



The Future of Genetic Testing in Taekwondo: Opportunities and Challenges

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Abstract: As far as we know, genetics in sports is a rapidly growing science field, due to new technologies and the cost decrease of such investigations. Onwards, genetic predispositions, besides the relations between the biological and chronological age play one of the main roles in talent identification processes. Utilization of such analyses in practice is unfortunately insignificant, perhaps because of the complexity of the genome and genotype-phenotype interrelations. Therefore, the aim of this investigation is to collect all relevant data about gene research in taekwondo. The authors tracked appropriate articles through three databases: Web of Science, PubMed and Google Scholar. A number of n=11 appropriate articles were found. Results suggest there is evidence that several genes may highly impact taekwondo performance, including ACE I/D, ACTN3, IGF-1, while the GABPb1, HSP90AA1 & HSP90AB1 and mtDNA haplogroups M, N9 and J have the moderate overall impact. Still, there are challenges in genetic testing of young athletes, of methodological and ethical nature, which should be avoided with a professional staff and correct approach towards such testings. Significant scores of listed genes shed a light towards the clarification of possible genetic impact on taekwondo success. Accordingly, the authors have established precise guidelines for future examination of genetics in taekwondo. This work presents the current knowledge about genetic examinations regarding taekwondo.

Keywords: genetics, sport success, genome, phenotype, sport performance

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INTRODUCTION

Human genome in the context of sports performance surely plays a significant role. On the one hand, an idea about genetic testing in sports is unfortunately and mostly still an idea or theoretical solution, with insignificant and limited practical impact at the present. On the other hand, there is growing evidence base about the influence of certain polymorphisms on sports performance. As applied molecular knowledge within sports sciences advances, the field of genetics became very popular with the claims that specific genes encompass associations of polymorphisms with sports performance, directing athletes to specialties according to their ability, developing methodologies for early detection of talents, and individualization of training for performance enhancement and injury prevention [1,2]. Moreover, nearly 200 genetic polymorphisms have been found to influence sports performance traits, and over 20 polymorphisms may condition the status of the elite athlete [3]. Further, early twin and family studies suggest that genetics accounts for between 30–80% of the variance in human athletic performance [4-8]. The physical performance phenotypes for which a genetic basis can be suspected include endurance capacity, muscle performance, determinants of tendon–ligament apparatus and physiological response to training. Consistent with the previous classification, the phenotypes of health-related fitness retained are grouped under additional categories, including cardiovascular (exercise heart rate, blood pressure and heart morphology), metabolism, anthropometry and body composition [9].

As genetic research recently became widely available and investigations concerning taekwondo became more extensive, the number of published gene-related studies within taekwondo has grown. There is one existing review featuring martial arts and related genetic research until 2021 [10], but soever, martial arts can widely differ concerning their different combat patterns and primary energy system contribution [11]. 21st-century World Taekwondo (WT) competitions demand extraordinary overall psychophysical features, and growing knowledge about the genetic conditionality of valuable traits will surely enable precise instructions and programming of training and diet for taekwondo competitors. Secondly, it will strengthen a path toward utilization of such analyzes within talent identification processes, and therefore enhance the quality of selected processes.

Accordingly to the previous statements, the aim of this investigation is to comprehend all relevant literature and evidence about genetic testing and its current usage in taekwondo.

MATERIAL AND METHODS

Search Strategy and Data Source

This narrative review is conducted in accordance with the guidelines for narrative biomedical reviews [12].

In the first phase, authors defined certain preconditions and keywords for the filtration of research papers according to the topic. Defined inclusion criteria were the following: published in English, open access papers/full-text papers, include empirical evidence and information about genetic research in terms of competitive taekwondo and/or include taekwondo athletes in their sample, correctly used research methodology, concern the success-related traits, and feature healthy participants.

The authors selected three topic-relevant databases for the extraction of papers: Web of Science, PubMed and Google Scholar. Further, Boolean operators [13] and specific keywords were used in search browsers are the following: 1) taekwondo AND: gene, genetics, genotype, genome, haplotype, haplogroup, polymorphism, SNP; 2) combat sport AND: gene, genetics, genotype, genome, haplotype, haplogroup, polymorphism, SNP.

Study selection and Data Extraction

In the second phase, researchers independently searched for papers to suit the selected inclusion criteria. Retrieved relevant papers were manually downloaded in separate folders, and folders of all authors were fused together, separately by a database. Duplicate papers were deleted, and all papers were evaluated and filtrated again by the authors. Finally, after the application of all previously listed methods, 11 scientific papers were extracted and analyzed.

RESULTS

Angiotensin-converting enzyme (insertion/deletion) (ACE I/D)

In the context of taekwondo, first investigation of ACE I/D polymorphism was conducted in 2010 [14] where authors compared frequencies of genotypes within ACE I/D polymorphism between subsamples of 49 sedentary people and 18 Turkish and Azerbaijan national team members. Analysis of frequencies showed no significant difference between national teams and the sedentary group, and ID heterozygous proved to be most frequent (54.50%). While the Turkish national members had the greatest proportion of ID genotype (75%), Azerbaijan team members had the greatest score of DD genotype (50%). As we know, I allele is associated with endurance performance [24-28], while the D allele is associated with power performance [29-31], which was also confirmed in review by Youn et al. in 2021 [10], based on research of Japanese wrestlers [31]. Further, Shahmoharadi et al. [16] investigated frequencies of the ACE gene II, ID, and DD genotypes between subgroups of Iranian elite athletes (taekwondo athletes belonged to mixed group n=32) and between athletes and control group. Mixed group had slightly higher proportion of I allele (53.13%), power-oriented athletes had equal amounts of I and D allele (50/50%), while endurance athletes had a greater proportion of D allele (63.51%). Also, athletes overall were confirmed to have greater proportions of I allele (47.44%) compared to controls (38.96%). Speaking of genotype, the most frequent among the mixed and power-oriented subgroups is ID heterozygous, while endurance athletes have DD homozygous as most represented. Results from these two papers reveal the similar distribution of II, ID, DD genotypes between samples and distribution in the Caucasian population, which are roughly 25%, 50%, and 25% respectively [32]. Similar frequencies were observed (II= 18%; ID= 45%; DD= 36%) by Elsayy & Shaban [17], who investigated ACE I/D genotype frequencies among n=11 Egyptian female national team members. Mentioned authors also conducted evaluations of strength and power and found no correlation between certain genotypes and selected latent motor dimensions. Furthermore, the latter authors [22] reported no significant difference ($p>0.05$) between athletes and non-athletes. II genotype frequency had the greatest proportion (49%) and authors also obtained greater I allele frequencies (71%), compared to D allele (29%). It must be highlighted that the last two mentioned papers reported results on Brazilian and Egyptian populations, which are relatively diverse populations in the context of population genetics. Within a genetic research there should always be a clear sample differentiation and detailed description of subjects, especially in terms of origins and their possible impact on research results outcome. D allele perhaps affects performance via an angiotensin II-mediated increase in muscle growth and strength. Conversely, a local increase in muscle efficiency, rather than a central cardiovascular control, contributes to the enhanced endurance associated with the I allele [32]. Genotype scores of this polymorphism were also observed in medicine. Clinical studies revealed a possible relationship of DD genotype with various diseases, such as chronic heart failure [33], abdominal aortic aneurysm [34], renal diseases [35], type 2 diabetes [36], etc. For now, there are unfortunately still a lot of doubts about this polymorphism and its possible connection with competitive combat performance, due to contrary results of different scientists. Speaking of ACE I/D investigations in the sport overall, there is a certain consensus about the I allele being related to endurance, while the D allele relates to power

[37]. Therefore, I allele seems to be more beneficial for disciplines that rely on aerobic systems with focus on speed and accuracy (e.g. taekwondo, karate, point fighting, light contact kickboxing;), while the D allele represents power, and is desirable among full contact disciplines where the power plays a main role, such as K-1, boxing, wrestling, etc. Not to confuse, taekwondo is *de jure* full contact discipline, but certain conditions directed its combat style toward speed and accuracy, while power became a secondary desired trait. So far, it can be concluded that the I allele, or II/ID genotype could be a desirable ACE I/D variant for competitive taekwondo, and possibly the overall health of competitors.

α-actinin 3 R577X polymorphism (ACTN3)

There is only one research of ACTN3 polymorphism conducted on a sample of taekwondo athletes, an investigation by Jung et al. in 2016 [20]. The purpose of this study was to analyze the possible interaction between ATCN3 gene polymorphism and muscle imbalance in the lower extremities. Variables of muscle imbalance were evaluated followed by an analysis of differences of the moment in hip, knee, and ankle joint during V-cut jumping and stop. The sample was divided into RX+RR and XX subgroups, also divided by their initial balance/imbalance. Reported results revealed no significant difference in muscle imbalance according to the genotype between all groups. However, allele analysis revealed that X allele with the knee muscle imbalance group showed a higher risk of injury risk during agility and strength movement in combat sports athletes. This work highlights the role of R allele in the prevention of knee joint injury incidence among combat (and taekwondo) athletes. Still, this is just a part of ACTN3's overall impact on athletes' fitness status. The ACTN3 gene encodes the actin-binding protein α-actinin-3, which is one of the predominant components of the Z-disk in human skeletal muscles. Further, there are two different versions of the ACTN3 gene – a functional R allele (production of α-actinin-3 protein) and an X allele (lack of production of α-ACTN 3 protein) [38]. Expression of this protein is restricted to the fast glycolytic fibers, which are responsible for generating rapid, forceful contractions, for example in sprinting and weightlifting [20]. Therefore, the R allele is associated with a greater proportion of type 2 fast muscle fibers (MHC- II), while the X allele represents an absence of α-ACTN 3 protein and consequently the absence of MHC- II. Furthermore, R allele is a relatively often studied allele, with growing evidence about its strong and positive relationship with sport success [38-43], also confirmed in review on combat sports by Youn et al., 2021. In terms of overall population, among individuals of European descent, less than a third of the population has two copies of the functional R allele (the RR genotype), while just over half the population has one copy of each of the two alleles (the RX genotype) [44]. Intriguingly, a significant proportion (~18%) of the human population is totally deficient in α-actinin-3 due to homozygosity for a premature stop codon polymorphism (R577X) in the ACTN3 gene [45], so genotype analysis on this particular gene seems to be a valuable and helpful process in terms of sports (taekwondo as well) performance capability and potential. Čular et al. [46] examined predictors of fitness status among taekwondo athletes, and concluded that speed and specific endurance are therefore most important abilities for success in combat taekwondo. Overall athlete's speed is a complex latent dimension, which mainly depends on the neuromuscular capabilities of the athlete. ACTN3 gene as a strong influence factor surely has a great potential for potential utilization in speed-relying combat sports.

Mitochondrial DNA haplogroups (mtDNA HG)

This term presents a group of similar haplotypes that share a common ancestor through their common mutations of single nucleotide polymorphism (SNP) within mtDNA. As well, the inheritance of mtDNA is conducted through maternal lineage. The presence of SNPs within a gene or a regulatory region may alter the amino acid sequence or the yield of the coded protein, ultimately affecting the activity or function of that protein. Thus, haplogroups are helpful in the definition of geographical genetic populations, while

haplotypes/ SNPs are in the investigation of the influence of genes on health or diseases [47]. Two extracted papers investigated haplogroup distribution among taekwondo athletes so far. First research was conducted by Kim et al. [15], where authors analyzed frequencies of M, M7, M8, M9, D, D4, G, G1, N, N9, Y, A, B and F haplogroups among 152 athletes (11 WT athletes) and 265 controls. There were significant differences in the distribution of mtDNA haplogroup frequencies overall between the endurance/middle power athletes (EMA) and controls (CON) and the combined EMA + sprint/power athletes (SPA) and CON groups, but not for the SPA and CON groups. Analysis revealed that EMA has the greatest frequency of the M and N9 haplogroup, while the B haplogroup seems to be underrepresented. It has been concluded that the distribution of mtDNA haplogroups affects elite endurance status among Korean people. Although this was an examination of a relatively small sample, such examinations contribute to a more accurate picture of haplogroup distribution among selected populations. Similar investigations should be conducted in other countries on various athlete populations in order to construct a unified database for every sport, continent and country. The second work regarding mtDNA HG from Table 1 [19] revealed results of mtDNA haplogroup genotyping within the Iranian population. The sample was composed of 100 (20 WT) athletes and 100 controls and the authors tested differences between frequencies of selected haplogroups between subsamples. Significant differences were observed for haplogroups U (underrepresented) and J (overrepresented) in the elite athletes' groups. Haplogroup J seems to be a desirable trait among Iranian athletes. Authors suggest that connection to certain extent might lay in desirable health-related traits previously investigated by other authors [48-51], such as the relation of haplogroup J with increased longevity and resistance to stress in certain populations. Haplogroup J was also examined in a series of investigations conducted by Finnish scientists [52-54] and they concluded that mtDNA haplogroups are one of the genetic determinants explaining individual variability in the adaptive response to endurance training, and mtDNA haplogroups J and K are markers of low-responders in exercise training. Also, BCAA catabolism is a surrogate marker of lower respiratory chain activity attributed to these haplogroups. Presented works confirm the hypothesis of a connection between certain haplogroups and athlete status. However, there are a lot of unexamined athletes and populations worldwide and this summarized knowledge unfortunately represents small percentage of complete haplogroup acquaintance within overall fitness status in taekwondo.

GA-binding protein transcription factor subunit beta 1 (GABPβ1) gene

Previous studies proved that the β1-subunit of the nuclear respiratory factor 2 (NRF2) is encoded by the GABPB1 gene, which is located on chromosome 15q21.2. Further, the polymorphisms located in this gene region may be associated with increased VO₂ [55-56]. GABPβ1 genotype AG and allele G were previously proven to be related to be advantageous for elite endurance athlete status and higher values of VO₂ [56-57]. The respective gene was analyzed by Guilherme et al. in 2020, on a sample of n=164 combat-sport athletes (n=47 WT) and n=965 controls. This is the first investigation of selected gene conducted on combat sports overall. Authors reported that GABPβ1 gene was associated with athletic status, with the minor G (rs7181866) and T (rs8031031) alleles overrepresented in athletes (p≤0.003), especially among world-class competitors (p≤0.000) [10]. Deacetylation of GABPβ1 facilitates complex formation with GABPA and its transcriptional activation, promoting proper mitochondrial function [58], which should be related to the enhanced metabolism of combat athletes and taekwondo athletes respectively. VO₂ however represents a valuable trait favorable for the vast majority of athletes regardless of sport. Consequently, future research of selected gene should concentrate on gene properties itself, expression ways, and its possible interactions with other & similar-to-VO₂ traits.

Table 1. Papers extracted for the current review (n=11).

Authors	n	Subject of research	Outcome
Gunay et al., 2010 [14]	67 (18 Tur/Azer national teams)	ACE I/D	-ID genotype most frequent -Azer athletes have increased DD genotype -no difference in con group
Kim et al., 2012 [15]	417 (11 tkd)	mtDNA haplogroups M, M7, M8, M9, D, D4, G, G1, N, N9, Y, A, B, F	-power sport athletes have increased M, N9 and lack of B -other show no difference
Shahmoradi et al., 2013 [16]	311	ACE I/D	-I allele increased among athletes -D allele increased among endurance athletes
Elsawy & Shaban, 2014 [17]	11	ACE (II, ID, DD genotypes)	-no correlation
Lee & Kim, 2015 [18]	44	IGF-I	-non-consistent connection
Arjmand et al., 2016 [19]	200 (20 tkd)	mtDNA haplogroups U, J	-U decreased among athletes -J increased among athletes
Jung et al., 2016 [20]	160 (40 tkd)	ACTN3 alleles	-no influence on the imbalance
Guilherme et al., 2020 [21]	1129 (47 tkd)	GABPb1	-increased among athletes -increased G and T, especially among elite athletes
Rocha et al., 2020 [22]	189 (20 tkd)	ACE I/D	-greater proportion of homozygotes among team athletes
Youn et al., 2021 [10]	14 313	PPARA, ACE, ACTN3, CKM, MCT1, FTO, GABPb1, COMT, FEV, SLC6A2, HTR1B, ADRA2A	-significant difference identified on 13 polymorphs, between exp and con
Hammad et al., 2022 [23]	11	Heat-shock proteins (HSP): HSP90AA1, HSP90AB1, PTGES3	-increased gene expression of HSP90AA1 & HSP90AB1 after VO2 treadmill test

tkd - taekwondo, Tur/Azer - Turkey/Azerbaijan national team members, exp - experimental group, con - control group, VO2 - oxygen intake.

Heat shock protein (HSP) genes: HSP90AA1 and HSP90AB1

Heat shock proteins (HSPs) respond to a variety of external and internal stresses to maintain homeostasis [23, 59]. Also, HSPs are molecular chaperones, binding to (holding) and refolding other cellular polypeptides (clients) with aberrant conformations [60, 61], processes which are dependent on hydrolysis of ATP [62]. HSP90 „family“ is influenced by the genes HSP90AA1 and HSP90AB1. HSP90AA1 expression may be regulated to maintain homeostasis by multiple factors such as hyperthermia, ATP depletion, hypoxia, and reactive oxygen species (ROS) generation [63, 64], while HSP90AB1 is necessary for the shuttle of client proteins between cytoplasm and nucleus [65, 66]. Both proteins share 60% overall homology and several regions of 50 amino acids (aa) or more share greater than 90% homology [62, 67]. But what do HSPs have in common with exercise and training conditions? During the physical exercise that organism detects as stress, HSPs are consequently increasingly expressed in plasma, monocellular cells, tissues and organs. HSP70/90 play a major role in immune regulation and cell protection during exercise and in the efficiency of regeneration and reparation processes [68]. There is unfortunately only one research about selected genes conducted on a sample of taekwondo athletes, by Hammad et al. reported in 2022 [23]. Authors of this work aimed to determine the effect of the VO2 test on the expression of genes related to heat shock proteins (HSPs) cycle (HSP90AA1, HSP90AB1, PTGES3) on a sample of n=11 taekwondo (black belt) male athletes. Further, the results reveal that levels of fold change expression were affected by the VO2 test. HSP90AA1, HSP90AB1 and PTGES3 mRNA

expression levels were significantly higher among taekwondo athletes immediately after the test ($p \leq 0.05$), while they tended toward homeostasis 2 hours after the test. The authors emphasize the fact that listed study demonstrates that maximal aerobic effort affects genetic expressions of HSPs and has a significant impact on several hematological and biochemical parameters. This paper is currently the only research to feature an investigation of HSPs/encoding genes for HSPs within taekwondo. Therefore, this is valuable information and guideline for future investigations, as HSP genes (HSP expression respectively) and intense exercise among taekwondo athletes seem to be connected and mutually influenced to a certain extent.

Insulin-like growth factor I gene (IGF-I)

Insulin-like growth factor I (IGF-1) is an important factor of the physiological mechanisms which affect child growth, and is controlled by the growth hormone (GH), also involved in growth stimulation [15, 69] as GH mediator. IGF-1 is the hormone most responsible for regulating cell growth and development, as well as for predisposing height. An athlete with abundant IGF-1 and other growth hormones and regulators will be tall [70], which is useful for taekwondo competitors as ectomorph phenotype became desirable trait for WT taekwondo combat due to their leg length [71]. Also, greater levels of this factor were found among sport winners in contrast to others [72]. Unfortunately, only one paper features a relationship between IGF-1 and taekwondo. Lee & Kim [15] in 2015 analyzed the effect of the regular taekwondo training for 16 weeks on physical fitness and growth index depending on the different IGF-1 gene polymorphisms. Results revealed that the difference between physical fitness and growth index according to the IGF-1 gene polymorphism after the taekwondo training is non-consistent and low impact, but however, authors stated that taekwondo training may affect the physical fitness and the growth index depending on the IGF-1 gene polymorphism. However, IGF-1 polymorphisms were examined in other sports as well to determine their possible connection with athletic performance. Ben-Zaken et al. [73] examined the role of IGF-1 receptor (IGF-IR) 275124A>C polymorphism, and AA genotype proportion was significantly greater among elite endurance athletes in regards to power athletes who had greater frequencies of the C allele, associated with muscle strength [74]. Selected (AA) genotype perhaps can be disadvantageous for power-oriented sports, and is not associated with endurance success, but rather performance. Polymorphisms in IGF-1 receptor may differentiate between the two edges of the endurance-power athletic performance running spectrum suggesting beneficial effects for endurance and prevent from success in power events [75]. Recent investigations by the same team [76] included six IGF-related polymorphisms (rs7136446, rs35767, rs6220, rs680, rs2854744, and rs1805086) and total genetic score results among athletes. The authors concluded that the IGF system seems important in land-speed sports events but not in swimming events. IGF-1 and the related growth factors IGF-2 and insulin, their receptors and multiple IGF-binding proteins constitute an extensive regulatory network involved in cell proliferation, differentiation and apoptosis. IGF-1 regulates normal growth during childhood and may exert a strong anabolic effect in adults [77]. In the context of taekwondo, IGF-1 and related factors seem to be disadvantageous for adult athletes, due to its anabolic effect which is not practical within the weight categories, and increased risk for tumor growth. Genetic testing of IGF-1 among young taekwondo athletes could be utilized in talent identification processes, due to its relation with final height predispositions. Moreover, monitoring of pubertal pace among young athletes can be successfully traced through the hormonal testing of selected factor.

DISCUSSION

There is unfortunately only one relatively recent and existing review about genetics in combat sports conducted by Youn et al. in 2021 [10], who extracted 8 polymorphisms (PPARA rs4253778, ACTN3 rs1815739, ACE rs4646994, CKM rs8111989, MCT1 rs1049434, FTO rs9939609, GABP β 1 rs7181866 and rs8031031) related to the athletic performance and 5 (COMT rs4680, FEV rs860573, SLC6A2 rs2242446, HTR1B rs11568817, ADRA2A rs521674) related to psychological traits. However, their conclusion suggests it is still not clear which genes could be explicitly connected with elite combat sports athletes and how do they affect the elite athlete's status or performance in combat sport. Similar psychophysical traits are desired by the vast majority of athletes, regardless of sport or discipline, because almost every competitive athlete wants to be fastest, strongest and best within their competition range. Taekwondo athletes are also among them, so gene variants that impact taekwondo also impact other sports, especially (striking) combat sports and *vice versa*.

Coaches, professional and voluntary staff within a sport community should be aware of challenges that arise from this field. Unfortunately, overall scientific knowledge about the impact of all possibly significant polymorphisms in terms of sports performance is still far from complete [78]. Existing assay packages to include analysis of „performance“ genes, offered by a growing number of clinics are often limited to several gene variants, and do not include practical/individual interpretation of results. There is an ongoing debate among scientists: is the genetic testing for talent selection ethically correct? It surely is, but it must be correctly conducted. Every healthy individual's phenotype has a predisposition for a certain activity or sport, while the final success within one depends on and is affected by many more factors. Endomorphs are therefore more suitable for the activities such as ball and hammer throwing, boxing, powerlifting, while the extreme ectomorphs should be directed towards volleyball, basketball, taekwondo, athletes with higher proportions of MHC-I fibers will be directed toward the endurance activities, etc. Further, such logic is applicable on all traits to be assessed through genetic testing. Professional and experienced staff should conduct selected processes with great caution towards the youth, and that is the only correct way to avoid any ethical error. It will reduce number of children who give up on sports on regular basis because they are not „good enough“, but maybe they are practicing (in this context) wrong sport. Thus, expressions of a certain gene vary from person to person, so even if the all significant genes were tested, gene scores can not reveal the whole picture of individual's overall elite athlete potential. There comes the need for a multidisciplinary approach in talent identification, and inclusion of various tests, including anthropometric, genetic, motor, physiological, psychological, and hormonal tests.

WT demonstrated its desire to become a modern sport, and the applicability of kinematics and electronics within taekwondo combat brought an evolution to the combat sports. Consequently, as WT became a relevant and popular sport, there is a growing need for the advancement of the current knowledge about favorable preconditions for competitive success in taekwondo, which are found in genetics to a certain extent. Current evidence about genetic examinations in taekwondo is summarized in this review. We can affirm that several gene polymorphisms (specific alleles and genotypes) and mtDNA haplogroups may influence the elite status of taekwondo athletes. This statement includes ACE I/D (I allele, II/ID genotype) associated with elite endurance, ACTN3 (R allele, RR genotype) related to the MHC- II, GABP β 1 (G (rs7181866) and T (rs8031031) alleles) and HSP genes (HSP90AA1, HSP90AB1) being associated with greater VO₂, and finally, IGF-1 related to skeletal longitudinality and maturation. Furthermore, analysis of mtDNA haplogroups revealed possible positive relationship between the J haplogroup and elite athlete status among Iranian populations, and M and N9 haplogroups within the Korean population. Although this data is valuable and useful, there is still no hierarchical scheme of factorial structure about the possible impact of relevant gene polymorphisms on sport

success, or athlete status at all. Also, the implementation of gene analysis within the processes of detection, selection, development & support of young taekwondo athletes would be of much value. A combination of gene testing and other advanced, non-invasive and accessible diagnostic tools will surely strengthen mentioned processes and minimize mistakes within. Therefore, the value of this review will be manifested within the guidelines for future genetic research in taekwondo, presented below.

Guidelines for the future genetic research in taekwondo:

1. Inclusion of genes and polymorphisms within previously proved to be advantageous for the sport overall, polymorphisms related to the muscular architecture and muscle properties, cellular metabolism, immune parameters, ultimate physical and physiological capabilities & psychological strength.
2. Inclusion of a wide spectrum of Y DNA and mtDNA haplogroups/haplotypes within research, and differentiation according to the different populations, countries, continents, etc.
3. Inclusion of polymorphisms and genotypes previously proved to have a significant role in the enhancement of certain favorable phenotypes among combat athletes from other sports besides taekwondo.
4. Analysis of epigenetic variations of the gene expression in the context of favorable traits within a specific athletic performance.
5. There is a number of studies focused on „athlete status“, or „fitness status“, but there is insufficient evidence regarding the relation between genetics and uttermost competitive success.
6. Analysis of morphologic phenotypes and their possible relation to the specific genes.
7. Further investigation of doubtful polymorphisms with contradictory research outcomes, or whose function and impact are not clearly described or determined yet.
8. Investigation of a possible connection between hematological and cardiovascular parameters and relevant polymorphisms.
9. Systematic compression of all existent data and determination of precise interrelation/factorial scheme between specific genes and performance variables (physiological, physical and psychological parameters).
10. Determination of genetic research impact within talent identification processes, as well as comparisons with a variety of non-invasive diagnostic tools and specific success-dependent sex, age and weight groups.

CONCLUSION

This article summarizes the knowledge about the current stage of genetic research and its applications in taekwondo and proposes guidelines for the future research. The authors suggest that several gene polymorphisms and mtDNA haplogroups may influence the elite status of taekwondo athletes, including ACE I/D, ACTN3, GABPb1, HSP90AA1 & HSP90AB1, IGF-1 and mtDNA haplogroups M, N9 and J. Challenges regarding genetic testing within talent identification processes were addressed and the key way to solve and pass them is to methodologically correctly perform it, by the professionals with expert knowledge level. Proposed guidelines for future research presented above follow the path of existing literature and experimental research presented in this review.

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Data Availability Statement: Data supporting reported results can be found within scientific bases in which authors have conducted the review, through the following links: <https://scholar.google.com/>; <https://pubmed.ncbi.nlm.nih.gov/>; <https://www.webofscience.com/wos/woscc/basic-search/>

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