Journal of Science and Medicine in Sport 21 (2018) 213–220

Contents lists available at ScienceDirect

Journal of Science and Medicine in Sport

journal homepage: www.elsevier.com/locate/jsams

Review

Nine genetic polymorphisms associated with power athlete status – A Meta-Analysis

Jan Weyerstraß[a,*], Kelly Stewart[a], Anke Wesselius[a], Maurice Zeegers[b]

[a] Department of Complex Genetics, School of Nutrition and Translational Research in Metabolism (NUTRIM), Maastricht University Medical Centre, The Netherlands

[b] Department of Complex Genetics, School of Nutrition and Translational Research in Metabolism (NUTRIM), CAPHRI School for Public Health and Primary Care, Maastricht University Medical Centre, The Netherlands

ARTICLE INFO

Article history:
Received 2 December 2016
Received in revised form 4 June 2017
Accepted 13 June 2017
Available online 21 June 2017

Keywords:
Muscular power
Single nucleotide polymorphism
Candidate gene study
Cohort
Case-control

ABSTRACT

Objectives: In this study the association between genetic polymorphisms and power athlete status with possible interference by race and sex was investigated to identify genetic variants favourable for becoming a power athlete.
Design: This meta-analysis included both, case-control and Cohort studies.
Methods: Databases of PubMed and Web of Science were searched for studies reporting on genetic polymorphisms associated with the status of being a power athlete. Thirty-five articles published between 2008 and 2016 were identified as eligible including a total number of 5834 power athletes and 14,018 controls. A series of meta-analyses were conducted for each of the identified genetic polymorphisms associated with power athlete status. Odds ratios (ORs) based on the allele and genotype frequency with corresponding 95% confidence intervals (95%CI) were calculated per genetic variant. Heterogeneity of the studies was addressed by Chi-square based Q-statistics at 5% significance level and a fixed or random effects model was used in absence or presence of heterogeneity respectively. Stratified analyses were conducted by race and sex to explore potential sources of heterogeneity.
Results: Significant associations were found for the genetic polymorphisms in the *ACE* (rs4363, rs1799752), *ACTN3* (rs1815739), *AGT* (rs699), *IL6-174* (rs1800795), *MnSOD* (rs1799725), *NOS3* (rs1799983, rs2070744) and *SOD2* (rs4880) genes.
Conclusions: Nine genetic polymorphisms have been identified in the meta-analyses to have a significant association with the status of being a power athlete. Nevertheless, more research on the investigated genes needs to be done to draw comprehensive conclusions.

1. Introduction

Typical power related sports can involve a short movement as sprinting and throwing but also a series of the same or different power movements over time, for example rowing.[1,2] The development of high muscular power can be seen as the main goal of any power athlete for achieving the maximum performance in their sport. Muscular power is an important component of fitness for power athletes as it is needed in any movement of a power related sport, requiring a well-trained muscular system.[3] This component refers to the ability to exert a maximal force at a given period of time, also equivalent to the energy output per unit of time or the rate of work.[4] Muscular power is mainly expressed as the power output, which is determined by physiological factors like muscle fiber size, length, muscle fiber type and the muscle fiber maximum contraction velocity (Vmax) with the athlete's relative proportions of the two muscle fiber types as one of the most important factors.[5] Literature suggests that the proportion of type I and type II muscle fibers is almost equal in healthy sedentary controls,[6] while power athletes of higher competitive level were estimated to have up to 80% type II muscle fibers[7] indicating that a high proportion of type II muscle fibers might be beneficial for power related sports. Type II muscle fibers can be divided in: a) oxidative IIa and b) glycolytic IIx muscle fibers. While IIx muscle fibers fatigue more quickly than IIa, they produce the highest force and are, therefore, most useful for very short explosive movements.[5] Muscle fiber size, shape and proportion of different fiber types are partially determined by the athlete's genotype, meaning that favorable genotypes for power related sports can be identified and used to optimize training programmes. In 2007, De Moor et al.[8]

* Corresponding author.
E-mail address: Jan.Weyerstrass@uni-wh.de (J. Weyerstraß).

https://doi.org/10.1016/j.jsams.2017.06.012
1440-2440/

estimated the genetic predisposition of athletic performance to be greater than 60% and only one third being due to environmental components such as training, nutrition and technological aids,[9,10] underlying the importance of sports genomics for researchers, athletes and coaches.[11] To date, several genes associated with power athlete performance have already been suggested.[12,13] One example of a commonly researched genetic variant in relation to the status of being a power athlete is the single nucleotide polymorphism (SNP) rs1815739, which alters the normal C-nucleotide in a T-nucleotide, in the *ACTN3* gene. The *ACTN3* gene encodes for the α-Actinin-3 protein, an actin-binding protein that plays a role in the human skeletal muscle. This protein is expressed in the type II muscle fibers where it helps to keep the myofibrillar actin filaments attached to each other.[14] A non-sense mutation results in a dysfunctional version of the protein, leading to a deficiency of the α-Actinin-3 protein which is substituted by alpha-actinin-2.[15] This deficiency slows metabolic and physiological properties of fast fibres resulting to a shift toward increased oxidative metabolism in fast muscle fibres and thereby decreasing the speed in which these muscle fibers can generate force.[16] Therefore, it is not surprising that MacArthur et al.[15] and Yang et al.[17] observed a higher frequency of the CC (RR) genotype at this SNP in sprint athletes, a typical power sport, compared to healthy sedentary controls. Many other genes have been linked to power athlete status, i.e. *ACE*, *ADRB1*, *ADRB2*, *ADRB3*, *AGT*, *CNTFR*, *FTO*, *IGF1*, *IGF-IR*, *IL6-174*, *GDF-8*, *GNB3*, *MCT1*, *MnSOD*, *NOS3*, *NRF-2*, *SOD2*.<

Although there is a lot of existing literature on genetic polymorphisms associated with power athlete status, studies generally investigate no more than one or two specific genetic variants or do not include a meta-analysis.[18–20] Identifying genetic variants associated with power athlete status is relevant for researchers, athletes and the coaching team to optimize the training process. This genetic knowledge may help athletes to develop their athletic potential most optimally. Therefore, the aim of this meta-analysis is to quantify the association between genetic polymorphisms and the status of being a power athlete.

2. Methods

2.1. Literature identification

Databases of PubMed and Web of Science were searched for eligible studies assessing genetic polymorphisms related to the status of being a power athlete during the period from the 2th of April 2016 until the 10th of August 2016.

Included search terms consisted of the names of several genetic polymorphisms, SNPs and "genetic polymorphism" in combination with "muscular power" and "power". Furthermore, additional studies were identified through cross-referencing of relevant reviews obtained in the search. No restriction was used with regard to the language or the date of publication.

2.2. Inclusion and exclusion criteria

Articles were considered eligible if they assessed genetic polymorphisms associated with the status of being a power athlete, which was defined as athletes competing at higher national and/or international competitive level, with the sport being identified as a power sport by the authors of each study. Included power athletes were sprinters, jumpers, throwers, track athletes, swimmers, rowers, short distance speed skaters, ice hockey players, rugby players, bodybuilders, power lifters and weightlifters. Articles using animals, diseased participants or review articles were excluded.

2.3. Data extraction

For all articles, the following information of the study was extracted: author and year, journal, country of the study, objective of the study, study design, total number of athletes and controls, type of athletes and controls, race and sex of participants, researched gene(s), reported subpopulations within the study population, major allele and the preferential genotype for power athlete status (reference group), genotype and allele frequencies among power athletes and controls and for each of the subgroups.

2.4. Statistical analysis

A series of meta-analyses were conducted for each of the identified genetic polymorphisms associated with power athlete status. The strength of association of the genetic polymorphisms with power athlete status was estimated by calculating odds ratios (ORs) with corresponding 95% confidence intervals (95%CI) per genetic variant, based on the allele and genotype frequencies. Heterogeneity of the studies was addressed by Chi-square based Q-statistics. A random effects model was used in case of statistically significant heterogeneity, while a fixed effects model was used otherwise. Stratified analyses were conducted by race and sex to explore potential sources of heterogeneity in the studies and create insight into the associations of each genetic variant on power athlete status under influence of the stratified factors. The statistical analyses were done in Stata 14 (Statacorp LP) with significance levels of 5%, which represents a p-value of <0.05.

3. Results

A total of 4728 articles were identified through the search in PubMed and Web of Science (Fig. 1). After deduplication, 2626 articles were scanned based on title and abstract, of which 2534 articles were excluded. From the 92 remaining articles, another 61 articles were excluded after full text selection due to the following reasons: used athletes were not clearly defined as power athletes or not of higher competitive level, a control group was missing, or allele and genotype frequencies were not reported. Four usable articles were identified through cross-referencing resulting in a final number of 35 articles published between 2008 and 2016.

Table 1 shows the characteristics of the 36 included studies regarding author, year, country, race as well as the total of investigated genes and the total of included athletes and controls.

Table 2 shows the results of the meta-analyses of the association between the genetic polymorphisms of the *ACE* (rs4363, rs1799752), *ACTN3* (rs1815739), *AGT* (rs699), *FTO* (rs9939609), *IL6-174* (rs1800795), *GNB3* (rs5443), *NOS3* (rs2070744) gene and power athlete status for all genes with two or more studies per SNP. In this table only the overall analyses for each gene are presented. The subgroup analyses for each gene can be found in Table 3. With regard to the SNP *ACE* rs4363, athletes carrying the AG genotype had a significantly 1.69 (95%CI = 1.12; 2.56) times greater chance of becoming a power athlete compared to athletes carrying the preferential genotype for power athlete status (AA). In the subgroup analysis by race, having the AG genotype yielded a significantly 2.18 (95%CI = 1.19; 3.99) lower chance of becoming a power athlete among the US African American group, but not among the Jamaican subgroup. At the SNP *ACE* rs1799752, an insertion (ID genotype) resulted in a significant association with power athlete status (OR = 0.64; 95%CI = 0.41; 0.99) compared to the preferential genotype for power athlete status (DD, no insertions) in Caucasians. Furthermore the ID genotype yielded significance among a European population (OR = 0.46; 95%CI = 0.25; 0.86) and