TTN genotype is associated with fascicle length and marathon running performance

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Running Head: TTN, fascicle length and marathon performance

Abstract

Titin provides a molecular blueprint for muscle sarcomere assembly and sarcomere length can vary according to titin isoform expression. If variations in sarcomere length influence muscle fascicle length, this may provide an advantage for running performance. Thus the aim of this study was to investigate if the titin (*TTN*) rs10497520 polymorphism was associated with muscle fascicle length in recreationally active men (RA; $n = 137$) and marathon personal best time in male marathon runners (MR; $n = 141$). Fascicle length of the vastus lateralis was assessed *in vivo* using B-mode ultrasonography at 50% of muscle length in RA. All participants provided either a whole blood, saliva or buccal cell sample, from which DNA was isolated and genotyped using real-time polymerase chain reaction. Vastus lateralis fascicle length was 10.4% longer in CC homozygotes, those carrying two copies of the C-allele, than CT heterozygotes ($p = 0.003$) in RA. In the absence of any TT homozygotes, reflective of the low T-allele frequency within Caucasian populations, it is unclear if fascicle length for this group would have been smaller still. No differences in genotype frequency between the RA and MR groups were observed ($p = 0.500$), although within the MR group the T-allele carriers demonstrated marathon personal best times 2 min 25 s faster than CC homozygotes ($p = 0.020$). These results suggest that the T-allele at rs10497520 in the *TTN* gene is associated with shorter skeletal muscle fascicle length and conveys an advantage for marathon running performance in habitually trained men.

Keywords: Gene polymorphism, muscle architecture, endurance athletes, mechanical efficiency

Introduction

The titin gene (*TTN*) encodes the largest described protein to date, which is the third most abundant protein within the myofilament of human striated muscle (Vikhlyantsev & Podlubnaya 2012). Titin provides a molecular blueprint for the assembly and organisation of the thin and thick filaments during myofibrillogenesis (Chauveau et al. 2014). Seven splice isoform variants of titin exist within human striated muscle, which each differ in size and elasticity (Chauveau et al. 2014; Vikhlyantsev & Podlubnaya 2012).

A missense C>T transition (rs10497520), where the more common C-allele is replaced by the T-allele, has been identified within human *TTN* and reportedly contributes to the variability in the training response of maximal oxygen consumption (VO_{2max}) in previously untrained individuals (Timmons et al. 2010). Within cardiac muscle, titin is suggested to be a key regulator of the Frank-Starling mechanism (Fukuda et al. 2001), and considering the substantial differences in the elasticity of cardiac titin isoforms (Wang et al. 1991), this C>T transition may contribute to the variability within titin isoform expression. Accordingly, differences in the titin isoforms expressed may explain the *TTN*-related increases in stroke volume (Rankinen et al. 2003) and consequently VO_{2max} following endurance exercise training (Timmons et al. 2010). Furthermore, if this *TTN* polymorphism influences titin isoform expression in cardiac muscle as speculated, there exists a distinct possibility that a similar influence is occurring within skeletal muscle tissue.

In skeletal muscle, the predominant titin isoform is N2A, of which a smaller (T1) and larger (T2) isovariant exist within humans (Fry et al. 1997). A recent study, which identified a *TTN* mutation that alters isoform splicing in rats, demonstrated an association between isoform size and sarcomere length; with significantly longer resting sarcomere lengths corresponding to the larger mutant titin isoforms (Greaser & Pleitner 2014; Greaser et al. 2008). Assuming a linear relationship between fascicle length and in series sarcomere number (Herzog et al. 1990), it follows that fascicles expressing larger titin isoforms could be longer than those expressing smaller titin isoforms. It is important to note, however, that there was no association between titin isoform size and resting

sarcomere length in wild-type rats, those without the larger mutant titin isoform in the aforementioned study (Greaser & Pleitner 2014). Furthermore, evidence exists demonstrating the non-uniform distribution of sarcomere length within fascicles of the same muscle and different muscles (Greaser et al. 2005; Wickiewicz et al. 1983), thus understanding the potential influence of titin on skeletal muscle architecture in humans appears complex.

If *TTN*-dependent differences in skeletal muscle fascicle length are apparent, variability in muscle functional phenotypes might also be expected. For instance, muscle maximal shortening velocity (V_{max}) is positively correlated with fascicle length (Bodine et al. 1982; Sacks & Roy 1982). Although no direct associations between *TTN* and fascicle length have been reported, the aforementioned C>T transition within the *TTN* gene has been identified as contributing significantly to a genetic predisposition for maximal isokinetic strength at $180°\cdot s^{-1}$ but not $60°\cdot s^{-1}$ (Thomaes et al. 2013), which could indirectly demonstrate that variability in V_{max} is influenced by genotype-dependent differences in fascicle length. Furthermore, enhanced efficiency of stretch-shortening contractions can be expected in individuals possessing shorter muscle fascicles due to the lower metabolic cost of producing a given force. More specifically, shorter fascicles produce the same force per unit cross-sectional area as longer fascicles, but when producing a given force, a smaller volume of muscle is activated in individuals possessing shorter fascicles (Pontzer et al. 2009; Roberts et al. 1998). Accordingly, vastus lateralis and gastrocnemius muscle fascicle length is shorter in elite distance runners than elite sprinters and untrained controls, and longer in elite sprinters than untrained controls (Abe et al. 2000). Shorter fascicles in elite distance runners are likely to contribute to improved mechanical efficiency, whereas the longer fascicles observed in elite sprinters is likely to contribute to enhanced V_{max}. To date, however, it remains unclear whether these differences in the muscle architecture of elite runners are the result of adaptations to training or genetic variation.

Consequently, the present study aimed to investigate if the *TTN* rs10497520 polymorphism was associated with muscle fascicle length in recreationally active men, and to investigate if *TTN* genotype distribution differed between recreationally active men and trained male marathon runners. It was

hypothesized that the *TTN* polymorphism would be associated with muscle fascicle length in recreationally active men, and the genotype associated with shorter fascicle length in this population would be overrepresented in trained marathon runners.

Materials and methods

The sample comprised 278 healthy, unrelated Caucasian men who were categorised as either recreationally active [RA; n = 137, age 20.6 (2.3) yr, height 1.79 (0.06) m, mass 75.1 (10.1) kg; mean (standard deviation; SD)] or habitually trained marathon runners [MR; n = 141, age 34.9 (7.8) yr; height 1.79 (0.07) m, mass 66.5 (6.7) kg]. RA participants were primarily recruited through mail-outs, posters and word-of-mouth. RA participants were excluded from participation if they had a body mass index (BMI) below 18.5 $kg \cdot m^{-2}$ or above 30 $kg \cdot m^{-2}$, self-reported as having a known musculoskeletal or neurological disorder and/or had undertaken any structured training in the preceding 12 months. MR participants comprised Olympic, international and national level marathon runners and were included if they had achieved marathon personal best times under 2 hr 36 mins (range ~2 hr 7 mins to ~2 hr 35 mins). MR participants were primarily recruited from London Marathon competitors at the London Marathon Expos during 2013-2015 and regional athletics clubs and organisations via mail-outs, posters and word-of-mouth. All participants gave written informed consent to participate in this study, which received approval from the Ethics Committee of Manchester Metropolitan University and complied with the Declaration of Helsinki.

Muscle fascicle length of the vastus lateralis (VL) was measured *in vivo* using B-mode ultrasonography (AU5, Esaote, Italy) for each RA participant. VL muscle length of the right limb was measured at rest following identification of the VL origin and insertion, whilst participants were standing upright with knees extended and relaxed (Abe et al. 2000). Whilst in this position, ultrasound scans were taken at 50% of VL muscle length, in the mid-sagittal plane, using a 40 mm wide, 7.5 MHz linear-array probe positioned perpendicular to the skin. Although the knee joint angle during standing does not correspond to that of optimal force production during running (Novacheck 1998; Tsuji et al. 2015), measurement of fascicle length in this position is highly reproducible. Each ultrasound scan

was recorded using a 25 Hz sampling frequency in audio video interleave (AVI) format and frame-capture software (Adobe Premiere Elements version 10, Adobe Systems) was used to capture single images for subsequent analysis. The distance between fascicular origin in the lower aponeurosis and insertion in the upper aponeurosis was measured as fascicle length using digitizing software (NIH ImageJ, version 1.44o, National Institute of Health, Bethesda, Maryland). Measurement of fascicle length in all instances required extrapolation of the superficial and deep aponeuroses to allow for estimation of fascicle length, due to fascicles extending beyond the ultrasound field of view (Reeves & Narici 2003). For each participant a minimum of three fascicles were measured and a mean of these was taken as fascicle length. Due to the field-based nature of data collection within MR, it was not possible to obtain measurements of fascicle length in this population.

All participants provided either a blood, saliva or buccal cell sample using the following protocols. For blood sampling, a 5 mL sample was taken from a superficial forearm vein into EDTA tubes (BD Vacutainer Systems, Plymouth, UK) and stored at -20°C. Saliva samples were collected following a minimum 30-minute abstinence from food and drink into Oragene DNA OG-500 collection tubes (DNA Genotek Inc., Ontario, Canada) in accordance with the manufacturer's guidelines and stored at room temperature. Buccal cell samples were collected in duplicate (Whatman Sterile, OmniSwab, GE Healthcare, USA) following a minimum 1-hour abstinence from food and drink. Participants were instructed to brush one OmniSwab collection tip firmly against the inside of the cheek for approximately 30 s and repeat with a second swab on the opposite cheek. Each collection tip was ejected into a 2 mL microcentrifuge tube and stored at -20°C.

The Qiagen QIAcube spin protocol (Qiagen, Crawley, UK), used for the extraction of genomic DNA from whole blood, saliva and buccal cell samples, was completed in accordance with the manufacturer's guidelines and used the buffers contained in the Qiagen DNA Blood Mini Kit. Each participant was genotyped for the *TTN* rs10497520 polymorphism, using real-time PCR on 96-well plates. The 10 μL reaction volume, for genotyping using DNA obtained from whole blood or saliva samples, contained 0.2 μL of participant DNA [9.9 (1.1) ng, amounts determined using ~20% of

participant DNA samples], 5 μL of TaqMan genotyping master mix (Applied Biosystems, Paisley, UK), 4.3 μL of nuclease-free H_2O (Qiagen) and 0.5 μL of TaqMan SNP genotyping assay (Applied Biosystems). For DNA samples obtained from buccal cells, the 10 μL reaction volume contained 1 μL of participant DNA [18.6 (4.6) ng], 5 μL of TaqMan genotyping master mix, 3.5 μL of nuclease-free H_2O and 0.5 μL of TaqMan SNP genotyping assay. In the control wells, the DNA sample was replaced by nuclease-free H_2O.

DNA amplification (StepOnePlus Real-Time PCR System, Applied Biosystems) was completed using the following protocol: an initial 10 min at 95°C followed by 40 cycles of denaturation for 15 s at 92°C, primer annealing and extension for 1 min at 60°C and plate read. *TTN* genotype was subsequently determined using StepOnePlus analysis software version 2.3 (Applied Biosystems). Genotypes were called based on reporter dye intensity and visualized using cluster plots. The TaqMan assays included VIC and FAM dyes that for rs1049752 indicated C and T alleles on the forward DNA strand, respectively. Thus, VIC/FAM were interpreted as: 5′- TCCAACTT[C/T]AGGTTCTT -3′. All samples were analysed in duplicate and 100% agreement between all duplicate samples was achieved.

Genotype frequency of the *TTN* rs10497520 polymorphism was assessed for compliance with Hardy-Weinberg equilibrium using a X^2 test. Due to the low number of TT homozygotes in the whole sample (RA, $n = 0$; MR, $n = 1$), CC homozygotes were compared to T-allele carriers within each sub-group (RA, CC vs. CT; MR, CC vs. CT+TT). Independent samples t-tests were conducted to determine any significant differences in physical characteristics (height, mass, BMI and age) between RA and MR, and according to genotype. Additionally, independent samples t-tests were conducted to identify any genotype differences in fascicle length in RA and marathon personal best time in MR. Pearson's X^2 tests were used to compare genotype frequencies between MR and RA. All statistical analyses were performed using SPSS version 21 and alpha was set at 0.05. Data are presented as mean (SD) unless otherwise stated.

Results

188 Genotype frequency of the *TTN* rs10497520 polymorphism was in Hardy-Weinberg equilibrium for
189 the whole sample and both the RA and MR sub-groups (Table 1). MR were older and had lower mass
190 (~9 kg) and BMI than RA (all differences $p \leq 1.0 \times 10^{-13}$), but there was no difference in height ($p =$
191 0.660). Genotype was not associated with mass, BMI or height either within the RA or MR
192 subgroups, nor in the combined sample of 278 participants ($p \geq 0.376$; Table 1).
193
194 In the RA sub-group, VL fascicle length was 10.4% longer in CC homozygotes than in CT
195 heterozygotes ($p = 0.003$; Figure 1). Furthermore, when VL fascicle length was normalised to VL
196 muscle length, VL fascicle length remained significantly longer in CC homozygotes than in CT
197 heterozygotes (11.7%, $p = 0.035$). There were no differences in genotype frequency between the RA
198 and MR groups ($X^2 = 1.385$, $p = 0.500$). However, marathon personal best time was significantly
199 lower in T-allele carriers compared to CC homozygotes in the MR group [2:26:28 (0:06:23) vs.
200 2:28:53 (0:05:50); $p = 0.020$; Figure 2].
201
202 **Discussion**
203 The aims of the present study were to investigate whether VL muscle fascicle length was associated
204 with *TTN* rs10497520 genotype in recreationally active Caucasian men, and to identify whether
205 differences in genotype frequency were evident between recreationally active individuals and trained
206 marathon runners. This study is the first to show a genetic influence on muscle architecture;
207 specifically, the results demonstrate that VL muscle fascicle length was significantly longer in *TTN*
208 CC homozygotes compared to CT heterozygotes in RA. This is also the first time marathon
209 performance in trained runners was associated with *TTN* genotype, with T-allele carriers performing
210 significantly better than CC homozygotes.
211
212 Titin acts as a template for myofibrillar protein assembly during sarcomere formation and provides an
213 attachment site for a plethora of myofibrillar proteins to maintain the structural integrity of the
214 sarcomere (Chauveau et al. 2014). This protein is therefore likely to play a key role in the architecture
215 of skeletal muscle, possibly affecting the serial arrangement of sarcomeres and, therefore, the length of

muscle fascicles (Greaser & Pleitner 2014; Greaser et al. 2008). Mean VL fascicle length in the RA group [7.1 (1.5) cm] was comparable to some previous reports of VL fascicle length (~7 cm) (Abe et al. 2000; Fukunaga et al. 1997), but less than others (~8 cm and ~9 cm) (Erskine et al. 2009; Reeves et al. 2004). Differences in participant positioning and muscle activation during the measurement of muscle fascicle length are likely to explain the reported differences between the present study and reports elsewhere (Fukunaga et al. 1997). Indeed, VL fascicle length was measured during standing with the knees extended and relaxed in the present study, which was similar to those studies reporting comparable fascicle lengths (Abe et al. 2000; Fukunaga et al. 1997). Those studies observing longer muscle fascicle lengths positioned the knee at 60-90° flexion and obtained measurements during maximal voluntary contraction (Erskine et al. 2009; Reeves et al. 2004).

The *TTN* genotype and allele frequencies observed in the present study were similar to previous reports in Caucasian populations (www.hapmap.org) (Gibbs et al. 2003). In the present study, individuals homozygous for the major C-allele had longer VL fascicles than heterozygotes, but as no individuals homozygous for the minor T-allele were present in the RA group, reflective of the low frequency of the T-allele within a Caucasian population, it is unclear if the VL fascicles of TT homozygotes would have been smaller still. Future research should attempt to replicate the observed association between *TTN* and fascicle length on larger cohorts that include a sufficient number of TT homozygotes. Based on the T-allele frequency we observed, future studies would require 2000 participants to recruit 20 TT homozygotes. A "stress the genotype" approach (Montgomery et al. 2002) could help prioritise recruitment of TT homozygotes prior to conducting time-consuming phenotype assessments. Furthermore, as fascicle length is known to vary between muscles (Erskine et al. 2009; Kawakami et al. 1998; Morse et al. 2008), future research should also include measurements of fascicle length from multiple muscles (i.e. gastrocnemius and soleus) to establish if the observed association with *TTN* genotype is consistent across different muscle groups, or specific to the vastus lateralis.

243 Nonetheless, it is possible that the presence of the T-allele affects *TTN* splicing thus increasing
244 expression of a smaller titin isoform within the muscle fascicles of heterozygotes. To date, seven
245 different titin splice isoforms have been identified within human striated muscle that each differ in size
246 (Vikhlyantsev & Podlubnaya 2012). Within human skeletal muscle, the predominant titin isoform is
247 N2A, of which two isovariants (T1 and T2) are known to exist (Fry et al. 1997). Thus, it is possible
248 that altered *TTN* splicing, due to the presence of the T-allele, may influence the expression of these
249 N2A isovariants and might explain the current observations. Earlier studies in rat cardiac muscle
250 support these possibilities by demonstrating a link between a *TTN* mutation and alternative isoform
251 splicing (Greaser et al. 2005) and, more recently, *TTN* was associated with both cardiac and skeletal
252 muscle sarcomere length in rats (Greaser & Pleitner 2014; Greaser et al. 2008). Individuals with
253 longer fascicles (CC homozygotes) would in theory experience a rightward shift in their length-tension
254 relationship and, potentially, larger optimal joint angles for maximal torque production. Such a shift
255 in the length-tension relationship has been linked to a reduction in injury occurrence, as a longer
256 optimum muscle length would ensure that less of the muscle's functional range would be along the
257 more unstable descending limb of the length-tension curve (Brughelli & Cronin 2007). Thus, in
258 populations at increased risk of injury, such as athletes, it may be necessary to tailor training
259 interventions specific to *TTN* genotype.
260
261 Considering the observed association between *TTN* genotype and VL fascicle length, it was
262 hypothesized that T-allele carriers would be overrepresented in habitually trained marathon runners
263 because shorter fascicles require less energy to produce a given force, which is likely to contribute to
264 improved mechanical efficiency in this population (Pontzer et al. 2009). No difference, however, in
265 *TTN* genotype distribution was observed between the RA and MR groups. Nonetheless, the MR T-
266 allele carriers (those expected to possess shorter fascicles according to our RA data) had marathon
267 personal best times 2 min 25 s faster than MR CC homozygotes. This observation is consistent with
268 previous reports of elite distance runners possessing shorter fascicles than both untrained individuals
269 and elite sprinters (Abe et al. 2000). Thus, possession of the T-allele, whilst not essential for
270 successful marathon running performance, might convey an advantage for marathon running when

combined with appropriate training and nutritional regimens as could be expected of the habitually trained runners included in the present study.

Despite observing associations between *TTN* genotype and VL fascicle length in RA and marathon personal best time in MR, it remains unclear whether marathon personal best time was enhanced in the MR T-allele carriers as a consequence of possessing a shorter fascicle length, as this was not directly measured in the MR group. As titin is suggested to be a key regulator of the Frank-Starling mechanism, the influence of *TTN* within cardiac muscle could provide an alternative explanation for the observed association between *TTN* genotype and MR personal best time. *TTN*-related increases in stroke volume following endurance training have been observed previously (Rankinen et al. 2003) and the rs10497520 polymorphism appears to contribute to the training response of VO_{2max} in previously untrained individuals (Timmons et al. 2010). Interestingly, however, Timmons et al. (2010) observed greater gains in VO_{2max} in CC homozygotes (those expected to have longer VL fascicles) than T-allele carriers (those expected to have shorter VL fascicles), with gains experienced by heterozygotes similar to those of TT homozygotes following training. For untrained participants, such as those in Timmons et al., training-induced increases in VO_{2max} are primarily due to increases in cardiac output via increases in stroke volume (Ekblom et al. 1968; Iwasaki et al. 2003) and might be accentuated in individuals possessing the CC genotype. However, in highly trained athletes with comparable rates of maximal oxygen uptake, as could be expected of the trained MR group, other factors such as lactate threshold and running economy are probably more important in determining performance (Conley & Krahenbuhl 1980). Moreover, improved running economy in individuals possessing lower ratios of titin isoforms (T1/T2) has recently been reported (Pellegrino et al. 2016), although more research is required to investigate whether the rs10497520 T-allele corresponds to lower T1/T2 ratios. Thus, despite a potential pleiotropic influence of *TTN* on both cardiac and skeletal muscle, possession of the T-allele (and consequently shorter VL fascicles) appears more important for marathon performance in trained individuals.

298 Finally, as RA CC homozygotes possessed longer VL fascicles, an association of this genotype with
299 successful sprint running performance is possible. Longer muscle fascicles are known to contribute to
300 enhanced V_{max} (Bodine et al. 1982; Sacks & Roy 1982), which is an important determinant of sprint
301 performance (Kumagai et al. 2000). Thus, trained sprinters with the CC genotype might possess
302 longer muscle fascicles and enhanced sprint ability compared to trained sprinters carrying the T-allele.
303 Future research should investigate the impact of *TTN* genotype on sprint performance in addition to
304 running economy, mechanical efficiency and V_{max}, to enhance our understanding of these associations.
305

306 **Conclusion and Perspective**

307 Here we report, for the first time, a genetic influence on human skeletal muscle architecture. The T-
308 allele at the rs10497520 polymorphism in *TTN*, the gene encoding the giant structural protein titin, is
309 associated with shorter VL muscle fascicles in recreationally active men, and faster marathon
310 performance (nearly 2.5 minutes faster) in habitually trained male runners with personal best times of
311 approximately 2.5 hours. Considering shorter muscle fascicles require less energy to produce a given
312 force, the genotype-dependent differences in marathon personal best times may be due to differences
313 in mechanical efficiency between T-allele carriers and CC homozygotes.
314

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Table 1. *TTN* rs10497520 genotype frequency and physical characteristics for RA and MR participants. Frequency data presented as count (%), all other data presented as mean (SD).

		All	CC	CT	TT	p	X^2
RA	Frequency (%)	137 (100)	110 (80.3)	27 (19.7)	0 (0.0)	0.441	1.637
	Height (m)	1.79 (0.06)	1.79 (0.06)	1.80 (0.07)	-	0.437	
	Mass (kg)	75.3 (10.1)*	75.0 (9.9)	76.3 (11.1)	-	0.376	
	BMI ($kg \cdot m^{-2}$)	23.5 (2.7)*	23.5 (2.7)	23.6 (3.0)	-	0.806	
	Age (yr)	20.7 (2.7)*	20.8 (2.6)	20.6 (3.1)	-	0.768	
	VL fascicle length (cm)	7.1 (1.5)	7.3 (1.6)	6.4 (0.9)	-	**0.003**	
	VL fascicle length/VL muscle length	0.17 (0.05)	0.18 (0.05)	0.16 (0.03)	-	**0.035**	
MR	Frequency (%)	141 (100)	108 (76.6)	32 (22.7)	1 (0.7)	0.756	0.561
	Height (m)	1.79 (0.07)	1.78 (0.07)	1.79 (0.06)	1.82	0.675	
	Mass (kg)	66.6 (6.7)	66.7 (6.8)	66.0 (6.6)	66.0	0.551	
	BMI ($kg \cdot m^{-2}$)	20.9 (1.9)	21.0 (2.0)	20.6 (1.6)	19.9	0.285	
	Age (yr)	34.9 (7.8)	34.3 (6.7)	37.0 (10.6)	31.0	0.196	
	Marathon PB Time (hr:min:s)	2:28:31 (0:06:17)	2:28:53 (0:05:50)	2:26:25 (0:06:12)	2:27:08	**0.020**	
TOTAL	Frequency (%)	278 (100)	218 (78.4)	59 (21.2)	1 (0.4)	0.385	1.908
	Height (m)	1.79 (0.07)	1.79 (0.07)	1.79 (0.06)	1.82	0.415	
	Mass (kg)	70.8 (9.6)	70.9 (9.4)	70.7 (10.4)	66.0	0.834	
	BMI ($kg \cdot m^{-2}$)	22.2 (2.7)	22.2 (2.7)	21.9 (2.7)	19.9	0.452	
	Age (yr)	27.9 (9.2)	27.5 (8.5)	29.5 (11.5)	31.0	0.196	

RA, untrained; MR, habitually trained marathoners; BMI, body mass index; PB, personal best; p relates to two-group analyses (CC vs. CT in RA and CC vs. CT+TT in MR) except for frequency analyses when this includes all genotype groups; * denotes significant difference between RA and MR ($p \leq 1.0 \times 10^{-13}$).

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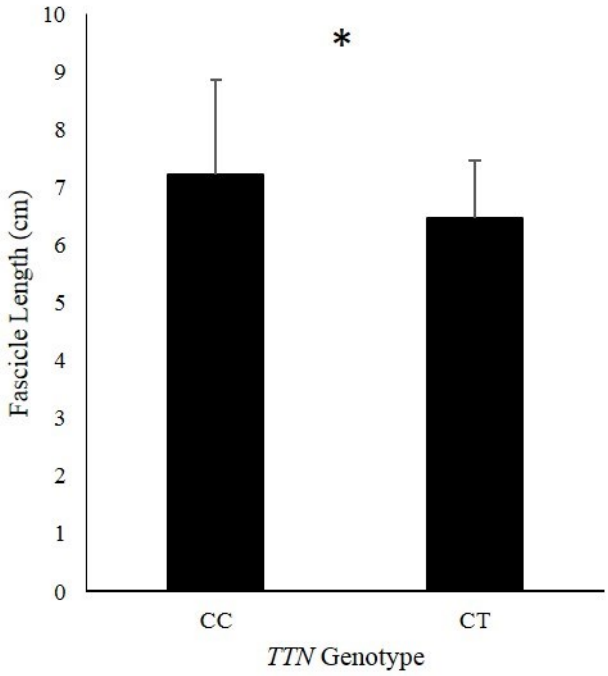
Figure 1. Comparison of VL fascicle length by *TTN* CC (*n* = 110) and CT (*n* = 27) genotype in RA (*p = 0.003). No TT homozygotes were identified. Columns and error bars are mean and SD.

Figure 2. Comparison of marathon personal best time between *TTN* CC genotype (*n* = 108) and T-allele carriers (*n* = 33) in MR (*p = 0.020). Columns and error bars are mean and SD.



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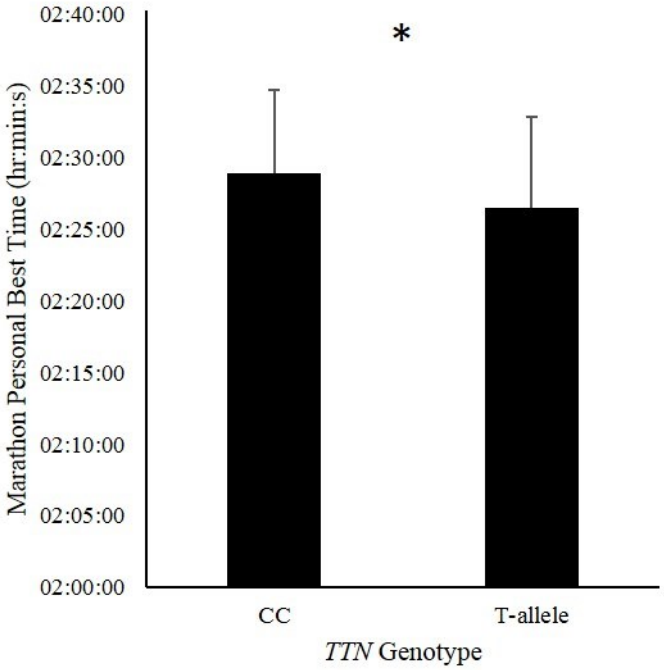
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Marathon Personal Best Time (hr:min:s)
*
CC
T-allele
TTN Genotype

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