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BIOPHYSICS OF MUSCLE CONTRACTION

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Annotation: This article analyzes the biophysical foundations of muscle contraction, including the structural organization of skeletal muscle, the sliding filament theory, the mechanism of excitation-contraction coupling, the energy supply of the contractile process, and the biomechanical properties of contraction. Based on the research findings, scientific and methodological conclusions for optimizing muscular activity in the practice of physical education and sport have been formulated.

Keywords: Muscle contraction, biophysics, actin, myosin, sarcomere, calcium ion, ATP, contraction mechanism.

Annotatsiya:
Ushbu maqolada muskullar qisqarishining biofizik asoslari, ya'ni skelet mushaklarining tuzilishi, siljuvchi ipchalar nazariyasi, qo'zg'alish-qisqarish bog'lanishi, energiya ta'minoti mexanizmlari hamda qisqarishning biomexanik xususiyatlari tahlil qilingan. Tadqiqot natijalari asosida jismoniy tarbiya va sport amaliyotida mushak faoliyatini optimallashtirish bo'yicha ilmiy-uslubiy xulosalar ishlab chiqilgan.

Аннотация:
В данной статье анализируются биофизические основы мышечного сокращения — строение скелетных мышц, теория скользящих нитей, механизм электромеханического сопряжения, энергетическое обеспечение и биомеханические свойства сокращения. На основе результатов исследования разработаны научно-методические выводы по оптимизации мышечной деятельности в практике физического воспитания и спорта.

Kalit so'zlar: muskul qisqarishi, biofizika, aktin, miozin, sarkomer, kalsiy ioni, ATF, qisqarish mexanizmi.

Ключевые слова: мышечное сокращение, биофизика, актин, миозин, саркомер, ион кальция, АТФ, механизм сокращения.

Introduction

The muscular system constitutes the fundamental biomechanical apparatus through which the human organism realizes all forms of motor activity, from the simplest reflex movement to the most complex sport technique. Understanding the biophysical

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mechanisms underlying muscle contraction is therefore of central importance not only for physiology and biophysics as fundamental sciences, but also for the applied theory and methodology of physical education and sport, where the rational organization of training loads directly depends on a correct understanding of how muscle fibers generate force and how this force is transformed into external mechanical work.

Muscle contraction is a complex, multilevel biophysical process in which chemical energy stored in the bonds of adenosine triphosphate (ATP) is converted into mechanical work through a strictly ordered sequence of molecular events occurring within the contractile proteins of the muscle fiber. The scientific explanation of this process has undergone considerable historical development: from the early mechanical and thermodynamic descriptions of muscle work in the first half of the twentieth century to the establishment of the sliding filament theory and the subsequent elucidation of the molecular cross-bridge cycle, which today remains the central paradigm of muscle biophysics.

The relevance of the present study is determined by the fact that a deep understanding of the biophysical foundations of muscle contraction allows specialists in physical education and sport to substantiate scientifically the selection of training methods, the dosage of physical load, and the means of preventing muscular fatigue and injury. Without a clear conception of the molecular and energetic mechanisms of contraction, the methodology of physical training risks remaining at a purely empirical level, disconnected from its natural-scientific basis.

Despite the considerable body of research accumulated in the field of muscle biophysics, a number of questions remain the subject of ongoing scientific discussion, in particular regarding the precise kinetics of the cross-bridge cycle, the mechanisms of muscular fatigue at the molecular level, and the biophysical basis of the differences between muscle fiber types. This determines the necessity of a systematic, generalized presentation of the existing scientific knowledge on the biophysics of muscle contraction, which constitutes the main purpose of the present article.

The purpose of the research is to study the biophysical mechanisms of skeletal muscle contraction, to analyze the structural, molecular, and energetic foundations of this process, and to examine its biomechanical manifestations relevant to the practice of physical education and sport. To achieve this purpose, the following tasks were set: to characterize the structural organization of the contractile apparatus of the muscle fiber; to reveal the molecular mechanism of contraction according to the sliding filament theory; to analyze the process of excitation-contraction coupling; to study the energetic foundations of muscle contraction; to examine the biomechanical relationships describing muscle force generation; and to formulate practically oriented conclusions for the field of physical education.

The scientific novelty of the article consists in a comprehensive presentation that integrates the molecular-biophysical, energetic, and biomechanical aspects of muscle contraction within a single logical structure oriented specifically toward the needs of physical education and sport pedagogy. The practical significance of the work lies in the

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fact that its results can be used by students, coaches, and teachers of physical culture as scientific and methodological material for a deeper understanding of the physiological basis of motor activity.

Research Methodology

The research was conducted using a complex of theoretical scientific methods. The method of theoretical analysis was applied to study the scientific and educational literature on physiology, biophysics, and biomechanics devoted to the mechanisms of muscle contraction. The historical-comparative method allowed the tracing of the evolution of scientific conceptions of muscle contraction, from the early mechanical theories to the modern molecular model. The method of systematization and generalization was used to integrate data from different levels of biological organization — molecular, cellular, and whole-muscle — into a unified, logically consistent description of the contraction process.

The theoretical basis of the study is formed by the classical works of foreign researchers in the field of muscle biophysics, together with the works of local scholars on human physiology and sport physiology, as well as the normative requirements of the State Educational Standard regarding the natural-scientific training of specialists in physical culture. The material collected in the course of the research was analyzed with attention to the internal logical connections between the structural, molecular, and functional levels of description of muscle contraction.

Main Part

1. Structural organization of the contractile apparatus of skeletal muscle

Skeletal muscle is a highly organized tissue composed of numerous parallel muscle fibers, each representing a single, multinucleated cell surrounded by a specialized membrane called the sarcolemma. Within each muscle fiber, the contractile apparatus is represented by a large number of thread-like structures known as myofibrils, which in turn are composed of repeating structural and functional units called sarcomeres, arranged in series along the length of the myofibril. The sarcomere constitutes the elementary contractile unit of skeletal muscle and is bounded on both sides by structures known as Z-discs.

Within the sarcomere, two principal types of protein filaments can be distinguished: the thin filaments, composed mainly of the protein actin together with the regulatory proteins troponin and tropomyosin, and the thick filaments, composed of the protein myosin[1]. The characteristic banding pattern observed under the microscope — alternating light and dark bands — reflects the regular, partially overlapping arrangement of these thin and thick filaments within the sarcomere.

The myosin molecule possesses a specific structure consisting of a long tail and a globular head, the latter functioning as a molecular motor capable of binding to actin

[1]Boron W.F., Boulpaep E.L. Medical Physiology. — Philadelphia: Elsevier, 2017. — P. 210-218.

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and of hydrolyzing ATP. It is precisely the cyclic interaction between the myosin heads of the thick filaments and the actin monomers of the thin filaments that constitutes the molecular basis of the force-generating process, which will be examined in detail in the following section.

2. The sliding filament theory and the molecular mechanism of contraction

The modern understanding of the mechanism of muscle contraction is based on the sliding filament theory, first formulated in the middle of the twentieth century[2], according to which the shortening of the sarcomere, and consequently of the whole muscle fiber, occurs not through a shortening of the individual actin and myosin filaments themselves, but through their relative sliding past one another, with the thin filaments being pulled deeper into the space between the thick filaments.

The molecular basis of this sliding process is provided by the so-called cross-bridge cycle, a cyclically repeating sequence of biochemical and mechanical events occurring at the level of the individual myosin head[3]. In the initial state, the myosin head, having hydrolyzed a molecule of ATP into adenosine diphosphate (ADP) and inorganic phosphate, is in a state of high potential energy and is weakly attached to a binding site on the actin filament. Upon the release of inorganic phosphate, the myosin head undergoes a pronounced conformational change — the so-called power stroke — during which it pulls the actin filament a small distance relative to the myosin filament, generating mechanical force.

Following the power stroke, ADP is released from the myosin head, and the myosin-actin complex enters a state of strong binding known as rigor. The binding of a new molecule of ATP to the myosin head causes its detachment from actin, after which the hydrolysis of this new ATP molecule restores the myosin head to its original high-energy configuration, allowing the cycle to repeat. The repeated, asynchronous cycling of a large number of cross-bridges within the sarcomere produces a smooth, continuous sliding of the filaments and, consequently, a macroscopically observable shortening of the muscle.

It should be particularly emphasized that ATP performs two distinct functions within this cycle: first, its hydrolysis provides the energy required for the conformational change underlying the power stroke, and second, the binding of a new ATP molecule is necessary for the detachment of the myosin head from actin. This latter function explains the biophysical basis of the phenomenon of rigor mortis, in which the depletion of ATP after death prevents the detachment of myosin from actin, resulting in a sustained state of muscular rigidity.

3. Excitation-contraction coupling

The initiation of muscle contraction begins with the arrival of a nerve impulse at the neuromuscular junction, where the neurotransmitter acetylcholine is released and

[2]Huxley A.F., Niedergerke R. Structural changes in muscle during contraction. — Nature, 1954. — Vol. 173. — P. 971-973.
[3]Huxley H.E. The mechanism of muscular contraction. — Science, 1969. — Vol. 164. — P. 1356-1365.

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triggers the generation of an action potential along the sarcolemma of the muscle fiber. This electrical signal is subsequently propagated into the depth of the muscle fiber through specialized invaginations of the sarcolemma known as transverse tubules, or T-tubules, which are structurally and functionally associated with the sarcoplasmic reticulum, an intracellular membrane system responsible for the storage of calcium ions.

The arrival of the action potential at the T-tubules triggers the opening of calcium release channels in the membrane of the sarcoplasmic reticulum, resulting in a rapid increase in the concentration of free calcium ions within the sarcoplasm surrounding the myofibrils[4]. This process, in which an electrical signal is translated into a chemical signal that ultimately produces a mechanical response, is termed excitation-contraction coupling and represents one of the central biophysical mechanisms linking neural control to muscular action.

The released calcium ions bind to the regulatory protein troponin, located on the thin filament, causing a conformational change that displaces the tropomyosin molecule and exposes the myosin-binding sites on the actin filament, which were previously blocked in the resting state of the muscle. Only after this exposure of the binding sites can the cross-bridge cycle described in the previous section proceed, which explains why the concentration of intracellular calcium constitutes the immediate biophysical trigger governing the transition of the muscle fiber from a relaxed to a contracted state.

The relaxation of the muscle fiber, correspondingly, depends on the active removal of calcium ions from the sarcoplasm back into the sarcoplasmic reticulum, a process carried out by specialized calcium pumps that consume additional ATP. This demonstrates that not only contraction, but also relaxation, is an energy-dependent biophysical process, and that the availability of ATP is essential for the normal cyclic alternation between the contracted and relaxed states of skeletal muscle.

4. Energetics of muscle contraction

The energetic supply of muscle contraction is provided through several interconnected biochemical pathways, whose relative contribution depends on the intensity and duration of the muscular activity. The most immediately available source of energy is the store of ATP directly present within the muscle fiber, which, however, is extremely limited and capable of sustaining maximal contraction for only a very short period of time, typically a few seconds.

The second, closely related energy source is the phosphocreatine system, in which the high-energy phosphate group of phosphocreatine is rapidly transferred to ADP, regenerating ATP without the need for oxygen[5]. This anaerobic alactic pathway provides energy for short, high-intensity efforts lasting up to approximately ten to fifteen seconds, after which its capacity becomes substantially depleted.

[4]Kamilova R.T. Fiziologiya asoslari. — Toshkent: O'qituvchi, 2020. — B. 142-150.

[5]Hill A.V. The heat of shortening and the dynamic constants of muscle. — Proceedings of the Royal Society of London, 1938. — Vol. 126. — P. 136-195.

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For contractile activity of longer duration, the muscle progressively relies on the anaerobic glycolytic pathway, in which glucose or glycogen is broken down to pyruvate and subsequently to lactate, yielding ATP at a relatively high rate but with the accompanying accumulation of metabolic by-products that contribute to the biophysical phenomenon of muscular fatigue. Finally, for prolonged, moderate-intensity activity, the aerobic oxidative pathway, occurring within the mitochondria of the muscle fiber, becomes the dominant source of ATP, providing a considerably larger total energy yield through the complete oxidation of carbohydrates and fats, at the cost of a slower rate of ATP production.

The interaction and sequential predominance of these three energy systems — the phosphocreatine system, anaerobic glycolysis, and aerobic oxidation — constitute the biophysical and biochemical basis for the classification of physical exercises according to their intensity and duration, a classification of direct practical relevance for the scientifically grounded planning of training loads in sport pedagogy.

5. Biomechanical and biophysical properties of muscle contraction

Beyond the molecular mechanism of contraction, muscle biophysics also examines the macroscopic mechanical properties of the whole muscle, expressed through several fundamental relationships. The force-length relationship describes the dependence of the maximal force a muscle is capable of generating on its initial length at the moment of stimulation, and it is directly explained by the degree of overlap between the actin and myosin filaments within the sarcomere: at excessively short or excessively long sarcomere lengths, the overlap between filaments becomes suboptimal, and consequently the number of cross-bridges capable of forming decreases, reducing the generated force.

The force-velocity relationship, first quantitatively described in the classical studies on muscle thermodynamics, expresses the inverse dependence between the velocity of muscle shortening and the force it can simultaneously produce[6]: the greater the external load against which the muscle contracts, the lower the velocity of shortening, and, conversely, under conditions of minimal load, the muscle is capable of shortening at its maximal velocity but generates comparatively little force.

From the point of view of biomechanics, three principal types of muscle contraction are traditionally distinguished. Isometric contraction occurs when the muscle generates force without any change in its overall length, as, for example, when an object is held motionless against gravity. Isotonic contraction, in turn, involves a change in muscle length while the force remains relatively constant, and is further subdivided into concentric contraction, in which the muscle shortens while generating force, and eccentric contraction, in which the muscle lengthens while continuing to resist an external force, a mode of contraction associated with particularly high mechanical stress on the contractile and connective tissue structures.

[6]Solodkov A.S., Sologub E.B. Sport fiziologiyasi. — Toshkent: Ilm-Ziyo, 2021. — B. 88-97.

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6. Muscle fiber types and their biophysical characteristics

Skeletal muscle fibers are commonly classified into several types on the basis of their biophysical and metabolic characteristics, most frequently distinguished as slow-twitch (type I) and fast-twitch (type II) fibers[7]. Slow-twitch fibers are characterized by a relatively low maximal speed of cross-bridge cycling, a high density of mitochondria, and a predominant reliance on aerobic oxidative metabolism, which makes them particularly well suited for prolonged, low-intensity activity requiring resistance to fatigue.

Fast-twitch fibers, by contrast, possess a considerably higher maximal speed of cross-bridge cycling and are capable of generating force more rapidly, but they rely predominantly on anaerobic glycolytic metabolism and consequently fatigue more quickly than slow-twitch fibers. Within the category of fast-twitch fibers, further subdivisions are often made according to the degree of oxidative capacity, reflecting a continuous spectrum of biophysical and metabolic properties rather than a strictly discrete classification.

The relative proportion of slow-twitch and fast-twitch fibers within a given muscle is determined largely by genetic factors, although it can be modified to a certain extent through systematic and appropriately directed physical training. This biophysical fact underlies the pedagogical principle according to which the selection of training methods should take into account the specific requirements of the sport discipline in question, whether it demands predominantly endurance-related qualities or predominantly speed-strength qualities.

7. Biophysics of muscular fatigue

Muscular fatigue represents a complex, multifactorial biophysical phenomenon characterized by a progressive decline in the capacity of the muscle to generate force or to sustain a given level of mechanical power output[8]. At the molecular level, fatigue is associated with several interrelated processes, including the depletion of phosphocreatine and glycogen reserves, the accumulation of metabolic by-products such as hydrogen ions and inorganic phosphate within the sarcoplasm, and a consequent disruption of the normal functioning of the calcium-release mechanism and of the cross-bridge cycle itself.

The accumulation of inorganic phosphate, in particular, is considered by contemporary muscle biophysics to interfere directly with the power stroke phase of the cross-bridge cycle, thereby reducing the force generated per individual cross-bridge, while the accumulation of hydrogen ions is associated with a reduction in the sensitivity of troponin to calcium, further impairing the efficiency of excitation-contraction coupling. Understanding these molecular mechanisms of fatigue provides an important scientific foundation for the development of rational recovery strategies within the training

[7]Aliyev N.A. Biofizika. — Toshkent: Yangi asr avlodi, 2019. — B. 175-183.
[8]Mahkamjonov K. Inson fiziologiyasi. — Toshkent: O'qituvchi, 2018. — B. 96-104.

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process, including the appropriate alternation of load and rest and the correct sequencing of exercises of differing intensity.

Comparative Analysis with Foreign Experience

The scientific study of muscle biophysics has developed through the combined contribution of several major research traditions. The classical British school of muscle physiology, associated with the pioneering thermodynamic and mechanical studies of muscle work in the first half of the twentieth century, established the fundamental quantitative relationships between force, velocity, and heat production during contraction, laying the empirical foundation upon which later molecular theories would be built.

The subsequent formulation and experimental confirmation of the sliding filament theory, achieved through detailed structural and biochemical investigations of isolated muscle fibers, marked a decisive shift from a purely mechanical to a molecular understanding of contraction, and this molecular paradigm continues to form the core of contemporary muscle biophysics taught in physiology and biophysics courses worldwide.

Within the local scientific and educational tradition, considerable attention has historically been given to the applied aspects of muscle physiology relevant to sport practice, in particular to the study of energy supply mechanisms during exercises of differing intensity and to the physiological substantiation of training methods for the development of strength, speed, and endurance qualities. The integration of the fundamental molecular-biophysical knowledge developed within the international scientific tradition with the applied, sport-oriented physiological research conducted locally represents a productive direction for further deepening the natural-scientific basis of physical education pedagogy in our country.

It should also be noted that modern biophysical research increasingly relies on advanced experimental techniques — including single-molecule mechanical measurements and high-resolution structural methods — that allow the direct observation of individual steps within the cross-bridge cycle. While such highly specialized experimental approaches remain primarily within the domain of fundamental biophysical science, their results progressively enrich the applied physiological knowledge that underlies the scientifically grounded practice of physical education and sport training.

Results and Discussion

The conducted analysis demonstrates that muscle contraction is a hierarchically organized biophysical process, in which molecular events occurring at the level of individual actin and myosin filaments are ultimately expressed as macroscopic mechanical work performed by the whole muscle. The sliding filament theory, together with the concept of the cross-bridge cycle, provides a coherent and experimentally well-supported explanation of how chemical energy stored in ATP is converted into mechanical force and displacement.

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The analysis further shows that the process of excitation-contraction coupling, mediated by the rapid release and subsequent reuptake of calcium ions, constitutes the essential link between neural control and the biophysical machinery of contraction, while the sequential involvement of the phosphocreatine, glycolytic, and oxidative energy systems determines the capacity of the muscle to sustain contractile activity of varying intensity and duration. These findings confirm that the practical planning of physical training loads should be grounded in a clear understanding of which energy system predominates under given conditions of exercise intensity and duration.

The examination of the force-length and force-velocity relationships, together with the classification of muscle fiber types, demonstrates that the mechanical output of skeletal muscle cannot be adequately understood without reference to its underlying molecular and structural organization. This confirms the necessity of including the fundamentals of muscle biophysics within the professional training of specialists in physical education, since a purely empirical, mechanically descriptive approach to the study of movement, without reference to its biophysical basis, inevitably remains incomplete.

Finally, the analysis of the molecular mechanisms of muscular fatigue indicates that fatigue should not be regarded as a simple, unitary phenomenon, but rather as the cumulative result of several distinct biophysical and biochemical processes occurring simultaneously at different levels of the contractile apparatus. This understanding provides an important scientific basis for the rational construction of training and recovery regimens aimed at delaying the onset of fatigue and accelerating post-exercise recovery.

Conclusion

Summarizing the conducted research, it can be concluded that the biophysics of muscle contraction represents a fundamental scientific basis for the theory and methodology of physical education and sport. The structural organization of the sarcomere, the molecular mechanism of the cross-bridge cycle, the process of excitation-contraction coupling, the multiple energy systems supplying the contractile process, and the biomechanical relationships governing muscle force generation together form a coherent, multilevel explanation of how the human organism produces movement.

On the basis of the results obtained, the following conclusions and recommendations may be proposed for the practice of physical education: training methods should be selected with explicit consideration of the predominant energy system required by a given type of physical exercise; the biomechanical properties of muscle, including the force-length and force-velocity relationships, should be taken into account when designing strength and speed training programs; the individual proportion of slow-twitch and fast-twitch muscle fibers should be considered, where possible, in the individualization of training programs; and a scientifically grounded understanding of the molecular mechanisms of fatigue should inform the rational planning of rest intervals and recovery strategies within the training process.

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Further development of this direction of research may be associated with a more detailed study of the age-related and sex-related biophysical characteristics of muscle contraction, as well as with the practical verification, within the conditions of sport pedagogy, of training methods explicitly grounded in the molecular and energetic principles examined in the present article.

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