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Introduction

The *APOE* gene encodes apolipoprotein E-based peptide and is a candidate marker for risk and severity of mild-traumatic brain injury (mTBI). ApoE is a 299 amino acid protein and has three common isoforms (Apo $\epsilon 2$, $\epsilon 3$, and $\epsilon 4$). Multiple meta-analyses have shown those possessing the $\epsilon 4$ allele ($\epsilon 4+$) have an increased risk of poor outcome >6 months after mTBI in^{1,2}. Recently, Merritt and Arnett³ showed that $\epsilon 4+$ athletes (as apposed to those without ($\epsilon 4-$)) suffered more severely, with a medium effect size for cognitive ($d = 0.60$) and a large effect size for physical symptoms ($d = 0.87$) within 3 months post-mTBI.

Current mTBI (concussion) incidence in elite rugby union (RU) ranges between 4.6 - 8.9 per 1000 playing hours⁴ with higher rates in elite rugby league (RL), ranging between 14.8 - 28.3^{4,5}. As *APOE* $\epsilon 4/\epsilon 4$ genotype and $\epsilon 4+$ individuals are at greater risk of experiencing more severe symptoms after mTBI, they are probably more likely to miss important training, selection and competitive events critical for their career progression. Thus, $\epsilon 4/\epsilon 4$ genotype and $\epsilon 4+$ individuals are potentially at a disadvantage compared to $\epsilon 4-$ individuals in terms of their ability to achieve success in elite competitive rugby.

Therefore, the aims of the present study were to establish the proportion of elite rugby athletes expected to be at higher risk of mTBI ($\epsilon 4+$) and to investigate if *APOE* genotype differed between elite rugby athletes and a control population.

Table 1 Genotype distribution of controls and rugby athletes sub-divided by code and international status, presented as genotype counts and percentage in parentheses.

Genotype	Controls	All athletes	RL athletes	RU athletes	RU Internationals	RU Non-Internationals
<i>APOE</i>						
$\epsilon 2/\epsilon 2$	1 (0.2)	1 (0.2)	0	1 (0.2)	1 (0.4)	0
$\epsilon 2/\epsilon 3$	69 (12.0)	71 (12.2)	14 (13.3)	57 (11.8)	19 (7.5)	38 (16.3)
$\epsilon 2/\epsilon 4$	14 (2.4)	8 (1.4)	1 (0.9)	7 (1.4)	1 (0.4)	6 (2.6)
$\epsilon 3/\epsilon 3$	350 (60.9)	338 (58.2)	53 (50.5)	290 (59.8)	156 (61.9)	134 (57.5)
$\epsilon 3/\epsilon 4$	127 (22.1)	144 (24.7)	34 (32.4)	113 (23.5)	68 (27.4)	45 (19.3)
$\epsilon 4/\epsilon 4$	14 (2.4)	19 (3.3)	3 (2.9)	16 (3.3)	6 (2.4)*	10 (4.3)
Total	575	581	105	484	251	233

RU, rugby union, RL rugby league. Eight athletes competed in both elite RL and RU and were included in both groups that were analysed separately. *Different from RU non-international ($P = 0.01$)

Method

Participants

Ethical approval was granted by the Manchester Metropolitan University, Glasgow University and the University of Cape Town ethics committees. Elite Caucasian male rugby players (League and Union; $n = 581$; stature 1.85 ± 0.07 m, mass 101.4 ± 12.5 kg) and controls ($n = 575$; stature 1.74 ± 0.10 m, mass 75.1 ± 13.5 kg) were recruited for the present study having given informed consent. The athletes comprised of players competing in the top league from Tier 1 rugby nations (51% international standard).

Sample collection, DNA isolation & Genotyping

Biological samples were obtained via venous blood, saliva (DNA Genotek Inc., Ontario, Canada) or buccal swab (Omni swab, Whatman, Springfield Mill, UK) and stored at -20°C until subsequent analysis. DNA was isolated using automated spin column protocol (Qiagen, West Sussex, UK). Genotyping was performed using real-time PCR on either a StepOnePlus real-time detector (Applied Biosystems) or Chromo4 (Bio-Rad).

Data analysis

Genotypic data was assessed for Hardy-Weinberg Equilibrium. Pearson's Chi-square (χ^2) was used to investigate genotypic and allelic frequencies using SPSS (SPSS Inc., Chicago, IL). Benjamini-Hochberg corrections were applied to correct for multiple testing. Odds ratios (OR) were calculated for estimations of the probability of an interaction between genes and elite rugby status. The alpha level was set at $P = 0.05$.

Results & Discussion

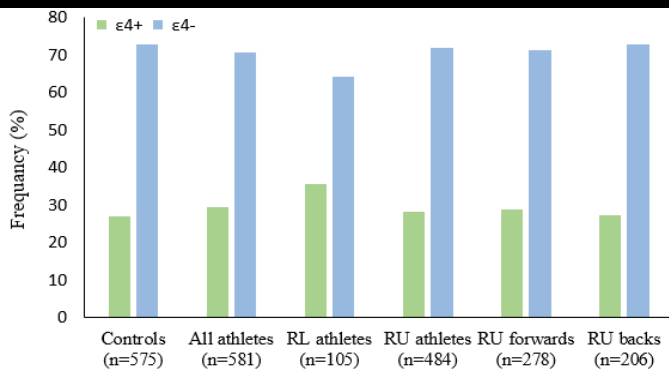


Fig 1 Presence or absence of $\epsilon 4$ allele in controls and athletes. Green bars represent $\epsilon 4$ carriers and blue bars represent those possessing no $\epsilon 4$ alleles.

No data violated H-W equilibrium. There were no differences in *APOE* genotype or $\epsilon 4+$ frequency when comparing all ($P = 0.27$), RU ($P = 0.15$) or RL athletes ($P = 0.54$) with controls (additive values presented; Table 1). However, prior to BH correction RL was different from controls ($P = 0.048$; OR = 0.67 95%CI 0.43-1.04). No genotype frequency or $\epsilon 4+$ differences were observed between RU backs and forwards ($P = 0.86$, $P = 0.70$, respectively, Fig 1).

Here we present the first large data set of *APOE* genotype and elite rugby athlete status. In contrast to our hypothesis, there were no differences in $\epsilon 4/\epsilon 4$ genotype or $\epsilon 4$ allele frequency between elite rugby athletes and non-athlete controls (Fig 1). Furthermore, there were no differences in $\epsilon 4/\epsilon 4$ genotype or $\epsilon 4$ allele frequency between RU playing positions (Fig 1).

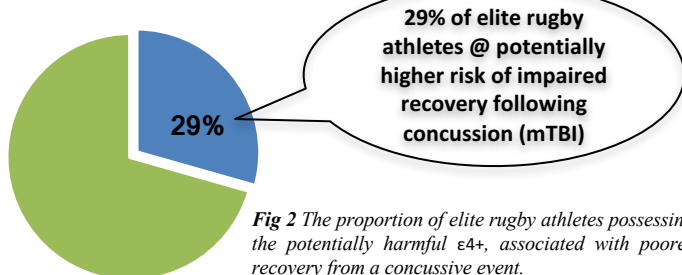


Fig 2 The proportion of elite rugby athletes possessing the potentially harmful $\epsilon 4+$, associated with poorer recovery from a concussive event.

It is noteworthy that there are considerable numbers of $\epsilon 4/\epsilon 4$ (3.3%) and $\epsilon 4+$ (29.4%) rugby athletes who may be at greater risk of cognitive and physical impairments following mTBI, compared to non-carriers³ (Fig 2). World Rugby (the international governing body of rugby union) estimates that there are 7.23 million rugby union players worldwide of all competitive standards (<http://www.worldrugby.org/development/player-numbers>). Assuming similar allele frequencies to the Caucasians we have studied amongst all players worldwide for the purpose of this discussion (i.e. ignoring geographic ancestry), over two million $\epsilon 4+$ rugby players may be at relatively greater risk of poorer outcome following mTBI than their $\epsilon 4-$ counterparts.

References

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