

## Sarcopenia and variation in the Human Leukocyte Antigen complex

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## Abstract

### Background

Aging is characterized by chronic inflammation plus muscle mass and strength loss, termed sarcopenia. Human Leukocyte Antigen (HLA) types are drivers of autoimmune disease, although with limited penetrance. We tested whether autoimmune diagnoses are associated with sarcopenia, and whether HLA types and related genetic variants associate with sarcopenia in autoimmune disease free older people.

### Methods

Data from 181,301 UK Biobank European descent volunteers aged 60 - 70 with measured hand-grip strength and impedance. Logistic regression analysis estimated HLA types sarcopenia associations, adjusted for confounders and multiple testing.

### Results

Having any autoimmune diagnosis was associated with sarcopenia (Odds Ratio 1.83, 95% Confidence Intervals 1.74-1.92,  $p=4.0*10^{-125}$ ). After excluding autoimmune diagnoses, six of 100 HLA types (allele frequency >1%) were associated with sarcopenia (low grip strength and muscle mass). Having two HLA-DQA1\*03:01 alleles increased odds of sarcopenia by 19.3% (OR 1.19, CI 1.09-1.29,  $p=2.84*10^{-5}$ ), compared to no alleles. Having  $\geq 6$  of the 12 HLA alleles increased sarcopenia odds by 23% (OR 1.23 CI 1.12-1.35,  $p=7.28*10^{-6}$ ).

Of 658 HLA region non-coding genetic variants previously implicated in disease, 4 were associated with sarcopenia, including rs41268896 and rs29268645 (ORs 1.08, CI 1.05-1.11,  $p=1.06*10^{-8}$  and 1.07, CI 1.04-1.09  $p=1.5*10^{-6}$ , respectively). Some HLAs associations with sarcopenia were greater in female participants.

## **Conclusion**

Autoimmune diagnoses are strongly associated with sarcopenia in 60 to 70 year olds.

Variation in specific HLA types and non-coding SNPs are also associated with sarcopenia in older carriers free of diagnosed autoimmune diseases. Patients with sarcopenia might benefit from targeted treatment of autoimmune processes.

## **Keywords**

UK Biobank, autoimmune, inflammation, Muscle

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## Introduction

Immuno-senescence and ‘Inflammaging’ are characterized by a low grade chronic pro-inflammatory state associated with ageing, which results from an imbalance between the inflammatory and anti-inflammatory networks (1)(2). The Human Leukocyte Antigens (HLA) have a major role in mediating the chronic inflammatory pathway in autoimmune disease via antigen presentation to the CD4<sup>+</sup>/8<sup>+</sup> T cells (3). The HLA complex has long been associated with autoimmune disorders and infectious disease (4). Examples of associations between certain HLA types and autoimmune disease include HLA-B\*27 and spondyloarthritis (SpA), HLA-B\*51 and Behcet’s disease (5), and HLA-DRB1\*15:01 and multiple sclerosis (6)(7). Many autoimmune diseases directly impact on muscle strength and physical functioning, however autoimmune diseases are generally not monogenic or fully penetrant, but rather are complex polygenic diseases influenced by environmental factors (despite having over 110 linked genes, excluding HLA types, the heritability of multiple sclerosis is approximately 28% (8)). We hypothesise therefore that both those with diagnosed auto-immune conditions and carriers of certain HLA types without diagnosed autoimmune diseases may have increased risk of age related conditions.

Sarcopenia, loss of muscle mass and strength during ageing, is associated with reduced physical functioning and is associated with increased risks of morbidity (including falls and fractures) and mortality (9)(10). The European Working Group on Sarcopenia in Older People (EWGSOP) defines age-related Sarcopenia to include both low muscle mass and low muscle function (9). The Baltimore Longitudinal Study of Aging (BLSA) found evidence that this can occur as early as age 40 in both men and women (11), with progressive decline over time. However studies of age-related sarcopenia commonly use an age range of 60 or older, to exclude causes of muscle weakness earlier in life (12). Previous studies have presented evidence for the role of inflammation in sarcopenia (13)(14), and it is becoming apparent that

contributors to disease vary in penetrance from Mendelian disorders to complex diseases (15). We hypothesise that certain HLA types may increase risks for sarcopenia, possibly via undiagnosed or subclinical autoimmune processes. While muscle loss is a classical feature of multiple sclerosis and some other autoimmune conditions, little is known of whether carrying certain HLA types predisposes to autoimmunity which in turn accelerates muscle loss in later life.

We aimed to test associations between diagnosed autoimmune conditions and sarcopenia in the exceptionally large UK Biobank study. We also aimed to test associations between common HLA types and sarcopenia in individuals independently of any diagnosed autoimmune condition, using three definitions of sarcopenia (European Working Group on Sarcopenia definition published in 2010; Low grip strength and lean muscle mass combined, grip strength only and lean muscle mass only). We hypothesise that the presence of certain HLA types are more common in sarcopenic individuals in later life, even in the absence of diagnosed autoimmune disease.

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## Methods

We used data from 451,447 UK Biobank participants of European descent, confirmed by principal components analyses of genome-wide genetic information from a selection of participants who self-identified as ‘white European’(16). The UK Biobank is a volunteer study where participants visited one of 22 assessment centres across the UK. A range of physiological and questionnaire data was collected, including genetic data from blood draws (17). Genotyping data was generated on the initial ~50,000 participants using the Affymetrix UK BiLEVE Axiom array and the ~450,000 participants of the remaining cohort were genotyped using the Affymetrix UK Biobank Axiom array - the two arrays sharing over 95% similarity (<http://www.ukbiobank.ac.uk>).

## Phenotype definitions

Sarcopenia was classified using the EWGSOP definition (9), based on having both low hand grip strength and skeletal muscle mass index (SMI). For grip strength the highest value from hand grip strength, left and hand grip strength, right was taken as the selected metric. Low grip strength was defined as under 30kg in Males and under 20kg in Females, as measured by Jamar J00105 hydraulic hand dynamometer.

Skeletal muscle mass (SMM) was calculated using the following equation from Janssen *et al* (18);

$$\text{SMM (kg)} = [(\text{Ht}^2 | R \times 0.401) + (\text{gender} \times 3.825 + (\text{age} \times -0.071))] + 5.102$$

Where Ht is standing height in centimetres measured at the initial assessment; *R* is Bioelectrical Impedance Analysis (BIA) resistance in ohms for the whole body taken by Tanita BC418MA body composition analyser at the initial assessment visit; for sex, men = 1

and women = 0; and age is in years. A Skeletal muscle mass index (SMI) was then calculated from the SMM.

$$\text{SMI} = \text{SMM}/\text{Ht-in-meters}^2$$

Low SMI was defined by Janssen *et al.* as under 8.87 in Males and under 6.42 in Females. Analysis was restricted to the age range of 60-70. We excluded a small number participants with max grip strength or lean mass (from BIA) greater than 4 standard deviations from the mean (SMI > 46.61; max grip > 73.91).

Three definitions of sarcopenia were developed based on the EWGSOP classification using both grip and lean muscle mass (grip strength 30kg for males and 20kg for females, Low SMI 8.87 for males and 6.42 for females), low grip strength only (grip strength 20kg for females and 30 kg for males) and low muscle mass only (Low SMI 6.42 for females and 8.87 for males). While DXA (Dual-energy X-ray absorptiometry) is the preferred alternative to CT and MRI for estimating muscle mass, EWGSOP deemed that BIA may be considered as a portable alternative to DXA.

The FNIH definition of sarcopenia (19) based on low grip strength and appendicular lean mass could not be analysed with the cohort due to less than 0.2% / 0.1% of the female / male participants meeting the criteria.

### **Auto-immune disease exclusions**

Some autoimmune diseases are known to influence muscle loss. We aimed to determine whether HLA-types were associated with sarcopenia in the absence of diagnosed autoimmune disease, and we therefore excluded participants with a diagnosis at the baseline assessment (self-reported or hospital diagnosed).

A list of 135 (including sub-groups) ICD-10 codes for autoimmune diseases were generated from previous review articles (20) and the codes used to exclude participants from the initial analysis (Supplementary Table 1). In addition, UK Biobank self-reported data was also used based on the autoimmune conditions in the ICD-10 list. Following the initial analysis an additional 55 autoimmune diseases associated with the HLA types were added to the exclusion criteria and formed the basis of the secondary analysis (Supplementary Table 2).

Logistic regression was performed on a selected subset of more common autoimmune conditions such as Rheumatoid Arthritis, Multiple Sclerosis, Coeliac disease, Type 1 Diabetes, Psoriasis and Ulcerative colitis. In order to include as many participants as possible with each condition all ICD-10 codes belonging to the superclass of each condition were included (for example, all ICD-10 codes for M06\* are included for Rheumatoid Arthritis), as well as any self-reported in the UK Biobank (Supplementary Table 10 for details).

### **HLA imputation**

Imputation of HLA types was performed centrally by the UK Biobank team. In brief, HLA\*IMP:02 (21) was used to impute the four-digit HLA types from genotype information, with a number of modifications: localization feature turned off; graph sampling error (mS) and graph building error (mB) probabilities were both set to 0.001; and the number of sampled haplotype pairs was set to 5 (22). Individuals are therefore coded as 0, 1 or 2 depending on the number of HLA alleles carried for each gene. The methods allow for imprecise coding (e.g. 1.92) to indicate the confidence in HLA type imputation. Some HLA type codes indicate unknown or other HLA types (e.g. \*99:01), and these were not included in analyses. HLA-types below 1% frequency were excluded from analyses to account for lower quality imputation for rarer alleles.

## Statistical Analysis

Logistic regression analyses were performed for each HLA type against sarcopenia, adjusted for age, sex, genotype array, and the first five principal components for ancestry. Cohorts were restricted to the age range 60 to 70 and of European descent. Participants with known autoimmune disease were excluded as previously described, based on Hospital Episode Statistics data (ICD-10 codes) and self-reported fields.

HLA types were modelled first assuming an additive effect, and secondly comparing participants with 2 alleles to those with 0. Participants with imprecise HLA imputations were recoded for the second, categorical analysis (i.e. estimated allele dose between 0 and 0.25 set to 0, values between 0.75 and 1.25 set to 1, and finally between 1.75 and 2 to 2; other doses were set to missing due to imprecise imputation). Correction for multiple testing was applied using the Benjamini-Hochberg method, for the additive and recessive models separately as these were independent hypotheses. Statistical analyses were performed in STATA (v14.1) and R (v3.3.2). Charts and figures were generated with package metafor (v2.0).

After analysing each HLA type for its association with sarcopenia we performed a literature search to identify any autoimmune diseases implicated by the significant HLA types not already included in the autoimmune exclusion criteria. HLA type associations with sarcopenia were reanalysed after participants with a diagnosis of these further autoimmune conditions had been excluded (Supplementary Table 2); these are the final results presented.

## **Sex specific cohort analysis**

HLA types associated with the three definitions of sarcopenia was analysed with sex-specific cohorts, after the removal of participants with autoimmune conditions. We tested for a statistical interaction between sex and HLA type on sarcopenia, in the models described previously.

## **Sensitivity analyses**

Sensitivity analysis was performed on the HLA types associated with sarcopenia across the three phenotypes, for smoking status (UKB data-field: 20116) and a combination of height and weight.

## **Non-coding SNPs associated with a phenotype in previous Genome-Wide Association Studies.**

The HLA types assessed so far were based on the protein-coding sequence of the HLA protein expressed. We also investigated non-coding SNPs within the HLA region that have previously been associated with traits in the GWAS catalogue; SNPs in the HLA region (4) between GRCh.v38: Chr6:29545629 (start of GABBR1 transcript ENST00000355973.7, minus 10Kb) and GRCh.v38: Chr6:33419924 (end of KIFC1 transcript

ENST00000428849.6, plus 10 Kb) were downloaded from the NHGRI-EBI GWAS

Catalogue(23). SNPs labelled with one or more of the following contexts were excluded stop\_gained, synonymous\_variant, missense\_variant, non\_coding\_transcript\_exon\_variant, frameshift\_variant or inframe\_deletion, in order to prioritise variants with a possible

regulatory role over variants involved in changes to protein coding. The 658 SNPs associated

with a reported trait ( $p$ -value  $< 5 \times 10^{-8}$ , Supplementary Table 3) and had available genotype data in the UK Biobank were included in the analysis (frequency  $\geq 1\%$  in order to account for lower quality imputation for rarer SNPs). These were tested for their association with sarcopenia using the methods described above for HLA type analysis. We used the Bonferroni adjusted cut-off for 658 tests of  $p$ -value  $< 7.6 \times 10^{-5}$ . Associations between these SNPs and sarcopenia-associated HLA types were also calculated. The GTEx database (24) was used to identify genes with expression affected by the alleles of the genetic variants. A threshold of  $3.66 \times 10^{-8}$  ( $0.05 / 4$  independent lead SNPs \* 341316 GTEx v7 eGenes) was used to select the most significant eQTLs.

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## Results

We selected 196,099 UK Biobank participants of European descent aged 60-70 with complete phenotype, diagnosis, and genotype data for investigation. Of these, 14,798 participants had at least one diagnosed autoimmune disease (including type-1 diabetes, multiple sclerosis, and rheumatoid arthritis, see methods for details). Participants with a diagnosed autoimmune disease had increased odds of meeting the EWGSOP sarcopenia criteria (Odds ratio 1.83, CI 1.74-1.92,  $p=4.0*10^{-125}$ ; Table 1). There were specific associations with Rheumatoid Arthritis (n=2,833): mean grip strength in this group was 22.1 (SD 11.3) Kg compared to 31.0 (SD 10.8) Kg ( $p < 0.001$ ) for all other participants in the European 60-70 age group. Associations were also present for multiple sclerosis, coeliac disease and psoriasis, but not for type 1 diabetes or ulcerative colitis.

After excluding those with autoimmune diagnoses, the remaining 181,301 participants had a mean age of 64.1 years and 95,340 were female (Table 2). Of 85,961 men included in the analysis, 3,510 were defined as having sarcopenia (4.08%), and of 95,340 women there were 11,540 defined as sarcopenic (12.10%).

Of 100 HLA types with allele frequency  $>1\%$ , six were associated with sarcopenia (EWGSOP definition) in logistic regression models adjusted for age, sex, genotyping array type, and population structure (genetic principal components 1-5), after accounting for multiple testing ( $FDR < 5\%$ ) (Figure 1). We compared participants with two alleles of each HLA-type to those with zero alleles; participants homozygous for HLA-DQA1\*03:01 have 19.3% (Odds Ratio 1.19, 95% Confidence Intervals 1.10-1.30,  $p=2.84*10^{-5}$ ) increased likelihood of sarcopenia, compared to those without HLA-DQA1\*03:01 (Supplementary Table 4.) and HLA-DRB4\*01:03 homozygotes had a 15.4% increased likelihood of sarcopenia (Odds ratio 1.15, CI 1.08-1.23,  $p=2.66*10^{-5}$ ). When the six HLA-types were

combined, participants with at least six alleles (of a possible 12 - each person can have up to two alleles of each HLA type) had 23% increased likelihood of sarcopenia (n= 5,685 participants of 181,301; OR 1.23, 95% CI 1.12-1.35,  $p=7.28*10^{-6}$ ).

Seven HLA-types were associated with the sarcopenia definition based on grip strength alone, and six were associated with the sarcopenia muscle mass definition, with no overlap between the alleles associated with the two phenotypes (Figure 1 and Supplementary Table 5). All of the top HLA type associations for the EWGSOP definition of sarcopenia were also present in the low grip phenotype, with the exception of HLA-C\*15:02 which did not reach significance after correction for multiple testing in the low grip phenotype analysis.

Conversely, the HLA types associated with low muscle mass (HLA-B\*27:05 OR 1.079, 95% CI 1.04-1.12,  $p=1.64*10^{-5}$ ; HLA-C\*01:02 OR 1.093, 95% CI 1.05-1.13,  $p=1.65*10^{-6}$  and HLA-C\*02:02 OR 1.059, 95% CI 1.02-1.10,  $p=1.46*10^{-3}$ ) were distinct from those associated with the EWGSOP definition of sarcopenia.

### **Sex specific analysis**

We tested for interactions between HLA types and sex on sarcopenia. Two HLA types, HLA-DQA\*03:01 ( $p=0.032$ ) and HLA-DRB1\*04:04 ( $p=0.038$ ), were nominally associated with sarcopenia (EWGSOP combined definition); indicating that the effect of these HLA types is significantly greater in females, compared to males. The other interactions were not significant, although we cannot rule out lack of statistical power due to the relatively low numbers of men with sarcopenia (Supplementary Table 5).

There were three additional HLA types associated with the EWGSOP combined definition of sarcopenia in the female only analysis (HLA-B\*15:01 OR 1.089, 95% CI 1.03-1.15,  $p=3.27*10^{-3}$ ; HLA-DRB1\*04:04 OR 1.107, 95% CI 1.03-1.19,  $p=3.65*10^{-3}$  and HLA-DQB1\*03:02 OR 1.07, 95% CI 1.02-1.12,  $p=3.2*10^{-3}$ ), which were not identified in the

analysis including both sexes (FDR-adjusted  $p > 0.05$ ). In the analysis of males only, there were no significant (FDR-adjusted  $p > 0.05$ ) associations between HLA-types and sarcopenia.

### **Sensitivity analyses**

In sensitivity analyses we investigated the effect of adjusting for height and weight; all the reported risk increasing associations between HLA-types and sarcopenia remained significant, with nominal changes to effect sizes (Supplementary Table 6). However, the three protective HLA-types associated with the sarcopenia grip definition were non-significant after adjusting for height and weight ( $p > 0.05$ ) in the combined cohort. In the Female only cohort the protective HLA type DRB1\*15:01 was the only HLA-type to lose significance. The Lean Muscle Mass only phenotype maintained the significance of the previously observed HLA-types, except in the case of HLA-C\*01:02 in the Female only cohort which lost its significant association with sarcopenia.

Adjustment for smoking status had no impact on the associations between HLA types and sarcopenia, for any of the three phenotypes analysed or across the three cohorts of all participants, female only and male only (Supplementary Table 6).

### **Non-coding Single Nucleotide Polymorphisms in HLA region**

We analysed 658 non-coding SNPs (frequency  $\geq 1\%$  in order to limit the number of statistical tests undertaken and to avoid misclassification from lower quality imputation for rarer SNPs) within the HLA region previously implicated in human traits at genome wide significance ( $p < 5 \times 10^{-8}$ ) available in the UK Biobank genotype data. We found 219 SNPs nominally ( $p < 0.05$ ) associated with the EWGSOP definition of sarcopenia (Supplementary

Table 7). 10 SNPs reached the Bonferroni adjusted cut-off of  $7.6 \times 10^{-5}$ . Of these, we identified 4 independent signals (Table 3), after removing those in linkage disequilibrium ( $R^2 > 0.4$ , see Supplementary Table 8). This included rs41268896 and rs2293751 with p-values  $< 5 \times 10^{-8}$  (ORs = 1.079 and 1.069, respectively).

We interrogated the GTEx eQTL (expression quantitative trait loci) database of SNP-expression associations to determine the likely genes affected by these 4 genetic variants (Table 3, see Supplementary Table 9 for full details), using a stringent significance threshold of  $p < 3.66 \times 10^{-8}$ . This included specific HLA genes, here listed with the tissue in which the strongest eQTL was found (HLA-DQA2 - Skeletal Muscle, HLA-DQB2 – Whole Blood, HLA-DQB1 – Whole Blood, HLA-DRB6 – Skeletal Muscle, HLA-DRB9 - Thyroid, HLA-DRB1- Skin, Sun exposed lower leg, and HLA-DQA1 - Lung), in addition to other genes with plausible mechanisms of action in sarcopenia (*ATF6B* – Skeletal Muscle, *CYP21A1P* – Subcutaneous Adipose, *BAG6* – Tibial Artery, *CSNK2B* – Left Heart Ventricle, *LY6G5C* - Thyroid, *PSORS1C1* - Thyroid, C2 - Testis). We also searched for protein QTLs in a recent paper by Sun *et al.* (25) and found that rs41268896 is highly correlated ( $R^2=0.8$  in UKB) with rs8111, a pQTL for ATF6A.

We also investigated the combined effect of the 4 non-coding SNPs; participants with at least 4 effect alleles (of a possible 8), showed an increased likelihood of sarcopenia of 11% (n= 74,820 participants of 181,301; OR 1.11, 95% CI 1.08-1.15,  $p=1.06 \times 10^{-9}$ ).

## Discussion

To the best of our knowledge, this is the first large human population study of HLA effects on sarcopenia in older people. First, we have shown that autoimmune diagnoses are strongly associated with sarcopenia in our sample of 60 to 70 year old community volunteers, with particularly large effect for rheumatoid arthritis (OR 3.09, 95% CI 2.87 to 3.34), plus multiple sclerosis, coeliac disease and psoriasis, but not for type 1 diabetes or ulcerative colitis.

After excluding participants with autoimmune diagnoses, we identified 6 HLA types associated with sarcopenia in 181,301 UK Biobank participants of European descent aged 60-70. Although these have modest effect sizes (per allele odds ratios from 1.054 to 1.15) they are common in the study population, ranging in frequency from 3.7% to 24.8%. In combination, participants with more than six of the HLA-types had markedly increased likelihood of sarcopenia (OR 1.23, 95% CI 1.12 to 1.35). We observed markedly different prevalence of sarcopenia in males and females (4% vs 12%); although a recent systematic review found that the average sarcopenia prevalence in males and females was approximately 10% (26), the individual studies varied considerably and it was not unusual to observe substantial sex differences. We performed sex-stratified analysis of HLA-types and found that all observed associations were only statistically significant in females, and for some this sex-interaction was statistically significant, suggesting that the effect of HLA-DQA1\*03:01 and HLA-DRB1\*04:04 are substantially greater in females compared to males. Unfortunately the study lacked the power required for the male only cohort to observe Odds Ratios within the ranges seen in the combined sex analysis.

We also identified 4 non-coding genetic variants in the HLA region of chromosome 6 associated with sarcopenia. These are known to affect the expression of multiple genes,

including *HLA* genes, in multiple tissues including skeletal muscle. Although more evidence is required for a clear causal link, this suggests that regulation in expression of *HLA* genes may also be an important driver of sarcopenia, not just the protein sequence (*HLA*-types). When taken in combination participants with more than four of the effect alleles had an 11% increased likelihood of sarcopenia.

The EWGSOP 2010 definition of sarcopenia (27), which combines low grip strength and low muscle mass, shares many of the associated *HLA* alleles with those seen in low grip strength definition alone. In contrast, there is little overlap with the low muscle mass definition. Often, grip strength alone is used to identify “frail” participants in population studies (28) as it is the maintenance of function that appears most important.

*HLA*-types associated with sarcopenia are also associated with conditions linked to joint pain and loss of function, such as rheumatoid arthritis (*DRB1\*04:01*), ankylosing spondylitis (*C\*15:02*), Behcet’s disease (*B\*51:01*, joint swelling and pain prevalence in 45-60% of cases (29)), and neuropathic pain (*DQB1\*03:02*, although a meta-analysis (30) only showed association to the two-digit allele *DQB1\*03*). Other *HLA* alleles associated with sarcopenia include *DQA1\*03:01*, which has been linked to pemphigus vulgaris, a painful autoimmune condition which can affect the skin, mouth and groin with blisters. In addition a previous study (31) of *HLA* types and the self-reported fields for Rheumatoid Arthritis in the UK Biobank has shown an association between *DQA1\*03:01* and the disease (OR 1.77, CI 1.70-1.85,  $p=1.5 \times 10^{-131}$ , moderate linkage disequilibrium with *HLA-DRB1\*04:01*  $r^2 = 0.5$  ).

*DQB1\*03:01* has only been shown to have an association previously as a protective allele against primary biliary cholangitis, although this study provides evidence of a novel association with sarcopenia. In this analysis we excluded participants with a self-reported or hospital diagnosis of autoimmune conditions, including those mentioned here, suggesting that

the associations observed here are not due to diagnosed conditions. More work is needed on whether these associations are due to a general pro-inflammatory effect or represent sub-clinical manifestations of specific autoimmune processes. More work is also needed on whether some patients with sarcopenia have evidence of autoimmune processes and might benefit from targeted treatment.

Some HLA types were protective for sarcopenia: increasing copies of DQB1\*06:02, DRB5\*01:01 and DRB1\*15:01 were all associated with reduced likelihood of sarcopenia, and have previously been implicated in a number of studies in the development of multiple sclerosis (6), although mainly as part of an extended haplotype including all three types.

When we compared participants carrying two alleles of each HLA to those with zero we found far greater effect sizes; for example the likelihood of being sarcopenic for DQA1\*03:01 rises from 6% to 19.3%, suggesting recessive effects. DRB4\*01:03 has been reported as appearing with increased frequency in a limited study of Brazilian patients with polyarteritis nodosa (32). Association of DRB4\*01:03 with rheumatoid arthritis has mixed evidence in the literature with recent studies showing no association (33), while slightly older and smaller studies in a different population showing a link (34). HLA-DQA1\*03:01 has been previously shown to increase the risk of type 1 diabetes (35), when present as part of the DR4 haplotype or in conjunction with DQB\*02:01 (36).

The analysis of low grip strength alone reinforced the associations seen in the EWGSOP sarcopenia definition analysis, with only a single additional association for DQA1\*01:02.

This type was protective against low grip strength and reported as associated with a multiple sclerosis-like condition in transgenic mice (37). HLA alleles were only associated with low muscle mass using the additive model, C\*01:02 and B\*27:05, both of which have previously been linked to forms of arthritis – psoriatic arthritis (38) and spondyloarthritis (39). Neither

type appeared in the associations for the combined EWGSOP phenotype of sarcopenia, suggesting potential independent effects.

In our analysis of non-coding genetic variation in the HLA-region we identified 4 genetic variants associated with sarcopenia. These SNPs also affect expression of genes other than HLAs, including *ATF6B*, which encodes a transcription factor in the unfolded protein response (UPR) pathway during endoplasmic reticulum (ER) stress and there has been speculation that ER stress may impair autophagy and myogenesis activity resulting in sarcopenia (40) (41). rs41268896 is strongly correlated with the rs8111 ( $R^2=0.8$ ), known to affect protein levels of ATF6A (25), which binds as a heterodimer with ATF6B. The rs41268896 A allele increases *ATF6B* expression, whilst the rs8111 T allele (co-inherited) decreases ATF6A protein levels, suggesting a complex relationship; more work is required to understand this. The *BAG6* protein product is also involved in elimination of misfolded proteins, including class-I HLA products (42) (43). *CYP21A2* has a role in producing cortisol and aldosterone as part of the hypothalamic-pituitary-adrenal (HPA) axis, disruption to the HPA has been linked to decline in physical function and aging (44)(45).

The strengths of this study include the large number of older participants with consistent sarcopenia measurements and medical records data available for analysis. However, it is a volunteer study and will therefore be healthier than the general population: effects of HLA types on sarcopenia may therefore be underestimated in this study. Future studies should investigate other definitions of sarcopenia, such as those from the FNIH (46) and the revised 2018 version of the EWGSOP definitions (47) which result in differing prevalence (19) due to different cut-points and muscle mass measurements, in older populations. Additionally, autoimmune diagnoses may be under-reported as diagnoses are either self-reported or from hospital in-patient records only; further studies will be required. Future work should clarify

the associations between HLA-types, circulating inflammatory cytokines, and frailty, ideally in a longitudinal study.

Given the biologically plausible and strong association between autoimmune diseases and sarcopenia, our finding in the autoimmune diagnosis free group are also plausible. Although all reported associations passed multiple statistical testing correction our results, especially in men, do require independent replication, as the effects observed may vary between cohorts, although sample size requirements for replication will be challenging.

Functional follow-up work on the HLA types that we have found associated with sarcopenia could give an indication of the underlying mechanisms at work. The mechanisms of effect of the HLA region and specific HLA types in seropositive Rheumatoid Arthritis (48) and other autoimmune diagnoses have been identified, and it needs to be established whether similar mechanisms explain associations with sarcopenia.

## **Conclusions**

Autoimmune diagnoses are strongly associated with sarcopenia in 60 to 70 year olds. In older participants without diagnosed autoimmune diseases we identified 6 HLA-types associated with EWGSOP sarcopenia definition. An additional four unique HLA types were associated with the low grip strength only and six types associated with the low Skeletal Muscle Index (SMI) definition only. Additional analysis of non-coding variants showed that SNPs involved the regulation of HLA, endoplasmic reticulum stress response and immune function genes are also associated with sarcopenia. Further studies into the long-term effects of HLA variation are required. More work is needed on whether some patients with sarcopenia have autoimmune processes and might benefit from targeted treatment.

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**Figure 1:** Forest plot of HLA types associated with Sarcopenia phenotypes.

Note: Logistic regression analysis of 100 HLA-types associated with sarcopenia (Benjamini-Hochberg correction for multiple testing applied). OR=Odds Ratio per allele of HLA-type, CI=Confidence Interval, EWGSOP=Combined sarcopenia definition: low grip and muscle mass. HLA types passing the FDR cut-off of 0.05 for each phenotype are marked with asterisks (\*)

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**Table 1:** Selected Autoimmune conditions and their association with the EWGSOP definition of sarcopenia (Low grip strength and Lean muscle mass) in the overall sample of 196,099 UK Biobank participants.

Description	Affected n	Odds Ratio (95% CIs)	P-value
<b>Rheumatoid Arthritis</b>	4,103	3.09 (2.87-3.34)	$6.00 \times 10^{-191}$
<b>Multiple Sclerosis</b>	588	2.14 (1.73-2.64)	$1.60 \times 10^{-12}$
<b>Coeliac disease</b>	1,001	1.82 (1.54-2.17)	$6.00 \times 10^{-12}$
<b>Psoriasis</b>	2,951	1.31 (1.16-1.48)	$1.20 \times 10^{-05}$
<b>Type 1 Diabetes</b>	1,565	1.14 (0.95-1.36)	$1.70 \times 10^{-01}$
<b>Ulcerative colitis</b>	2,077	1.13 (0.97-1.32)	$1.00 \times 10^{-01}$
Any autoimmune	14,798	1.83 (1.74-1.92)	$4.0 \times 10^{-125}$

Note: Supplementary Table 10 has full details of additional sarcopenia definitions.

**Table 2:** UK Biobank Participants Characteristics, excluding those with autoimmune conditions

	<b>n</b>	<b>min-max</b>	<b>mean (SD)</b>			
<b>Age of study participant (years)</b>	181,301	60-70	64.11 (2.85)			
<b>BMI (Kg/m<sup>2</sup>)</b>	181,301	12.81-68.41	27.52 (4.46)			
<b>Grip strength (Kg)</b>	181,301	0-73	31.09 (10.71)			
<b>Skeletal muscle mass (Kg)</b>	181,301	8.57-46.13	21.96 (6.00)			
			<b>Sarcopenia EWGSOP</b>			
	<b>n</b>	<b>%</b>	<b>No</b>		<b>Yes</b>	
			<b>n</b>	<b>%</b>	<b>n</b>	<b>%</b>
<b>Gender</b>						
<i>Female</i>	95,340	52.59	83,800	87.90	11,540	12.10
<i>Male</i>	85,961	47.41	82,451	95.92	3,510	4.08
<i>Combined</i>	181,301	100.00	166,251	91.70	15,050	8.30
<b>Highest education level attained</b>						
<i>None</i>	48,224	26.60	43,150	89.48	5,074	10.52
<i>Secondary</i>	28,870	15.92	26,096	90.39	2,774	9.61
<i>College-level</i>	26,810	14.79	25,006	93.27	1,804	6.73
<i>Professional/University</i>	75,075	41.41	69,882	93.08	5,193	6.92
<i>No data</i>	2,322	1.28	2,117	91.17	205	8.83
<b>Smoking status</b>						
<i>Never</i>	90,242	49.77	82,112	90.99	8,130	9.01
<i>Previous</i>	75,618	41.71	70,031	92.61	5,587	7.39
<i>Current</i>	14,602	8.05	13,356	91.47	1,246	8.53
<i>No data</i>	839	0.46	752	89.63	87	10.37

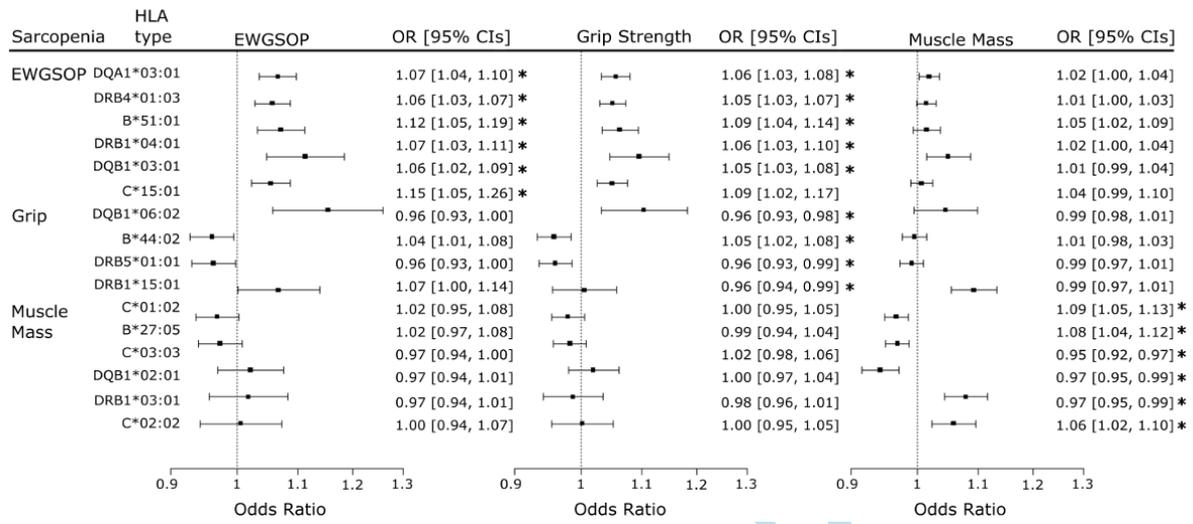
Note: UK Biobank participants aged 60-70 of European descent with complete grip strength, skeletal mass, genotype (HLA), and autoimmune diagnosis data. Participants with a diagnosis of autoimmune diseases were excluded from analyses.

**Table 3:** Non-coding SNPs within the HLA region associated with EWGSOP definition of sarcopenia ( $p \leq 1.0 \times 10^{-5}$ ) with gene expression information

RS id	A1/A0	CHR:POS	Trait	OR	95% CI	p-value	Expressed gene(s) $P < 3.66 \times 10^{-8}$	Tissue type*
rs41268896 ¥	A/G	6:32070069	Atopic dermatitis	1.08	1.05-1.11	$1.06 \times 10^{-8}$	ATF6B, CYP21A1P, BAG6, HLA-DQA2	MS, AS, AT, WB
rs2844479	C/A	6:31572956	Height	1.07	1.04-1.09	$6.11 \times 10^{-7}$	BAG6, ATF6B, <b>CSNK2B</b> , LY6G5C	AT, MS, HLV, TH
rs9268645 †	G/C	6:32408527	T1 diabetes	1.06	1.04-1.09	$1.50 \times 10^{-6}$	HLA-DQA2, HLA-DQB2, <b>HLA-DQB1</b> , HLA-DRB6, HLA-DRB9, HLA-DRB1, HLA-DQA1	MS, WB, WB, MS, TH, SE, LN
rs2072633	G/A	6:31919578	Coronary artery disease	1.06	1.03-1.08	$3.58 \times 10^{-6}$	CYP21A1P, ATF6B, HLA-DQA2, PSORS1C1, C2	AS, MS, WB, TH, TE

Note: A1=Effect allele, A0=Reference allele, POS=build 37 base pair, OR=Odds Ratio, CI=95% Confidence Intervals. Trait = the top identified trait from the GWAS catalogue. \* Tissue type: Adipose Subcutaneous=AS; Artery Tibial=AT; Colon Sigmoid=CS; Esophagus Muscularis=EM; Muscle\_Skeletal=MS; Nerve Tibial=NT; Skin Sun exposed lower leg=SE; Thyroid=TH; Whole Blood=WB; Heart Left Ventricle=HLV; Testis=TE; Lung=LN. † correlated with DQA1\*03:01 ( $R^2=0.42$ ). ¥ in LD with protein QTL for AFT6A ( $R^2=0.8$  with rs8111 in UKB) (25). GTEx genes for each variant shown, which reached a threshold of  $3.66 \times 10^{-8}$  for the Nominal P-value in GTEx (with the most significant tissue type for that eQTL shown also) – see Supplementary Table 9 for all eQTL associations. Expressed genes in bold are downregulated in GTEx by the Effect Allele, all others are upregulated.

**Figure 1**



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