the CON group vs. the RUP group. The CC genotype was significantly over-represented (p = 0.019) in the CON group (24%) compared to the RUP group (3%). Inferred haplotype analyses showed no significant difference in the frequency distributions of the *VEGFA* or *KDR* haplotype combinations between the CON vs. TEN groups or the CON vs. RUP groups.

Discussion This pilot study did not find a statistical association with any of the five tested polymorphisms within the *VEGFA* and *KDR* genes using the Achilles tendinopathy risk model. However, the preliminary results are suggesting that the *VEGFA* rs699947 polymorphism may be implicated in acute injuries as noted in the Achilles tendon rupture cases. This hypothesis would be in alignment with the previous ACL risk model observations [Rahim, 2014]. These loci therefore need further interrogation in larger sample sizes. Studies are underway to explore the five polymorphisms within two independent case-control samples sets, in order to elucidate the potential biological significance of the angiogenesis-associated cell signalling pathway in the aetiology of Achilles tendon injuries (overuse and acute).

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84 *TIMP2* AND *GDF-5* GENE VARIANTS AND ACHILLES TENDON PATHOLOGY: REPLICATION STUDY IN A BRITISH CASE-CONTROL POPULATION

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Introduction Achilles tendon pathology (ATP) encompasses a range of tendon overuse injuries that can be sub-classified into separate pathologies [Weinfeld, 2014]. To date, a number of single nucleotide polymorphisms (SNPs) have been associated with ATP [Raleigh and Collins, 2012] but, with the exception of the *COL5A1* rs12722 variant, limited work has been published on attempting to replicate these findings in cohorts other than those recruited from either South Africa or Australia. We selected variants within the *TIMP2* (rs4789932) and *GDF-5* (rs143383) genes, that have previously been shown to associate with ATP [El Khoury *et al*, 2013 and Posthumus *et al*, 2010], and attempted to replicate previous associations in a newly recruited British-based, case-control, Caucasian cohort.

Methods We recruited 133 ATP Caucasian patients from the County Clinic in Northampton along with 131 physically active controls from various sports clubs within the East Midlands region. DNA samples were collected from saliva (DNA genotek Ltd) and Taqman technology, using allele specific probes and primers, was used to genotype all DNA samples. Reactions were run on a StepOne Plus real-time PCR instrument (ABI). Genotypes were called according to post run cluster profiles and data were analysed using Chi-squared (c^2) analysis or Fisher's exact test. Significance was accepted at $p < 0.05$. All procedures were approved by the University of Northampton Research Ethics Committee.

Results For the *TIMP2* rs4789932 variant we found no association between genotype and case or control status in the entire cohort (p = 0.279). However, in sex specific analysis we did find that the CC genotype was associated (p = 0.043) with male ATP cases compared to controls (Table 1). For the *GDF-5* rs143383 variant, we found no association between genotype and case or control status in the entire cohort (p = 0.538) or in either male (p = 0.319) or female (p = 0.737) specific analysis (data not shown). Genotypes did not associate with any other potential confounding variables.

Abstract 84 Table 1 Genotype and allele frequency distribution of the Tvariant in a British case (ATP) and control (CON) cohort. Values are expressed as frequency with number (n) in parentheses

	All CON	All ATP	Male CON	Male ATP
TIMP2 rs4789932	n = 131	n = 121	n = 83	n = 74
CC	26.7 (35)	24.8 (30)	20.5 (17)	37.8 (28)
CT	54.2 (71)	45.5 (55)	60.2 (50)	43.2 (32)
TT	19.1 (25)	29.8 (36)	19.3 (16)	18.9 (14)
P- value	–	0.279	–	**0.043**
HWE	0.301	0.329	0.062	0.375
T allele	46.2 (121)	52.5 (127)	49.4 (82)	40.5 (60)
P-value	0.158	–	0.116	–

Conclusions The *TIMP2* rs478992 CC genotype was associated with male cases of ATP. Although this locus was previously associated with ATP in cohorts recruited from the Southern Hemisphere it was the CT genotype that was the risk factor and the association was not sex specific [El Khoury *et al*, 2013]. This result might be related to differences in unknown environmental exposures between the cohorts investigated that may modify the effect of the genotype. We found no evidence of an association between ATP and the *GDF-5* variant. These data should be viewed as preliminary findings and will need to be repeated in a larger cohort.

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85 IS THERE AN ASSOCIATION BETWEEN TENDINOPATHY AND DIABETES MELLITUS? A SYSTEMATIC REVIEW

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Introduction An association between tendinopathy and diabetes mellitus (DM) has been noted across multiple studies; see review by.[1]

This review aimed to identify and synthesise all available data on this topic.

Methods Nine databases were comprehensively searched for English language journal articles reporting both a tendon and diabetes related variable. Reference lists and citation tracking were used to increase the sensitivity of the search. Articles were excluded if they were: case reports, conference proceedings, animal studies or if they lacked a control group.

Results The search yielded 680 papers of which 33 were included in the final review. Meta-analysis of 4 studies identified a greater prevalence of diabetes in people with tendinopathy (OR 1.37, CI 1.05, 1.80, Figure 1). Similarly, meta-analysis of 12 studies

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Notes