Manuscript title: Genetic associations with technical capabilities in English academy football players: a preliminary study

Running title: Genetic associations with technical capabilities

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Abstract

BACKGROUND: Technical capabilities have significant discriminative and prognostic power in youth football. Although, many factors influence technical performance, no research has explored the genetic contribution. As such, the purpose of this study was to examine the association of several single nucleotide polymorphisms (SNPs) with technical assessments in youth football players.

METHODS: Fifty-three male under-13 to under-18 outfield football players from two Category 3 English academies were genotyped for eight SNPs. Objective and subjective technical performance scores in dribbling, passing, and shooting were collated. Simple linear regression was used to analyse individual SNP associations each variable, whereas both unweighted and weighted total genotype scores (TGSs; TWGSs) were computed to measure the combined influence of all SNPs.

RESULTS: In isolation, the *ADBR2* (rs1042714) C allele, *BDNF* (rs6265) C/C genotype, *DBH* (rs1611115) C/C genotype, and *DRD1* (rs4532) C allele were associated with superior (8-10%) objective dribbling and/or shooting performance. The TGSs and/or TWGSs were significantly correlated with each technical assessment (except subjective passing), explaining up to 36% and 40% of the variance in the objective and subjective assessments, respectively.

CONCLUSIONS: The results of this study suggest inter-individual genetic variation may influence the technical capabilities of youth football players and proposes several candidate SNPs that warrant further investigation.

Keywords: Genomics; polygenic profile; skill acquisition; soccer; talent identification.

## Introduction

In football (soccer), technical skills (e.g., dribbling, passing, and shooting) are some of the most frequently performed actions during match-play [1]. There has been a significant increase in the frequency of technical skills completed within national and international competitions over time. For instance, from the 2006/07 to the 2012/13 season in the English Premier League there was an increased incidence of dribbling (~20%) and passing (~30%) [2]. Moreover, in the context of international competition, ball speeds (~15%) and passing rates (~35%) increased significantly between 1966 and 2010 in World Cup final matches [3].

The continued rise in the number of technical actions performed during match-play in football may be driven by their association with the relative success of the team. Indeed, Rampinini et al. [4] reported that more dribbling, passing, and shooting were associated with a higher league position ($1^{st}$ to $5^{th}$ vs. $16^{th}$ to $20^{th}$) in the Italian Serie A. Moreover, technical actions such as passing and shooting frequency were related to a team's league position ($1^{st}$ to $6^{th}$ vs. $7^{th}$ to $18^{th}$) in the Greek Superlegue first division [5]. Similar findings have also been reported in youth football, whereby teams that attempted a greater number of shots attained a higher placing ($1^{st}$ to $4^{th}$) at the under-17 Al Kass International Cup [6].

Technical capabilities also have significant discriminative power with regards to individual playing levels and perceived potential within youth football. For instance, Vaeyens et al. [7] showcased that a technical testing battery (ball juggling, lob pass, shooting accuracy, and slalom dribble) could distinguish under-13 to under-16 ability groups (i.e., elite, sub-elite, and non-elite). More recently, Kelly et al. [8] reported that 'higher-potential' under-12 to under-16 players in the same academy performed significantly better at the same four technical tests than 'lower-potentials'. In addition, Keller et al. [9] revealed that the Loughborough Short Passing Test, long passing test, shooting test, and speed dribbling test were able to differentiate under-18 youth football players, with the highest playing level achieving the highest scores.

From a talent identification perspective, perhaps the most important factor is the significant prognostic value of technical skill possessed at younger ages on career progression and attainment. As an example, Huijgen et al. [10] reported that during ages 14 to 18 years in the Netherlands future professional players outperformed amateur players in dribbling. Similarly, Forsman et al. [11] revealed that at age 15 years in Finland future professional players outperformed non-professional players in dribbling and passing. In Germany, at the under-12

to under-15 age groups future professionals outperformed both semi-professionals and non-professionals in ball control, dribbling, and shooting [12,13].

Given the evidence supporting the influence of technical skills on a football match as well as their discriminative and prognostic power, it is not surprising coaches and scouts view technical skill as an integral part of evaluating a player's current performance and future potential [14]. However, technical capabilities are the result of a complex and multifactorial relationship between several factors [15]. Indeed, age, maturation, lean body mass, hours of practice, type of practice, and playing position have all been associated with influencing technical skill in some capacity [16]. Although, a potentially important factor that is currently under-researched throughout talent identification and development in football is the contribution of genetics [17–19].

More specifically, inter-individual genetic variation is responsible for differences in all observable human traits to some extent [20]. Heritability studies have reported relatively high estimates for the influence of genetics on traits theoretically associated with technical capability, such as motor control and motor learning (~70%) [21,22]. A number of genetic polymorphisms have also already been identified that influence several of these traits, particularly polymorphisms in genes that encode for dopamine receptors and degradation enzymes within the dopaminergic system. These polymorphisms are consistently associated with traits such as motor control and motor learning due to the role of dopamine in several brain processes, including learning, movement, plasticity, and reward [23]. Therefore, as a by-product, these genetic polymorphisms may also be related to technical ability in football.

Several genetic polymorphisms have been associated with physiological and injury phenotypes in football, as well as overall athlete status due to their influence on these underpinning traits [17,18]. However, the extent to which genetic variants may contribute to technical capabilities within the context of football is very limited. In Australian Rules Football (AFL), Jacob et al. [24] found associations between several single nucleotide polymorphisms (SNPs) in the *ACE*, *ADRB2*, *ADRB3*, *BDNF*, *COMT*, and *DRD2* genes and the Nathan Buckley kicking skill assessment. Although SNPs appear to impact technical skills in AFL, it is currently unclear to what extent inter-individual genetic variation influences technical skill specifically in football. Moreover, the genetic polymorphisms that are ultimately responsible for any association are yet to be identified. Identifying a panel of SNPs associated with technical performance may enhance athlete development processes in football by enabling more individualised training programmes. Therefore, this preliminary study examined

associations between genetic polymorphisms and technical assessments in youth football players.

## Materials and methods

### Participants

Fifty-three male under (U)-13 to U-18 (aged 16.28 ± 1.27 years) outfield football players from two Category 3 English academies were examined [U-13 (n = 2), U-14 (n = 2), U-15 (n = 9), U-16 (n = 10), U-17 (n = 7) and U-18 (n = 23)]. Objective technical performance scores (n = 26) were collected from one academy and subjective technical coach ratings (n = 27) were collected from the other academy, in adherence with each club's standard player assessment protocols. Informed assent from all players, consent from parents/guardians, and gatekeeper consent from each academy was collected prior to the commencement of the study. All experimental procedures were conducted in accordance with the guidelines in the Declaration of Helsinki and ethical approval was granted by Birmingham City University via the Health, Education, and Life Sciences Academic Ethics Committee. This study was conducted in accordance with the recommendations for reporting the results of genetic association studies defined by the STrengthening the REporting of Genetic Association studies (STREGA) Statement.

### Objective data

Objective data on three football-specific technical tests were collected: (a) slalom dribble, (b) lob pass, and (c) shooting accuracy. The slalom dribble test required players to control the ball through nine cones (2 m apart) from the start to the end line and return. Each player completed two trials and the quickest was recorded for analysis, measured via timing gates (Brower TC Timing System, Draper, Utah, USA). In the lob pass test, players had ten attempts (five with each foot) to kick the football from a distance of 20 m into a target area divided into three concentric circles. Each circle was different in diameter (3 m, 6 m, and 9.15 m) and each attempt received points (3, 2, and 1, respectively) depending on the circle in which the ball originally landed. In the shooting accuracy test, players had ten attempts (five with each foot) to kick the ball at a 16 m wide goal target from a shooting distance of 20 m central to the goal. The goal was divided into five parallel zones: centre (2 m wide), two areas on each side of the centre (3 m wide), and two areas 4 m wide at each extreme (4 m wide) that award different points (3, 2, and 1, respectively). All tests have been previously utilised in football research as valid indicators of technical skill in youth football populations [7,8].

## Subjective data

Subjective data on the technical skills of dribbling, passing, and shooting were collected. Coaches from each age group (who possessed the minimum of a UEFA B licence) used a 5-point Likert scale to rate the technical abilities of each player: 1 = significant weakness; 2 = requires attention; 3 = competent; 4 = accomplished; and 5 = excellent. Each coach independently completed their technical ratings. The average rating on each technical skill from all coaches was then recorded for analysis. The coach-based subjective ratings used in this study have been utilised previously by researchers in youth football and demonstrate good reliability and validity [25].

## Genetic procedures

### *Genotyping*

Saliva was collected from players via sterile, self-administered buccal swabs, following a minimum of 30 minutes since food or drink ingestion. Within 36 hours, saliva samples were sent to AKESOgen, Inc. (Peachtree Corners, GA, USA) for DNA extraction. Using Qiagen chemistry, DNA was extracted on an automated Kingfisher FLEX instrument (Thermo Fisher Scientific, Waltham, MA, US). The manufacturer's recommended guidelines and procedures were followed throughout. To measure the extracted DNA's quality and quantity, PicoGreen and Nanodrop measurements were taken. Input to the custom testing array occurs at 200 ng in 20 μL. Amplification, fragmentation, and resuspension were performed using Biomek FXP. GeneTitan instrumentation (Thermo Fisher Scientific, Waltham, MA, US) was used to stain and scan the arrays, with hybridisation performed in a Binder oven at 48 degrees for 24 hours, following the Affymetrix Axiom high throughput 2.0 protocol. Data analysis was then performed using a raw CEL file data input into the Affymetrix Axiom Analysis Suite (Affymetrix, Santa Clara, CA, US).

### *Polymorphism selection*

To identify polymorphisms potentially associated with technical skills in football, empirical research, review articles, book chapters, and the GWAS catalog (https://www.ebi.ac.uk/gwas/) were examined. After an extensive search of the literature, the following polymorphisms were selected: Adrenoceptor beta 2 (*ADRB2*; rs1042714), Angiotensin I converting enzyme (*ACE*; rs4341), Brain derived neurotrophic factor (*BDNF*; rs6265), Catechol-O-methyltransferase (*COMT*; rs4680), Dopamine beta-hydroxylase (*DBH*; rs1611115), Dopamine receptor D1 (*DRD1*; rs4532), Dopamine receptor D2 (*DRD2*; rs1076560), and Dopamine receptor D3

(*DRD3*; rs6280) (see Supplementary Table 1 for more information). These gene names and symbols are in accordance with those officially approved by the Human Gene Nomenclature Committee (HGNC; https://www.genenames.org). Standard genomic quality control (QC) procedures and thresholds were applied when selecting polymorphisms: SNP call rate (>95), sample call rate (>95), fisher's linear discriminant (>3.6), and minor allele frequency (>0.05).

*Total genotype score*

A total genotype score (TGS) was calculated to assess the combined influence of the included SNPs on each dependent variable. Since Williams and Folland [26] first proposed and implemented the TGS, the mathematical algorithm has undergone various modifications to try and improve its accuracy. For instance, one approach has included incorporating a mathematical weight for each SNP based on its partial influence in a regression model [27,28]. Both unweighted and weighted TGS approaches have demonstrated sufficient discriminatory power. As such, both an unweighted and weighted TGS were calculated and implemented in this study (referred to herein as TGS and TWGS, respectively).

To generate both the TGS and TWGS, each genotype of a respective SNP initially received a score between 0-2 based on the observed genotype associations with a dependent variable. Genotypes of co-dominant models (AA vs. Aa vs. aa) were assigned three scores (i.e., homozygous-associated genotypes received a score of two, the heterozygote received a score of one, and the alternate homozygous genotype received a score of zero), whereas genotypes of dominant (AA vs. Aa-aa) and recessive (AA-Aa vs. aa) models were assigned a score of two (i.e., associated genotype[s]) or zero (i.e., alternate genotype[s]).

For the TGS, the genotype scores (GS) were then summed and transformed into a 0-100 scale by dividing the total score by the maximum possible score and multiplying by 100.

$$TGS = (combined\text{-}GS / maximum\text{-}GS) * 100$$

For the TWGS, a similar procedure to Varillas Delgado et al. [28] was used. Each GS was multiplied by the standardised beta coefficients (β) of each SNP following multiple regression with each dependent variable to create weighted genotype scores (WGS). The WGSs were then summed and transformed into a 0-100 scale by dividing the total score by the maximum possible score and multiplying by 100. Greater values in both models indicate a polygenic profile more advantageous to technical performance in football.

$$TWGS = (combined\text{-}WGS / maximum\text{-}WGS) * 100$$

Data analysis

Each SNP was tested for adherence with Hardy-Weinberg equilibrium (HWE) using an exact test. Linkage disequilibrium (LD) was analysed using LDlink and data from the 1000 Genomes Project European ancestry population [29]. All other data were analysed using Jamovi version 1.8.1 and IBM SPSS version 25. Normality was assessed with the Shapiro-Wilk test and homoscedasticity was assessed using Levene's test. Akaike information criterion (AIC) was used to select which genetic model (i.e., co-dominant, dominant, recessive) best fits the data and would be subjected to hypothesis testing. However, if MAF $\leq 0.25$, a dominant model was utilised to retain statistical power. Simple linear regression was performed to assess the association of genotype models with each objective and subjective dribbling, passing, and shooting assessments. Age was controlled for in the objective analysis by adding it as a covariate. Multiple regression was used to calculate the standardised beta coefficients (β) of each SNP for the TWGS models. Simple linear regression was then performed to assess the association of each TGS and TWGS with each dependent variable. Pearson's correlation coefficient (*r*) with thresholds values of ≤0.1 (trivial), >0.1-0.3 (small), >0.3–0.5 (moderate), >0.5–0.7 (large), >0.7–0.9 (very large), and >0.9–1.0 (almost perfect) were used to measure correlation [30]. The coefficient of determination ($R^2$) was computed to determine the variance explained by each TGS and TWGS. Statistical significance was set at $p < .05$.

**Results**

Genotype and allele distributions of all SNPs were in HWE and all SNPs were in linkage equilibrium. Assumptions of normality and homoscedasticity were not violated. Descriptive statistics for objective and subjective technical variables and genotype frequencies are displayed in Supplementary Table 2 and Table 3, respectively.

Objective associations

*Dribbling*

There was a significant association between *DRD1* ($F_{(1, 23)} = 6.51$, $p = .018$), *ADBR2* ($F_{(1, 23)} = 6.32$, $p = .019$), *DBH* ($F_{(1, 23)} = 4.64$, $p = .042$), and dribbling performance (see Table 1). More specifically, *DRD1* T/T homozygotes were 10% slower than C allele carriers ($B = 1.37$), *ADBR2* G/G homozygotes were 9.5% slower than C allele carriers ($B = 1.46$), and *DBH* C/C homozygotes were 8.2% faster than T allele carriers ($B = -1.27$). There were also significant associations with both the TGS ($F_{(1, 24)} = 7.02$, $p = .014$) and the TWGS ($F_{(1, 24)} = 8.74$, $p = .007$). While the TGS had a moderate negative correlation ($r = -.48$) and explained 23% of the

variance, the TWGS had a large negative correlation ($r$ = -.52) and explained 27% of the variance (see Figure 1).

*Passing*

There were no significant associations between any single SNP or the TGS ($F_{(1, 24)}$ = 1.33, $p$ = .260) and passing performance. However, there was a significant association with the TWGS ($F_{(1, 24)}$ = 5.23, $p$ = .031), which had a moderate positive correlation ($r$ = .42) and explained 18% of the variance.

*Shooting*

There was a significant association between *BDNF* ($F_{(1, 23)}$ = 6.78, $p$ = .016), *DBH* ($F_{(1, 23)}$ = 4.52, $p$ = .044), and shooting performance. More specifically, *BDNF* C/C homozygotes achieved 9.5% higher scores than T allele carriers ($B$ = 2.27) and *DBH* C/C homozygotes achieved 8.2% higher scores than T allele carriers ($B$ = 1.96). There were also significant associations with the TGS ($F_{(1, 24)}$ = 10.86, $p$ = .003) and the TWGS ($F_{(1, 24)}$ = 13.74, $p$ = .001). Both the TGS and TWGS had large positive correlations ($r$ = .56; $r$ = .60) and explained 31% and 36% of the variance, respectively.

***Insert Table 1 near here***

***Insert Figure 1 near here***

Subjective associations

*Dribbling*

There were no significant associations between any single SNP and dribbling rating (see Table 2). However, there were significant associations with the TGS ($F_{(1, 25)}$ = 8.91, $p$ = .006) and the TWGS ($F_{(1, 25)}$ = 16.71, $p$ < .001). More specifically, both the TGS and TWGS had large positive correlations ($r$ = .51; $r$ = .63) and explained 26% and 40% of the variance, respectively (see Figure 2).

*Passing*

No significant associations were identified between any single SNP, the TGS ($F_{(1, 25)}$ = 2.38, $p$ = .135), or the TWGS ($F_{(1, 25)}$ = 3.08, $p$ = .092) and passing rating.

*Shooting*

There were no significant associations between any single SNP and shooting rating. However, there were significant associations with the TGS ($F_{(1, 25)}$ = 7.85, $p$ = .010) and the TWGS ($F$

$_{(1, 25)}$ = 11.97, $p$ = .002). The TGS had a moderate positive correlation ($r$ = .49) and explained 24% of the variance, whereas the TWGS had a large positive correlation ($r$ = .57) and explained 32% of the variance.

***Insert Table 2 near here***

***Insert Figure 2 near here***

**Discussion**

This preliminary study investigated the association of eight SNPs, both individually and collectively, with objective and subjective assessments of technical capabilities in youth football players. In doing so, this study has shown for the first time: (a) genetic variations may be associated with the technical capabilities of youth football players, (b) the genetic variants that may be responsible for inter-individual variability in technical skill, (c) phenotypic distinctions in the characteristics of objective and subjective assessments may alter allelic associations, and (d) advantageous genotypes may have an additive effect on technical performance in football, irrespective of assessment method. As such, these preliminary findings may have important implications for future football genomic studies.

The single SNP analysis revealed four SNPs associated with objective dribbling and shooting assessments, but there were no associations with the objective passing assessments. This may reflect the different phenotypic characteristics of the tests and/or the much wider distribution of scores in the passing test compared to dribbling and shooting, which would have decreased statistical power in the passing test. The SNPs associated with either of the dribbling and shooting objective assessments were: *ADBR2* (rs1042714), *BDNF* (rs6265), *DBH* (rs1611115), and *DRD1* (rs4532). Studies in this area, with this type of unique sample, are typically underpowered, which can make it difficult to clearly make conclusions about what these findings mean. However, in early stages of development in a field, informed speculation based on prior knowledge may be important for informing future work. As a result, we have made informed speculation about our findings as a way of guiding subsequent work in this area.

The C allele of *ADBR2* (rs1042714) was associated with a faster completion time in the slalom dribble test and exhibited the largest effect of any SNP on this phenotype. These results correspond with those of Jacob et al. [24], who reported that C allele carriers performed significantly better during a skill assessment in AFL. The findings of both studies indicate that *ADBR2* (rs1042714) may play a role in motor control and/or development. To the authors'

knowledge, the association of *ADBR2* (rs1042714) with motor skills has yet to be investigated outside of the sport domain. The G allele has, however, been associated with an increased risk of autism [31]. Although speculative, the proposed underpinning mechanisms of this association may help elucidate the results of this study, as autism is in part characterised by deficits in skill acquisition [32]. The *ADRB2* gene encodes the beta-2-adrenergic receptor, which is widely expressed in the brain as part of the catecholamine system and acts as a receptor for adrenaline, noradrenaline, and dopamine [33]. The *ADRB2* (rs1042714) SNP modulates receptor activity and sensitivity [34], whereby the G allele is associated with increased responsiveness to ligand and delayed desensitisation and downregulation. As the G allele is more responsive, it may increase vulnerability to the associated effects of overstimulation (i.e., altered cell replication, differentiation, morphology and distribution), causing neurodevelopmental disorders by modifying neural architecture [31], and consequently deficits in technical ability in football. Other research has also shown that *ADBR2* (rs1042714) may be associated with changes in white matter and cognitive functions, although specific allelic associations have been inconsistent [35]. As such, further research with larger samples is required to validate the association of *ADBR2* (rs1042714) with technical ability in football as current mechanistic explanations are speculative.

The C/C genotype of *BDNF* (rs6265) was associated with a higher score in the shooting accuracy test and exhibited the largest effect of any SNP on this phenotype. These results are in accordance with a plethora of research that suggests the T allele is associated with a decreased motor learning capacity. The *BDNF* gene encodes for the BDNF protein, which influences cortical synaptic plasticity [36]. Carriers of the *BDNF* (rs6265) T allele have shown lower increases in the amplitude of motor-evoked potentials and motor map reorganisation following motor training [37]. Moreover, following transcranial magnetic stimulation, there was no change in the neurological excitability of individuals possessing the T allele, whereas there was a 67% increase in C allele carriers [38]. This suggests T allele carriers may have a lower motor learning adaptation capacity due to less neurobiological excitability, which may be related to altered cortical synaptic plasticity. Indeed, it has been reported that the T allele produces a lower activity-dependent release and recruitment of BDNF in neurons, altered glutamatergic and GABAergic synaptic transmission, and changes of cortical and hippocampal morphology resulting in deficits in learning and memory [39]. As such, the association of *BDNF* (rs6265) with technical ability in football may be explained by its potential influence on motor learning. The C/C genotype has also been associated with power assessments in youth football

players [40], indicating the C allele may be advantageous in this population across a number of sport-specific actions.

The C allele of *DRD1* (rs4532) was associated with a faster completion time of the slalom dribble test. The *DRD1* gene encodes the DRD1 protein, which helps regulate synaptic dopamine levels by subserving dopamine neurotransmission across motor cortices and the basal ganglia [41]. The *DRD1* (rs4532) SNP is in a 5′ untranslated regulatory region that may affect mRNA stability and translation, as the C allele has been associated with several disorders associated with increased brain dopamine neurotransmission [42]. Increased dopamine levels have been found to promote motor learning and motor cortex plasticity, so long as an excess of dopamine is not accumulated [43]. Indeed, when *DRD1* (rs4532) was incorporated into a TGS, with the C allele classified as an advantageous genotype, the TGS was associated with greater motor learning [23]. As such, the findings of this study suggest a role for *DRD1* (rs4532) on technical ability in football due to the potential association with dopamine levels and consequently motor learning.

The C/C genotype of *DBH* (rs1611115) was associated with a faster completion time of the slalom dribble test and a higher score in the shooting accuracy test. The *DBH* gene encodes the DBH enzyme which catalyses the oxidative hydroxylation of dopamine to norepinephrine [44]. DBH enzymatic activity modulates norepinephrine levels and influences executive and motor function [45]. It has been estimated that the *DBH* (rs1611115) SNP explains between 30 to 50% of the variance in DBH activity, with the T allele associated with decreased DBH activity [46]. Since DBH plays an important role in the metabolism of dopamine and norepinephrine, decreased DBH activity may facilitate structural or functional neuronal damage, and consequently neurodevelopmental and neurodegenerative disorders [44]. Therefore, as the C allele may be associated with higher DBH activity and consequently improved motor function, this mechanism may explain the association of *DBH* (rs1611115) with technical ability in football.

There were no associations between a single SNP and the subjective coach ratings of any technical skill. This may in part be due to the specific characteristics of a different cohort, but it is also likely because of the unique criteria coaches use to judge player and technical ability. Unfortunately, coaches have found it difficult not only to describe technical proficiency, but also explicitly report the criteria they use to assess athlete abilities [14]. Indeed, as a recent review highlighted [47], there is a lack of knowledge and clear understanding of how coaches subjectively assess the abilities of players throughout the literature, and as a result, the

underlying mechanism(s) remains unknown. Therefore, the specific phenotypic characteristics coaches evaluate in players to infer technical ability, may be subtly different from those that facilitate improved performance in objective tests.

Research has indicated that objective and subjective assessments of player ability in football have similar prognostic validity [48]. However, the levels of agreement between subjective and objective assessments of current performance have only been confirmed using physical assessments [25]. Moreover, Dugdale et al. [25] reported that coaches' subjective assessments of physical assessments only corresponded with the extremities (i.e., highest and lowest objective performances), suggesting that subjective assessments may lack sensitivity when discriminating between players of similar ability. Although these findings are yet to be replicated with technical assessments, they may help explain the non-significant results of this study due to the narrow distribution of subjective scores.

The TGSs and TWGSs were associated with several objective and subjective technical assessments. This suggests the technical skills of dribbling, passing, and shooting in football are polygenic traits and the SNPs in this study have an additive effect on each skill. This finding is in accordance with a previous investigation on the collective influence of genetic polymorphisms on motor learning, which found advantageous alleles of genetic variants associated with dopamine neurotransmission influence the motor system in an additive manner [23]. This study also showed weighting SNPs by their partial influence improved the relationship between each GS model and the respective technical phenotype under investigation. This finding is congruent with previous research comparing unweighted and weighted TGSs using a similar approach. For instance, Massidda et al. [27] found a TWGS explained 10% and 15% more of the variance than a TGS in countermovement jump and squat jump height, respectively. In this study, the TWGSs explained 4-13% and 2-14% more of the variance than the TGSs in the objective and subjective assessments, respectively. These findings suggest each advantageous allele of a given SNP may have a different degree of influence on a specific technical phenotype. Moreover, these findings showcase that dribbling, passing, and shooting all have subtly different phenotypic characteristics, resulting in each having unique advantageous genotypes and polygenic profiles. However, some SNPs also have a pleiotropic effect, whereby they influence separate technical phenotypes in a similar manner (e.g., *DBH* C/C genotype on objective dribbling and shooting performance).

This study has several limitations which should be acknowledged when interpreting its results. The main limitations derive from the size of the samples and the number of association

tests performed without adjustment for multiple comparisons. However, the sample sizes used in this study are similar to that of other preliminary studies in this research area [e.g., Jacob et al. [24]] and indeed football genetics as a whole [see McAuley et al., [17] for a review]. Furthermore, adjustments for multiple comparisons in exploratory research are not recommended [see Althouse, [49]], as reducing Type 2 errors is the priority to ensure an important novel association is not missed, which can be confirmed or rejected in subsequent higher-powered studies. Nevertheless, the observed associations could be false positives or might only be specific to the samples under investigation, and consequently may not be generalisable to other football cohorts. As such, further research is required with independent and larger football cohorts to replicate and assess the external validity of these results before practical applications can be recommended. Building this research base with studies using transparent methodologies is important so they can contribute to research synthesis approaches in the future to draw more valid and reliable conclusions [50]. There are many other factors that may influence performance in technical assessments that could not be controlled for. For instance, recent research has shown that maturation status is associated with distinct genetic profiles in youth football players [40]. Capturing and adjusting for maturation status as well as chronological age and other confounding variables may provide greater context to findings.

## Conclusions

This study indicates inter-individual genetic variation may influence the technical capabilities of youth football players. These findings suggest *ADBR2* (rs1042714), *BDNF* (rs6265), *DBH* (rs1611115), and *DRD1* (rs4532), in isolation, may be significant predictors of dribbling and shooting performance when using objective assessment methods. In addition, the polygenic models of all the SNPs included in this study were shown to be significant predictors of technical capabilities, irrespective of assessment method. As such, these SNPs may prove to be a useful starting point in establishing a genetic profile tool capable of assisting with technical performance assessment and development. However, before the results of this study can be considered for practical applications, replications via higher-powered research designs are necessary.

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**Table I.** Objective simple regression analysis

| Gene (SNP) | Model | Skill | *B* | *SE B* | β | *t* | *p* |
|---|---|---|---|---|---|---|---|
| *ADBR2* (rs1042714) | G/G vs. G/C-C/C | Dribbling | 1.46 | 0.58 | 0.74 | 2.51 | **.019*** |
| | | Passing | 0.46 | 2.14 | 0.08 | 0.21 | .833 |
| | | Shooting | -1.92 | 0.95 | -0.82 | -2.03 | .054 |
| *ACE* (rs4341) | G/G vs. G/C-C/C | Dribbling | -0.62 | 0.67 | -0.32 | -0.93 | .360 |
| | | Passing | 0.06 | 2.22 | 0.01 | 0.03 | .978 |
| | | Shooting | -0.49 | 1.06 | -0.21 | -0.47 | .645 |
| *BDNF* (rs6265) | C/C vs. C/T-T/T | Dribbling | 0.21 | 0.63 | 0.11 | 0.33 | .741 |
| | | Passing | 0.02 | 2.07 | 0.00 | 0.01 | .994 |
| | | Shooting | 2.27 | 0.87 | 0.97 | 2.60 | **.016*** |
| *COMT* (rs4680) | G/G vs. G/A-A/A | Dribbling | 0.42 | 0.80 | 0.21 | 0.52 | .606 |
| | | Passing | -0.76 | 2.63 | -0.14 | -0.29 | .775 |
| | | Shooting | -1.07 | 1.24 | -0.46 | -0.86 | .396 |
| *DBH* (rs1611115) | C/C vs. C/T-T/T | Dribbling | -1.27 | 0.59 | 0.64 | 2.15 | **.042*** |
| | | Passing | 1.01 | 2.09 | -0.19 | -0.48 | .633 |
| | | Shooting | 1.96 | 0.92 | -0.84 | -2.13 | **.044*** |
| *DRD1* (rs4532) | T/T vs. T/C-C/C | Dribbling | 1.37 | 0.54 | 0.69 | 2.55 | **.018*** |
| | | Passing | -1.70 | 1.95 | -0.31 | -0.87 | .395 |
| | | Shooting | 0.20 | 0.95 | 0.08 | 0.21 | .839 |
| *DRD2* (rs1076560) | C/C vs. C/A-A/A | Dribbling | -0.82 | 0.59 | 0.42 | 1.39 | .177 |
| | | Passing | -2.97 | 1.91 | 0.55 | 1.56 | .133 |
| | | Shooting | -1.30 | 0.92 | 0.55 | 1.41 | .173 |
| *DRD3* (rs6280) | T/T vs. T/C-C/C | Dribbling | -0.37 | 0.61 | -0.19 | -0.62 | .544 |
| | | Passing | 0.52 | 1.99 | 0.10 | 0.26 | .795 |
| | | Shooting | -0.68 | 0.94 | -0.29 | -0.72 | .480 |

*Note.* Bold values and * highlight statistical significance at $p < .05$. *B* = unstandardised beta; *SE B* = standard error; β = standardised beta.

**Table II.** Subjective simple regression analysis

| Gene (SNP) | Model | Skill | *B* | *SE B* | β | *t* | *p* |
|---|---|---|---|---|---|---|---|
| *ADBR2* (rs1042714) | C/C vs. C/G-G/G | Dribbling | 0.29 | 0.18 | 0.63 | 1.62 | .118 |
| | | Passing | 0.12 | 0.18 | 0.27 | 0.66 | .514 |
| | | Shooting | 0.35 | 0.17 | 0.77 | 2.05 | .051 |
| *ACE* (rs4341) | G/G vs. G/C-C/C | Dribbling | -0.28 | 0.21 | -0.61 | -1.34 | .194 |
| | | Passing | 0.04 | 0.21 | 0.08 | 0.18 | .859 |
| | | Shooting | -0.25 | 0.21 | -0.54 | -1.17 | .254 |
| *BDNF* (rs6265) | C/C vs. C/T-T/T | Dribbling | -0.22 | 0.19 | -0.48 | -1.15 | .261 |
| | | Passing | 0.22 | 0.19 | 0.49 | 1.18 | .249 |
| | | Shooting | 0.01 | 0.20 | 0.03 | 0.07 | .946 |
| *COMT* (rs4680) | G/G vs. G/A-A/A | Dribbling | -0.19 | 0.19 | -0.42 | -0.99 | .332 |
| | | Passing | -0.05 | 0.19 | -0.12 | -0.28 | .784 |
| | | Shooting | 0.16 | 0.19 | 0.36 | 0.85 | .405 |
| *DBH* (rs1611115) | C/C vs. C/T-T/T | Dribbling | 0.07 | 0.19 | 0.15 | 0.36 | .721 |
| | | Passing | -0.10 | 0.19 | -0.22 | -0.54 | .593 |
| | | Shooting | 0.05 | 0.19 | 0.11 | 0.25 | .802 |
| *DRD1* (rs4532) | T/T vs. T/C-C/C | Dribbling | -0.07 | 0.20 | -0.15 | -0.35 | .732 |
| | | Passing | 0.15 | 0.19 | 0.33 | 0.77 | .448 |
| | | Shooting | 0.22 | 0.19 | 0.48 | 1.13 | .268 |
| *DRD2* (rs1076560) | C/C vs. C/A-A/A | Dribbling | 0.21 | 0.18 | 0.44 | 1.14 | .265 |
| | | Passing | -0.10 | 0.18 | -0.21 | -0.53 | .599 |
| | | Shooting | -0.13 | 0.18 | -0.29 | -0.72 | .477 |
| *DRD3* (rs6280) | T/T vs. T/C-C/C | Dribbling | -0.11 | 0.18 | -0.24 | -0.60 | .553 |
| | | Passing | 0.11 | 0.18 | 0.25 | 0.63 | .536 |
| | | Shooting | -0.23 | 0.18 | -0.49 | -1.27 | .215 |

*Note.* *B* = unstandardised beta; *SE B* = standard error; β = standardised beta.

TITLES OF FIGURES

Figure 1. Objective total genotype score (TGS) and total weighted genotype score (TWGS) correlations with dribbling, passing, and shooting assessments. TGS and TWGS correlations are displayed on the left and right, respectively. * Statistically significant at $p < .05$.

Figure 2. Subjective total genotype score (TGS) and total weighted genotype score (TWGS) correlations with dribbling, passing, and shooting assessments. TGS and TWGS correlations are displayed on the left and right, respectively. * Statistically significant at $p < .05$.