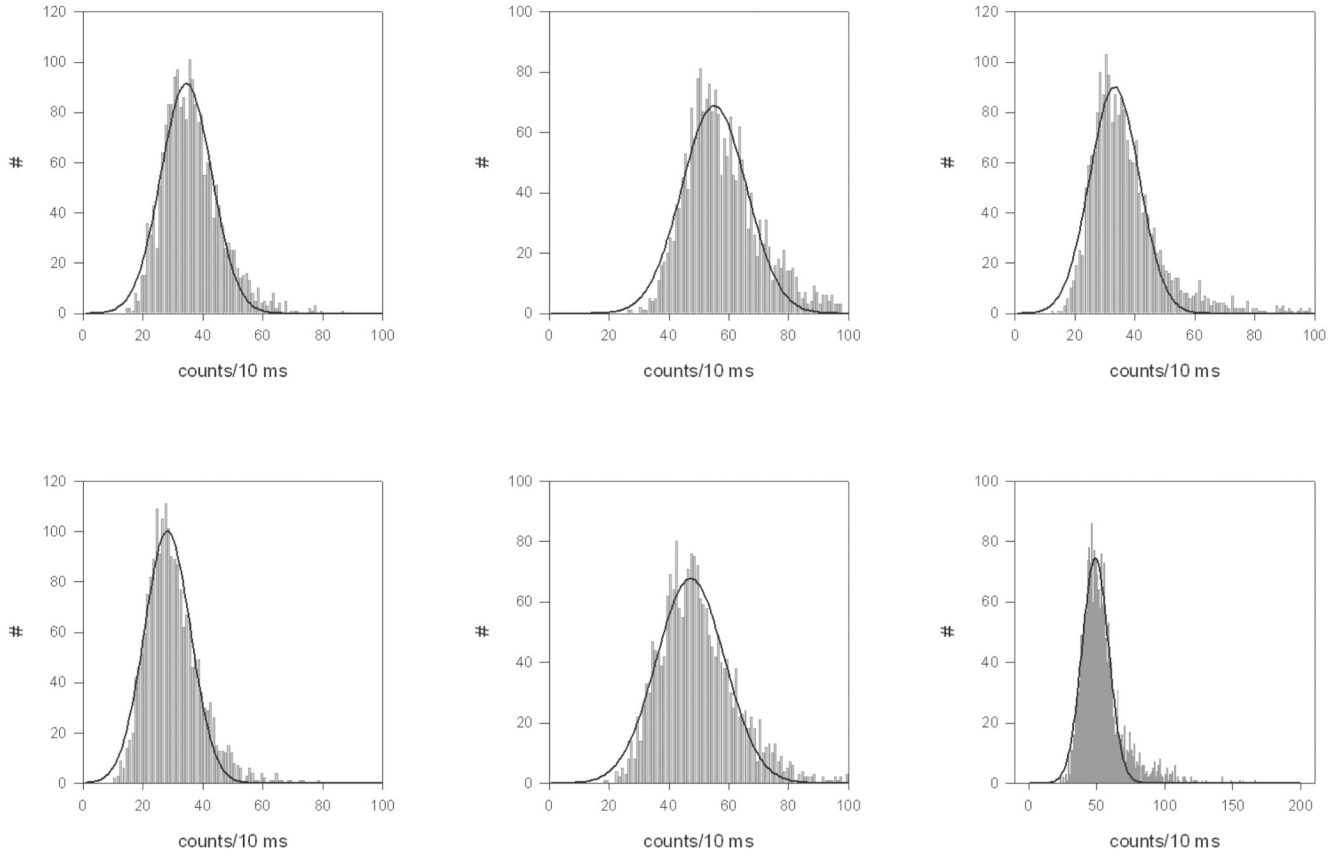

Fig. 7.

Examples of histograms of $I_{\perp}$ of contracting R58Q myofibrils. The solid line shows the fit to the 3 parameter Gaussian $y=aexp[-0.5(x-x_o/b)^2]$. LV muscle.

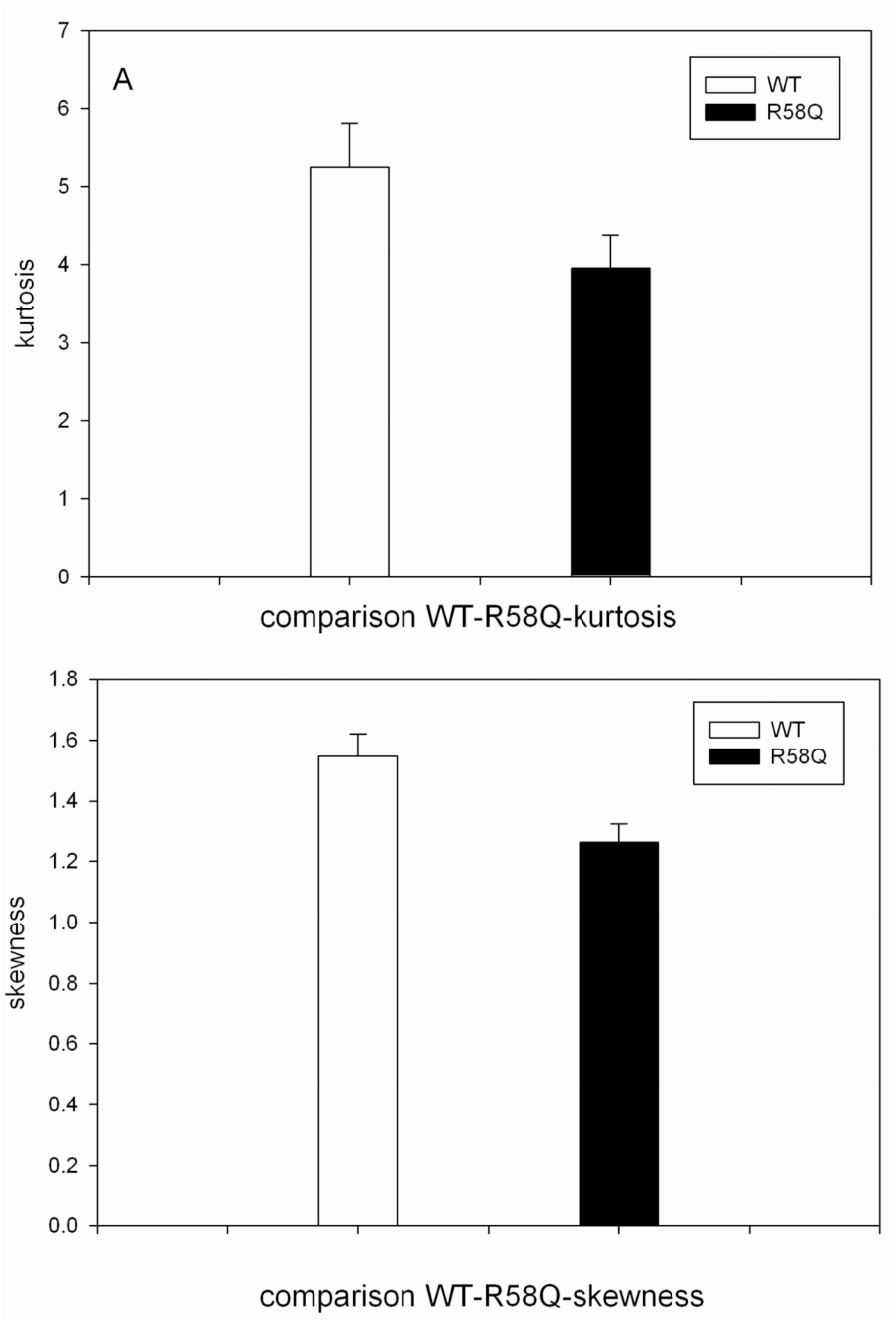

Fig. 8.
Comparison of average values of kurtosis (**A**) and skewness (**B**) for R58Q hearts.

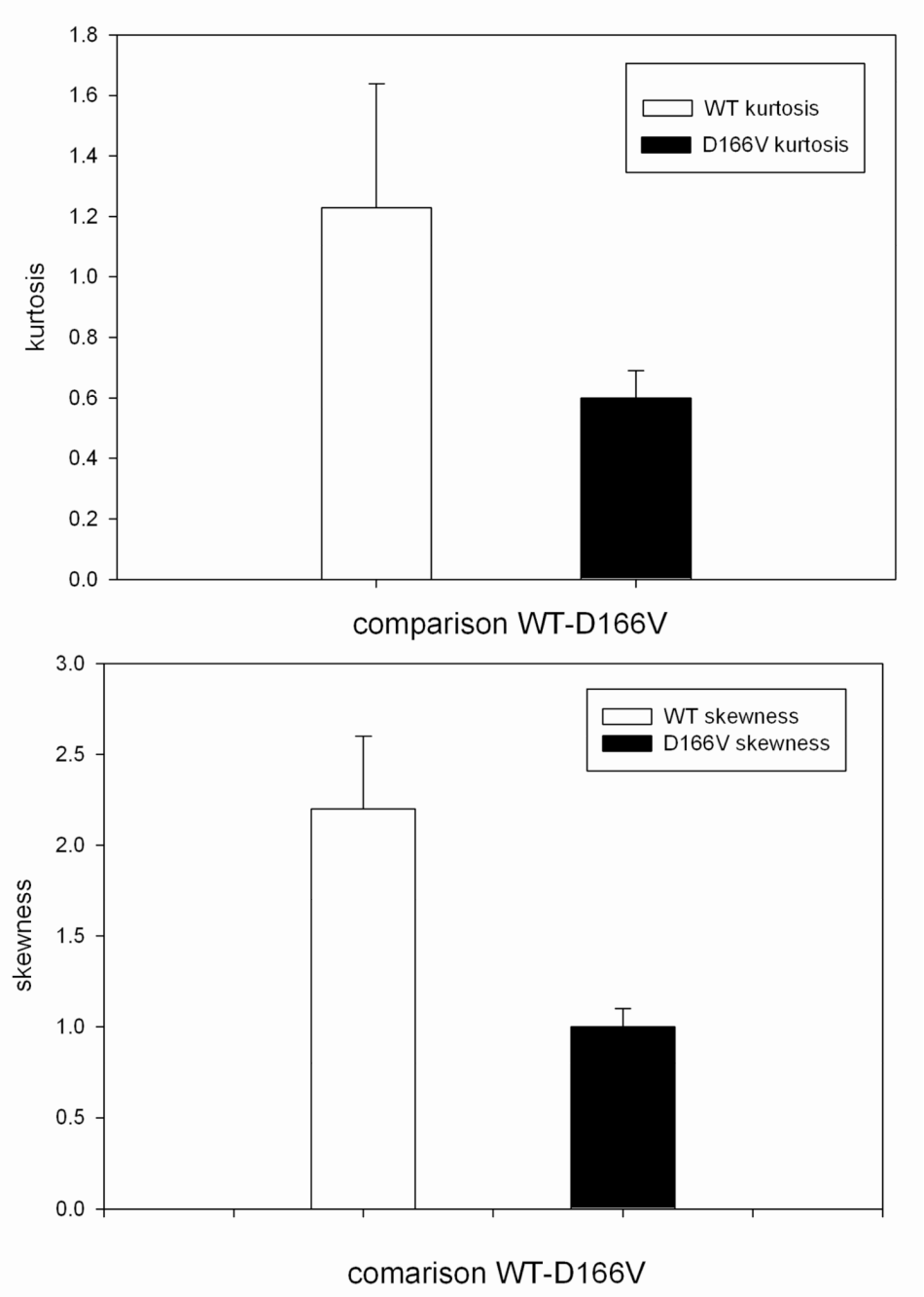

Fig. 9.
Comparison of average values of kurtosis (**A**) and skewness (**B**) for D166V hearts.

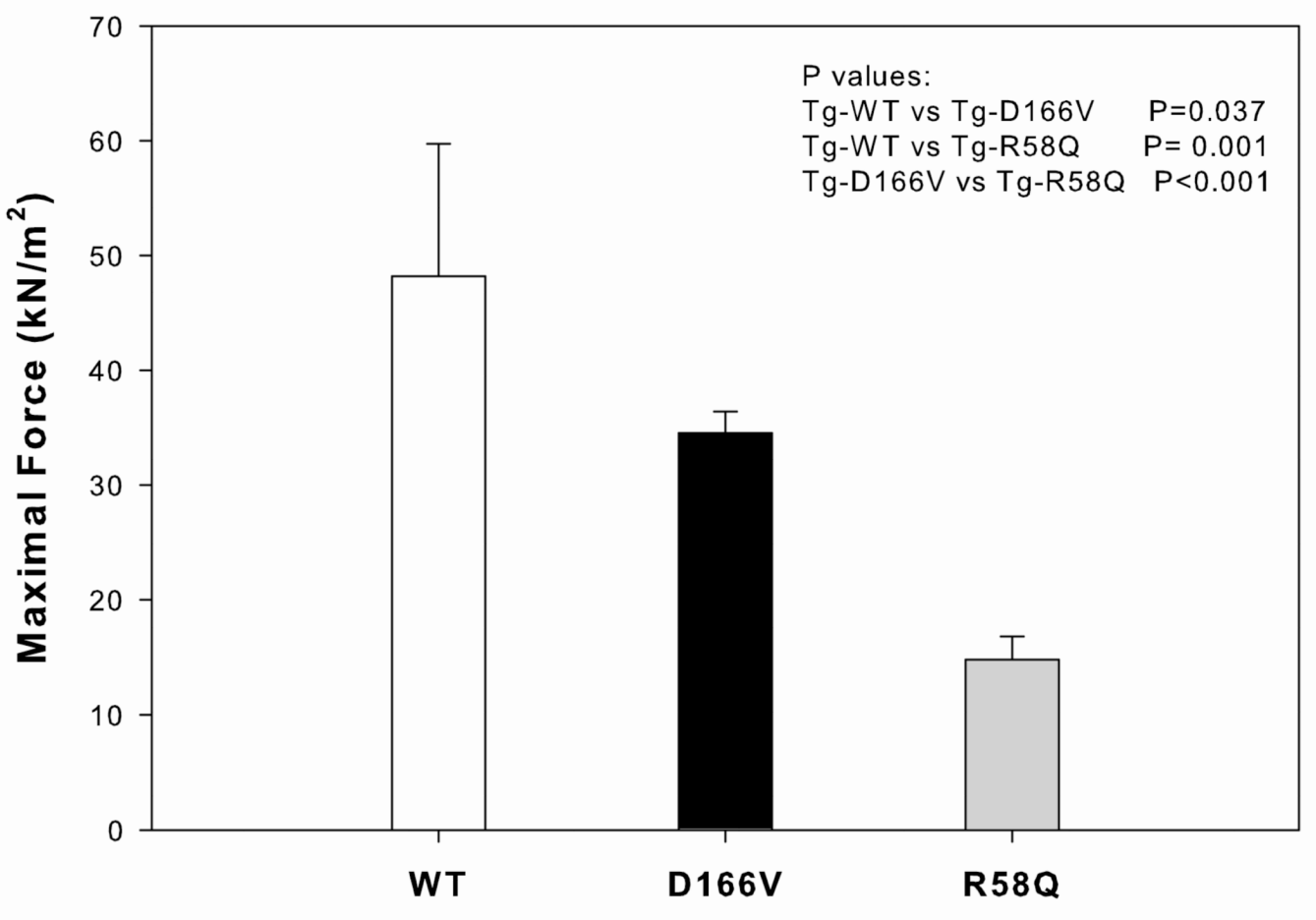

Fig. 10.

Maximal steady-state force measured in skinned papillary muscle fibers from Tg-D166V and Tg-R58Q mice compared to Tg-WT mice. The values of force (in KN) per cross-sectional area (in m^2) of fibers were: Tg-WT: 48.17±11.55(SD) n=9 fibers; Tg-D166V: 34.51±1.88 (SD) n=4 fibers, and Tg-R58Q:14.79±1.97(SD) n=7 fibers.

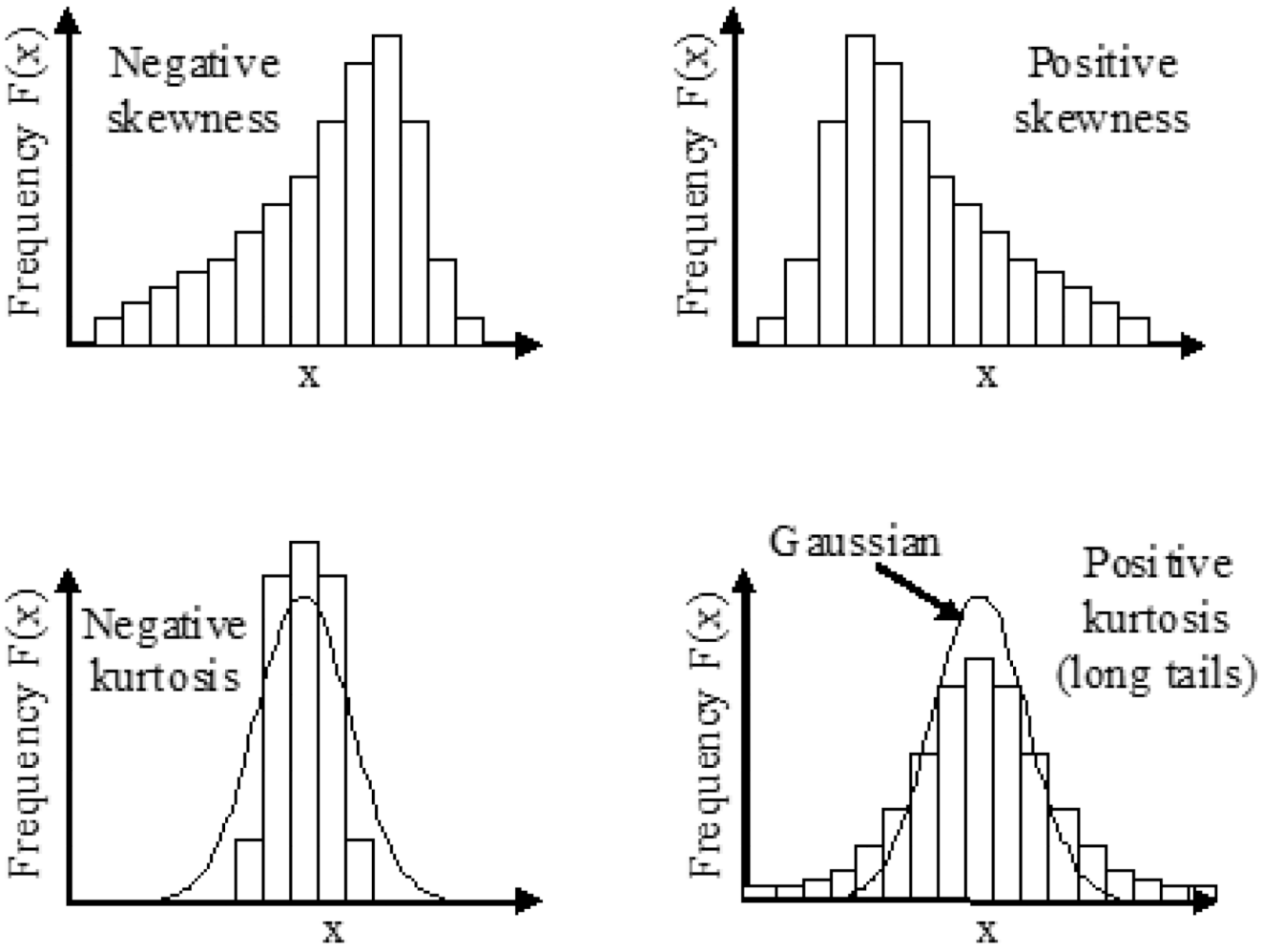

Fig. 11.
Definition of skewness and kurtosis.

Table 1

Comparison of kurtosis and skewness of rigor and contracting Tg-WT left ventricular muscle. Errors are SD's and N is the number of experiments.

Tg-WT LV muscle	Kurtosis	Skewness	N
Rigor	0.130±0.084	0.265±0.055	262
Contraction	4.562±1.605	1.571±0.286	262

Table 2

Comparison of kurtosis and skewness of contracting Tg-WT and Tg-mutant myofibrils.

Transgenic muscle	Kurtosis	Skewness	N
WT (R58Q)	5.2±0.5	1.5±0.07	218
R58Q	3.9±0.4	1.2±0.06	218
WT (D166V)	1.2±0.4	2.2±0.4	36
D166V	0.6±0.09	1.0±0.1	36

Errors are SE and N is the number of experiments.