Genetic predisposition and its effect on performance in outdoor activities

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Abstract

Presented article is focused on the possibilities of genetic predispositions affecting sport performance and its use in selecting of talents for specific sports. Attention is paid to the specific genes which are involved in the level of speed-strength or endurance abilities applied in outdoor activities such as mountain climbing, skiing, canoeing etc. Genetic motion preconditions are in the article represented by presence of polymorphisms R577X ACTN3 gene, I / D ACE gene and C / G gene PPARα. ACTN3 gene and its R allele was the only one associated merely with speed-strength preconditions. At PPARα and ACE gene was found assumption, according to present allele, for connection to both speed-strength and the endurance abilities. The main contributor to exert influence of gene is the presence of alleles found in the aforementioned genes.

Key words:
polymorphism, sport performance, gene, speed-strength abilities, endurance abilities, predispositions.

Souhrn

Předkládaný článek je zaměřený na možnosti genetických predispozic ovlivňujících sportovní výkon a jejich využití při výběru talentů pro konkrétní sportovní odvětví. Pozornost je věnovaná konkrétním genům podílejících se na úrovni rychlostně-silových nebo vytrvalostních schopností. Genetická podmíněnost pohybových předpokladů je v článku zastoupena přítomností polymorfismů R577X genu ACTN3, I/D genu ACE a C/G genu PPARα. Gen ACTN3 a jeho alela R byla jako jediná spojena pouze s rychlostně silovými předpoklady. U genů PPARα a ACE byl nalezen předpoklad, dle přítomné alely, pro spojení jak s rychlostně silovými, tak s vytrvalostními schopnostmi. Hlavní podíl na uplatnění vlivu genu má přítomnost alel výše zmíněných genů.

Klíčová slova:
polymorfismus, sportovní výkon, gen, rychlostně-silové schopnosti, vytrvalostní schopnosti, predispozice.

Introduction

The accelerating trend, new scientific approaches, new technologies and specialized sports institutions show that sports practice and sports performance are by its nature interdisciplinary matter with new possibilities of data processing (Dovalil et al., 2009). Development of high performance athletes affect not only environmental factors such as training, nutrition and the environment he lives in but also genetic potential that influence every athlete since birth. Elite sports performance is a phenotype of physical capability determined by genetic potential (MacArthur & North, 2005). Thus the biological base of physical capability always develops in genetically determined range of assumptions, ie. that the extent of plasticity properties of cells, tissues, organs or their systems, as well as the regulatory mechanisms involved in the determination of

their properties (such as composition, metabolism and functions) is defined genetically. Phenotype of an individual, which might have a genetic base for endurance capabilities used on long running trails, muscle strength needed for climbing and downhill skiing, physiological possibilities to repeat series in high intensity or ability tendons and ligaments to withstand damage, provides us with information relevant to the selection of specific sport (Lippi, Longo, & Maffuli, 2010). Physical abilities are not hereditary in definitive form, but only certain disposition / abilities for relevant feature are transmitted and these dispositions /abilities are encoded in the genes and it depends essentially only on chance or parent estimation whether will be used for the appropriate sports activity or specific sport. Skeletal muscle is an organ that reacts on external stimuli and changes very sensitively and at the same time it

is an example of unity and structure of body. Initial stage of tissue differentiation and thus the skeletal muscles, but also degree of individual maximum, are encoded within the genotype of cells.

Current scientific findings show that genetic information in the form of several genotypes is an integral part affecting sport level of every athlete and therefore it is necessary to take account of new researches in molecular genetics and integrate them into methods used for the prediction of motional abilities (Měkota & Novosad, 2005).

Grasgruber and Cacek (2008) reported that muscle protein composition, blood supply to the heart and lungs, as well as the activity of key enzymes involved in energy production are significantly genetically influenced ingredients of sports performance. Effect of genetic factors is considered to be stronger in early childhood, because environmental effects are not yet fully applied and therefore measure of genetic determination has a considerable importance in the selection of sports talents and sports activities. According to the existing findings, best athletes of different specializations have different fibers composition (Dovalil et al., 2009). Effect of genetics for a particular physical performance is estimated around 40-50%. For anaerobic performance, in the form of short-term anaerobic action in 10s, is estimated higher than 50% (Bouchard, Malina, & Pérusse, 1997). Měkota and Novosad (2005) reported that mostly is genetically determined maximum anaerobic and lactate performance, which is crucial for the implementation of speed-strength movements. Lippi et al. (2010) reported that genetic testing in sports could allow identification of individuals with optimal physiology and morphology, as well as individuals with higher ability to react and assimilate to practice, thereby reduce the chance of injury.

Currently used detailed analysis of physiological parameters basically represents the integrated measurement of the effects of multiple genes and environmental influences on the phenotype, while genetic tests examine only isolated individual determinants. There may be situations in which genetic testing can provide invaluable information about the genes influencing performance using physiological way that is badly characterized, or it is difficult to measure it directly, whose physiological tests are only weakly predictable for performance in adulthood (MacArthur & North, 2005).

Genetic determination

Genetic predispositions or assumptions for sports performance are sets of genes built within the DNA molecule, which are involved in formation of features, functions or morphology of cellular tissues. These features, morphology or function are usually encoded by several genes and simultaneously can have several different forms, several polymorphisms and, thus, several different phenotypic manners. Information encoded in DNA is determined by order of the nucleotides (A, C, G, T) in the chain, in other words, sequence which forms the respective gene (Alberts, 1998). Genes contain instructions in form of a linear nucleotides order for the proteins production whose features are determined by their three-dimensional structure and they are responsible for their biological function. Most of the genes is made up by relatively short DNA segments that encode individual proteins and larger segments of NOT coding DNA, so called regulatory regions. Encoding genes, so called exons that encode individual proteins constitute only 3% of the human genome, remaining 97% of NOT coding DNA are called introns which have unknown or unspecified function (Ganong, 2005). The genotype of an individual is a set of alleles that form genetic makeup in loci of chromosomes and the allele is one of alternative versions of the gene which may occur in a given locus. If in the population were at least two relatively common alleles for a given locus, we could say that the locus evinces polymorphism or literally „many forms". Gene is a unit of heredity. It is a sequence of chromosomal DNA necessary for the production of a functional product (Nussbaum, 2004). Right these polymorphisms, or small changes in the DNA structure are responsible for different phenotypic variants such as height of athlete, muscle mass, strength, sports position etc. Most common types of DNA sequences are SNP (single-nucleotide) polymorphisms and insertion or loss (insertion/deletions) thus, I/D polymorphisms. Phenotypic manifestations, such as muscle strength, speed and endurance are generally polygenic it means that observed phenotype is being influenced by many genetic factors. Heritability was strongly proved in speed-strength abilities (Ahmetov et al., 2012). Most studied are genetic effects on cardio-respiratory functions and skeletal muscles, which are very important for performance in many sports. Connection of genotype with motion testing is difficult according to motor skills which can be affected by training. To date, more than 20 genetic variants were associated with the phenotype of sports performance, whereas the most studied genotypic variants are ACE, ACTN3 and PPARα.

Polymorphism ACE I/D
(Angiotensin-I-Converting Enzyme)

Polymorphism ACE I / D is one of the most studied genetic variant affecting sports performance. ACE gene has two alleles differing by presence (insertion, an allele I) or absence (deletion, an allele D) of 287-bp Alu recurrent element in intron 16 (MacArthur & North, 2005). Circulating angiotensin I-converting enzyme shows a tonic regulatory function in circulatory homeostasis through vasoconstrictor synthesis of angiotensin II, Circulating angiotensin I-converting enzyme shows a tonic regulatory function in circulatory homeostasis through the synthesis of vasoconstrictor angiotensin II, which control the aldosterone synthesis and degradation of vasodilatory kinins. I allele is associated with a lower tissue activity than allele D (Ahmetov, 2012b). ACE I/D polymorphism may also affect athletic performance by local effects on the skeletal level. I allele was associated with significantly greater modifications in muscle resistance and efficiency of muscle contraction in response to training and with the increased number of muscle fibers type I („slow") in m. vastus lateralis at untrained individuals. In contrast, D allele was associated with larger increases of strength m. quadriceps femoris in response to nine weeks isometric strength training program (MacArthur & North, 2005). Jones and Woods (2003) suggest that the I allele supports resistance by increasing of the efficiency of skeletal muscle, partly probably due to effect on the composition of the types of muscle fibers, while the D allele may increase the speed activity via increasing of muscle strength.

It was proved that ACE D allele is associated with high serum and tissue ACE activity, hypertension, type 2 diabetes, obesity, coronary artery disease and myocardial infarction. Excess ACE I allele was detected at endurance athletes compared with controls in several studies and this fact indicates that the ACE I allele is favorable for aerobic performance (Ahmetov, 2012b).

The first study that showed an increased frequency of allele I was conducted at 25 British alpine climbers compared to controls. Afterwards similar results were reported at 64 endurance Australian rowers compared with healthy controls. Conversely, increased D allele was detected at 35 elite swimmers for short distances (less than 400m). Which suggests that ACE I allele and the ACE D polymorphism ACE I / D have differing effect on athletic performance. Athletes with allele I prefer endurance load and athletes with allele D tend to shorter sprint disciplines (MacArthur & North, 2005). In study of elite rowers (n = 107), the frequency of ACE II genotype was significantly higher than the frequency in the control group (Ahmetov, 2007). Several studies have shown that the D allele may be related to greater strength and muscle bulk and I allele was rather associated with endurance athletes. Another relation was found between the D allele and left ventricular growth in response to exercise. Significant association was found in several studies where individuals were put in intentional physical training. The association apparently does not occur at untrained healthy individuals. This implies an indication of any effect of the ACE genotype on cardiacal function involving an interaction between the genotype and training (MacArthur & North, 2005).

Polymorphism ACTN3 R577X (α-actinin-3)

α-actinin is omnipresent conserved cytoskeletal protein that transversely binds actin filaments and occurs in skeletal, cardiac and smooth muscle cells. It is located in Z-disc and in bodies of similar density, wherein it is forming a structure similar to a grid and it stabilizes the muscle contractile apparatus. Furthermore α-actinin is also associated with lots of cytoskeletal and signaling molecules, cytoplasmic spheres trans-membrane receptors and ion channels thereby it reflects important structural and regulatory role in cytoskeletal organization and muscle contraction. In family of α-actin proteins can be found encoded α-actin forming at least six different protein products, which can be divided into muscular and non-muscular cytoskeletal isoforms (Sjöblom, Salmazo, & Djinović-Carugo, 2008). Due to the above mentioned issue we are interested only in muscular α-actinin namely α-actinin-2 and α-actinin-3 α-actinin-2 is the major isoform in cardiac and skeletal oxidative muscle fibers and α-actinin-3 is manifested predominantly in glykolitic skeletal muscle and is responsible for creating of force at high speeds. Thus, there are two genes in humans that decode skeletally-muscular α-actinin: ACTN2, which manifests itself in all fibers and ACTN3, which is restricted to fast muscle fibers. This indicates that the presence of α-actinin-3 has a positive effect on the function of skeletal muscle during creation of power contraction at high speeds thereby provides an evolutionary advantage thanks to increased sprint performance (Yang et al., 2003).

α-actinin-3 is probably the most interesting version for our topic from the sports point of view,

because it is essentially most specialized member of α-actinin whose manifestations are usually reserved for fast glycolytic fibers of skeletal muscle (MacArthur & North, 2004). Common genetic variation in the ACTN3 gene, which was identified, leads to replacement of arginine stop-codon in amino acid 577. Therefore, we can speak about the X allele which contains sequential change completely inhibiting the production of functional protein α-actinin-3-(Ahmetov et al. 2012). Complete lack of α-actinin-3 homozygotes (ACTN3 577XX) does not result in phenotypic disease, suggesting that related sarcomeric isoforms of α-actinin-2 may compensate for the absence of α-actinin-3 (MacArthur & North, 2004).

Several case studies reported that ACTN3 XX RR genotype is over-represented or ACTN3 XX is underrepresented at athletes focused on speed--power activity compared with controls. For example, in a study of elite rowers, the frequency of ACTN3 XX genotype, allele unfavorable for the development of power and speed, twice lower in the control group (Ahmetov, 2008). Although there were contradictory results, so the hypothesis that the ACTN3 XX R allele may confer some advantage in speed-power sports was supported by several studies (Ahmetov et al., 2012). Ahmetov et al. (2012b) further states that the study was conducted, in which the number of muscle fibers in the cross section of vastus lateralis was compared (determined immunochemically) with the type of polymorphism. It was shown that the number of IIX fibers and area was higher than at genotype RR than at genotype XX, suggesting that bearers of ACTN3 XX genotype exhibit a higher proportion of slow muscle fibers.

Polymorphism PPARα intron 7 C/G (Peroxizom proliferation-activating receptor α)

Receptor type α (PPARα) activated by peroxisome proliferator is a ligand activated by transcription factor that regulates the expression of genes participating in fatty acid absorption and oxidation, glucose metabolism and lipid metabolism, growth of left ventricle and weight control (Ahmetov, 2012). Endurance training increases the use of non-plasma fatty acids and may increase oxidative capacity of skeletal muscle by regulation of gene expression PPARα. PPARα expression level is higher in muscle fibers type I than type II muscle fibers. Ahmetov (2012b) reported that the growth of the left ventricle after induced exercise in heal-

thy young men were strongly associated with the intron 7 polymorphism C/G (rs 4253778) gene PPARα. Individual C homozygotes had a three times higher and heterozygotes had a double increase of the left ventricle volume than homozygotes with the G allele. Furthermore, it was shown that PPARα C allele is related to type diabetes 2 and atherosclerosis.

Ahmetov study (2012) found that PPARα C allele is overrepresented in Russian power- oriented athletes and this allele is associated with an increase in the proportion of fast muscle fibers in m. vastus lateralis at physically active healthy men. Eynon et al. (2010) adds that the allele C in C/G polymorphism of PPARα gene is associated with higher level of plasma lipids, with increasing volume of the heart and increased risk of coronary artery disease. It also states that the level of expression PPARα is higher in muscle fibers type I than type II, where the homozygotes of allele G PPARαC/G polymorphism have significantly higher proportion of slow muscle fibers. Recent studies have shown that frequency of PPARα GG genotype was significantly higher in Russian endurance-oriented athletes, elite Israeli endurance athletes and Polish elite rowers than in controls or sprinters. In subjects with GG PPARα genotype was the percentage of muscle fibers type I higher than in the homozygotes with genotype CC (Ahmetov, 2012b).

Other possible genotypic variants associated with sports performance

Other significant but less-studied polymorphisms are HIF1A Pro582Ser (gene for factor 1α induced by hypoxia), CNTF A / G (ciliary neurotrophic factor), CKM A / G (gene for muscle isoform creatine kinase) or VDR Fok1 f / F (gene for the vitamin D receptor), and many others.

Conclusion

Area of sport science nowadays involves a large number of biological and environmental factors that influence and determine sports performance in any sport. Findings from this area may be used as an aid in talent identification and in preparation of training programs that maximize individual potential and minimize the possibility of injury. Using genetic variants that strongly affect sports performance, along with the existing battery of physiological, biochemical and psychological tests, we can support selection and direction of young people interested in sport. By exploring some of the rules from genetics and effects of gene action

on sports performance, but also speed of fitness or regeneration, coaches can design effective training plans, methods for recovery or suitability of compensatory exercises. From above stated data about described genes it is obvious that genes affecting sports performance may have an influence on other physiological processes, which can represent a connection with the emergence of certain diseases and thus affect health of individual.

Genetic variants of genes ACE, ACTN3 and PPARα described in the article are just a little piece of genes involved in sports performance of climbing, canoeing or other outdoor sport. Certainly it does not serve to advance eliminate people with „unfavorable" genotype from sports teams. On the contrary, obtained information about genetic dispositions could serve to recognize boundaries of individuals and help them choose a career that is not stressful, but make their lives happier (Havelkova, 2007). Another interesting field of genetics is nutritional genomics, where common food starts or modulates transcription of target genes or directly affects changes of chromatin structure and thus provides another opportunity to create specific training plans, regeneration methods or recuperative therapy (Bouchard, Perusse, & Malina, 1997).

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