biomechanics has nothing in common with these processes—here chemical energy is transformed directly into mechanical work; there is no thermal stage. How can such a mechanochemical process be performed?

The contractile fibrillar proteins serve as the working substances of the biological mechanochemical systems. At first it was suggested that work is done as a result of the folding and unfolding of the polymeric chains because of their electrostatic properties. Proteins are polyelectrolytes; they contain amino acidic residues, which can have positive or negative charges at the R groups. The residues Arg and Lys, for example, can be positively charged, and the residues Glu and Asp negatively.

Let us imagine a polymeric chain. Residues with charges of the same sign repel each other, and therefore the chain becomes elongated. If the charges are compensated by small ions, the mutual repulsion vanishes and the chain becomes folded in a coil because of the conformational motility of its links as a result of internal rotations around single bonds.

Such processes have been realized. In a model mechanochemical engine constructed by Kachalsky and Oplatka, the polyelectrolytic fiber (collagen) submerges alternately into salt solution and into pure water (Fig. 32). In the salt solution the fiber contracts; in water it becomes elongated again. The engine works continuously, and it can lift the load till the moment when, as the result of transfer of ions by the fiber into water, the concentrations in both reservoirs become equal.

This is a beautiful experiment, but biological contractile systems work otherwise. The cross-striated muscle is the best studied biological mechanochemical system. Three groups of facts concerning muscular contraction are known: first, information about the struc-

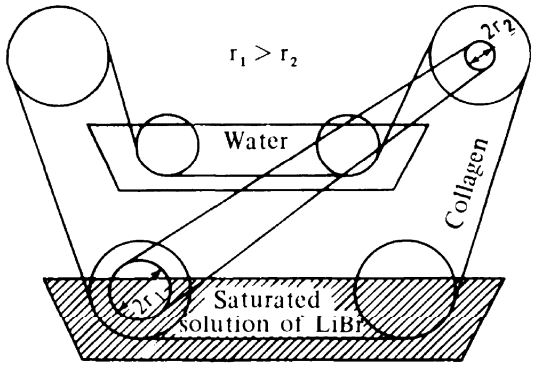

Fig. 32 The mechanochemical engine.

tural changes in the contracting muscular fiber obtained with the help of the electron microscope and x-ray diffraction; second, information about the biochemical processes in muscle; and third, the results of direct measurements of the mechanical and thermal properties of muscle. Electronic microscopy shows that the cross-striated muscle is formed by thin fibers—myofibrils—and they are arranged in a complicated but very regular structure. The myofibrils are built by thin and thick protein threads, known respectively as actin and myosin. The thin threads contain also regulatory proteins, such as tropomyosin, troponine, and actinine. Bridges are formed between the thin and thick threads. During contraction of the fiber, the threads slide in relation to each other and the muscle contracts like a field glass. This is shown schematically in Fig. 33. The "sliding model" of muscular contraction was suggested and confirmed in the works of Huxley, Hanson, and others.

The main biochemical process occurring in muscle was discovered in 1939 by Engelhardt and Ljubimova. They showed that myosin acts as an enzyme (ATPase), splitting ATP. During ATP splitting, energy is liberated. Now it is clear that the mutual shift of the protein threads and the pulling or pushing force can be produced only by conformational changes occurring in contractile proteins, that is, in the threads or bridges formed between them. The molecular mechanism by which the chemical energy released during the dephosphorylation of ATP is transformed into the energy of conformational motion remains unknown. Here we meet again with electronic–conformational interactions, that is, the transformation of the electronic energy of ATP into the conformational energy of proteins. Mechanochemistry is directly connected with enzymatic activity and evidently cannot exist without it.

It has been established that the nervous impulse is the cause of electrochemical processes in muscle. They begin by the appearance

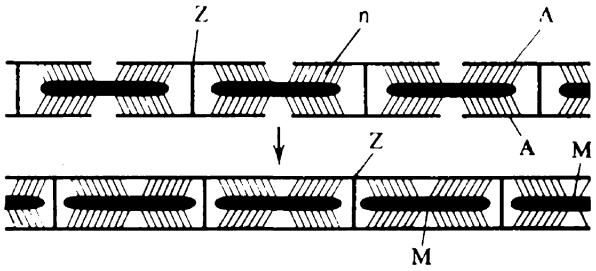

Fig. 33 Shortening of the muscle fiber. Z, membranes; A, thin threads of actin; M, thick threads of myosin; and n, bridges.

of the Ca^{2+} ions in the liquid medium surrounding the protein threads. The Ca^{2+} ions are necessary for the functioning of actomyosin, for it closes the bridges between the thick and thin protein threads.

The mechanical properties of the muscle were studied in detail by Hill, who established the fundamental equation connecting the velocity of the muscle shortening with the stress applied by the load P. Hill's equation is valid for comparatively small changes of the muscle length. For steady shortening with a constant velocity V, the equation has the form

$$(P + a)V = b(P_0 - P) \tag{52}$$

Here a and b are constants, and P_0 is the maximum load that can be supported by the muscle without it shortening or lengthening (if $P = P_0$, $V = 0$). For the sartorius muscle of the frog, $a \cong 0.25P_0$. The dependence of V on P is hyperbolic. At $P = 0$, the velocity of shortening is maximal:

$$V_{\max} = \frac{b}{a} P_0$$
$$\cong 4b \tag{53}$$

The constant b depends strongly on temperature; it doubles if the muscle is heated by 10° (in the region of physiological temperatures).

The empirical equation (52) has a very simple form. We may think that it expresses some relatively simple regularity. Really, this equation can be obtained by the theory based on the sliding model shown in Fig. 33. The pulling effort is produced as a result of the closing and subsequent opening of the bridges between the thick and thin protein threads. Let the number of the possible bridges in a sarcomere—the part of the fiber between Z-membranes to which the thin threads are attached (Fig. 33)—be n_0. Hence the maximum load that can be maintained by the muscle, or the maximum stress developed by it, is

$$P_0 = n_0 f_0 \tag{54}$$

where f_0 is the force developed by one bridge. Similarly, the applied force can be expressed in the form

$$P = n_0 f \tag{55}$$

where f is the external force per bridge. At any given moment, under the load P, not all n_0 bridges are working; only a smaller number n of them are.

Hence

$$\frac{n}{n_0} = w \leq 1 \tag{56}$$

The ratio w is equal to 1 only at $P = P_0$, when all bridges are working.

The closing and opening of the bridge means the presence in the system of the force of friction, which is proportional to the velocity of shortening. Now we can write the balance of forces using Newton's second law

$$m\dot{V} = P' - P - \gamma V \tag{57}$$

where m is some mass, $\dot{V}$ is the acceleration, P' the force developed by the bridges, and γV the friction force. Under stationary conditions, the acceleration $\dot{V}$ is equal to zero. Both P' and γV are proportional to the number n of working bridges. Calculating for one bridge, we get Eq. (57) in the form

$$nf_0 - n_0 f - n\beta v = 0 \tag{58}$$

where v is the rate of shortening of one sarcomere, and $\beta = \gamma/n$ is the coefficient of friction due to one bridge. It follows from Eq. (58) that

$$v = \frac{1}{\beta}\left(f_0 - \frac{f}{w}\right) \tag{59}$$

The value of w [Eq. (56)] depends on the force f. The most simple and natural guess is that w depends linearly on f, that is,

$$w(f) = A + Bf \tag{60}$$

If $f = f_0$, $w = 1$ and $f = 0$ when the rate of shortening is maximal, then $w = \tau < 1$ is the smallest fraction of working bridges. We get the values of A and B:

$$1 = A + Bf_0$$

$$\tau = A$$

and

$$w = 1 + (1 - \tau)\frac{f}{f_0} \tag{61}$$

Putting Eq. (61) into Eq. (59), after simple transformations we get

$$v = \frac{f_0}{\beta} \frac{\tau}{1-\tau} \frac{f_0 - f}{f + \frac{\tau}{1-\tau} f_0} \tag{62}$$

This equation is similar to Hill's equation (52), in which (in calculation per sarcomere)

$$\begin{aligned} a &= \frac{\tau}{1-\tau} f_0 \\ b &= \frac{\tau}{1-\tau} \frac{f_0}{\beta} \end{aligned} \tag{63}$$

At $a \cong 0.25 f_0$, $\tau \cong 0.2$. We get also that at $f = 0$,

$$v_{\max} = \frac{f_0}{\beta} \tag{64}$$

This calculation shows that Hill's equation describes the plastic flow—the motion of the protein threads with friction. The equation does not contain elasticity. The strong dependence of the constant b on temperature is determined by the natural dependence of the friction coefficient on temperature. Further theoretical analysis allows us to express b by molecular constants connecting this quantity with the energy of activation necessary for the dephosphorylation of ATP [19].

Many difficulties must be overcome along the way to understanding heat production during muscular contraction. The muscle works like an electric motor. The bigger is the load in the network, the greater is the current consumed by the motor. The bigger is the load lifted by the muscle, the greater is the power developed by it, and simultaneously the greater is the heat produced by the muscle. One thing is clear: both the work of the muscle and the evolved heat are derived from one source—the energy of ATP.

Notwithstanding the enormous number of books and papers devoted to muscular contraction, we are far from constructing an artificial device that works like a muscle. This would be very tempting—the efficiency of the muscles of some animals reaches 75%.

More detailed information about the physics of muscular contraction can be found in the literature [19, 21].

We end this chapter with a few words about the flight muscles of insects. They perform many contractions in a second—everybody has heard the buzzing of mosquitoes. It has been established that the

frequency of contraction of insect muscles surpasses the frequency of the arrival of the nervous impulse by hundreds of times. In other words, we meet here with a clear case of an autooscillatory process. Its investigation is a fascinating problem of biophysics, as is the study of nonstationary contractions of the muscles of vertebrates.

By considering muscular contraction, we have seen the role of experimental and theoretical physics in the studies of the biological (bioenergetic) processes.