

Genome-Wide Association Study Reveals a Novel Association Between MYBPC3 Gene Polymorphism, Endurance Athlete Status, Aerobic Capacity and Steroid Metabolism

Al-Khelaifi F., Yousri N.A., Diboun I., Semenova E.A., Kostryukova E.S., Kulemin N.A., Borisov O.V., Andryushchenko L.B., Larin A.K., Generozov E.V., Miyamoto-Mikami E., Murakami H., Zempo H., Miyachi M., Takaragawa M., Kumagai H., Naito H., Fuku N., Abraham D., Hingorani A., Donati F., Botrè F., Georgakopoulos C., Suhre K., Ahmetov I.I., Albagha O., Elrayess M.A.
Kazan Federal University, 420008, Kremlevskaya 18, Kazan, Russia

Abstract

© Copyright © 2020 Al-Khelaifi, Yousri, Diboun, Semenova, Kostryukova, Kulemin, Borisov, Andryushchenko, Larin, Generozov, Miyamoto-Mikami, Murakami, Zempo, Miyachi, Takaragawa, Kumagai, Naito, Fuku, Abraham, Hingorani, Donati, Botrè, Georgakopoulos, Suhre, Ahmetov, Albagha and Elrayess. Background: The genetic predisposition to elite athletic performance has been a controversial subject due to the underpowered studies and the small effect size of identified genetic variants. The aims of this study were to investigate the association of common single-nucleotide polymorphisms (SNPs) with endurance athlete status in a large cohort of elite European athletes using GWAS approach, followed by replication studies in Russian and Japanese elite athletes and functional validation using metabolomics analysis. Results: The association of 476,728 SNPs of Illumina DrugCore Gene chip and endurance athlete status was investigated in 796 European international-level athletes (645 males, 151 females) by comparing allelic frequencies between athletes specialized in sports with high ($n = 662$) and low/moderate ($n = 134$) aerobic component. Replication of results was performed by comparing the frequencies of the most significant SNPs between 242 and 168 elite Russian high and low/moderate aerobic athletes, respectively, and between 60 elite Japanese endurance athletes and 406 controls. A meta-analysis has identified rs1052373 (GG homozygotes) in Myosin Binding Protein (MYBPC3; implicated in cardiac hypertrophic myopathy) gene to be associated with endurance athlete status ($P = 1.43 \times 10^{-8}$, odd ratio 2.2). Homozygotes carriers of rs1052373 G allele in Russian athletes had significantly greater $VO_2\max$ than carriers of the AA + AG ($P = 0.005$). Subsequent metabolomics analysis revealed several amino acids and lipids associated with rs1052373 G allele (1.82×10^{-05}) including the testosterone precursor androstenediol (3beta,17beta) disulfate. Conclusions: This is the first report of genome-wide significant SNP and related metabolites associated with elite athlete status. Further investigations of the functional relevance of the identified SNPs and metabolites in relation to enhanced athletic performance are warranted.

<http://dx.doi.org/10.3389/fgene.2020.00595>

Keywords

elite athletes, endurance, GWAS, metabolites, metabolomics, SNP

References

- [1] Al-Khelaifi F., Diboun I., Donati F., Botre F., Abraham D., Hingorani A., et al. (2019b). Metabolic GWAS of elite athletes reveals novel genetically-influenced metabolites associated with athletic performance. *Sci. Rep.* 9:19889.
- [2] Al-Khelaifi F., Diboun I., Donati F., Botre F., Alsayrafi M., Georgakopoulos C., et al. (2018). A pilot study comparing the metabolic profiles of elite-level athletes from different sporting disciplines. *Sports Med. Open* 4:2.
- [3] Al-Khelaifi F., Donati F., Botre F., Latiff A., Abraham D., Hingorani A., et al. (2019a). Metabolic profiling of elite athletes with different cardiovascular demand. *Scand. J. Med. Sci. Sports* 29 933-943.
- [4] Ahmetov I. I., Fedotovskaya O. N., (2015). Current progress in sports genomics. *Adv. Clin. Chem.* 70 247-314. 10.1016/bs.acc.2015.03.003 26231489
- [5] Ahmetov I., Kulemin N., Popov D., Naumov V., Akimov E., Bravy Y., et al. (2015). Genome-wide association study identifies three novel genetic markers associated with elite endurance performance. *Biol. Sport* 32 3-9. 10.5604/20831862.1124568 25729143
- [6] Bergh U., Ekblom B., Astrand P. O., (2000). Maximal oxygen uptake "classical" versus "contemporary" viewpoints. *Med. Sci. Sports Exerc.* 32 85-88.
- [7] Bouchard C., Tremblay A., Despres J. P., Theriault G., Nadeau A., Lupien P. J., et al. (1994). The response to exercise with constant energy intake in identical twins. *Obes Res.* 2 400-410. 10.1002/j.1550-8528.1994.tb00087.x 16358397
- [8] Bouchard C., Daw E. W., Rice T., Perusse L., Gagnon J., Province M. A., et al. (1998). Familial resemblance for VO₂max in the sedentary state: the HERITAGE family study. *Med. Sci. Sports Exerc.* 30 252-258. 10.1097/00005768-199802000-00013 9502354
- [9] Bouchard C., An P., Rice T., Skinner J. S., Wilmore J. H., Gagnon J., et al. (1999). Familial aggregation of VO₂max response to exercise training: results from the HERITAGE Family Study. *J. Appl. Physiol.* 87 1003-1008. 10.1152/jappl.1999.87.3.1003 10484570
- [10] Bouchard C., Sarzynski M. A., Rice T. K., Kraus W. E., Church T. S., Sung Y. J., et al. (2011). Genomic predictors of the maximal O₂ uptake response to standardized exercise training programs. *J. Appl. Physiol.* 110 1160-1170. 10.1152/jappphysiol.00973.2010 21183627
- [11] Carrier L., Mearini G., Stathopoulou K., Cuello F., (2015). Cardiac myosin-binding protein C (MYBPC3) in cardiac pathophysiology. *Gene.* 573 188-197. 10.1016/j.gene.2015.09.008 26358504
- [12] Cummins C. L., Volle D. H., Zhang Y., McDonald J. G., Sion B., Lefrancois-Martinez A. M., et al. (2006). Liver X receptors regulate adrenal cholesterol balance. *J. Clin. Investigat.* 116 1902-1912. 10.1172/jci28400 16823488
- [13] Evans A. M., DeHaven C. D., Barrett T., Mitchell M., Milgram E., (2009). Integrated, nontargeted ultrahigh performance liquid chromatography/electrospray ionization tandem mass spectrometry platform for the identification and relative quantification of the small-molecule complement of biological systems. *Anal. Chem.* 81 6656-6667. 10.1021/ac901536h 19624122
- [14] Fatima A.-K., Yousri N. A., Albagha O., Semenova E. A., Kostryukova E. S., Kulemin N. A., et al., (2019). Genome-wide association study reveals novel genetic markers associated with endurance athlete status. *Res. Sqre.* 10.21203/rs.2.14107/v1
- [15] Georgiades E., Klissouras V., Baulch J., Wang G., Pitsiladis Y., (2017). Why nature prevails over nurture in the making of the elite athlete. *BMC Genomics* 18(Suppl. 8):835.
- [16] Guth L. M., Roth S. M., (2013). Genetic influence on athletic performance. *Curr. Opin. Pediatr.* 25 653-658. 10.1097/mop.0b013e3283659087 24240283
- [17] Hamel P., Simoneau J. A., Lortie G., Boulay M. R., Bouchard C., (1986). Heredity and muscle adaptation to endurance training. *Med. Sci. Sports Exerc.* 18 690-696.
- [18] Handa R. J., Sharma D., Uht R. A., (2011). role for the androgen metabolite, 5alpha androstane 3beta, 17beta diol (3beta-diol) in the regulation of the hypothalamo-pituitary-adrenal axis. *Front. Endocrinol.* 2:65.
- [19] Hedman K., Tamas E., Bjarnegard N., Brudin L., Nylander E., (2015). Cardiac systolic regional function and synchrony in endurance trained and untrained females. *BMJ Open Sport Exerc. Med.* 1:e000015. 10.1136/bmjsem-2015-000015 27900120
- [20] Kastenmuller G., Raffler J., Gieger C., Suhre K., (2015). Genetics of human metabolism: an update. *Hum. Mol. Genet.* 24 R93-R101.
- [21] Landrum M. J., Lee J. M., Benson M., Brown G. R., Chao C., Chitipiralla S., et al. (2018). ClinVar: improving access to variant interpretations and supporting evidence. *Nucleic Acids Res.* 46 D1062-D1067.

- [22] Lortie G., Bouchard C., Leblanc C., Tremblay A., Simoneau J. A., Theriault G., et al. (1982). Familial similarity in aerobic power. *Hum. Biol.* 54 801–812.
- [23] Mannan A. U., Roussa E., Kraus C., Rickmann M., Maenner J., Nayernia K., et al. (2004). Mutation in the gene encoding lysosomal acid phosphatase (Acp2) causes cerebellum and skin malformation in mouse. *Neurogenetics* 5 229–238. 10.1007/s10048-004-0197-9 15503243
- [24] Maron B. J., Pelliccia A., (2006). The heart of trained athletes: cardiac remodeling and the risks of sports, including sudden death. *Circulation* 114 1633–1644. 10.1161/circulationaha.106.613562 17030703
- [25] McNamara J. W., Li A., Lal S., Bos J. M., Harris S. P., van der Velden J., et al. (2017). MYBPC3 mutations are associated with a reduced super-relaxed state in patients with hypertrophic cardiomyopathy. *PLoS One* 12:e0180064. 10.1371/journal.pone.0180064 28658286
- [26] Mitchell J. H., Haskell W., Snell P., Van Camp S. P., (2005). Task force 8: classification of sports. *J. Am. Coll. Cardiol.* 45 1364–1367. 10.1016/j.jacc.2005.02.015 15837288
- [27] Moss R. L., Fitzsimons D. P., Ralphe J. C., (2015). Cardiac MyBP-C regulates the rate and force of contraction in mammalian myocardium. *Circ. Res.* 116 183–192. 10.1161/circresaha.116.300561 25552695
- [28] Ogawa T., Spina R. J., Martin W. H., III Kohrt W. M., Schechtman K. B., Holloszy J. O., et al. (1992). Effects of aging, sex, and physical training on cardiovascular responses to exercise. *Circulation* 86 494–503. 10.1161/01.cir.86.2.494
- [29] Pelliccia A., Maron B. J., Spataro A., Proschan M. A., Spirito P., (1991). The upper limit of physiologic cardiac hypertrophy in highly trained elite athletes. *N. Engl. J. Med.* 324 295–301. 10.1056/nejm199101313240504 1824720
- [30] Pelliccia A., Culasso F., Di Paolo F. M., Maron B. J., (1999). Physiologic left ventricular cavity dilatation in elite athletes. *Ann. Intern. Med.* 130 23–31.
- [31] Pelliccia A., (1996). Determinants of morphologic cardiac adaptation in elite athletes: the role of athletic training and constitutional factors. *Int. J. Sports Med.* 17(Suppl. 3) S157–S163.
- [32] Peeters M. W., Thomis M. A., Beunen G. P., Malina R. M., (2009). Genetics and sports: an overview of the pre-molecular biology era. *Med. Sport Sci.* 54 28–42. 10.1159/000235695 19696506
- [33] Pitsiladis Y. P., Tanaka M., Eynon N., Bouchard C., North K. N., Williams A. G., et al. (2016). Athlome Project Consortium: a concerted effort to discover genomic and other “omic” markers of athletic performance. *Physiol. Genomics* 48 183–190. 10.1152/physiolgenomics.00105.2015 26715623
- [34] Prud’homme D., Bouchard C., Leblanc C., Landry F., Fontaine E., (1984). Sensitivity of maximal aerobic power to training is genotype-dependent. *Med. Sci. Sports Exerc.* 16 489–493. 10.1249/00005768-198410000-00012 6542620
- [35] Rankinen T., Roth S. M., Bray M. S., Loos R., Perusse L., Wolfarth B., et al. (2010). Advances in exercise, fitness, and performance genomics. *Med. Sci. Sports Exerc.* 42 835–846. 10.1249/mss.0b013e3181d86cec 20400881
- [36] Rankinen T., Fuku N., Wolfarth B., Wang G., Sarzynski M. A., Alexeev D. G., et al. (2016). No evidence of a common DNA variant profile specific to world class endurance athletes. *PLoS One* 11:e0147330. 10.1371/journal.pone.0147330 26824906
- [37] Ray D., Culine S., Tavitaian A., Moreau-Gachelin F., (1990). The human homologue of the putative proto-oncogene Spi-1: characterization and expression in tumors. *Oncogene* 5 663–668.
- [38] Repa J. J., Berge K. E., Pomajzl C., Richardson J. A., Hobbs H., Mangelsdorf D. J., (2002). Regulation of ATP-binding cassette sterol transporters ABCG5 and ABCG8 by the liver X receptors alpha and beta. *J. Biol. Chem.* 277 18793–18800. 10.1074/jbc.m109927200 11901146
- [39] Sato K., Iemitsu M., Aizawa K., Ajisaka R., (2008). Testosterone and DHEA activate the glucose metabolism-related signaling pathway in skeletal muscle. *Am. J. Physiol. Endocrinol. Metab.* 294 E961–E968.
- [40] Semenova E., Fuku N., Ahmetov I., (2019). “Genetic profile of elite endurance athletes,” in *Sports, Exercise, and Nutritional Genomics: Current Status and Future Directions*, eds Barh D., Ahmetov I., (Cambridge, MA: Academic Press), 73–104. 10.1016/b978-0-12-816193-7.00004-x
- [41] Semenova E. A., Miyamoto-Mikami E., Akimov E. B., Al-Khelaifi F., Murakami H., Zempo H., et al. (2020). The association of HFE gene H63D polymorphism with endurance athlete status and aerobic capacity: novel findings and a meta-analysis. *Eur. J. Appl. Physiol.* 120 665–673. 10.1007/s00421-020-04306-8 31970519
- [42] Tanaka M., Wang G., Pitsiladis Y. P., (2016). Advancing sports and exercise genomics: moving from hypothesis-driven single study approaches to large multi-omics collaborative science. *Physiol. Genom.* 48 173–174. 10.1152/physiolgenomics.00009.2016 26812985
- [43] Theofilopoulos S., Arenas E., (2015). Liver X receptors and cholesterol metabolism: role in ventral midbrain development and neurodegeneration. *F1000Prime Rep.* 7:37.
- [44] Tang J., Chu G., (2002). Xeroderma pigmentosum complementation group E and UV-damaged DNA-binding protein. *DNA Repair (Amst)*. 1 601–616. 10.1016/s1568-7864(02)00052-6
- [45] Wang G., Tanaka M., Eynon N., North K. N., Williams A. G., Collins M., et al. (2016). The future of genomic research in athletic performance and adaptation to training. *Med. Sport Sci.* 61 55–67.

- [46] Wu C. K., Huang Y. T., Lee J. K., Chiang L. T., Chiang F. T., Huang S. W., et al. (2012). Cardiac myosin binding protein C and MAP-kinase activating death domain-containing gene polymorphisms and diastolic heart failure. *PLoS One* 7:e35242. [10.1371/journal.pone.0035242](https://doi.org/10.1371/journal.pone.0035242) 22529996
- [47] Zhang W., Elimban V., Nijjar M. S., Gupta S. K., Dhalla N. S., (2003). Role of mitogen-activated protein kinase in cardiac hypertrophy and heart failure. *Exp. Clin. Cardiol.* 8 173-183.