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Relationship between sports gene polymorphism expression and physiological function of long-distance runners: A biomechanical analysis

Yu Dong, Shexiong Wang*, Tiantian Yin

College of Ministry of Sports, Wuhan Donghu University, Wuhan 430212, China

* **Corresponding author:** Shexiong Wang, 13307197879@163.com

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Abstract: This paper aims to explore the effect of the expression of sports gene polymorphisms related to long-distance running on the physiological functions of athletes, especially on the physical adaptability of marathon runners. With the progress of genetic research, more and more scholars are paying attention to the effect of sports genes on the physical fitness and cardiopulmonary endurance of athletes, but there is still a lack of research on marathon runners. Therefore, this study used amplified fragment length polymorphism (AFLP) technology, combined with phenotypic data, to analyze the differences in sports gene polymorphisms between long-distance runners and the general population, and explored the relationship between gene expression and physiological function. In this paper, the AFLP technique was used for analysis. The results showed that under the same other conditions, the average value of foot force test in Group X and Group Y was 75.6 kg and 46.9 kg, respectively, with standard deviation of 18.5 and 10.4. The *P* value was 0.026, less than 0.05, indicating a significant difference between the two groups. This may indicate that there was a correlation between the expression of sports gene polymorphism and the physiological function of long-distance runners, and the relationship between the two was always positive.

Keywords: long-distance runner; exercise gene; angiotensin converting enzyme; polymorphic expression; physiological function

1. Introduction

The physiological functions of long-distance runners are closely related to the expression of sports gene polymorphisms, and the genetic background of sports genes plays an important role in the physiological functions of long-distance runners. In recent years, with the deepening of genetic research, more and more studies have begun to focus on the relationship between sports genes and the physiological functions of long-distance runners. At present, most studies focus on the gene polymorphisms that improve physical fitness and cardiopulmonary endurance, while there are relatively few studies on the relationship between sports gene polymorphisms and physiological functions of marathon runners. China's long-distance running started late and has long been restricted by venues, equipment, and selection, resulting in insufficient reserves of long-distance running talents, affecting the competitiveness of long-distance running projects.

With the continuous deepening of genetic research, more and more scholars have begun to pay attention to the relationship between sports genes and the physiological functions of long-distance runners. The view that the physiological functions of long-distance runners are closely related to the polymorphic expression of their sports genes has been widely recognized.

At present, there are still relatively few studies on the specific association between sports gene polymorphisms and the physiological functions of long-distance runners, especially in long-distance running projects such as marathons. Therefore, the research in this paper has important theoretical and practical significance. By deeply analyzing the relationship between the expression of sports gene polymorphism and its physiological function in long-distance runners, this study aims to provide a scientific basis for the selection and training of long-distance runners, help athletes better realize their potential, improve their sports performance, and reduce the risk of sports injuries. In addition, this study is expected to provide new ideas and methods for researchers in related fields and promote the further development of sports genetics research.

The main contributions of this paper are as follows:

- 1) Exploration of the relationship between gene polymorphism and physiological function: This study deeply explored the impact of sports gene polymorphism related to long-distance running on the physiological function of athletes, filling the gap in the research between sports genes and the physiological adaptability of long-distance runners.
- 2) Combination of genetic testing and phenotypic data: By using AFLP technology and combining the phenotypic data of athletes, the correlation between gene polymorphism and physiological function was analyzed, providing empirical evidence for the relationship between genes and physiological functions.
- 3) Experimental proof of significant differences: The results showed that under the same other conditions, the differences in foot strength tests among athletes with different genomic types were statistically significant, indicating that there is a significant positive correlation between sports gene polymorphism and the physiological function of long-distance runners.

2. Related work

Today, with the rapid development of the world sports world, more and more sports begin to be valued by people. Among them, long-distance running, as a sport that can be participated in by the whole people, has been liked by most people and has been studied. The purpose of van Poppel Dennis's study was to review information on risk factors of lower limb running injury in short distance and long distance runners. Among short and long distance runners, he has identified several risk factors leading to lower limb injuries, but the quality of evidence of these risk factors related to running-related injuries was limited. Running injuries seem to have multiple origins in both short and long distance runners [1]. The dynamic of rest/load index usually depended on the technical level of athletes. The more successful athletes had a high level of sympathetic response and central circuit activity, and took the load of adjusting heart rate as the performance of functional reserve mobilization. Healthy and powerful load response ability and high-level mobilization ability were the most important parameters for the success of race training and competitive activities. Bakayev's study [2] evaluated the comprehensive evaluation of heart rate variability in short (5 min) and long (week) recordings. The results showed that compared with athletes trained at medium altitude, long-distance

runners trained in flat terrain were more suitable for sports conditions with higher pressure on the regulation system [2]. Kenneally's research [3] aimed to analyze the training intensity distribution (TID) of a group of seven world-class middle-distance runners in 50 weeks. Kenneally [3] analyzed training data, including training volume, intensity and frequency. The research results showed that in the training analysis of a group of world-class runners, different TIDs were displayed when the evaluation was related to race pace and physiological area [3]. However, the studies were all superficial analysis of some long-distance runners and lack of correlation research, so a scientific method was urgently needed for analysis and verification.

In recent years, with the deepening and development of genomics research, it was possible to use genetic variation to predict individual physiological functions. At present, many scholars have found the influence of some gene polymorphisms on sports through analysis and research. It was generally believed that the state of elite athletes was a multifactor phenotype, which depended on many environmental and genetic factors. The study of Balberova et al. [4] found that the identification of genetic biomarkers related to muscle system regulation can help neurologists, exercise doctors and coaches develop personalized strategies to select children, adolescents and young people for endurance, strength and speed sports (for example, short distance, medium distance or long distance running). This personalized approach would improve sports performance and reduce the risk of sports injury of musculoskeletal system [4]. There was a lot of information about the molecular and biological structure and function of aquaporin-1 (AQP1) gene and AQP1 channel. Regulating the flow of water through the cell membrane was essential to support the fluid balance between cells and within cells, which was essential for health and sports performance. Rivera Miguel A.'s research found that AQP1 gene and AQP1 channel seem to support steady-state mechanism, but they were not fully understood. These mechanisms helped to gain advantages in endurance exercise. AQP1 function was very important in the process of sports and had a profound impact on the performance of endurance running. AQP1s was an under-recognized structure that played an important role in cell homeostasis during resting state and endurance running exercise. It also provided support for the hypothesis statement and further research work of the possible influence of AQP1 gene and AQP1 channel on cardiopulmonary endurance performance [5]. The research showed the applicability of gene polymorphism in sports, which laid a solid foundation for analyzing the relationship between the expression of sports gene polymorphism and the physiological function of long-distance runners.

3. Construction of exercise gene and AFLP

3.1. Construction of sports gene

(1) Exercise gene.

At present, angiotensin-converting enzyme (ACE) is the most studied gene in the world. Renin-angiotensin system (RAS) can not only promote the proliferation of cardiac and vascular cells, but also promote the contraction of cardiac and vascular cells. ACE is its main enzyme. ACE plays a vital role in improving athletes' sports ability, enhancing myocardial contractility and improving athletes' oxygen transport

ability [6]. With the different expression of ACE gene, its effect on human body would also be different [7]. Therefore, whether there is correlation and difference between the frequency of ACE gene I/D (Insertion/deletion) polymorphism of ordinary long-distance runners and that of marathon long-distance runners, which provides a basis for scientific selection of Chinese long-distance runners [8,9].

(2) Definition of sports talent selection.

From the scientific nature of sports selection, sports selection can be divided into “scientific selection” and “experience selection”.

Experience selection refers to the selection of materials by coaches according to their own experience, through qualitative or quantitative indicators and using simple methods. The scientific selection of materials is compared with empirical materials. It is based on scientific theories and relatively advanced methods. Through certain inspections and tests, it achieves a high success rate. According to the timing and task of the selection, it can be divided into early athletes and excellent athletes.

The selection of early athletes refers to the preliminary screening of potential children from the early childhood stage, that is, from the overall observation and testing to the final long-term and systematic special training. The selection of excellent athletes refers to the selection of athletes with good talent and acquired quality for high-level training after certain basic and early special training.

(3) Genetic selection method.

Genetic selection has a high stability in sports selection, and has been paid more and more attention in modern sports selection. In recent years, in many studies, it can be found that athletes’ physical quality, body shape, physiological, biochemical indicators and other genetic factors would have a great impact on their performance. Genes have a great influence on the performance of athletes. Some data show that the higher the degree of heredity, the greater the impact on performance [10,11]. Its classification is shown in **Figure 1**:

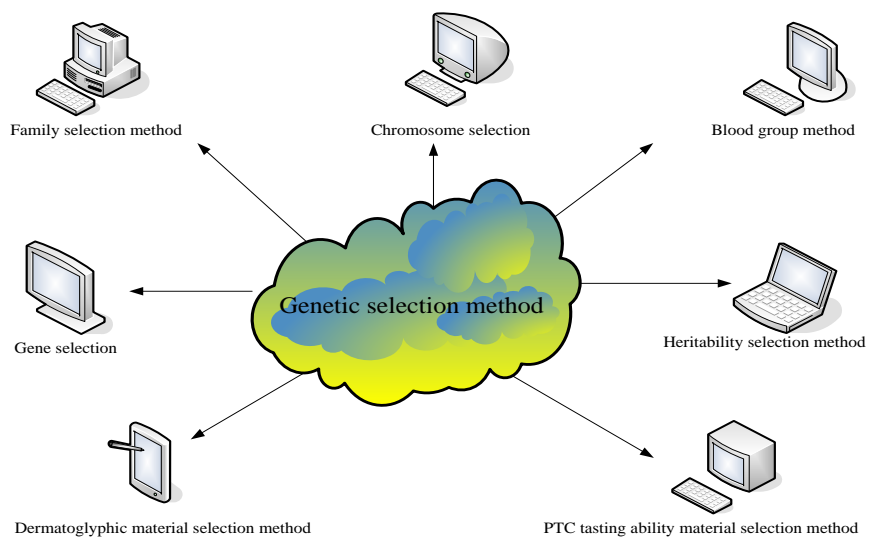


Figure 1. Classification of genetic selection methods.

3.2. Construction of AFLP technology

(1) Introduction of AFLP.

AFLP is a new DNA molecular marker technology developed on the basis of RFLP (Restriction fragment length polymorphism) and RAPD (Randomly amplified polymorphism) technology. Although AFLP technology has not been developed for a long time, it has made a great breakthrough in DNA molecular marker method and has become the most ideal and efficient molecular marker at present. It combines the reliability of restriction enzyme digestion with the high specificity under the more strict annealing conditions of polymerase chain reaction (PCR), and overcomes the complex and time-consuming defects of traditional RFLP technology. At the same time, it also solves the credibility problem caused by the non-specific amplification of RAPD technology. These advantages make it a powerful tool for current molecular systematics research. The analysis process of AFLP is shown in **Figure 2**:

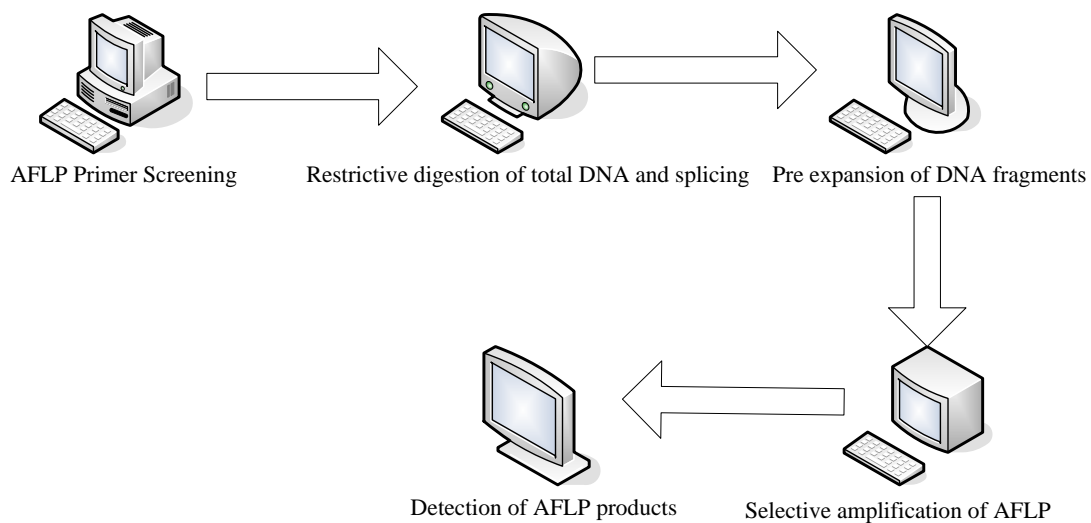


Figure 2. Analysis process of AFLP.

(2) AFLP data processing and analysis.

1) Molecular variance.

The molecular variance analysis (AMOVA, Analysis of Molecular Variance) in Arlequin software can be used to analyze the genetic diversity sources of physiological functions of long-distance runners [12,13].

2) Polymorphism meter.

$$\alpha = \frac{\beta}{\chi} \times 100\% \quad (1)$$

Among them, α is the proportion of multiple positions, β and χ represent the number of amplified polymorphic fragments and the total number of amplified fragments, respectively.

3) Nei index and Shannon index

By inputting the statistical results of 0/1 into Popgen software, the amplified primer Shannon polymorphism index O and Nei index J can be obtained, and the distribution of genetic variation among populations can be analyzed.

The genetic diversity of long-distance runners is calculated by Nei method, and the formula is:

$$J = \sum_{o=1}^m \left(1 - \sum_{o=1}^n p_o^2 \right) / m \quad (2)$$

p_o is the number of alleles at the o site, and m is the number of detected alleles. Calculate the total genetic diversity Ju in the population, and people can get:

$$Ju = \sum [1 - (q_o^2 + p_o^2)] / m \quad (3)$$

m is the total number of loci, q_o^2 and p_o^2 are the dominant and recessive frequencies of O loci in the total population.

Calculate the genetic diversity Fdu between populations, and the expression is:

$$Fdu = Ju - Jd \quad (4)$$

Jd is the genetic diversity within the population.

Calculate the gene differentiation Hdu between populations, and the expression is:

$$Hdu = Fdu / Ju \quad (5)$$

The expression of Shannon polymorphism index O is:

$$O = 1 - \sum q_o \quad (6)$$

Among them, the phenotype of q_o product bands.

4) Genetic similarity and genetic distance.

In this paper, popgen is used to calculate the genetic similarity D and genetic distance F between individual species and between various species.

$$D = \frac{2Mok}{Mo + Mk} \quad (7)$$

$$F = 1 - D \quad (8)$$

Mo and Mk are the total number of amplified bands owned by o and k individuals or populations respectively, and Mok is the number of bands shared by both.

5) Cluster analysis.

Through the calculation of the formulas and in combination with the popgen software, the cluster diagram of the genetic relationship between the expression of sports gene polymorphism and the physiological function of long-distance runners can be generated [14,15].

3.3. Introduction to ACE gene

(1) Polymorphism of ACE gene.

ACE is an important enzyme, namely angiotensin converting enzyme. The polymorphic marker sites of ACE gene can be divided into II homozygotes, ID heterozygotes and DD homozygotes.

(2) ACE distribution in vivo.

ACE is widely distributed in the human body. At present, it has been confirmed that the renin-angiotensin system exists in the heart, brain, lung, kidney, prostate, jejunum and ileum, adrenal gland, testicle, uterus and other tissues and organs of the human body. It has high content in heart, lung, kidney, jejunum and ileum, uterus and other tissues. The content of ACE in prostate, adrenal gland and testis is relatively low.

(3) The Mechanism of ACE Gene Affecting Exercise.

Different genotypes of ACE play different roles in sports mechanism. Now there are two views:

The first gene is type D. The expression of D allele in ACE gene is invisible. The D allele has high ACE activity, which can transform inactive angiotensin I into active angiotensin II, resulting in left ventricular hypertrophy during endurance and strength training. It can also promote the hypertrophy of myocardial cells, the production of collagen and connective tissue, and the contraction of myocardium. It makes the sympathetic nerve endings secrete norepinephrine, thus further improving the muscle contractility.

The second is the I allele. The I allele showed obvious advantages in ACE. The results showed that in type I alleles, the proportion of slow muscle was significantly higher than that of other genes, and the main role was to affect exercise through muscle efficiency, while the skeletal muscle of endurance athletes had a greater contractive function. The mechanism is as follows: ACE enzyme activity in the I allele decreases, CO content increases, mitochondrial respiratory function is enhanced, and muscle oxygen absorption is enhanced. By reducing the uncoupling protein of central muscle and skeletal muscle, it can enhance the contraction function of cardiac muscle and skeletal muscle, and increase the absorption of nutrients by muscle. It can also increase the aerobic capacity of the body and increase the endurance sports ability.

(4) Relationship between ACE gene polymorphism and physiological function of long-distance runners.

A large number of studies have shown that ACE gene has a significant correlation with the physiological function of long-distance runners. The results showed that the tissue and serum ACE activity of the carriers of I allele was lower than that of the normal population. They perform more frequently among long-distance runners and are more sensitive to sports. After the same physical exercise, their sports ability is significantly enhanced.

There is a close and complex relationship between gene expression and muscle cells. Genes produce specific proteins and other biomolecules through expression, which play a key role in the growth, development, contractile function and energy metabolism of muscle cells. At the same time, the state and demand of muscle cells will also feedback and regulate the expression of related genes, forming a dynamic balance, which jointly affects the performance and adaptability of muscles.

The relationship between gene expression and muscle cells is mainly reflected in the growth, differentiation and functional performance of muscle cells. Gene expression is the process of synthesizing genetic information from genes into functional gene products, and the products are usually proteins. These proteins play a vital role in muscle cells, such as regulating the size, shape and function of muscle

cells, and promoting the proliferation of muscle fibers and protein synthesis, making muscles stronger and more durable. In addition, gene expression also involves the synthesis of key proteins for muscle contraction, such as actin and myosin, which interact when nerve impulses arrive, causing muscle contraction.

As for force signal transduction pathways, in the broader signal transduction pathways, the signal transduction pathways of muscle cell proliferation include cell growth factor signaling pathways, cell cycle regulation pathways, etc. These pathways affect the proliferation and differentiation of muscle cells through a series of complex molecular mechanisms when responding to external growth factors, hormones and other signals. These signal transduction pathways are closely related to gene expression, because the regulatory mechanism of gene expression controls the synthesis and activity of key molecules in these pathways, thereby affecting the proliferation, differentiation and function of muscle cells. Therefore, gene expression and signal transduction pathways work together on muscle cells to maintain their normal physiological functions and adapt to changes in the external environment.

4. Experiment and association between ACE gene polymorphism and physiological function of long-distance runners

4.1. Objects and methods

(1) Research object.

In addition to being Han Chinese, having the same origin as athletes, being between 18 and 24 years old, having no history of professional training or family sports training, and passing the physical examination, the screening criteria for experimental subjects also need to be specified as follows [16]:

Excellent long-distance runners group (Group X): professional long-distance runners selected from Heilongjiang Province and Harbin City, half male and half female, with world-class or national-level athletes, covering excellent results in different events such as 5 km, 10 km and marathon.

General population control group (Group Y): College students with no sports training background selected from universities in Heilongjiang Province and Harbin City, 30 men and women each, to ensure consistency with the athlete group in terms of basic information such as region and ethnicity. Eliminate the influence of these factors on the experimental results.

Such screening criteria are designed to ensure that the experimental subjects have certain similarities in genetic background, living environment, etc., but also have significant differences in athletic ability, so as to more accurately explore the relationship between sports gene polymorphisms and the physiological functions of long-distance runners. Basic information as shown in **Table 1**:

Table 1. Basic information of excellent long-distance runners.

	Personal main item			Athlete level	
	5 km	10 km	Marathon	World-class	National level
Male	6	8	10	20	15
Female	14	12	10	10	15
Total	20	20	20	30	30

(2) Research methods.

1) Literature method.

The research on ACE gene, sports material selection, long-distance running and other aspects was carried out in Heilongjiang Provincial Library, Harbin Institute of Physical Education Library, Heilongjiang University of Traditional Chinese Medicine Library and other libraries.

2) Experimental method.

It includes DNA extraction, PCR amplification, PCR-ALFP research method, foot strength test and other related indicators.

3) Mathematical statistics.

The data in this paper were processed by the Windows software package of SPSS, and the results of selected subjects were analyzed by H-W (Hardy-Weinberg) test. In this paper, the alleles and genotypes among groups were analyzed by using the card method. This paper used SPSS average T test to test the results of foot force measurement. $P < 0.01$ indicated a very significant difference, $0.01 < P < 0.05$ indicated a significant difference, and $P > 0.05$ indicated no difference.

4.2. Treatment of experimental samples

The blood samples in the experiment were carried out by senior students in the early stage of the laboratory, while DNA was carried out by colleagues in the laboratory.

(1) Take blood.

5 mL of venous blood was extracted from each group for DNA extraction and DNA library construction. All blood samples are collected by professionals.

(2) DNA extraction.

In this paper, EDTA (Ethylene Diamine Tetraacetic Acid), heparin, citrate anticoagulant and other methods have no adverse effects on the subsequent DNA operation and PCR process. Anticoagulant samples can be stored at 2 °C–8 °C for 2 months, but DNA would gradually lose as the storage time goes on. In order to reduce the loss of DNA, people would carry out long-term storage. The storage method is –50 °C ultra-low temperature storage.

The raw materials required by the operators are as follows: 1.5 mL sterile micro-centrifuge tube (for 300 mL blood sample), Hardy-Weinberg balance test of 374.2 ACE gene I/D polymorphism frequency distribution.

4.3. Experimental results

In this paper, Hardy-Weinberg equilibrium test was used to statistically analyze the frequency distribution of ACE gene I/D polymorphism, and the results were

shown in **Table 2**:

Table 2. Chi-square test of genetic balance of ACE gene survey data.

	II	ID	DD	Total	Q2	Group X	Group Y
Observation number (O)	22	20	18	60			
Expected number (E)	20	24	16	60	1.85	2.63	2.15
$ O - E ^2/E$	0.2	0.67	0.25	11.2			

It can be seen from **Table 2** that the frequency distribution of ACE gene I/D polymorphism in all subjects reached genetic balance. Since the chi-square value of group X and group Y was greater than Q2, $P > 0.05$, the gene frequency distribution reached the genetic balance, indicating that the subjects selected in this paper were representative of the population.

The frequency distribution of ACE genotype and allele in 60 people in Group X and Y was studied in this paper. The results were shown in **Figures 3** and **4**:

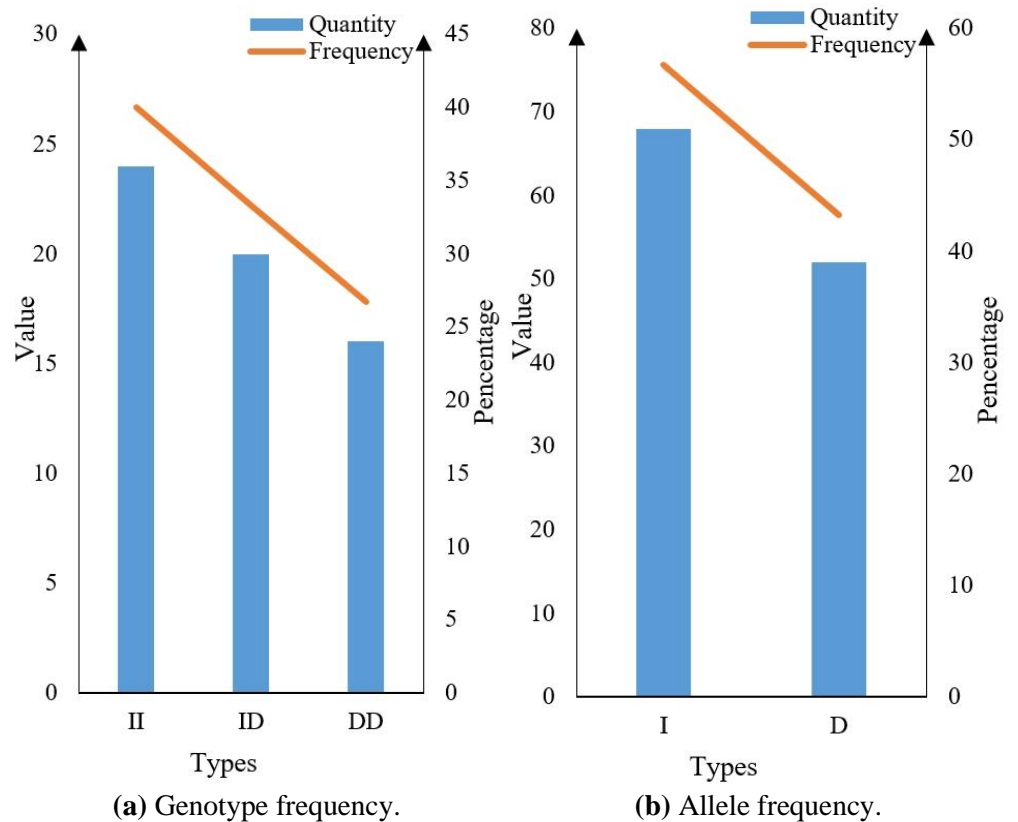


Figure 3. Distribution of ACE gene I/D polymorphism in Group X.

According to **Figure 3a**, there were 24 people of type II, accounting for 40%. There were 20 people of ID type, accounting for 33.3%, and 16 people of DD type, accounting for 26.7%. It can be seen from **Figure 3b** that the frequency of allele type I was 56.7% and that of allele type D was 43.3%. It can be seen from **Figure 3** that the distribution frequency of three ACE genotypes in Group X was type II > ID > DD. The frequency of allele I was significantly higher than that of allele D, which

indicated that there are more allele I than type D genes in athletes, and type I allele was the main characteristic of athletes.

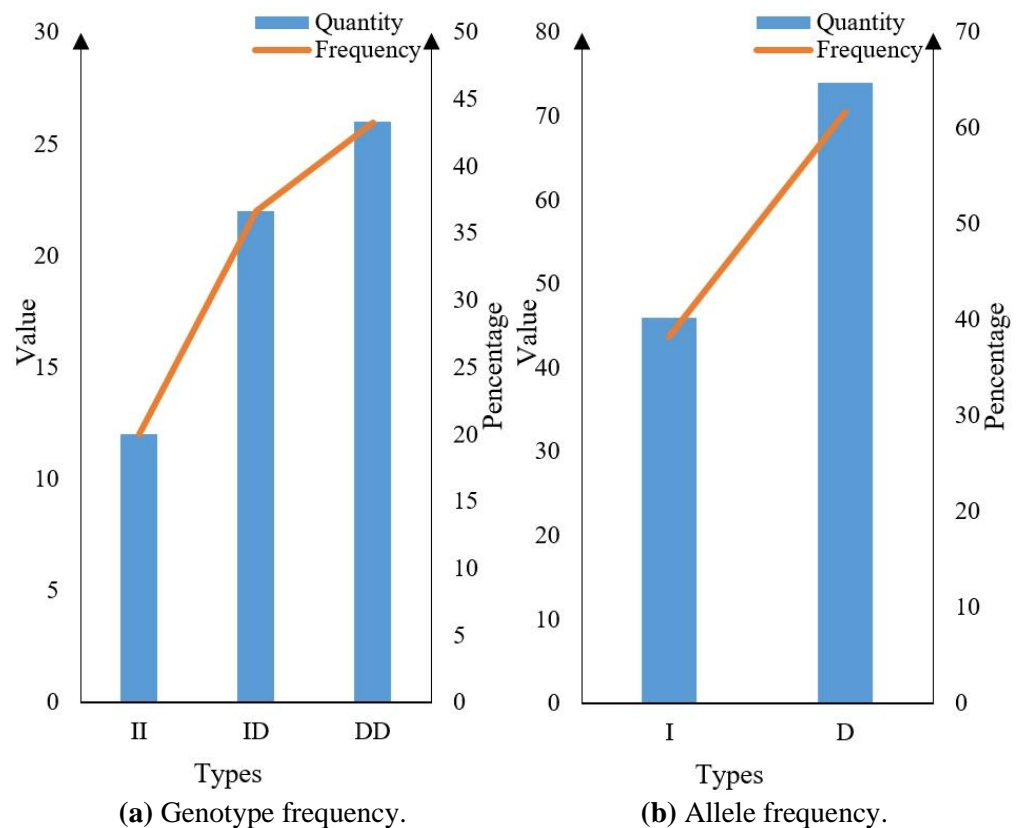


Figure 4. Distribution of ACE gene I/D polymorphism in group Y.

According to **Figure 4a**, there were 12 people of type II, accounting for 20%, and 22 people of type ID, accounting for 36.7%. There were 26 people with DD type, accounting for 43.3%. According to **Figure 4b**, the frequency of allele type I was 38.3%, and that of allele type D was 61.7%. It can be seen from **Figure 4** that the distribution frequency of three ACE genotypes in group Y showed an opposite trend compared with that in group X. The frequency of type I allele was much lower than that of type D allele. It showed that the I allele of group Y was smaller than the D allele, and the D allele was dominant in the general population.

4.4. T test of mean value of foot force in group X and group Y

(1) Endurance test methods and precautions.

It can turn on the power, press the “key”, and a flashing signal would appear on the screen. When the number is “0”, it would start to work.

The subjects’ feet are about 15 cm apart, standing on the chassis of the measuring instrument, and their arms and hands are extended in front of the same thigh. The tester contacts the handle of the back measuring instrument with the finger of the subject, and the distance between the handle of the back measuring instrument and the rack sensor is the zipper length of the measuring instrument. During the test, the subjects straightened their hands, palms facing inward, held the handle with both hands, extended their feet, straightened their upper body, and

stretched their legs as much as possible. Two tests were carried out in this paper. The maximum record was in kilogram without decimal point.

Matters needing attention:

- 1) Before the test, the subjects must be fully prepared.
- 2) During the test, subjects should not bend their elbows or knees.
- 3) Before each test, it should press the “key” to clear it and set it to 0.

(2) Analysis of two experimental results.

In order to further understand the correlation between the expression of sports gene polymorphism and the physiological function of long-distance runners, this paper made statistics on the comparison of the foot strength test between the athlete group and the control group, and the comparison of the average number of foot strength of each genotype between the athlete group and the control group. This paper also compared the genotype frequency of athletes with that of foot strength test and the genotype frequency of control group with that of foot strength test. The results were shown in **Figures 5 and 6**:

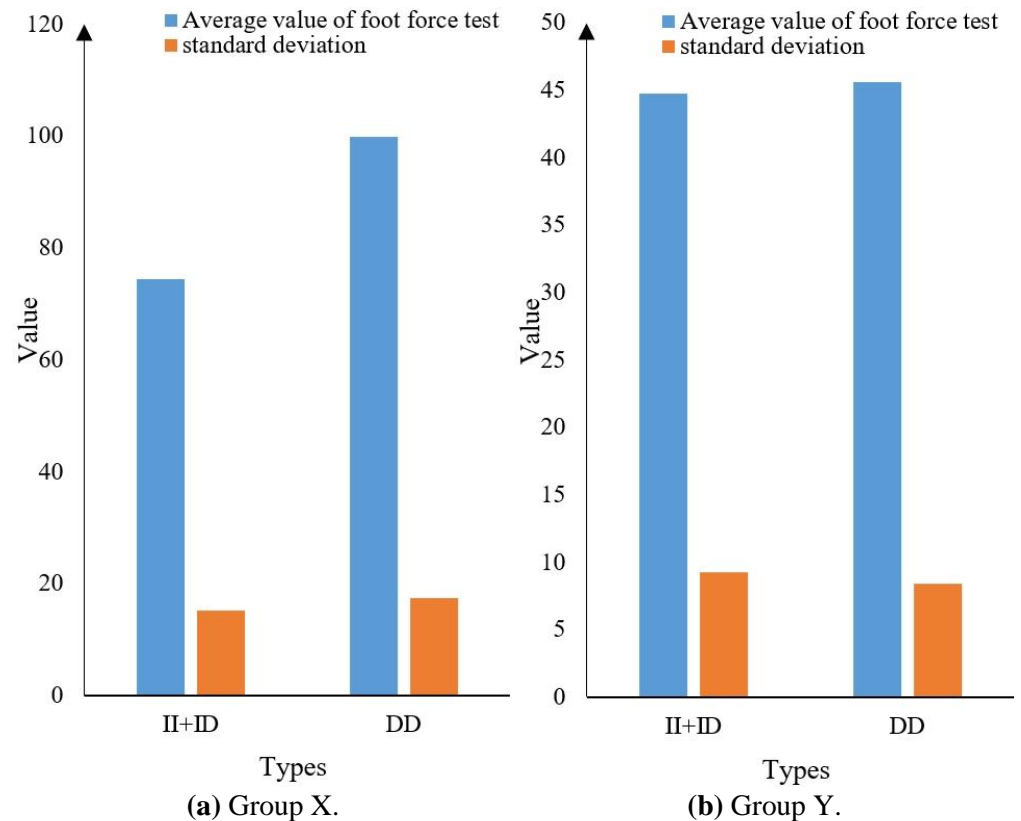
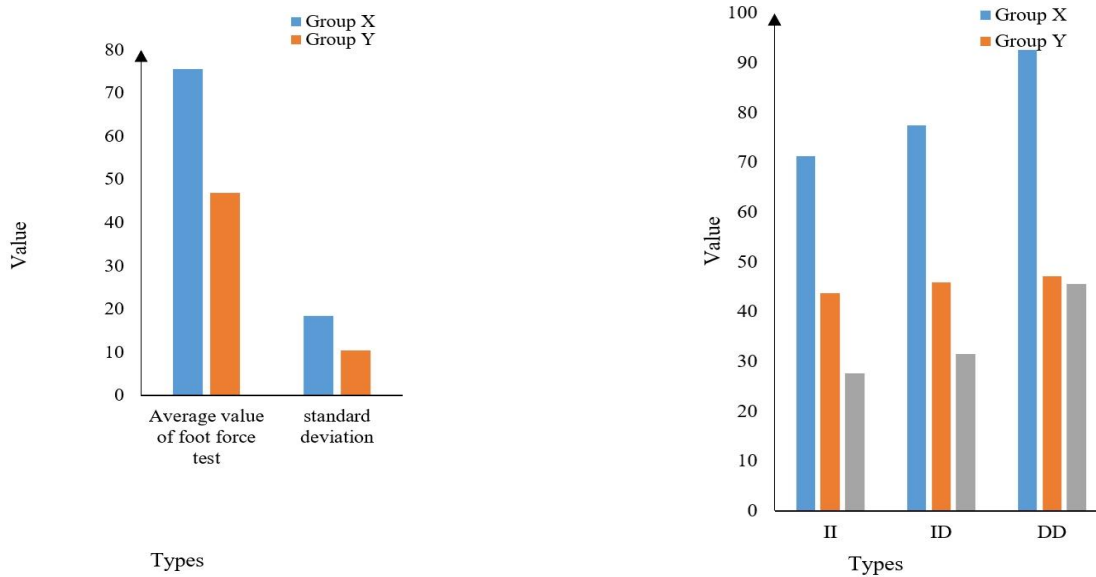


Figure 5. Comparison of genotype frequency and foot strength test between two groups.

It can be seen from **Figure 5a** that the average values of II + ID and DD genotypes in Group X were 74.4 kg and 99.9 kg, respectively, with standard deviation of 15.3 and 17.5. It can be seen from **Figure 5b** that the average values of II + ID and DD genotypes in Group Y were 44.8 g and 45.6 kg, respectively, with standard deviation of 9.3 and 8.4. The average values of genotype II + ID and DD in group X were significantly higher than those in group Y, indicating that the foot

strength of the elite long-distance runner group was greater than that of the general population.



(a) Comparison of foot force test between group X and group Y. (b) Comparison of average foot force of each genotype between group X and group Y.

Figure 6. Comparison of the two groups of foot strength tests and the comparison of the average foot strength of each genotype.

It can be seen from **Figure 6a** that the average value of foot force test in Group X and Group Y was 75.6 kg and 46.9 kg respectively, with standard deviation of 18.5 and 10.4 respectively. From **Figure 6b**, people can see that the average number of foot force of type II, ID and DD athletes in Group X was 71.3 kg, 77.5 kg and 92.7 kg respectively. The average foot strength of type II, ID and DD athletes in group Y was 43.7 kg, 45.9 kg and 47.1 kg respectively, with an increase of 27.6 kg, 31.6 kg and 45.6 kg respectively. It can be seen from **Figure 6** that the average number of foot strength of each genotype athlete group was different from that of the control group, and the growth range of the difference was also different. The DD genotype had the largest growth range.

The data in **Figures 5** and **6** can be tested by SPSS average *T* test, and the results were shown in **Figure 7**:

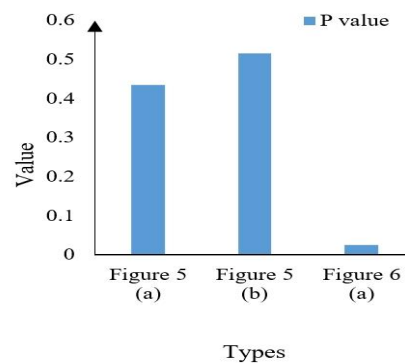


Figure 7. Group X and Y and their genotype frequency and *P* value of foot strength test.

It can be seen from **Figure 7** that the *T*-test *P* value of the II + ID and DD genotype foot force test in Group X was 0.435, which was significantly greater than 0.05. The *T*-test *P* value of II+ID and DD base type foot force test in group Y was 0.516, which was also significantly greater than 0.05. This may indicate that there was no significant difference between the two groups, and there was no significant difference in genotype between the two groups. The *T*-test *P* value of foot force test in Group X and Group Y was 0.026, which was far less than 0.05, indicating that there was a significant difference between the two groups. It shows the association between the expression of sports gene polymorphism and the physiological function of long-distance runners.

By detecting and comparatively analyzing genetic polymorphisms in elite long-distance runners and the general population, this article aims to reveal how specific genetic variations affect an individual's aerobic capacity, muscle endurance, and energy metabolism efficiency. These analyzes not only focus on variation at a single genetic locus, but also consider the interactions of multiple genetic loci to provide a more comprehensive understanding of the mechanisms by which genetic factors play a role in distance runner performance.

Furthermore, the experiment also explored the correlation between genetic polymorphisms and physiological indicators, such as maximum oxygen uptake, lactate threshold, and muscle enzyme activity. These physiological indicators are key parameters for measuring individual aerobic exercise capacity and muscular endurance, and are closely related to the competitive performance of long-distance runners. Through comparative analysis, significant correlations between some genetic polymorphisms and these physiological indicators were found, which provides important clues for understanding the physiological adaptation mechanism of long-distance runners. These findings not only help to deepen our understanding of the human body science of exercise, but may also provide scientific basis for future personalized exercise training and nutritional intervention strategies.

5. Conclusions

This study reveals the close relationship between specific gene variations and the physiological functions of long-distance runners through in-depth analysis of genetic polymorphisms in elite long-distance runners and controls in the general population. Research has found that certain genetic polymorphisms are significantly related to key physiological indicators such as maximum oxygen uptake, lactate threshold, and muscle enzyme activity of long-distance runners, providing a new perspective for understanding the physiological adaptation mechanism of long-distance runners. However, this study still has some limitations. The sample size is relatively limited, which may limit the generalizability and accuracy of the results; in addition, the possible impact of non-genetic factors such as environment and nutrition on athlete performance was not considered. Future research should further expand the sample size and include more genetic loci and environmental factors for comprehensive analysis to more comprehensively analyze the genetic basis of long-distance runners. At the same time, exploring the relationship between genetic polymorphisms and training response will provide scientific basis for the

development of personalized training plans and nutritional intervention strategies, and promote the sustainable development of the field of sports human science.

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