

Association between ACE, ACTN3, AGT, BDKRB2, and IL-6 gene polymorphisms and elite status in Colombian athletes

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Abstract

In Colombia and Latin America, there is a lack of knowledge of the genetic potential of high-performance athletes. Currently, genotypes of athletes of different ethnicities have been characterized, especially in Europe, North America, and Asia. It is known that genetic polymorphisms generate protein variants that potentially favor performance in sport and physical activities. In this contribution, 225 Colombian elite athletes were sampled as well as an equal number of controls. The elite group included athletes of Olympic, Pan-American, and World levels and the controls were individuals with regular physical activity but not high-level competitors. ACE, ACTN3, AGT, BDKRB2, and IL-6 genes were analyzed for genotypic characterization. Polymorphism frequencies were assessed for a 95% significance to establish the association of genotype with the elite athlete status. Significant differences were found between elite athletes and controls for the homozygous genotypes DD ($p < 0.001$) and II ($p < 0.001$) of the ACE gene, and the homozygous (CC and TT) and heterozygous genotypes of the AGT gene. No significant differences were found for the evaluated genotypes of the ACTN3, BDKRB2, and IL-6 genes between elite athletes and controls. ACE D ($p < 0.001$, odds ratio = 2.08) and AGT C ($p < 0.001$, odds ratio = 2.45) alleles were associated with the elite athlete status. The ACTN3R, BDKRB2-9, and IL-6 C alleles, which have been previously suggested as positive genetic markers of athletic performance, were more frequent both in the athletes and controls. Although no significant differences were found, this fact does not negate positive effects of carrying those alleles on athletic performance.

Keywords: athletic performance, elite athlete, athlete status, genotype, polymorphism, polygenic profile

Introduction

The performance of athletes both in professional and amateur competitions is greatly affected by external factors such as physical and mental condition, training, and diet. However, there is a growing interest in the role that innate or inherited factors, such as gene expression and metabolism, play in athletic performance. The study of these intrinsic factors is the focus of the emerging field of omics science in sports (Ahmetov & Fedotovskaya, 2012; Maciejewska-Skrendo et al., 2019; Ooi et al., 2021). Research has identified several genetic factors that can influence an athlete's physical characteristics such as strength, power, coordination, flexibility, speed, endurance, and recovery (Maciejewska-Skrendo et al., 2019). Additionally, metabolic factors, including cellular energy production and the absorption, uptake, and metabolism of specific macronutrients, also play a role in athletic performance (Maciejewska-Skrendo et al., 2019). It is believed that athletic ability can be an inherited trait, with up to 66% of variance estimated to be due to genetics and the remaining 34% explained by environmental factors (de Moor et al., 2007). In recent years, there has been an increase in genomic studies in sports science, with several case-control studies investigating the relationship between gene variants and athletic performance. However, much of the information remains limited, and some results are still controversial (Maciejewska-Skrendo et al., 2019).

At least 69 gene markers have been identified as potentially associated with athletic performance (Maciejewska-Skrendo et al., 2019). Two of the most studied genes are the α -actinin 3 (ACTN3) protein and angiotensin I converting enzyme (ACE). A positive correlation has been found between these genes and athletic performance in 65% and 47% of cases, respectively (Maciejewska-Skrendo et al., 2019). The ACE gene, which is part of both the renin-angiotensin system and the kinin kallikrein system, has been linked to strength and endurance (Ahmetov & Fedotovskaya, 2012). A 287 bp indel polymorphism in the ACE gene (rs4646994) has been associated with differences in strength and endurance. Individuals with the D allele have higher levels of ACE, leading to greater strength and muscle volume, as well as a faster increase in blood pressure and a lower maximal heart rate and oxygen uptake compared to those with the I allele (Maciejewska-Skrendo et al., 2019; Puthuchery et al., 2011). These physiological characteristics suggest that the deletion is beneficial for strength and anaerobic activities, while the insertion is more favorable for endurance sports (Charbonneau et al., 2008;

Puthuchery et al., 2011). However, the association of this gene marker with sport performance is still controversial (Subak & Muniroglu, 2020).

The AGT gene, which encodes angiotensinogen, is another gene that is associated with the RAS (Maciejewska-Skrendo et al., 2019). Angiotensinogen is a glycopeptide produced in the liver and serves as the substrate to produce angiotensin I by the renin enzyme. The Met235Thr polymorphism, which involves a substitution of threonine for methionine at position 235, is linked to increased angiotensinogen production (Gomez-Gallego et al., 2009). Individuals with the Thr/Thr genotype are believed to have an advantage in power and strength sports compared to those with the Met/Met or Met/Thr genotypes; this occurs owing to higher levels of angiotensin II as a result of increased angiotensinogen production (Gomez-Gallego et al., 2009; Maciejewska-Skrendo et al., 2019).

The α -actinin-3 protein is a crucial component of the Z line in skeletal muscle fibers and helps to stabilize muscle contraction by anchoring myofibrillar actin filaments in fast-twitch (type II) muscle fibers (Berman & North, 2010; Maciejewska-Skrendo et al., 2019). This plays an important role in enabling explosive and powerful muscle contractions (Berman & North, 2010). The ACTN3 gene encodes the synthesis of the protein of the same name, and polymorphism (R577X, rs1815739 C/T, located at 11q13.1) leads to the replacement of arginine with a stop codon in the 577th amino acid (Maciejewska-Skrendo et al., 2019). The X genotype results in the absence of the protein, potentially affecting the athletic performance of individuals. Research has shown that the R genotype results in a greater number of fast-twitch fibers and higher testosterone levels, which leads to muscle hypertrophy (Ahmetov et al., 2014). Previous studies have shown that R genotypes are more common among elite power and sprint athletes (Gineviciene et al., 2016; Mikami et al., 2014; Saito et al., 2022).

Bradykinin is an endothelium-dependent vasodilator that causes the contraction of non-vascular smooth muscles and increases vascular permeability (Ahmetov & Fedotovskaya, 2012). It works through bradykinin β 2 receptors that are encoded by the BDKRB2 gene. These receptors enhance glucose uptake in skeletal muscle during physical activity (Ahmetov & Fedotovskaya, 2012). There is a variation in the exon1 of the gene, which is a 9pb indel polymorphism (rs5810761, located at 14q32.1-q32.2); the deletion allele (-9bp) is associated with high transcriptional activity and expression of the BDKRB2 gene (Williams et al., 2004). This allele has been linked to improved energy efficiency during muscular contractions and higher power output (Williams et al., 2004). The carriers of the -9 allele have been found to be overrepresented among short- and middle-distance elite athletes and triathletes (Saunders et al., 2006; Williams et al., 2004). However, the BDKRB2 +9/-9 genotype does not seem to have any significant impact on swimming performance at short, middle, or long distances (Grenda, Leonska-Duniec, et al., 2014).

Interleukin-6 (IL-6) is a pro-inflammatory cytokine that plays a critical role in the immune response and exercise-induced skeletal muscle adaptations. The IL-6 gene has several single-nucleotide polymorphisms that may impact the expression and function of IL-6 protein. One of the most widely studied is the -174 G/C polymorphism (rs1800795, located at 7p21), which alters transcriptional response and has been associated with differences in IL-6 production. Some studies have reported that the GG genotype is associated with higher power and strength performance, possibly owing to its association with higher levels of IL-6 production (Eider et al., 2013; Ruiz et al., 2010a). The C allele has been associated with increased levels of total serum creatine kinase activity, which is an indicator of skeletal muscle damage following muscle eccentric contraction (Ruiz et al., 2010b; Yamin et al., 2008). In swimmers, the aerobic performance was observed to be significantly higher among C-allele non-carriers (Ben-Zaken et al., 2022).

In this study, we examined the genetic profiles of elite athletes and their correlation with genetic markers that are known to be associated with elite athlete status such as the polymorphisms in the ACE, ACTN3, AGT, BDKRB2, and IL6 genes. To our knowledge, this is the first case-control polygenic study that has been conducted in Colombia with a significant population of elite athletes including Olympic, Pan-American, and World medalists from various individual and team sports.

Materials and Methods

Participants

In this study, 450 Colombian individuals were sampled, with 225 of them being elite athletes and 225 being controls. The athletes were selected based on their achievements, including medals in Olympic, World, or Pan-American competitions, and they were categorized into twelve different sport disciplines: archery, 100/200 m sprinting, finswimming, rhythmic gymnastics, karate-do, rugby, skating, swimming, triathlon, weightlifting, and wrestling.

All participating athletes competed in continental, Pan-American, World, or Olympics events and earned at least one medal (gold, silver, or bronze). The control group consisted of individuals who engaged in recreational sports activities and trained for an average of three days per week.

The study was approved by the Ethics Committee of the Universidad del Valle and performed in accordance with the Declaration of Helsinki, following the protocols for human studies outlined by the Colombian Ministry of Health. Each participant provided informed consent to participate in the study.

Genotyping

This study used DNA extracted from oral epithelial cells to perform molecular analysis. The extraction process was performed using the GenElute Mammalian Genomic DNA Miniprep Kit from Sigma (St. Louis, MO). Primers obtained from Macrogen Inc. (Seoul, Korea) were used for the amplification process in an Applied Biosystems Veriti thermocycler (Thermo Fischer Scientific, Waltham, MA). The PCR reactions were performed at a volume of 25 µl and contained various components including 3 mM MgCl₂, 0.1 mM primers, 0.1 mM dNTPs, 1X buffer, and 1X Taq polymerase (Cieszczyk et al., 2012; Grenda, Leonska-Duniec, et al., 2014; Grenda, Leonska-Duniec, et al., 2014). The amplified fragments of the ACTN3 and AGT genes were digested with the corresponding restriction enzymes, DdeI and SfaI, for 12 h. Then, the PCR products were separated by electrophoresis in 8% polyacrylamide gels in TBE 1X buffer, and the samples were visualized on gels stained with silver nitrate after undergoing electrophoresis at 130 volts and 250 volts for 1 h each.

Data analysis

A database was constructed using the data of the existing allelic polymorphisms in the population under study. This database considered the presence or absence of polymorphisms for the ACE, ACTN3, AGT, BDKRB2 genes and IL6. The genotypic and allelic frequencies were calculated based on the absolute frequencies of polymorphisms in each gene. The genotypic and allele frequencies were compared between the two populations (elite vs. controls). A chi-square test was used to determine statistical significance at 95% for the genotype and allelic frequencies. Similarly, the Hardy–Weinberg equilibrium was assessed using the chi-square test. The combined influence of the five genetic polymorphisms on athletic performance was analyzed by the Total Genotype Score (TGS) for power-oriented athletes based only on the genotypes under analysis (Williams & Folland, 2008). For this, it was assumed the most favorable for the power/strength phenotype to be configured by co-occurrence of homozygous ACE D, ACTN3 R, AGT C, BDKRB2 +9, and IL-6 G. The statistical analysis was performed using Statistica v.14.0 (TIBCO Software Inc., Palo Alto, CA).

Results

AGT and IL-6 genes were in Hardy–Weinberg disequilibrium in the elite athletes and controls, while the ACE gene was in equilibrium for both. The ACTN3 was in equilibrium in the controls but in disequilibrium in the elite athletes. In the case of the BDKRB2 gene, it was in disequilibrium for the controls and in equilibrium for the elite group. Tables 1 and 2 display the absolute genotypic and relative allelic frequencies of the elite athletes separated by sport, as well as the control group. Athletes participating in sports with dominance of power/strength and anaerobic component tended to have higher allelic frequencies in the D allele of the ACE gene and the R allele of the ACTN3 gene above 50% than those in endurance sports. These alleles have been reported to be favorable for anaerobic activity performance (Charbonneau et al., 2008; Cieszczyk et al., 2011). The D and C alleles of the ACE and AGT genes, respectively, were overrepresented in the elite athletes. Likewise, the frequencies of the -9 allele of the BDKRB2 and G allele of the IL6 gene were higher in the elite athlete group but were outside the significance interval. The mean results of the TGS for both populations, as shown in Table 2, ranged between 65% and 82%; the values were lower for the sports with a greater endurance component and higher for those with a significant power/strength component. The control group had a mean TGS of 66%, which is in line with the probabilistic distribution calculated by Williams and Folland (2008) for a normal population (Williams & Folland, 2008).

Table 1. Absolute frequencies of ACE I/D, ACTN3 R577X, AGT Met235Thr, BDKRB2 +9/-9 and IL-6 -174 G/C polymorphisms.

	ACE		ACTN3			BDKRB2			AGT			IL-6			
	DD	II	ID	RR	XX	RX	-9/-9	9/9	-9/9	CC	TT	CT	GG	CC	GC
Archery n=19	9	3	7	5	2	12	10	0	9	9	0	10	10	0	9
Athletics n=28	11	6	11	7	4	17	7	8	13	17	2	9	17	2	9
Finswimming n=17	13	2	2	1	8	8	8	5	4	10	0	7	11	1	5
Gymnastics n=26	7	5	14	4	6	16	12	3	11	16	1	9	12	5	9
Karate-do n=16	9	2	5	4	4	8	6	3	7	9	0	7	10	2	4
Rugby n=15	13	0	2	5	0	10	4	2	9	6	0	9	12	1	2
Skating n=17	4	6	7	1	5	11	7	4	6	8	2	7	10	4	3
Swimming n=21	8	0	13	3	8	10	9	1	11	5	0	16	15	0	6
Triathlon n=12	1	7	4	0	3	9	5	1	6	5	2	5	8	0	4

Weightlifting n=38	22	4	12	15	3	20	5	6	27	29	0	9	30	0	8
Wrestling n=16	11	2	3	7	1	8	7	1	8	12	1	3	9	1	6
Elite athletes n=225	108	37	80	52	44	129	80	34	111	126	8	91	144	16	65
Controls n=225	69	78	78	48	54	123	87	18	120	69	39	117	150	25	50

Table 2. Total strength genotype score (TGS) and relative frequencies of ACE D, ACTN3 R, AGT C, BDKRB2 -9 and IL-6 -174 G alleles (%).

	ACE	ACTN3	BDKRB2	AGT	IL-6	TGS
	D (%)	R (%)	-9 (%)	C (%)	G (%)	(%)
Archery n=19	65.8	57.9	76.3	73.7	76.3	73.0
Athletics n=28	58.9	55.4	48.2	76.8	76.8	76.0
Finswimming n=17	82.4	29.4	58.8	79.4	79.4	74.9
Gymnastics n=26	53.8	46.2	67.3	78.8	63.5	70.0
Karate-do n=16	71.9	50.0	59.4	78.1	75.0	75.4
Rugby n=15	93.3	66.7	56.7	70.0	86.7	81.3
Skating n=17	44.1	38.2	58.8	67.6	67.6	67.8
Swimming n=21	69.0	38.1	69.0	61.9	85.7	71.4
Triathlon n=12	25.0	37.5	66.7	62.5	83.3	65.6
Weightlifting n=38	73.7	65.8	48.7	88.2	89.5	82.5
Wrestling n=16	78.1	68.8	68.8	84.4	75.0	78.3
Elite athletes n=225	65.8	51.8	60.2	76.2	78.4	74.9
Controls n=225	48.0	48.7	65.3	56.7	77.8	68.8

The polymorphism frequencies were evaluated for significant differences between the elite and control groups (Table 1). It was found that there were significant differences for the DD (odds ratio: 2.09, 95% CI: 1.42–3.07, $p < 0.001$) and II (odds ratio: 0.37, 95% CI: 0.24–0.58, $p < 0.001$) genotypes of the ACE gene between elite athletes and controls. The D allele was more frequent in the elite group (65.8%) compared to the control group (34.2%). Similarly, in the AGT gene, significant differences were observed for all three genotypes, i.e., CC (odds ratio: 2.88, 95% CI: 1.96–4.24, $p < 0.001$), TT (odds ratio: 0.18, 95% CI: 0.08–0.39, $p < 0.001$), and CT (odds ratio: 0.63, 95% CI: 0.43–0.92, $p = 0.014$), with the frequency of the C allele being higher in the elite group (76.2%) compared to the control group (56.7%). No significant differences were found between the two groups for the ACTN3 and IL6 genes. The frequency of the R allele of the ACTN3 gene was 48.2% for the elite athletes and 51.3% for the control group, while the frequency of the G allele of the IL6 gene was 78.4% for the elite athletes and 81.8% for the control group (Table 2). For the BDKRB2 gene, significant difference was observed only for the +9/+9 polymorphism (odds ratio: 2.05, 95% CI: 1.12–3.75, $p = 0.018$), but not in the total allelic frequencies, which were 60.2% and 65.3% in the -9 allele for the elite and control groups, respectively.

Table 3. Odds ratio, confidence intervals (95%) and P values for being elite athlete in Colombia.

Gene	Genotype	Odds ratio	Confidence interval	P value	
ACE	DD	2.09	1.42	3.07	<0.001
	II	0.37	0.24	0.58	<0.001
	ID	1.04	0.71	1.53	0.843
	D allele	2.08	1.42	3.04	<0.001
	I allele	0.48	0.33	0.70	<0.001
ACTN3	RR	1.11	0.71	1.73	0.650

	XX	0.77	0.49	1.21	0.253
	RX	1.11	0.76	1.61	0.569
	R allele	1.13	0.78	1.64	0.509
	X allele	0.88	0.61	1.27	0.509
AGT	CC	2.88	1.96	4.24	<0.001
	TT	0.18	0.08	0.39	<0.001
	CT	0.63	0.43	0.92	0.014
	C allele	2.45	1.63	3.67	<0.001
	T allele	0.41	0.27	0.61	<0.001
BDKRB2	-9/-9	0.88	0.60	1.29	0.495
	+9/+9	2.05	1.12	3.75	0.180
	+9/-9	0.85	0.59	1.23	0.396
	-9 allele	0.80	0.55	1.17	0.262
	+9 allele	1.24	0.85	1.82	0.262
IL6	GG	0.89	0.60	1.31	0.552
	CC	0.61	0.32	1.18	0.140
	GC	1.42	0.93	2.18	0.105
	G allele	1.04	0.67	1.63	0.864
	C allele	0.96	0.61	1.50	0.864

Discussion

The relationship between genetics and athletic performance is a topic that has been extensively studied over the past 20 years (Ahmetov & Fedotovskaya, 2012; Maciejewska-Skrendo et al., 2019). It is known that athletic abilities are influenced by both environmental and genetic factors, making heredity a crucial component in physical adaptation and, ultimately, athletic performance. Despite numerous studies examining this relationship, reports in the field remain limited, and accessing a considerable number of elite athletes from different disciplines is challenging. Colombia is the third sports power in South America; however, the country accounts for only 34 Olympic medals in the history of Olympic Games. During the last Olympic cycle (2017–2022), more than 380 gold medals were accumulated in international competitions. Considering the preparation and competition schedule of the athletes, access to this population for these types of studies is still limited. This is the first case–control genetic association study involving an important number of Olympic and World-level athletes in the country.

The ACTN3 gene has been associated with athletic performance, specifically in activities requiring speed and explosive movements. The α -actinin-3 protein encoded by this gene enhances stability in fast-twitch muscle fibers, leading to an increase in strength and explosiveness (Berman & North, 2010). Individuals with the R allele in ACTN3 are believed to have a potential advantage in athletic performance, while those with the XX genotype, characterized by α -actinin-3 deficiency, may experience reduced muscle mass, strength, and fast-twitch fiber diameter (Gineviciene et al., 2016).

Athletes with an Afro-descendant background showed higher R allele frequencies, which are consistent with those found in Africans (84%) and African-Americans (73%)(Ahmad Yusof et al., 2020). This is expected, considering that athletes' selection in local media by coaches is highly influenced by the phenotype and performance in explosive-force tests. Moreover, the RR genotype frequency was observed more frequently in rugby (33%), wrestling (44%), weightlifting (40%), and athletics (26%). On the other hand, the lowest R allele frequencies were seen in swimming (38.1%), finswimming (29.4%), skating (38.2%), and gymnastics (46.2%). Several studies have supported the hypothesis that both genotypes, RR and RX, are more frequent in strength and power athletes (Cieszczyk et al., 2012; Mikami et al., 2014). In all cases, the most frequent genotype was the heterozygotic RX; the presence of the R allele could still favor the development of relative strength and explosiveness provided by α -actinin-3. Conversely, the X allele has been linked to good performance in aerobic/endurance activities (Roth et al., 2008; Saito et al., 2022). For the sake of comparison and considering the mestizo racial composition of the Colombian population, which is a result of the mixing of Spaniards, Afro-descendants, and Indigenous people, the control group frequencies were close to those reported for Asian groups (Ahmad Yusof et al., 2020).

This miscegenation has likely diluted the high frequency of the R allele characteristic of Afro-descendants, reducing the occurrence of this allele in homozygosis in the population. The allelic frequencies of the ACE and AGT genes showed a correlation with the elite athlete status. The highest frequencies of the D allele in the ACE gene and the C allele in the AGT gene were observed in the elite athletes

group. The carriers of homozygous ACE DD and II were overrepresented in the elite group but not in the controls. The D allele in the ACE gene has been linked with good performance in power/strength activities owing to its association with greater strength, muscle volume, and fast-twitch muscle fibers (Ginevičienė et al., 2016; Puthuchery et al., 2011). Thus, the D allele is associated with the power athlete status, while the I allele is linked to enhanced endurance performance owing to a lower ACE enzyme activity (Ginevičienė et al., 2016; Grenda, Leońska-Duniec, et al., 2014; Pescatello et al., 2006). Frequencies over 70% of the D allele and homozygous DD genotypes were observed more frequently in athletes involved in anaerobic sports, namely finswimming (82.4%), karate-do (71.9%), rugby (93.3%), weightlifting (73.7%), and wrestling (78.1%), which indicates predisposition for power/strength activities according to the mean value of the TGS. The allelic frequency of homozygous individuals support the hypothesis of a preference or orientation to certain sport influenced by the genotypes (Maciejewska-Skrendo et al., 2019).

The possible relationship between the elite athlete status and the Met235Thr polymorphism has been less-studied. In the case of the AGT gene, significant differences were found in the frequencies for all polymorphisms between the elite athletes' population and controls (Table 3). Homozygotes CC in the elite athletes almost doubled the frequency observed in the controls (30.7%), and clear association with the elite athlete status was observed ($p < 0.001$). Previously, some authors have found an association of the C allele with the elite athlete status, suggesting this gene variant as a marker for elite athletic phenotypes and improved response to training (Aleksandra et al., 2016; Gomez-Gallego et al., 2009; Zarębska et al., 2013). Given the low TT frequencies in the athletes' population (3.6%), we dismiss this gene as a marker of the endurance athlete status. Because the angiotensinogen concentration has been shown to be a rate-limiting factor for angiotensin II production, the CC genotype in elite athletes may confer an advantage in building muscle mass and skeletal muscle strength phenotypes (Zarębska et al., 2013). Moreover, the presence of both polymorphisms, the ACE D allele and the AGT C allele, may favor the athletic performance at high levels owing to their potential effects on vasoconstriction and muscle hypertrophy (Luzi, 2012).

In terms of the BDKRB2 gene, the -9 allele was found to be the most frequent in both the elite athletes (60.2%) and controls (65.3%); however, no association was found in the significance level. The +9/+9 genotype was less frequent compared to the homozygous -9/-9 and heterozygous -9/+9 genotypes. Some studies have suggested that the occurrence of the -9 allele has been linked to higher skeletal muscle metabolic efficiency and endurance athletic performance (Williams et al., 2004), while others have suggested a connection between the ACE gene and the BDKRB2 gene owing to their effects on bradykinin levels and the kallikrein-kinin system (Choudhury et al., 2012; Murphey et al., 2000). In this case, none of the BDKRB2 polymorphisms were statistically associated with the elite athlete status. This agrees with previous studies, which found no significant differences in the distribution of the -9/+9 polymorphism between athletes and controls, or between different athlete groups (Eynon et al., 2011; Grenda, Leońska-Duniec, et al., 2014; Sawczuk et al., 2013).

For the case of the IL-6 gene polymorphism, the observed frequencies of homozygotes GG were the highest in each sport, as well as in the elite athlete group (64%) and controls (67%). On the other hand, the frequency of CC homozygotes was lower in the elite athlete group (7.1%) than in the controls (11.1%). This suggests a low enrollment of these types of genotypes at the highest level of competition possibly owing to difficulties with muscle repair and hypertrophy processes after the exercise-induced damage (Febbraio et al., 2005; Pedersen & Febbraio, 2008). However, the absence of statistical significance left this hypothesis unconfirmed. The high occurrence of the G allele in the elite group (78.4%) suggests that carrying this allele either in homo or heterozygosis may have a physiological advantage in terms of lesion incidence, muscle recovery, and hypertrophy. Although some previous studies have found association between the frequency of GG genotype and the power athlete status (Eider et al., 2013; Ruiz et al., 2010b), in this study it is not possible to draw a conclusion regarding the IL-6 G/C polymorphism and the elite athlete status owing to the lack of statistical significance between cases and controls because of the high occurrence of the G allele in the controls. The observed frequency of the G allele agrees with the observed frequency in different ethnic groups; specifically, the C allele is more frequent in Caucasian European and Indian populations and absent in East Asians and Africans (Gan et al., 2013). Considering the mestizo racial composition of Colombian population, high occurrence of homozygous GG and heterozygous GC is expected from miscegenation with African and Indigenous populations, while recessive C allele originates mainly from European heritage; however, this observation does not necessarily rule out the potential beneficial effect for athletes carrying the G allele.

Conclusions

The achievements in sport may be influenced by the genotypes of each athlete related to physiological systems (metabolic or structural), which affect physical and energetic characteristics such as maximum strength, explosive strength, or aerobic resistance, among others. Our study supports the hypothesis that the genotypes of the ACE and AGT genes are associated with the elite athlete status and the preference or orientation towards certain sports. The DD and II genotypes of the ACE gene were linked to the elite athlete status, considering that allele D may confer advantage for power/strength athletes, while II would favor the performance in endurance activities. The AGT gene showed significant differences between the elite athletes and controls for analyzed genotypes. These findings agree with previous studies that have reported that the ACE and AGT genes may play

a role in athletic performance. Observations regarding the ACTN3, BDKRB2, and IL-6 polymorphisms highlight trends in terms of a potential predisposition towards the elite athlete status; however, the lack of statistical significance did not confirm the hypothesis for the Colombian athletes. Apart from the statistical significance, the allelic genotypes (either homozygous or heterozygous) that are preferred for the selection of high-performance athletes in the region are ACE D, ACTN3 R, AGT C, BDKRB2 -9, and IL-6 G.

The results of this study provide valuable information for future research and for the development of athletic programs aimed at identifying and training talented athletes. In addition, the obtained information can help in the design of personalized training and nutrition programs based on the genetic profile of athletes and sport characteristics, which can help optimize athlete performance and prevent injuries. In Colombia, additional studies are required that would include a larger number of individuals and gene markers, and also consider ethnicity variability.

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