

The genetics of sports injuries and athletic performance

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Summary

Purpose: in the last two decades, several evidences have been provided to support the relationship between single nucleotide polymorphisms and the susceptibility to develop injuries participating in sport and performance related to sports activity. We report up-to-date review of the genetics factors involved in tendon injuries and athletic performance.

Methods: we searched PubMed using the terms “sports injuries”, “athletic performance” and “genetics” over the period 1990 to the present day. We also included non-English journals.

Results: most of the currently established or putative tendinopathy susceptibility loci have been analyzed by candidate gene studies. The genes currently associated with tendon injuries include gene encoding for collagen, matrix metalloproteinase, tenascin and growth factors. Several genes have been related to the physical performance phenotypes affecting endurance capacity and

muscle performance. The most studied include *ACE* and *ACTN3* genes.

Conclusions: genetics determines the response of an individual to the surrounding environment. Recently, some of the individual genetic variations contributing to the athletic performance and the onset of musculoskeletal injuries, particularly in tendon and ligament tissues, have been identified. However, the identification of the genetic background related to susceptibility to injuries and physical performance of the athletes is challenging yet and further studies must be performed to establish the specific role of each gene and the potential effect of the interaction of these.

KEY WORDS: sports injuries, athletic performance, genetics, single nucleotide polymorphisms.

Introduction

Tendinopathies account for a substantial proportion of overuse injuries associated with sports¹, and are a common cause of disability²⁻⁴. Most major tendons, such as the Achilles, patellar, rotator cuff and forearm extensor tendons (amongst others) are vulnerable to overuse, which induces pathological changes in the tendon⁵.

The term tendinopathy as a generic descriptor of the clinical conditions (both pain and pathology) associated with overuse in and around tendons⁶. The histological descriptive term ‘tendinosis’ (a degenerative pathology with a lack of inflammatory change) and ‘tendonitis’ or ‘tendinitis’ (implying an inflammatory process) should only be used after histopathological confirmation⁶. However, it should be kept in mind that, despite the use of the term ‘tendinosis’, at histopathological examination the essence of a tendinopathic lesion is a failed healing response, with haphazard proliferation of tenocytes, intracellular abnormalities in tenocytes, disruption of collagen fibres, and subsequent increase in non-collagenous matrix⁷⁻⁹. Tendinopathic tendons have an increased rate of matrix remodelling, leading to a mechanically less stable tendon which is probably more susceptible to damage¹⁰. Histological studies of surgical specimens in patients with established tendinopathy consistently show either absent or minimal inflammation¹¹⁻¹³. They generally also show hypercellularity, a loss of the tightly bundled collagen fiber appearance, an increase in proteoglycan content and, commonly, neovascularisation^{14,15}. Inflammation seems to play a role only in the initiation, but not propagation and progression, of the disease process¹⁶.

Competing theories have been proposed to explain the pathogenesis of tendon pathology at specific stages and presentations of the condition¹⁷⁻²⁰. A continuum of tendon pathology from asymptomatic tendons to tendon tears has been proposed^{21,22}.

Failed healing and tendinopathic features have been associated with chronic overload, but the same histopathologic characteristics also has been described when a tendon is unloaded: stress shielding seems to exert a deleterious effect¹¹. Unloading a tendon induces cell and matrix changes similar to those seen in an overloaded state, and decreases the mechanical integrity of the tendon^{21,22}.

Genetics is the science of heredity and variation in living organisms. It investigates gene function, genome structure, chromatin organisation, recombination rate, mutation processes, and evolutionary history, to provide a coherent understanding of the human genome and its complex relationship with human biology, physiology and disease. In the last two decades, several evidences have been provided to support the relationship between single nucleotide polymorphisms and the susceptibility to develop injuries participating in sport and performance related to sports activity²³.

In this current concepts review, we report up-to-date review of the genetics factors involved in tendon injuries and athletic performance.

Candidate genes associated to tendon injuries

Most of the currently established or putative tendinopathy susceptibility loci were analyzed by candidate gene studies. Identify genetic susceptibility loci to injury could lead to customize exercise recommendations for specific patient populations. Prevention strategies like avoidance of weight-bearing and high-impact sports for individuals who have risk profile genotypes would take advantage of this information.

COL1A1 (Collagen type I alpha 1 gene)

Collagen type I fibrils are a major constituent of bone matrix and form strong parallel bundles of fibers in tendons and ligaments. The major two genes that regulate collagen production are the collagen $\alpha 1$ (*COL1A1*) and the collagen $\alpha 2$ (*COL1A2*) gene. The *COL1A1* and *COL1A2* encode collagen $\alpha 1$ and collagen $\alpha 2$ polypeptides, respectively, which associate in a 2:1 ratio to form collagen type I²⁴. The *COL1A1* gene (located on chromosome 17q21.33) contains a polymorphism in the region of intron 1 (rs1800012), a predicted binding site for the transcription factor Sp1²⁵. Some studies have shown that the functional Sp1-binding site polymorphism is associated with various complex disorders including osteoporotic fractures²⁵, osteoarthritis²⁶, myocardial infarction²⁷, lumbar disc disease²⁸ and stress urinary incontinence²⁹. It was proposed that the G to T substitution within the intronic Sp1-binding site increases the affinity for the

transcription factor Sp1, resulting in increased *COL1A1* gene expression and the production of a weaker type I collagen homotrimer consisting of three $\alpha 1$ chains instead of the conventional heterotrimers (two $\alpha 1$ and one $\alpha 2$ chains)^{25,30}. Recently, this polymorphism, has been associated with cruciate ligament ruptures³¹, shoulder dislocation³¹, anterior cruciate ligament ruptures³² in two different populations study. Khoschnau et al.³¹ reported that the *COL1A1* Sp1 TT genotype was associated with a substantially reduced risk of cruciate ligament ruptures and shoulder dislocation ruptures, they found a substantial 85% reduced risk (95% CI 34% to 97%) of injury for those with the rare TT genotype compared with those with GG genotype. Individuals with the rare genotype TT showed a 4% prevalence in the 325 Swedish controls analyzed whereas in the 358 injured patients was underrepresented showing only 1 case in the cruciate ligament ruptures group (0.4%; n=233) and 1 case in the shoulder dislocation ruptures group (0.8%; n=126). Posthumus et al.³² reported a similar data, showing that the relative genotype frequencies of the *COL1A1* Sp1 binding site polymorphism within the asymptomatic 130 white South African controls was of the 4.6% for the TT genotype while none of the 117 Caucasian patients with surgically diagnosed anterior cruciate ligament ruptures showed a TT genotype. In fact the TT genotype was significantly underrepresented in the anterior cruciate ligament ruptures group compared with the control group (P=0.031; OR=0.08; 95% CI 0.01 to 1.46). Finally, Posthumus et al.³³ had shown no significant association in the allelic or genotype frequencies of the Sp1 binding site polymorphism in 126 patients with Achilles tendinopathy and 126 healthy Caucasian controls. These results suggested that the *COL1A1* polymorphism potentially protects from cruciate ligament, shoulder dislocation, and anterior cruciate ligament ruptures^{31,32}. A recent short communication reported the combined effect, from the above three published studies, of the rare TT genotype of the *COL1A1* Sp1 binding site polymorphism on the risk of acute soft tissue ruptures (cruciate ligament, shoulder dislocation and Achilles tendon ruptures)³⁴. A Fisher's exact test was used to analyse any differences in the genotype frequencies (TT vs GT and GG) of the 581 combined control and injured groups in the three published studies. The injured groups were analysed as: 1) 350 cruciate ligament ruptures^{31,32}; 2) 476 cruciate ligament ruptures and shoulder dislocation^{31,32} and 3) all 517 soft tissue ruptures (cruciate ligament, shoulder dislocation and Achilles tendon)³¹⁻³³. The rare TT genotype was significantly underrepresented in the cruciate ligament group (0.3% TT genotype; n=1) when compared with the control group (4.1% TT genotype; n=24) of all three published studies (OR=15.1; 95% CI 2.0 to 111.7; P<0.001). Similar results were obtained when the cruciate ligament and shoulder dislocation group (0.4% TT genotype; n=2; OR=10.2; 95% CI 2.4 to 43.4; P<0.001) or the all soft tissue ruptures group (0.4% TT genotype; n=2; OR=11.1; 95% CI 2.6 to 47.2; P<0.001) were compared with the control

group. In summary, the combined results from three recently published studies, show that the TT genotype of the *COL1A1* Sp1 binding site polymorphism is underrepresented in acute soft tissue ruptures, in particular of the cruciate ligament group. The clinical relevance of this finding is that the *COL1A1* TT genotype seems to have a protective effect on his carriers. However, further larger sample sizes studies must be evaluated for this rare polymorphism, before addressing his protective role on ligament, tendon and other soft tissue ruptures.

COL5A1 (Collagen type V alpha 1 gene)

Based on its known biological function and chromosome location *COL5A1* gene has been selected as specific candidate gene for Achilles tendon injuries, anterior cruciate ligament rupture, and altered musculotendinous flexibility in four different reports coming from the same research institute³⁵⁻³⁸. The *COL5A1* gene encodes for the $\alpha 1$ chain of type V collagen, which is a minor fibrillar collagen found in ligaments and tendons, as well as other tissues³⁹. Type V collagen, which makes up approximately 10% of the collagen content in ligaments, intercalates into the core of type I collagen fibrils, where it is believed to be involved in the organization and regulation of type I collagen fibril diameters⁴⁰. Furthermore, some investigators have reported an association of the ABO blood group with Achilles tendon injury⁴¹, the ABO blood group is determined by a single gene located on the end of the long arm of chromosome 9 (9q34) close to the chromosomal localization of the *COL5A1* gene and other genes that will be discussed further in this review. The *COL5A1* gene contains a BstUI and a DpnII restriction fragment length polymorphisms (RFLPs) within its 3'-untranslated region (UTR)⁴². Some studies investigated whether genetic variants within the *COL5A1* gene were associated with Achilles and quadriceps tendon injuries, anterior cruciate ligament rupture, and altered musculotendinous flexibility^{35-38,43}.

In particular, Mokone et al.³⁵ investigated whether the BstUI (rs12722, C to T substitution) and/or the DpnII (rs13946, C to T substitution) polymorphisms were associated with Achilles tendon injuries in 111 Caucasian patients and 129 healthy Caucasian controls from a South African population. The main biological finding was a significant difference in the allele distribution of the three *COL5A1* BstUI RFLP alleles (A1, A2, and A3 deriving from two single nucleotide polymorphisms substitution: rs12722 and rs557488 01) when controls subjects were compared with the Achilles tendon injuries group ($P=0.006$). The frequencies of the A1 and A3 alleles were higher in the Achilles tendon injuries group (A1, 76.1% and A3, 5.9%) than in the controls group (A1, 67.1% and A3, 3.1%), while the frequencies of the A2 allele (corresponding to the C allele of the rs12722 single nucleotide polymorphism substitution) was significantly higher in the controls subjects (A2, 29.8%) than in the

patients group (A2, 29.8%). Based on this statistical evidence the authors concluded that individuals with the CC genotype were therefore less likely of developing symptoms of tendon pathology (OR=1.9; 95% CI 1.3 to 3.0; $P=0.004$)³⁵ (35). Finally, there were no significant differences in the genotype frequencies of the *COL5A1* DpnII RFLP alleles between the controls subjects and the Achilles tendon injuries group³⁵.

Moving from first evidence September et al.³⁶ decided to study the association of the *COL5A1* gene and the Achilles tendinopathy in two different population, white South African and Australian³⁶. The authors selected 7 genetic variants within the *COL5A1* gene, the already investigated rs12722 (BstUI RFLP) and rs13946 (DpnII RFLP) plus 5 other variants (rs10858286, rs3196378, rs11103544, rs4504708 and rs3128575). The first two variants rs12722 and rs13946 were already analyzed in the South African population by Mokone et al.³⁵ and as mentioned the rs12722 was strongly associated with chronic Achilles tendinopathy in this study, while the rs13946 was not associated. Thus, the authors evaluated these two variants in a second case-control population study of subjects from Australia, while the other 5 variants were investigated in both South African and Australian population³⁶. There was a highly significant difference in the genotype distribution of rs12722 between the Australian controls and Australian Achilles tendon injuries group ($P=0.001$). Moreover, individuals with a CC genotype had a significantly decreased risk of developing chronic Achilles tendinopathy than those with a T allele (TC or TT genotype) in both the Australian (OR=0.42; 95% CI 0.20 to 0.86; $P=0.017$) and South African (OR=0.38; 95% CI 0.18 to 0.77; $P=0.008$) groups. As for the South African population there was no significant association of the marker rs13946 (DpnII RFLP) and tendinopathy disease in the Australian population³⁶.

A significant difference in the genotype distribution between the Australian controls and Australian Achilles tendon injuries groups was noted for rs3196378, which spans a putative mRNA binding site ($P=0.016$). The AC genotype was significantly associated with the increased risk of developing Achilles tendon injuries in the Australian population (OR 2.3; 95% CI 1.3 to 4.1; $P=0.004$). These data were not confirmed in the South African study. None of the differences in genotype distribution between the Australian controls and tendon injuries groups for markers rs10858286, rs4504708 and rs3128575 were significant. For this reason, these markers were not analysed in the South African group. In conclusion, the relevant finding of this report was that the *COL5A1* BstUI RFLP is associated with Achilles tendinopathy in two independent populations.

Finally, Laguette et al.⁴⁴ investigated the relationship between the sequence of the *COL5A1* 3'-UTR and the mRNA stability, comparing patients with Achilles tendinopathy and asymptomatic controls.

The predominant forms were T-allele in patients with Achilles tendinopathy and C-allele in the controls. The authors reported a significantly increased mRNA

stability for T-allele and proposed that it could be a molecular mechanism underlying musculoskeletal soft tissue injuries.

Recently, Posthumus et al.³⁷ have shown that the CC genotype of *COL5A1* BstUI RFLP polymorphism was also significantly underrepresented in female, but not male, athletes with anterior cruciate ligament rupture. The authors genotyped for the *COL5A1* BstUI and DpnII RFLPs 129 white participants (38 of which were women) with surgically diagnosed anterior cruciate ligament ruptures and 216 physically active control participants (84 of which were women) without any history of anterior cruciate ligament injury. When the female and male participants were analyzed together, there were no significant differences in genotype or allele frequencies, whereas when the female and male participants were analyzed separately, the BstUI RFLP CC genotype was overrepresented in the control participants within the female (OR=6.6; 95% CI 1.5 to 29.7; P=0.006), as has been already shown in the previous reports^{35,36} but no association was found in the male participants³⁷. These data should be interpreted with caution because of the small sample size of the female participants.

The polymorphisms within the 3'-UTR were further analyzed from Collins et al.³⁸ to investigate the possible association with musculotendinous range of motion, because altered musculotendinous flexibility, defined as "the ability to move a joint through its complete range of motion" (ROM)⁴⁵, has been cited as an intrinsic risk factor for musculotendinous injuries⁴⁶⁻⁴⁸. The ROM measurements were recorded in all the subjects like sit and reach (SR) test⁴⁵ and passive straight leg raise (SLR) test⁴⁹. The sit and reach (SR) and the passive straight leg raise (SLR) were measured on 119 Caucasian subjects with either a past, current or no history of Achilles tendon injuries³⁸. The subjects were genotyped for the DpnII RFLP (rs13946), BstUI RFLP (rs12722) and two other variants the Acil RFLP (rs3196378, C or A variant) and MboII RFLP (rs11103544, C or T variant)³⁸. The only significant genotype differences distribution was noted in the passive SLR and SR measurements between *COL5A1* BstUI RFLP genotype groups, with the heterozygous group (TC genotype) less flexible than the homozygous (TT and CC genotypes) groups. There were, however, no significant differences in any of the ROM measurements between the genotype groups of the other three polymorphisms³⁸. Authors concluded that the *COL5A1* BstUI RFLP was independently associated with lower limb ROM within that cohort. Subsequently, Brown et al.⁵⁰ investigated the association between *COL5A1* BstUI RFLP and SR ROM in healthy and physically active subjects. They found that the *COL5A1* BstUI RFLP genotype was associated with SR ROM in subjects over 35 years, with the greater SR ROM associated with TC genotype and the lower with CC (P=0.017). Moreover, *COL5A1* genotype interacted significantly with age and sex for SR ROM. Given these results, authors stated that the *COL5A1* BstUI RFLP contribute to determine the ROM in older, healthy and physically

active subjects. Finally, Brown et al.⁵¹ also investigated the relationship between *COL5A1* genotype, ROM, and ultra-marathon running performance. They reported better endurance running performance in patients with lower ROM (TT genotype) when compared with participants with TC and CC genotypes. Moreover, T allele was found significantly (P=0.044) over-represented in conditions of faster performance and lower flexibility.

COL12A1 (Collagen type XII alpha 1 gene)

As the *COL5A1* gene and the *COL1A1* gene any other proteins involved in similar biological processes can be studied to test the association between the selected candidate gene and the Achilles tendon injuries and or anterior cruciate ligament rupture. For this reason it was decided to investigate additional candidate genes such as *COL12A1* and *COL14A1* gene^{52,53}. Types XII and XIV collagens belong to a family of non-fibrillar collagens are associated with the surface of the collagen fibril and are members of the Fibril Associated Collagens with Interrupted Triple helices (FACITs) subfamily⁵⁴. Type XII collagen is a homotrimer consisting of 3 α 1 (XII) chains and is encoded by a single gene, *COL12A1*, mapped to chromosome 6q12-q13⁵⁵. Similar to type V collagen, type XII collagen is believed to regulate fibril diameter (fibrillogenesis)⁵⁶⁻⁵⁸. September et al.⁵² investigated the association of two *COL12A1* single nucleotide polymorphism (SNP rs970547 and SNP rs240736) with Achilles tendon injuries, and reported not significant association in the selected group⁵².

Since tendons and ligaments have a similar hierarchical structure²⁴, and previous work suggested that there might be common genetic risk factors for acute soft tissue ruptures³⁴, Posthumus et al. investigated the *COL12A1* gene as a possible additional genetic risk factor for anterior cruciate ligament rupture as well⁵³. One hundred and twenty-nine (38 of which were female) participants with clinically and surgically diagnosed anterior cruciate ligament rupture, as well as 216 (83 of which were female) physically active control participants without any history of anterior cruciate ligament injury were included in this case-control genetic association study. All participants were genotyped for two previously characterised non-synonymous single nucleotide polymorphisms (SNPs), located within exon 29 (rs240736, a T to C single nucleotide substitution) and exon 65 (rs970547, a A to G single nucleotide substitution) of *COL12A1*. The rs970547 is a missense substitution of Gly to Ser at position 3058 and the rs240736 it a missense substitution of Thr to Ile at position 1738⁵². The differences in genotype or allele frequencies of the rs240736 SNP between the two groups were statistically significant only when the female participants were analysed separately from the male. The AA genotype of the rs240736 SNP increased the risk of developing anterior cruciate ligament injury of 2.4 fold in the female participants (OR 2.4; 95% CI 1.0 to 5.5;

$P=0.048$), while in the male did not have any effects⁵³. The other rs970547 was not associated with the disease independently by the gender. The authors reported that the AA genotype of rs240736 SNP within the terminal exon 65 of the *COL12A1* gene was associated with a 2.4 fold increased risk of anterior cruciate ligament injury in female, but not male participants. Since the small sample size further investigation are required either for confirmation and/or exclusion of the *COL12A1* gene association with anterior cruciate ligament injury.

COL14A1 (Collagen type XIV alpha 1 gene)

Based on its known biological function *COL14A1* gene has been selected as specific candidate gene for Achilles tendon injuries⁵². Unlike the fibrillar collagens, types XIV collagen is associated with the surface of the collagen fibril and are members of the Fibril Associated Collagens with Interrupted Triple helices (FACITs) subfamily⁵⁴. Type XIV collagen is a homotrimeric molecule consisting of $\alpha 1$ (XIV) chains and is encoded by a single gene, *COL14A1*, mapped to chromosome 8q23^{59,60}. September et al. decided to investigate two informative exonic SNPs of the *COL14A1* gene, the A to C transversion at position 90 of the exon 14 (rs4870723) that cause a missense substitution of Asn to His at position 563, and the intronic SNP as well with high heterozygosity the A to T transversion at position 93 of the intron 43 (rs1563392). The authors selected for this case-control study a total of 137 physically active Caucasian unrelated individuals with chronic Achilles tendinopathy and 44 acute Achilles tendon rupture, and 131 physically active Caucasian without any history of clinical symptomatic Achilles tendon injuries were selected as controls⁵². There were no significant differences in the genotype or allele distribution of the *COL14A1* SNPs between any of the affected and control subjects suggesting that the *COL14A1* gene is not associated to increased risk of developing Achilles tendinopathy⁵².

TNC (Tenascin C gene)

Some investigators have reported an association of the ABO blood group with Achilles tendon injury⁴¹, these findings suggest that either the ABO gene or a closely linked gene(s) may be associated with tendon injury. In addition, has been reported that persons with blood group O are more susceptible to tendon injuries^{41,61-63}. The ABO blood group is determined by a single gene located on the end of the long arm of chromosome 9 (9q34) close to the chromosomal localization of the already discussed *COL5A1* gene and of the *TNC* gene, closely linked to the ABO gene on chromosome 9q32-q34.3⁶⁴. The extracellular matrix glycoprotein tenascin-C is expressed in a variety of tissues, including tendons⁶⁵, and is encoded by the tenascin-C (TNC) or hexabrachion (HXB) gene. Tenascin-C binds other compo-

nents of the extracellular matrix and cell receptors, and it plays an important role in regulating cell-matrix interactions⁶⁶. In normal adult tendons, it is expressed predominately in regions responsible for transmitting high levels of mechanical force, such as the myotendinous and osteotendinous junctions⁶⁷⁻⁶⁹. The *TNC* gene contains a guaninethymine (GT) dinucleotide repeat polymorphism (a tandem repeat consisting of a repeated 2-base pair sequence of varying lengths in different people) within intron 17. The influence of this polymorphism in the expression of the gene or the biological function of tenascin-C is, to our knowledge, unknown. Mokone et al.⁷⁰ investigated the association of the GT dinucleotide repeat polymorphism of the *TNC* gene with Achilles tendon injuries. The authors selected 114 physically active white patients with symptomatic Achilles tendon injuries (72 chronic Achilles tendinopathies and 42 acute Achilles tendon ruptures) and 127 apparently healthy physically active white subjects without any history of symptomatic as a control. Eighteen different alleles of the GT dinucleotide repeat polymorphism within the *TNC* gene were identified within the two groups. There was a significant difference in the distribution of the alleles between the Achilles tendon injuries and control groups ($\chi^2=51$; $P=0.001$), with the alleles containing 12 and 14 GT dinucleotide repeats being significantly more frequent in the Achilles tendon injuries group ($\chi^2= 21.6$; $P<0.001$). The alleles containing 13 and 17 repeats were, on the other hand, significantly less frequent in the Achilles tendon injuries subjects ($\chi^2=42.4$; $P<0.001$). Alleles were grouped according to those significantly overrepresented, containing 12 or 14 GT dinucleotide repeats (O), those significantly underrepresented, containing 13 or 17 repeats (U), or alleles evenly distributed (E), and were then paired by genotype and the genotype distribution were analyzed between case and control. Subjects with a genotype of UU or UE were significantly underrepresented in the Achilles tendon injuries group (OR=6.2; 95% CI 3.5 to 11.0; $P<0.001$). With respect to the O alleles, subjects who were either homozygous or heterozygous were overrepresented in the Achilles tendon injuries. The novel finding of this study was that the allele distributions of the GT dinucleotide repeat polymorphism within the *TNC* gene were significantly different between the subjects presenting with symptoms of Achilles tendon injuries and the asymptomatic subjects. Alleles containing 12 and 14 GT repeats were overrepresented in subjects with Achilles tendon injuries, while the alleles containing 13 and 17 repeats were underrepresented⁷⁰.

MMP3 (Matrix metalloproteinase 3 gene)

Besides the genes which encode for the extracellular matrix proteins already discussed, the genes that encode for any protein that regulates tendon and ligament biological processes, such as adaptation, healing and remodelling are probably also associated with

them injuries^{71,72}. Raleigh et al.⁷³ investigated the role of the matrix metalloproteinases (MMPs) proteins in the etiology of tendinopathy. The MMPs have regulatory roles in maintaining extracellular matrix (ECM) homeostasis. The MMPs are known to consist of over 20 distinct endopeptidases that can catalyse a broad spectrum of both ECM and non-ECM substrates⁷⁴. One of the family, MMP3, can catalytically degrade multiple substrates including: types II, IV, V, IX, X collagens, laminin, fibronectin, proteoglycan, decorin and aggrecan^{74,75}. The *MMP-3* gene is located at the long arm of chromosome 11 (11q22.3), in cluster together with five other *MMP* genes (*MMP-7* and *MMP-10*, -11, -12, -13)⁷⁶. The promoter region of *MMP-3* is characterized by a 5A/6A promoter polymorphism at position -1171, in which one allele has six adenosines (6A) and the second has five adenosines (5A). Has been shown that expression of the *MMP3* gene can be substantially altered by the 5A/6A promoter polymorphism⁷⁷ and this variant has been associated with a number of pathological states^{78,79}. Interestingly, reduced levels of *MMP3* mRNA^{80,81}, and immunochemically detectable *MMP3* protein have been observed in resected Achilles tendinopathy tissue compared to control tissue⁸¹. Raleigh et al.⁷³ investigated the relationship between variants within the *MMP3* gene and Achilles tendinopathy or Achilles tendon rupture. One hundred and fourteen Caucasian subjects diagnosed with Achilles tendon injuries were recruited (including 75 with chronic Achilles tendinopathy and 39 with partial or complete ruptures of the Achilles tendon). An additional, 98 apparently healthy, unrelated, Caucasian subjects were recruited as controls. Three exonic SNPs were identified and selected for this case-control study. The rs679620 (E45K) and the rs602128 (D96D) within exon 2 and rs520540 (A362A) within exon 8, all with an high heterozygous frequency and therefore considered potentially informative⁷³.

There were no significant differences in the genotype and allele distributions of the selected SNPs between the Achilles tendon injuries and control groups. Since differences have been detected in genotype distributions between subjects with chronic Achilles tendon or Achilles tendon ruptures⁵², the Achilles tendon pathology group was sub-divided into 75 patients with chronic Achilles tendinopathy and 39 patients rupture sub-groups. There were significant differences in the distribution of the genotype ($P=0.031$) and allele ($P=0.037$) frequencies of the *MMP3* rs679620 SNP between the control and 75 patients with chronic Achilles tendinopathy. The GG genotype was significantly more frequent in the chronic Achilles tendinopathy (37.3%; $n=28$) when compared to the control group (19.4%; $n=19$) (OR=2.5; 95% CI 1.2 to 4.9; $P=0.010$). The CC genotype of SNP rs591058 was over-represented in the chronic Achilles tendinopathy (35.6%; $n=26$) compared to the CON (19.6%; $n=19$) (OR=2.3; 95% CI 1.1 to 4.5; $P=0.023$) and the AA genotype of SNP rs650108 was over-represented in the chronic Achilles tendinopathy (9.5%; $n=7$) compared to the CON (2.1%; $n=2$) (OR=4.9;

95% CI 1.0 24.1; $P=0.043$). There were, however, no significant differences in the distribution of the genotype and allele frequencies of the three *MMP3* SNPs between the control and the 39 patients rupture subgroup. The authors evaluated the *MMP3* rs679620 G/A and *COL5A1* rs12722 C/T genotype pairs, together with their frequencies within the 75 patients with chronic Achilles tendinopathy and control groups, as well as their estimated risk (OR) and the risk order. The *MMP3* rs679620 A allele (AA or AG genotype) combined with the *COL5A1* rs12722 CC genotype had the lowest risk for Achilles tendinopathy⁷³. In conclusion, the authors reported the evidence that variation within the human *MMP3* gene is associated with Achilles tendinopathy. They also studied and discovered an interaction of the *MMP3* variant and the *COL5A1* gene variant to increase risk of Achilles tendinopathy. Further study and repetition of this work in other, larger population analysis must to be done to confirm these associations.

Recently, Malila et al.⁸² investigated the relationship between -1612 5A/6A polymorphism of the *MMP-3* gene and anterior cruciate ligament (ACL) rupture, evaluating 86 patients with ACL ruptures and 100 healthy controls without history of ligament or tendon injuries. They found that 5A+ (5A/5A, 5A/6A) genotype and 5A allele frequencies were significantly higher in subjects participating in contact sports when compared with those participating in non-contact sports. Given these results, the authors proposed the -1612 5A/6A polymorphism as risk factor for ACL rupture.

***TGFB1* (Transforming growth factor beta 1 gene)**

To study further candidate genes as possible predisposing factors to Achilles tendon pathology, Posthumus et al.⁸³ selected a functional polymorphism of the *TGFB1* gene (the *TGFB1* rs1800469 variant) and investigated the association with Achilles tendon pathology within an Australian and a South African case-control cohort study. The TGF- β superfamily, which includes various growth/differentiation factors (GDFs), plays an essential role in tissue (including tendon) growth and homeostasis. Two members of this family, TGF- β 1 (an isoform of TGF- β) and GDF-5, have been shown to increase mechanical strength after gene transfection in experimentally injured animal Achilles tendons⁸⁴⁻⁸⁶. The *GDF-5* gene will be discussed further in this review, TGF- β 1 is released in response to a number of stimuli (including mechanical loading⁸⁷) and is known to increase cell proliferation, migration and the synthesis of extracellular matrix. The gene coding for TGF- β 1, *TGFB1*, is located on chromosome 19q13. The 5' untranslated region (UTR) of the *TGFB1* gene contains a functional promoter single nucleotide polymorphism (SNP) (rs1800469, C to T substitution) that has been associated with various multifactorial pathologies⁸⁸⁻⁹⁴. Moreover, retrospective regression analysis estimated the mean acid-activated

TGF- β concentration to be approximately twice as high in the TT genotype compared with the CC genotype of the *TGFB1* rs1800469 variant⁹⁵. Posthumus et al.⁸³ enrolled subjects from the Australian cohort study³⁶, in particular selected 59 Caucasian patients all of which were diagnosed with chronic Achilles tendonopathy and 142 healthy subjects as controls. While from the South African cohort study^{35,70} selected 112 Caucasian subjects diagnosed with Achilles tendon pathology and 96 healthy subjects as controls. The genotype and allele frequency of the *TGFB1* rs1800469 variant shows no significant differences between the Achilles tendon pathology and controls groups within the South African and/or the Australian cohorts⁸³. In conclusion, the study suggests that the *TGFB1* polymorphism rs1800469 is unlikely a predisposition factor for the Achilles tendon pathology disease, especially in subjects of European descent.

GDF-5 (Growth/differentiation factor-5 gene)

The specific role of GDF-5 in tendon is largely unknown^{55,96}. GDF-5 is involved in the maintenance, development and repair of bones, cartilage and various other musculoskeletal soft tissues (including tendons)^{55,96,97}. The gene coding for GDF-5, *GDF5*, is located on chromosome 20q11. Mutations within the *GDF5* gene are known to cause several inherited developmental disorders⁹⁸⁻¹⁰⁰. A possible role of GDF-5 in tendon and ligament biology was first suggested by Wolfman et al.¹⁰¹. In this study, ectopic administration of GDF-5 resulted in the synthesis of new tendon tissue. The 5' UTR of the *GDF5* gene contains a functional promoter SNP (rs143383; T to C substitution) that has been associated with multifactorial disorders such as osteoarthritis¹⁰² and congenital hip dysplasia¹⁰³, as well as phenotypic data such as height, hip axis length and fracture risk¹⁰³. The function of this SNP has been reported by luciferase reported assays¹⁰⁴ and differential allelic expression analysis^{105,106}. The T allele of the *GDF5* rs143383 was correlated with reduced expression of the *GDF5* gene within a wide range of soft tissues^{105,106}. To further investigate the role of GDF-5 in tendon, Posthumus et al.⁸³ decided to determine whether the functional polymorphisms rs14338 of the *GDF5* gene was associated with Achilles tendon pathology within an Australian and a South African case-control cohort study. Given the known functional effect of the chosen SNP, the hypothesis was that the TT genotype of the *GDF5* rs143383 variant increases the risk of Achilles tendon pathology. There were significant genotype differences between the Australian chronic Achilles tendonopathy and Australian controls groups for the *GDF5* rs143383 variant ($P=0.027$). Although similar frequencies and trends were observed within the South African cohort, there were no significant genotype or allele differences. When the data from the Australian and the South African cohort were combined, both genotype ($P=0.013$) and allele ($P=0.019$)

frequencies were significantly different between the case and control groups. Similar results were observed when individuals with a TT genotype for the *GDF5* rs143383 variant were compared with individuals with a C allele (combined TC and CC). Within the Australian cohort, the TT genotype increased the susceptibility to Achilles tendonopathy by 2.24 times (OR=2.24; 95% CI 1.21 to 4.16; $P=0.011$). Although there was a similar pattern in the South African cohort, the TT genotype was not significantly over-represented in the Achilles tendonopathy. The TT genotype remained significantly over-represented when both cohorts (Australian and the South African) were analysed together (OR=1.82; 95% CI 1.23 to 2.74; $P=0.004$). The main finding of this study was that the *GDF5* gene was associated with Achilles tendon pathology within an Australian population, independently, and when combined with an additional South African population⁸³.

Candidate gene associated to physical performance

Physical and athletics performance depend upon a variety of biological and mechanical tissue properties. Such properties may be metabolic or anatomical, including, for example choice of substrate and efficiency of use or tendon length, tendon elasticity, muscle tension properties and fibre types. All of these different phenotypes are related by a complex interplay among the environment and the individual genetic profile. The general hypothesis is that there is an inheritance component affecting physical and athletic fitness that is able to interact with environmental factors, particularly with training. Until the 1990s, the study of such complex traits was based almost entirely on twin and family analyses and on association studies. In the last decade, it has been possible to investigate complex traits, such as physical performance, using molecular biological techniques. Candidate gene loci have been identified related to a variety of performance phenotypes which might relate to athletic phenotype. The most recent update of the 'Human Gene Map for Performance and Health-Related Fitness Phenotypes reported a total of 221 autosomal and X-linked genes and 18 mitochondrial markers that have shown to be associated with a relevant genotype in at least one study, whereas 119 QTL have been reported for exercise- or physical activity related traits¹⁰⁷. Here we mainly review the most studied genes that have been considered to have a direct influence on physical performance or fitness phenotypes of the athlete. In particular, we will review the literature related to association studies and the *ACE* gene, which is most extensively studied of any other gene, with at least 60 articles examining the effect of an insertion/deletion polymorphism on fitness and performance traits. In addition to *ACE*, another gene has been recently characterized by a great attention in numerous scientific articles related to physical and athletic fitness, the *ACTN3* gene.

ACE (Angiotensin-converting enzyme gene)

The most extensively studied gene in sports and physical performance is the *ACE* gene^{108,109}. In 1998, Montgomery et al. were the first to publish evidence for an association of improved physical performance and *ACE* gene¹¹⁰. This gene map on chromosome 17q23.3 and encodes an enzyme, the Angiotensin 1-converting enzyme involved in catalyzing the conversion of angiotensin I into a physiologically active peptide angiotensin II. Angiotensin II is a potent vasopressor and aldosterone-stimulating peptide that controls blood pressure and fluid-electrolyte balance. This enzyme plays a key role in the renin-angiotensin system. Many studies have associated the insertion/deletion (I/D) polymorphism of a 287 bp Alu repeat element in intron 16 of this gene with individual variability in exercise-related phenotypes, and particularly in muscle phenotypes. Besides regulating blood pressure, the *ACE* is expressed in skeletal muscle, where it may influence its function and biomechanical properties¹¹¹⁻¹¹³. The *ACE* D allele is associated with higher concentration of circulating and tissue *ACE*, thus increased angiotensin II levels¹¹²; this allele would theoretically favour performance in more power or strength-oriented sports such as weightlifting. Indeed, the D allele has been associated with elite "sprint" athletic performance^{108,109} and power-related phenotypes in non-athletic populations, like lower risk of skeletal muscle damage induced by eccentric contractions¹¹⁴, or greater gains in knee extensor strength after training in old (≥ 60 years) individuals¹¹⁵. Conversely, the I allele is theoretically associated with a decrease in circulating levels of angiotensin II with reduction in vascular resistance, which might facilitate cardiac output during strenuous exercise¹¹². The I allele could also favour muscle efficiency, a key determinant of long-distance running performance¹¹⁶, indicating that these allele, as has been frequently reported, is more frequent in elite endurance athletes^{108,117}, while the D allele is more frequent among those engaged in more power oriented sports^{108,118}. These results were recently confirmed in a study carried out on 39 Portuguese Olympic swimming candidates, who were stratified into two homogeneous groups: short distance swimmers (SDS), between 50 and 200 m (mainly anaerobic events) and middle distance swimmers (MDS), 400-1.500 m (mixed anaerobic and aerobic events)¹¹⁹. Moreover a group of 32 non-elite swimmers were studied and classified as well, and a control group (n = 100) was selected from the Portuguese population. The authors found higher DD genotype (P=0.029) and allelic frequency (P=0.021) of the elite short distance swimmers (SDS) when compared with controls¹¹⁹. These results support previous observations, demonstrating an association of the D allele with elite short-distance swimmer status^{109,118,120}, and the relation of the D allele with more power oriented sports. However, the power of the performed test was <0.80, hence as the author mentioned, these data should interpret cautiously. Another recent study by Papadimitriou et

al.¹²¹ suggested a weak association of the DD genotype with more power oriented sports. The authors assessed 101 Greek athletes (including 73 power-oriented athletes and 34 sprinters) and 181 controls, showing that sprinters had higher frequency of the DD genotype when compared with the control group (55.8% vs 31.5%). Furthermore, there was a trend of increased frequency of both II and DD genotypes in the elite endurance athletes group, as compared to the controls, even though these results were not statistically significant.

However, evidences about the association of *ACE* polymorphisms and athletic phenotype are not definitive. Amir et al.¹²², observed that the D allele is more frequent in Israeli marathon runners than in sprinters. Moreover, some authors demonstrated that the *ACE* I/D polymorphism and A22982G polymorphisms are not associated with elite endurance athlete status in Kenyans¹²³ and Ethiopians¹²⁴.

Uncovering the influence of a gene on an heterogeneous phenotype can be difficult, a rare well defined extreme phenotype is easily associated with a rare gene mutation, but the challenge of associating the *ACE* I/D polymorphism with different sport disciplines and/or continuous variable like left ventricular mass (LV), Maximal Oxygen Uptake (VO_{2max}), or Bone Mineral Density (BMD) is not so simple: the polymorphism is common with I allele frequency of 50%, and sport performance and continuous variable can depend on several environmental and biological factors including exercise, sex, age race, to overcome such noise these studies needs very large population sample (several hundreds) to reach sufficient statistical power for making solid conclusion. One possible approach is conducting genome-wide linkage analysis studies, which are used to analyze the linkage between hundreds of polymorphisms and a given disease phenotype, eg, obesity or type 2 diabetes. To this end, a recent genome-wide linkage scan study estimated the heritability of athlete status at 60%¹²⁵. The authors studied 1.210 single-nucleotide polymorphisms (SNPs) in 4.488 British adult female twins and elite status was assumed for those reaching county or national level. However future association studies should be done to clarify the possible role of the genes identified in this study with the athlete status.

ACTN3 (Alpha-actin 3 protein gene)

The alpha-actin 3 gene (*ACTN3*) named the "speed gene"^{126,127} recently has received the most attention for his association with sports performance. This gene encode the α -actinin-3 protein, which is, together the α -actinin-2 protein, an important structural component of the Z disc, where they anchor actin thin filaments, helping to maintain the myofibrillar array^{128,129}. Several independent studies have established that the absence of alpha-actinin-3 protein is detrimental to sprint and power performance in athletes and in the general population¹³⁰⁻¹³⁶. In humans, α -actinin-2 is expressed in all skeletal muscle fibers,

while α -actinin-3 is expressed only in type 2 fibers. The α -actinin-3 gene (*ACTN3*) has attracted considerable attention due to a frequent nonsense polymorphism R577X (rs1815739) that may influence muscular performance¹³²⁻¹³⁵, this is due to a cytosine to thymine transition at codon 577 of the *ACTN3* gene that results in the replacement of an arginine residue (R allele) by a premature stop codon (X allele), thus individuals homozygous for the X allele do not produce ACTN3 protein in their muscle, and in these cases the *ACTN2* gene which is expressed in both type I and II myofibers, it can compensate for the loss of the ACTN3 protein in type II fibers in individuals who are 577X homozygotes. It has been proposed that the physiological consequences of an α -actinin-3 deficiency include differences in fibre type composition of human muscle¹³⁷. ACTN3 deficiency in mice leads to a shift in muscle metabolism towards aerobic pathways, resulting in enhanced distance running ability, but reduced muscle force generation¹³⁸. The R577X polymorphism is found in every human population, with a wide variation, from 1% in Africans to 25% in Asian. Yang et al.¹³⁰ were the first to demonstrate highly significant associations between ACTN3 genotype and athletic performance, 50% (53/107) of elite white sprint athletes had the RR genotype, compared with 30% (130/436) and 31% (60/194) of healthy white control participants and elite endurance athletes, respectively. While elite endurance athletes had a slightly higher frequency of the XX genotype (24%) than did controls (18%). From this research, it appears that the presence of the ACTN3 protein (577R) might be associated with greater success in activities requiring sprint or power performance. On the other hand the ACTN3 deficiency (577X) may provide some sort of advantage for endurance athletes. These results were confirmed in several human association studies that have shown a positive association between the 577X allele and elite endurance athlete performance¹³³⁻¹³⁵ and several other studies have shown a positive association between the 577R allele with power athletic status^{130,132-135,139} and sprint performance¹⁴⁰. Recently, Eynon et al.¹⁴¹, have evaluated the ACTN3 R577X polymorphism in the Israeli population, in particular were analyzed 155 athletes (119 men and 36 women) and 240 non-athletic healthy individuals as controls. Considering that the athletes were divided into two groups: 1) endurance-type group that included 74 long distance runners whose main events were the 10.000 m run and the marathon; 2) sprint-type group that included 81 sprinters whose main event was the 100-200 m dash, the authors demonstrated a significantly higher proportion of the XX genotype in the first group of endurance athletes (32 %) compared with the sprinters (14%; $P=0.005$) and the controls (18 %; $P=0.006$) groups. Furthermore, according to their individual best performance, athletes within each group were further divided into two subgroups: top level (those who had represented Israel in world track and field championships or in the Olympic Games) and national-level. A comparison between the top-level and na-

tional-level sprinters revealed that the R allele is more frequently found in the top-level sprinters. However, top-level and national-level endurance athletes had similar allele and genotype frequencies. The data support the hypothesis that the *ACTN3* R allele is associated with top-level sprint performance but that the X allele and XX genotypes may not be critical to endurance performance. Several other studies have provided no evidence for associations between endurance athlete performance and XX genotype, suggesting that this association is not as strong as the association with reduced performance in sprint and power activities^{133,142-147}. On the other hand, Shang et al.¹⁴⁸, while were investigating the frequency of the *ACTN3* R577X polymorphism among Han Chinese athletes, reported that the XX genotype (21.2 vs. 15.8%; $P=0.02$) and X allele (51.3 vs. 41.1%; $P=0.019$) were significantly over-represented in female endurance athletes compared to controls, while no genotype-related differences were observed in male endurance athletes. Consequently it is possible that all the different results in the previous case-control studies of *ACTN3* genotype were due to sexual and racial specific differences. Ahmetov et al.¹⁴⁹ also demonstrated that *ACTN3* XX genotype frequency was significantly lower in Russian subelite and elite speed skater sprinters compared with control subjects (2.6 vs 14.5%; $P=0.034$). The authors also showed a positive relationship between the preferred racing distance (PRD) and the proportion of slow-twitch muscle fibres ($r=0.593$, $P<0.0005$) in 34 subelite Russian speed skaters (20 men and 14 women), competing in races of different length (500-10.000 m). Finally, they demonstrated that R577X polymorphism was associated with muscle fibre composition (the amount of slow-twitch fibres in RR, RX and XX genotypes was 12.8%, 13.2% and 16.3% respectively; $\rho=0.215$; $P=0.049$) and PRD of all athletes ($\rho=0.24$, $P=0.010$), showing that *ACTN3* XX genotype carriers have a higher proportion of type I fibres and prefer to skate long-distance races.

Recently, the impact on physical performance of combination of polymorphisms involving *ACTN3* gene and other several genes has been investigated^{150,151}. Ginevičienė et al.¹⁵¹ studied the association between the polymorphisms of *ACE* and *ACTN3* genes in elite athletes and controls from the Lithuanian population. They reported that athlete carriers of the *ACE* I/I and I/D as well as *ACTN3* X/X and R/X genotypes have better results in terms of grip strength and vertical jump. Chiu et al.¹⁵⁰ assessed the *ACE*, *ACTN3*, peroxisome proliferator-activated receptor delta (*PPARD*), and peroxisome proliferator-activated receptor gamma coactivator-1 alpha (*PPARGC1A*) genes and physical performance in 170 Taiwanese sedentary adolescent girls. At the individual gene analysis, they reported better performance in hand-grip strength, 30- and 60-s sit-up tests, and standing long jump for subjects with the *ACE* D/D, *ACTN3* R/R and *PPARD* T/C genotypes. In the gene combination analysis, the authors demonstrated that individuals with *ACE* D/D, *ACTN3* R/R and *PPARD* T/T genotype

have significantly greater performance in handgrip strength.

So far, other genetic variants in the *ACTN3* gene have not been investigated in relation to endurance performance, power athletic status and sprint performance. Further investigations are needed to clarify the possible role of other polymorphisms and the combination of polymorphisms in determining sports performance.

Other gene related to fitness phenotype

It is thus evident that strong genetic influences interact with environmental stimuli to alter performance traits and other phenotype responses to training. Understanding the genetics factor would give new insight in the explanation of differences in athletic performance. It is important to understand which are the genes strongly influencing critical physiological pathway, for example *ACE* and *ACTN3* genotypes could become an important guide for determining the best suited discipline a young athletes should follow. However, we have just began to recognise some important genetic component involved in the athletic performance and we need more longitudinal studies of large cohorts of young athletes before we could benefit of a genetic testing.

The creatine kinase isoenzyme MM (*CK-MM*) gene encodes the cytosolic muscle isoform of CK responsible for the rapid regeneration of ATP during intensive muscle contraction. Human studies of *CK-MM* gene sequence variation have shown a significant association between polymorphisms in this gene, increased cardiorespiratory endurance as indexed by maximal oxygen uptake following 20 weeks of training¹⁵², peak performance and less decline in force generation¹⁵³. In particular, the A/G polymorphism in the 3' untranslated region of *CK-MM* contributes to individual running economy responses to endurance training¹⁵⁴. Recently, Miranda-Vilela et al.^{155,156} have also showed that *CK-MM* TaqI polymorphism could indirectly influence performance affecting the susceptibility to exercise-induced inflammation.

Myosin light chain kinase (MLCK), a calcium-calmodulin dependent multi-functional enzyme, plays a critical role in the regulation of smooth muscle contraction. Polymorphisms in this gene, especially the C37885A allele, are associated with post-exercise strength loss. Heterozygotes for this polymorphism also demonstrate greater strength loss compared with the homozygous wild type (CC)¹⁵⁷.

Adenosine monophosphate deaminase 1 (*AMPD1*) is a highly active enzyme in the skeletal muscle that plays an important role in the adenine nucleotide catabolism. A nonsense C to T transition in nucleotide 34 (C34T) in exon 2 of *AMPD1* gene converts the codon CAA into the premature stop-codon TAA. Subjects with the TT genotype at the C34T *AMPD1* gene have diminished exercise capacity and cardiorespiratory responses to exercise in the sedentary state¹⁵⁸. Moreover, carriers of the T allele have a limited train-

ing response of ventilatory phenotypes during maximal exercise¹⁵⁸ and a reduced submaximal aerobic capacity¹⁵⁹. Recently, Ciężczyk et al.¹⁶⁰ reported a significant deficiency of the T allele in the Polish elite and non-elite rowers compared to control samples, showing that it can be considered a negative factor to athletic performance. The same group also confirmed these results in high-level Polish power-oriented athletes, suggesting that the C allele may contribute to attain elite status in power-oriented sports¹⁶¹.

The insulin-like growth factor 1 protein (IGF-1) increases muscle mass and possibly strength. Accordingly, carriers of the 192 allele of the *IGF-1* promoter microsatellite are characterized by greater quadriceps-muscle strength gains compared with non-carriers¹⁶². However, this study included older subjects (aged 52-81), who have different metabolic characteristics, especially in terms of growth factor levels, cytokines, prior habitual activity, etc., than young aspiring athletes. Therefore, this study does not provide good evidence that variation at this locus influences likelihood of success in sport. On the other hand, Huskonen et al.¹⁶³ demonstrated that genotype CC of polymorphism rs7136446 of *IGF1* gene increases the maximal force production.

Peroxisome proliferator-activated receptor (PPAR)-delta (*PPARD* gene) and PPAR-gamma coactivator-1-alpha (*PPARGC1A* gene) are determinants of mitochondrial function in animals and in vitro, and play a crucial role in training-induced muscle adaptation. PPAR-delta, in particular, regulates expression of genes involved in lipid and carbohydrate metabolism, affects insulin sensitivity by modifying glucose uptake in skeletal muscle. A functional +294T/C polymorphism in this gene (allele C) is associated with higher transcriptional activity compared to T allele. Akhmetov et al.¹⁶⁴ reported a significantly higher frequency of *PPARD* C allele in endurance-oriented athletes than in controls (18.3% vs 12.1%; $P < 0.0001$), showing that the +294T/C polymorphism of *PPARD* gene is associated with predisposition to endurance performance. Moreover, Chiu et al.¹⁵⁰ reported better performance in handgrip strength, 30- and 60-s sit-up tests, and standing long jump in Taiwanese adolescent girls with *PPARD* T/C genotype, whereas a combination of *ACE* D/D, *ACTN3* R/R and *PPARD* T/T genotype have significantly greater performance in handgrip strength.

PPAR-gamma coactivator-1-alpha (*PPARGC1A* gene) is an important factor regulating the expression of genes for oxidative phosphorylation and ATP production in target tissues through coactivation of nuclear receptors. Muscle-specific expression of PGC-1 alpha improves the performance during voluntary as well as forced exercise challenges. Additionally, *PGC-1 alpha* transgenic mice exhibit an enhanced performance during a peak VO_2 exercise test, demonstrating an increased peak oxidative capacity, or whole body oxygen uptake¹⁶⁵. Maciejewska et al.²³ investigated the genotype distribution of Gly482Ser polymorphism of *PPARGC1A* gene in Polish and Russian athletes, showing that its frequency is signifi-

cantly lower in the athletes compared with unfit controls ($P < 0.0001$). The under-representation of 482Ser allele was observed among the endurance, strength-endurance, and sprint-strength athletes. Thus, the authors concluded that Gly482 allele may be associated with endurance performance, while 482Ser allele may affect the aerobic capacity.

The adrenergic receptors are involved in several performance-related pathways and are therefore of particular interest as candidate genes for performance phenotypes. The β 2-adrenergic receptor (*ADRB2*) gene is a candidate for variation in endurance performance levels because of its contribution to the regulation of energy expenditure and lipid mobilization from human adipose tissue¹⁶⁶. The Arg16Gly polymorphism in this gene may be associated with endurance performance status in white men¹⁶⁷.

The Nuclear Respiratory Factors NRF1 and NRF2 coordinate the expression of nuclear and mitochondrial genes relevant to mitochondrial biogenesis and respiration. Carriers of a polymorphism in the sequence of translation initiator ATG in the *NRF2* gene have higher training response in running economy than non-carriers, thus potentially explaining some of the inter-individual variance in endurance capacity¹⁶⁸.

The hypoxia inducible factors (HIFs) are a family of proteins regulating the mechanisms of response to hypoxia occurring in circumstances of increased oxygen demand, such as muscles working at high intensity. HIF-1 α is the primary transcriptional response factor for acclimation to hypoxic stress, which up-regulates glycolysis and angiogenesis in response to low levels of tissue oxygenation. The increase of expression of erythropoietin and glycolytic enzyme genes, induced by HIFs, achieves high levels of anaerobic performances, allowing increase of anaerobic power output in a short-term period. Removal of HIF-1 α causes an adaptive response in skeletal muscle akin to endurance training, and provides evidence for the suppression of mitochondrial biogenesis by HIF-1 α in normal tissue¹⁶⁹. Since HIF-2 α , encoded by the endothelial PAS domain protein-1 (*EPAS-1*), is a sensor capable of integrating cardiovascular function, energetic demand, muscle activity and oxygen availability into physiological adaptation, DNA variants in *EPAS-1* influence the relative contribution of aerobic and anaerobic metabolism and hence the maximum sustainable metabolic power for a given event duration¹⁷⁰.

The haemoglobin plays a crucial role in endurance performance, because the increase in its concentration in blood is associated with enhanced VO_2 max and endurance capacity, which is also proportional to the increase in the oxygen carrying capacity of the blood. Subjects homozygous for intron2, +16C/C or -551C/C in the haemoglobin gene have decreased oxygen cost of running, thus explaining part of the individual variation in the cardiorespiratory adaptation to endurance training¹⁷¹.

Three quantitative trait loci have been related to glucose and insulin metabolism phenotypes in response to endurance training exercise. A promising locus for

glucose effectiveness (an insulin-independent effect whereby glucose mediates its own disposal from plasma) influencing exercise training response was identified on 19q13 at the skeletal muscle glycogen synthase (*GYS1*) gene locus, which regulates glycogen storage in skeletal muscles. Two additional possible loci on 6p and 7q were captured for disposition index, which measures overall glucose homeostasis exercise training responses¹⁷².

The acetylcholine receptor subtype M2 (*CHRM2*) plays a key role in the cardiac chronotropic response and DNA sequence variation at the *CHRM2* locus is a potential modifier of heart rate recovery in the sedentary state and after short-term endurance training in healthy individuals¹⁷³. In its role as an endothelial cell proliferation and migration factor, vascular endothelial growth factor (VEGF) can affect peripheral circulation. Therefore, individuals with at least one copy of the AAG or CGC promoter region haplotype have higher VO_2 max before and after aerobic exercise training than subjects with only the AGG and/or CGG haplotype¹⁷⁴.

The mitochondrial uncoupling proteins 2 and 3 (*UCP2* and *UCP3*) can affect the physical performance, by negatively regulating the production of reactive oxygen species and mitochondrial ATP synthesis. Recently, Dhamrait et al.⁴³ assessed the efficiency of skeletal muscle contraction, both before and after a period of endurance training, in 85 young, healthy, sedentary adults with *UCP3-55C>T* (rs1800849) and/or *UCP2-866G>A* (rs659366) polymorphisms. The authors demonstrated that these polymorphisms at the *UCP3/2* gene locus are associated with training-related improvements in skeletal muscle performance.

Interleukin-6 (IL-6) is involved in muscle repair and hypertrophy following exercise-induced damage¹⁷⁵. The -174 G/C polymorphism (rs1800795) of the IL6 gene is associated with increased transcriptional response *in vitro*^{9,176} and *in vivo*⁴ settings. Ruiz et al.¹⁷⁷ evaluated the frequencies of -174 G/C genotype and allele in Spanish elite endurance and power athletes, and non-athletic controls. Both GG genotype and G allele were significantly higher in the power athletes than the endurance athletes or controls. On the other hand, there was no difference between the control and endurance athletes. Thus, the authors concluded that the G allele of the IL6 -174 G/C polymorphism may favour sprint/power sports phenotype, which is mainly characterized by muscle hypertrophy/strength. However, this association was not confirmed in a replication study performed on Israeli elite endurance and power athletes¹⁷⁸.

Some other gene polymorphisms have been associated with sport performance, although results are still preliminary or controversial. These include polymorphisms in the α 2a-adrenoceptor gene (*ADRA2A*)¹⁷⁹, bradykinin beta 2 receptor (*BDKRB2*) and endothelial nitric oxide synthase 3 (*NOS3*) genes¹⁸⁰, vitamin D receptor gene^{181,182}, and ATPase, Ca²⁺ transporting, cardiac muscle, slow twitch 2 (*ATP2A2*), the NUA family, SNF1-like kinase, 1 (*NUAK1*), and the protein phosphatase 1, catalytic subunit, gamma isoform (*PPP1CC*) genes¹⁸³.

Conclusion

According to Darwin's theory of natural selection, individuals with favourable traits are more likely to survive and reproduce than those without them. Today, it is accepted that genetics determines the response of an individual to the surrounding environment. However, the identification of the genetic background related to susceptibility to injuries and physical performance of the athletes is challenging. Recently, the development of technology for rapid DNA sequencing and genotyping has allowed the identification of some of the individual genetic variations that contribute to athletic performance and the onset of musculoskeletal injuries, particularly in tendon and ligament tissues. Although these findings could explain why an individual is able to excel in one sport discipline (i.e. sprint) rather than in a different one, and why an individual develops more injuries than another one, many other factors should be taken into account. Sport performances are also the result of hours spent in focused, prolonged, intensive training, and a favourable genotype is not enough to produce a champion. On the other hand, appropriate prevention strategies play a critical role in reducing injury rates, independently by the genetics.

Although further studies must be performed to establish influence and interaction of genes across a range of athletic parameters, genetic analyses will help to identify individuals with advantageous physiology, morphology and maybe psychology, those with a greater capacity to respond/adapt to training and those with a lower chance of suffering from injuries. Recently, the British Association of Sport and Exercise Sciences (BASES) Molecular Exercise Physiology Interest Group produced a position stand to advise on current issues in genetic research and testing in sport and exercise science (BASES position stand on Genetic Research and Testing in Sport and Exercise Science). This statement clearly highlights that genetic testing (i) might be useful for the development of genetic performance tests, (ii) may also be applied for pre-participation risk screening and may prevent sudden deaths during sport; (iii) might in future also be used to identify those who are most likely to benefit medically from exercise programmes; (iv) may become more important in anti-doping activities where it could be used for identification purposes (genetic fingerprinting) and more direct antidoping testing.

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