International Journal of
Health Systems and Medical Sciences

ISSN: 2833-7433
Volume 2 | No 1 | January -2023

Sports Genetics is the Key to High Achievements of Athletes

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Abstract: Sports genetics is one of the young sciences. Genetic factors are generally known to affect strength and endurance, but only a few studies have examined the relationship between genetic factors and athletic performance in young athletes. One of the intensively developing areas of modern genetics is the development of molecular genetic approaches that make it possible to determine a person's predisposition to various types of activity, which is determined by the need to substantiate a system for selecting people for playing sports and correcting the training process. This approach is the most promising, since it allows you to determine the genetic predisposition to the performance of large physical activities and to carry out a targeted differentiated selection of children for sports at the earliest stages of their sports activity. Currently, predictive medicine is actively developing, the purpose of which is to identify possible diseases in a particular patient by the DNA structure, as well as to develop a set of preventive or health-improving measures based on these studies. Such preventive measures are also important in sports, so sports genetics can achieve high results using scientific methods.

Keywords: sports genetics, predicting athletes' capabilities, selection of young athletes, DNA polymorphism, genetic predisposition.

Genetic factors are generally known to affect strength and endurance [8], but only a few studies have examined the relationship between genetic factors and athletic performance in young athletes. Among the potential polymorphisms potentially associated with muscle function and physical performance, the most studied are angiotensin-converting enzyme (ACE), variant R577X of the actinin-3 gene (ACTN3), and muscle creatine kinase isoform (CK-). MM), peroxisome proliferator-activated receptor α (PPARα) and more recently SLC2A4 [9-14]. It has been demonstrated that alternative polymorphic variants of these potential polymorphisms are associated with sprint / strength or endurance disciplines with reasonable replication in different groups of athletes [15-18]. Indeed, the I allele of the insertion (I) / deletion (D) polymorphism in the ACE gene is one of the most putative factors determining aerobic capacity in performance-oriented endurance [28]. Likewise, the PPAR-G, ACTN3 X, and CK-MM A alleles are involved in improving aerobic performance [16, 17, 19]. On the other hand, it is assumed that ACE D, PPARα C, ACTN3 R and CK-MM G are more related to strength-oriented characteristics [8, 16, 20]. Given that the contribution of specific genes to athletic performance has been investigated primarily in athletes who are at the two endpoints of the human athletic performance continuum, less is known about the application of sports genomics in more complex disciplines that do not exhibit specific phenotypes. Thus, the aim of the present study was to compare the allele and genotype frequencies of four known

polymorphisms in athletes from various mixed sports disciplines in order to investigate the genetic markers that are suitable for distinguishing the predominant components of these sports.

One of the rapidly developing areas of modern genetics is the development of molecular genetic approaches to determine a person's predisposition to various types of activity. So, in particular, in recent years, a search has been carried out for molecular genetic markers that determine a person's ability to perform high sports loads (Montgomery, 2000; Rogozkin, 2004), which is determined by the need to justify a system for selecting people for sports and correcting the training process. This approach is the most promising, since it allows you to determine the genetic predisposition to high physical activity and to carry out a targeted differentiated selection of children for sports at the earliest stages of their sports activity. It should be noted that in 2000 a human genetic map was created, in which genes were introduced, which in at least one study revealed associations with physical indicators and / or influenced human health (Rankinen, Bray et al, 2006). In an early 2000 version, the map included 29 genes. The 2005 version, 6th - amended, includes 165 autosomal genes, 5 - located on the X chromosome, as well as 17 mitochondrial genes. To date, work of this kind is being carried out only in five countries: the USA, Great Britain, Australia, Russia (Scientific Research Institute of Physical Culture - under the leadership of Doctor of Biological Sciences, Professor V.A. Rogozkin; laboratory of molecular genetic research of the Department of Genetics at the Bashkir State Pedagogical University - under the leadership of Doctor of Biological Sciences, Professor Gorbunova V.Yu.) and Kazakhstan. On the site 4 www.genoterra.ru - the register of leading scientific institutions, the laboratory of molecular genetic research of the Department of Genetics of BSPU is included in the list of groups engaged in the search for genetic markers that determine people's predisposition to sports activities.

A lot of data, including the results of recent studies, confirm the influence of polymorphism of some genes on the physical characteristics of an athlete and, as a consequence, on the predisposition of the athlete's body to strength loads or to endurance training. Its proclamation as a branch of knowledge took place at the Olympic Scientific Congress "Sport in Modern Society", which was held in Tbilisi in 1980. Also there was created the "International Scientific Society for Sports Genetics and Somatology."In 1983, Claude Bouchard first coined the term “genetics of fitness and physical performance”. Then he published two reviews in one issue of the journal "Exercise and Sport Science Reviews", where he presented generalizing facts, firstly, about individual differences in response to physical activity, and secondly, about the heritability of many qualities involved in the process of physical activity [3].1995 was marked by the beginning of the international project HERITAGE (HEalth, RIsk Factors, Exercise Training And GEnetics) led by Claude Bouchard. The project involved several research centers and more than 800 volunteers who were subjected to physical activity for several weeks. K. Bouchard and his colleagues searched for polymorphic loci associated with physical activity, and published hundreds of works on the topic of heritability of human physical factors. Progress in understanding this issue has been significant.It is necessary to take into account that the development and manifestation of the physical qualities of a person depends on both genetic and environmental factors. The more genetic factors influence physical qualities (high degree of heritability), the less successfully these qualities are trained, and vice versa [1].

Sports genetics allows you to calculate the limit for each person to perform any type of exercise, depending not only on the nature of the task, but also on the genetic components. The human genotype largely determines such important characteristics for athletes as strength, endurance, composition of muscle fibers and muscle mass, flexibility, neuromuscular coordination, and reaction speed [2]. Over the past few decades, certain hereditary factors have been identified that are responsible for the development of the above qualities in humans. Therefore, sports genetics provides useful information on how to improve the performance of performances, which athletes to select for competitions and which of them will be able to cope with the task at hand. The selection of young, promising in their hereditary qualities athletes (at the same time the minimum risk of intense physical activity for their health) is an important issue in sports medicine, which can be solved by modern methods of genetics. The introduction and active use of molecular genetic technologies

makes it possible to create an optimal training program specifically for each athlete, in which the body's energy resources will be used as efficiently as possible, which will allow achieving high sports results.

I would also like to note that in connection with the active development of genetics as a science and methods of its study, genetic research is becoming more and more accessible. At the moment, sports genetics is present not only in elite sports, but also in amateur sports. Fitness is an important part of a healthy lifestyle, and you should approach the issue of its correct organization responsibly. In this case, on the basis of genetic research, a geneticist can recommend a specific diet, diet, exercise regimen, as well as the nature of the exercises, taking into account the individual characteristics of the organism. In addition, sports genetics makes it possible to identify diseases to which a person is genetically predisposed (for example, cardiovascular diseases, bronchial asthma, obesity). Based on the data obtained, it is possible to recommend preventive measures to prevent these diseases for each individual person.

In 1998, the journal "Nature" published a scientific article "Human gene for physical performance" by a young British scientist Hugh Montgomery. He presented the results of his work with a team of authors (19 people) on the study of the role of the ACE gene (angiotensin converting enzyme) in sports activities. H. Montgomery and his colleagues investigated a group of alpine climbers [4]. The size of the article is just one page, which states that one of the polymorphic alleles of the ACE gene - allele I provides endurance, and allele D - the speed-strength qualities of an athlete. The conclusion was based on the fact that in athletes who are successful in sports requiring endurance, the frequency of allele I is higher than in the control group, and in athletes of high-speed types, allele D predominates [5].

This publication attracted the attention of the entire scientific community and society as a whole. The world media reported on the discovery of the "sport gene" (ACE gene), thanks to which it was now possible to identify a predisposition to a particular sport or physical activity in any person. Among domestic scientists, Eduard Georgievich Martirosov should be noted, who created on the basis of VNIIFK (All-Russian Scientific Research Institute of Physical Culture and Sports) in 1972 the Laboratory of Sports Anthropology (later called the Laboratory of Sports Anthropology, Morphology and Genetics) [6].

Later, research in the field of sports genetics was started in the laboratory of prenatal diagnostics of the Research Institute of Obstetrics and Gynecology. BEFORE. Ott (St. Petersburg), as well as in the laboratories of the Institute of Biochemistry. A.N. Bach of the Russian Academy of Sciences (Moscow), at the All-Russian Research Institute of Physical Culture (Moscow), Research Institute of Transplantology and Artificial Organs (Moscow) and the Russian State University of Physical Culture (Moscow) [7]. Now such laboratories are located not only in Moscow and St. Petersburg, but also in other large scientific centers in Russia. Sports genetics is developing quite rapidly, since the number of newly studied genes that characterize the physical qualities of a person is growing exponentially: in 1997 - 5 genes; in 2000 - 24 genes; B 2004 - 101 genes [8]. To date, about 200 genetic markers (DNA polymorphisms) associated with the development and manifestation of physical qualities are known [9].

In sports, to achieve the highest possible performance, talented athletes must be selected correctly and in a timely manner, and then included in long-term, planned training programs [10]. Today, due to the fact that investments in sports and individual athletes reach serious sums, the issue of effective selection of athletes is more relevant than ever [10]. Each of us is individual, we carry unique genetic information. And our uniqueness can be studied with the help of DNA diagnostics methods, which shows the characteristics of metabolism, the state of organ systems, the properties of the psyche. In sports genetics, molecular genetic methods such as PCR, real-time PCR, RFLP analysis, QTL mapping, NGS, NNGS, biochip technology, as well as cytogenetic (karyotyping, fluorescent in situ hybridization or FISH), genealogical and biochemical research methods.

It is impractical and irrational to perform DNA typing for all possible genes responsible for the athletic characteristics of a person. The information obtained must be correctly interpreted and

conclusions drawn in relation to each individual case. Moreover, the analysis of one gene is not sufficiently informative. Genetic analysis provides information about the hereditary predisposition to a particular sport. For example, skeletal muscle is made up of two distinct types of muscle fibers: fast and slow. Slow fibers are characterized by little force of contraction, but low fatigue, they are involved in the performance of low-intensity strength work for a long time. Fast fibers, on the other hand, are distinguished by greater force of contraction and high fatigue; they are used when performing short high-intensity strength work [11]. For muscles, which are dominated by slow fibers, aerobic exercise will be most effective. These sports include swimming, rowing, tennis, long-distance running, cycling, and walking. And for muscles, which are dominated by fast muscle fibers, anaerobic loads (strength training) are most effective. Wrestling, sprint running, powerlifting, arm wrestling, rock climbing are examples of physical activity based on anaerobic muscle metabolism.

The type of muscle fibers prevailing in our body is genetically determined (this is associated with the ACE gene polymorphism). Thus, the results of a distance runner (long-distance runner) in a 2000-meter run negatively correlate with his own results in a 100-meter run. When the type of physical activity matches the hereditary predisposition, the person can achieve the best results and get the most from the training in the shortest possible time. Recent studies have demonstrated the high effectiveness of diet and physical activity in correcting metabolic disorders. When lifestyle changes in individuals with early disorders of carbohydrate metabolism, the risk of type 2 diabetes mellitus (type 2 diabetes) decreases by 58%. However, it is also known that in a number of patients, diet and increased physical activity are ineffective and do not prevent the development of the disease. Today, a new approach to building a diet based on the individual characteristics of a person is proposed. The influence of nutritional components on gene expression is being studied by a new science - nutrigenomics. Nutrients can induce metabolic changes by affecting the activity of certain genes. In addition, the genetic variability of the food itself can have an impact on human health. Nutrients can affect the genome of the gut microbial flora, which also causes metabolic changes. Thus, the subject of nutrigenomics is the study of interactions between food genomes, the human genome, and the genomes of the gut microbiota. Changes in gene activity that occur during the growth and development of an organism are called epigenetic. Epigenetics studies changes in gene expression that occur without disrupting the nucleotide sequence of deoxyribonucleic acid (DNA). There are three mechanisms of epigenetic changes: DNA methylation, histone modification, and RNA interference (suppression of gene expression using small molecules of ribonucleic acid). It is assumed that dietary components can influence DNA methylation processes [13]. First, nutrients are essential for the provision and regulation of the synthesis of S-adenosylmethionine, a universal methyl donor. Second, they can influence the utilization of methyl groups through changes in the activity of DNA methyltransferase. The third possible mechanism is associated with the activation of DNA demethylation [12]. Currently, a large number of genes have been identified, the polymorphism of which is associated with the development of metabolic disorders. It turned out that food components can change the activity of these genes. Studies have been published that demonstrate interactions between a number of genes associated with obesity and type 2 diabetes and some foods. Variants of such interactions are presented below as examples. Fatty acid binding protein type 2 (FABP2) is an intracellular protein produced in enterocytes. It is involved in the transport and metabolism of long chains of fatty acids and can also maintain cellular homeostasis by acting as a lipid sensor.

The FABP2 gene is located on chromosome 4q28-q31. Polymorphism of this gene is associated with an increased risk of developing type 2 diabetes. This is because the protein it encodes is involved in the absorption of fatty acids and therefore can affect insulin sensitivity and glucose metabolism. Three genotypes are distinguished: normal, or the so-called wild type (Ala54 / Ala54), heterozygous (Ala54 / Thr54) and homozygous (Thr54 / Thr54). Heterozygous and especially homozygous Thr54 genotype is associated with the development of insulin resistance, type 2 diabetes, and, possibly, increased cardiovascular risks. A meta-analysis of 31 studies, which examined 13,451 people, demonstrated that a mutation in the FABP2 gene, namely the presence of the Thr54 allele, is associated with more pronounced insulin resistance, increased fasting plasma insulin levels and increased glycemic levels 2 hours after glucose loading [20]. It has been established that FABP2

expression may depend on adherence to a specific diet. D. de Luis et al. investigated the dynamics of body weight and a number of metabolic markers in response to a hypocaloric diet (1459 kcal / day) rich in polyunsaturated fats (22.7% of the total fat consumed per day) in obese individuals with FABP2 (Thr54) gene polymorphism ... The decrease in body mass index, body weight, and waist circumference was significantly more pronounced in the group with the Thr54 allele, compared with those with the wild type of the FABP2 gene allele. Moreover, only carriers of the Thr54 allele, while adhering to a diet enriched with polyunsaturated fats, showed a significant decrease in total cholesterol, low-density lipoprotein cholesterol, and insulin [21]. In another study, it was shown that people with obesity and FABP2 gene polymorphisms (Ala54 / Thr54 and Thr54 / Thr54) who followed a hypocaloric diet (1342 kcal) with a high content of monounsaturated fats (67.5%) did not have a significant change in biochemical markers , despite the improvement in anthropometric indicators. On the contrary, in the carriers of the wild allele for this gene, on the background of adherence to the proposed diet, in addition to the decrease in body weight, the levels of insulin, leptin, and insulin resistance significantly decreased [2, 4]. Thus, on the basis of nutrigenomic studies, it should be concluded that individuals with FABP2 gene polymorphism (Ala54 / Thr54 and Thr54 / Thr54) are shown a diet high in polyunsaturated fatty acids (about 20% of the total fat consumed per day). To do this, it is enough to introduce fatty fish into the diet (about 750 g per week) or regularly take fish oil. Peroxisome proliferator-activated receptors (PPARs) belong to the group of nucleus receptors. PPAR proteins are involved in reading the genetic code in many genes. They play a significant role in glucose and lipid homeostasis: they determine the need of muscle tissue for glucose and its sensitivity to insulin, regulate adipocyte differentiation and glucose homeostasis, bind lipid-lowering drugs and fatty acids, regulate the production of a number of adipokines, and participate in the regulation of bone metabolism. Natural ligands of PPAR are polyunsaturated fatty acids and prostaglandins [26]. There are three subgroups of these receptors: PPARα, PPARδ and PPARγ. The PPARγ isoform is synthesized in fat cells and is involved in their differentiation. In addition, this protein is a mediator of insulin resistance. PPARγ regulates the synthesis of adipokines in adipocytes: interleukin-6 (IL-6), tumor necrosis factor-α, plasminogen activator type 1 inhibitor. In an experiment on animals, it was proved that after a diet high in fat in mice, there is an increase in PPARγ-mRNA in adipose tissue [27]. Polymorphism of the PPARγ gene is characterized by the substitution of cytosine nucleotide for guanine, which leads to the substitution of the amino acid proline for alanine in the protein. In obese Caucasians, the PPARγ (Pro12Ala) gene polymorphism is associated with a lower risk of developing type 2 diabetes, and with the homozygous genotype (Ala12Ala), insulin sensitivity is even higher compared to the wild genotype [28]. It was found that the ratio of polyunsaturated to saturated fats in the diet can affect the concentration of blood lipids in carriers of the Ala12 allele of the PPARγ gene. In the RISCK study (Reading, Imperial, Surrey, Cambridge, King's), this effect was studied in 367 ethnic Europeans with an increased cardiometabolic risk. According to the results obtained, the concentrations of total cholesterol and triglycerides in carriers of the Ala12 allele of the PPARγ gene decreased with an increase in the ratio of polyunsaturated to saturated fats in the diet (from ≤0.33 to> 0.65) and did not depend on a decrease in saturated fat in the diet [9]. Therefore, carriers of the Ala12 allele of the PPARγ gene should eat foods with a high ratio of polyunsaturated to saturated fats to reduce triglycerides and total cholesterol levels.

In the regulation of metabolic processes, leptin (LEP), an adipokine, plays an essential role in regulating the body's fat reserves, namely, it controls the amount of food consumed and the expenditure of energy reserves. Leptin is produced by adipocytes in white adipose tissue, enters the bloodstream and transported to the brain, where it regulates the production of a number of neurotransmitters. On the one hand, a deficiency in leptin secretion leads to severe obesity. On the other hand, in overweight and obese individuals, leptin levels rise and so-called leptin resistance develops. It is known that the effect of leptin is not limited to adipose tissue; it also participates in the functioning of the reproductive system, mammary glands, immune system, intestines, kidneys, lungs, and skeletal bones [10]. The LEP gene is located on chromosome 7. Polymorphism of the LEP gene on chromosome 7 is associated with the replacement of adenine with guanine at position 2548 in the promoter. This leads to changes in leptin activity and affects the perception of satiety,

decreasing the central nervous system's control over appetite. LEP gene polymorphism can be associated with a decrease in leptin secretion and the development of obesity, and homozygous mutations of the LEP gene predispose to the development of obesity at an early age [11]. A relationship between the LEP A19G polymorphism and sugar cravings has been established [12]. The effects of leptin are due to interactions with its receptor. The leptin receptor gene polymorphism (LEPR) associated with the replacement of glutamine with arginine at position 223 alters the sensitivity of the receptor to leptin, can disrupt signal transduction, and contribute to the development of leptin resistance. The association of the LEPR gene polymorphism with the development of obesity has been confirmed in various ethnic groups [13, 14]. These disorders predispose to the development of obesity, accompanied by leptin resistance and hyperleptinemia. It turned out that a diet high and low in polyunsaturated fats affects the activity of polymorphic variants of the LEPR gene [15]. Polymorphism of the dopamine D2 receptor gene (DRD2) - TaqI A1 - is associated with various types of addictions (alcohol, cocaine, opioids). According to a number of researchers, mutations in this gene may be associated with eating disorders. C.L. Carpenter et al. showed that the combination of DRD2 and LEPR polymorphisms increases the risk of obesity [16].

The FTO gene is responsible for the amount of fat in the body and the propensity for obesity. It is expressed in the nuclei of the hypothalamus and islets of the pancreas. FTO gene polymorphism (AA rs-9939609) is associated with obesity, and according to the results of some studies, with type 2 diabetes. Patients with type 2 diabetes, who had this type of polymorphism, ate food rich in fat (more than 34% of daily calories; odds ratio (OR) 2.17, 95% confidence interval (CI) 1.02-4.63) and poor in fiber (less than 16 g / day; OR 2.42, 95% CI 1.05–5.57) [17]. In a study involving 7052 people with a high risk of cardiovascular complications, the presence of associative links between type 2 diabetes, gene polymorphism, and dietary habits was established [18]. In individuals not adhering to the Mediterranean diet, an association was found between the presence of the FTO gene polymorphism (rs-9939609) and type 2 diabetes: the relative risk of type 2 diabetes was 1.21 (95% CI 1.03–1.4). In contrast, there was no such relationship among those on the Mediterranean diet. A similar pattern persisted after standardization of the sample by body mass index. The same relationship took place in the presence of polymorphism in the melacortin-4 receptor gene. Therefore, adherence to the Mediterranean diet eliminates the negative effect of polymorphic alleles of the FTO gene (rs-9939609). IL-6 is an adipokine synthesized by both adipocytes and fibroblasts, endothelial cells, pericytes and immunocompetent cells. IL-6 production and, accordingly, its plasma level increase in obese individuals and in patients with type 2 diabetes. IL6 gene polymorphism is associated with an increased risk of obesity. One study showed that the addition of 750 ml of apple juice with a high content of polyphenols (802.5 mg) to the daily diet for 4 weeks reduced the volume of adipose tissue in individuals with the IL6 gene polymorphism (C / C), and in others variants of the alleles of this gene, no changes were observed [19]. Personalized diet means that nutrition is tailored to the individual needs of a particular person, depending on the stage of life, lifestyle and life situation in which the person finds himself. It is obvious that such an approach to building a diet can significantly increase the effectiveness of treatment and prevention of metabolic disorders. At present, recommendations on nutrition have been developed based on the presence of certain gene polymorphisms, and the spectrum of gene polymorphisms has been determined, which should be studied in persons with metabolic disorders or with a high risk of their development. However, more research is needed to study different dietary regimens when certain gene polymorphisms are found.

Conclusion. The genetic approach to the problem of selection of athletes will undoubtedly save you from performing ineffective work and ensure high rates of training for young athletes. With the help of genetic tests, it is possible to determine not only the predisposition to a particular sport, but also to identify possible health problems that can become a serious obstacle to sports victories.

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