Identification of a novel locus on chromosome 2q13 which predisposes to clinical vertebral fractures independently of bone density

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ABSTRACT

Objectives: To identify genetic determinants of susceptibility to clinical vertebral fractures, an important complication of osteoporosis. **Methods:** Here we conduct a genome-wide association study in 1,553 postmenopausal women with clinical vertebral fractures and 4,340 controls, with a 2-stage replication involving 1,028 cases and 3,762 controls. Potentially causal variants were identified using eQTL data from transiliac bone biopsies and bioinformatic studies. **Results:** A locus tagged by rs10190845 was identified on chromosome 2q13 which was significantly associated with clinical vertebral fracture ($p=1.04x10^{-9}$) with a large effect size (odds ratio 1.74, 95% CI 1.06 – 2.6). Bioinformatic analysis of this locus identified several potentially functional SNPs which are associated with expression of the positional candidate genes *TTL* (Tubulin Tyrosine Ligase) and *SLC20A1* (Solute Carrier Family 20 Member 1). Three other suggestive loci were identified on chromosomes 1p31, 11q12 and 15q11. All these loci were novel and had not previously been associated with BMD or clinical fractures. **Conclusion:** We have identified a novel genetic variant that is associated with clinical vertebral fractures by mechanisms that are independent of BMD. Further studies are now in progress to validate this association and evaluate the underlying mechanism.

KEYWORDS: Osteoporosis, Gene polymorphism, Bone Mineral Density, *TTL*, *SLC20A1*

1. INTRODUCTION

Osteoporosis is a common disease with a strong genetic component. It is characterised by low bone mineral density (BMD), deterioration in the microstructural architecture of bone and an increased risk of fragility fractures. Vertebral fractures are an early and important complication of osteoporosis.[1] They are characterised by loss of height and deformity of the affected vertebrae and associated with increased risk of other fractures.[2] It has been estimated that between 8-30% of patients with radiological evidence of vertebral fractures (so called morphometric fractures) come to medical attention for reasons that are incompletely understood.[3,4] In contrast, other patients with vertebral fractures come to medical attention because of symptoms such as back pain, kyphosis, and height loss, and are defined as having clinical vertebral fractures.[5-7] Clinical vertebral fractures are associated with a markedly increased risk of future fractures and increased mortality.[8] Major advances have been made in identifying genetic variants that regulate BMD and some variants have also been identified that predispose to non-vertebral fractures.[9-20] However, the genetic determinants of vertebral fractures are poorly understood. A previous genome-wide association study (GWAS) published by Oei and colleagues involving a discovery cohort of 8,717 cases and 21,793 controls failed to identify any significant genetic predictors of radiographic vertebral fracture at a genome-wide significant level.[21] However, in this study, the vertebral fractures were defined simply on the basis of morphometric analysis of spinal radiographs. It is well recognised however that the morphometric techniques employed in this study may have identified vertebral deformities that were not fractures.[22] The aim of the present study was to re-evaluate the predictors of clinical vertebral fractures by genome wide association study to try and gain new insights into this important and poorly understood clinical problem.

2. PATIENTS AND METHODS

The study involved a discovery phase with 1,553 clinical vertebral fracture cases and 4,340 controls, a first replication phase of 694 cases and 2,105 controls, and a second replication phase of 334 cases and 1,657 controls, as summarised in Supplementary Table 1. The genome wide association study was performed using standard methodology as detailed in the Supplementary Text 1.

3. RESULTS

3.1. Characteristics of the study populations

The mean (±standard deviation) age of the patients with clinical vertebral fractures was 71.3±9.3 years with a bone mineral density T-score at the lumbar spine of -2.72±1.4; and at the femoral neck of -2.57±1.1. The controls were not matched with the cases by age and did not undergo phenotyping for vertebral fracture on the basis that clinical vertebral fractures are uncommon in the general population (estimated incidence of 9.8/1000 person-years in 75-84 year olds)[23]. While it is possible that clinical vertebral fractures may have occurred in some controls in later life this is unlikely to have substantially affected the results of the analysis, other than to have potentially slightly reduced its power.[24] This approach has been used previously for genome-wide studies in various common diseases including diabetes, Paget's disease, and rheumatoid arthritis.[25,26]

We identified 334 clinical vertebral fracture female cases from the UK Biobank cohort with a mean age (±standard deviation) of 58.8±7.7 years, and they were age-matched with 1,657 female controls from the same cohort.

3.2. Genome-wide association analysis of the discovery sample

Since different genotyping platforms were used in the analysis of the different cohorts that constitute the discovery sample, association analysis was conducted following imputation of all genotypes into the CEU panel of HapMap II reference (see Patients and Methods section). Following imputation, we analysed 2,366,456 SNPs and identified 31 with suggestive evidence of association with vertebral fracture ($p \leq 10^{-4}$). Details are summarised in Supplementary Table 2, the Manhattan and quantile-quantile plots are shown in Supplementary Figures 2 and 3. Each study was corrected by genomic control; genomic inflation factors ranged between λ=1.001 to λ=1.046 for genotyped SNPs and λ=1.006 to λ=1.036 after imputation.

3.3. Replication and combined analysis

We analysed the 31 suggestively associated SNPs identified in the discovery cohort (Supplementary Table 4) and seven additional SNPs that had been significantly associated with clinical fractures in a previous GWAS (Supplementary Table 5) in the replication sample.[10] Four SNPs showed nominal association ($p<0.05$) with clinical vertebral fractures at replication (Table 1). The combined discovery and replication analysis corrected for age identified one SNP (rs10190845) on chromosome 2q13 with genome-wide significant evidence of association with clinical vertebral fractures ($p=1.27 \times 10^{-8}$). The predisposing allele had a frequency of 0.034 in cases compared with 0.022 in controls and the odds ratio for susceptibility to fracture was 1.75 [95% CI: 1.44-2.12] (Figure 1). The results were similar without age correction ($p=4.9 \times 10^{-8}$; odds ratio 1.66 [95% CI: 1.38-1.99]). Conditional

analysis on rs10190845 did not reveal any secondary association signals at the locus (Supplementary Figure 4). Three other SNPs on chromosomes 1p31, 11q12 and 15q11 were suggestively associated with vertebral fracture in the combined analysis (Table 1 and Supplementary Figures 5 and 6). None of these regions have previously been found to be associated with BMD or fracture in previous GWAS.[10,13]

The top SNP (rs10190845) maps to a region which contains eleven potential candidate genes (Figure 2). This region has previously been implicated as a genetic regulator of bone density by Estrada and colleagues[10] who reported that rs17040773 within *ANAPC1* (Anaphase Promoting Complex Subunit 1) was associated with femoral neck BMD ($p=1.5x10^{-9}$), but not with clinical fractures (p=0.79). rs17040773 is not in linkage disequilibrium with rs10190845 in our population ($r^2=0.006$), and, in keeping with this, when we performed conditional analysis on rs17040773, we confirmed that rs10190845 remained significantly associated with clinical vertebral fractures ($p=2.09x10^{-8}$; odds ratio 1.73 [95% CI: 1.43-2.09]). In order to test whether the variants associated with clinical vertebral fractures played a role in BMD, we tested the rs10190845 variant for association with volumetric vertebral bone mineral density in females on the dataset from Nielson and colleagues.[27] We did not find any association for the variant and BMD (p=0.23). This suggests that rs10190845 constitutes an independent signal which predisposes to clinical vertebral fracture by mechanisms that are independent of an effect on BMD.

Table 1. Variants showing suggestive or significant association with vertebral fracture

				Discovery (n = 5,893)			Replication (n= 2,799)			Combined* (n= 8,692)				UK Biobank replication (n= 1,991)			Total** (n= 10,683)			
Chr	**SNP**	**Position**	**A**	**AF**	**p**	**OR (95% CI)**	**AF**	**p**	**OR (95% CI)**	**p**	**OR (95% CI)**	**I2**	**Q p**	**AF**	**p**	**OR (95% CI)**	**p**	**OR (95% CI)**	**I^2**	**Q p**
2	rs10190845	112192944	A	0.03	$2.4x10^{-5}$	1.70 (1.33-2.17)	0.05	$1.60x10^{-4}$	1.84 (1.34-2.53)	$1.27x10^{-8}$	1.75 (1.45-2.12)	5.9	0.39	0.05	0.027	1.66 (1.06-2.60)	$1.04x10^{-9}$	1.75 (1.45-2.12)	0.0	0.48
11	rs7121756	57980425	A	0.29	$5.2x10^{-5}$	1.22 (1.11-1.35)	0.28	0.011	1.23 (1.05-1.45)	$1.27x10^{-6}$	1.23 (1.13-1.33)	0.0	0.67	0.29	0.35	1.09 (0.91-1.32)	$4.39x10^{-7}$	1.22 (1.13-1.32)	49.0	0.03
15	rs2290492	92464744	A	0.23	$3.4x10^{-5}$	1.24 (1.12-1.37)	0.21	0.021	1.23 (1.03-1.46)	$1.61x10^{-6}$	1.24 (1.13-1.35)	53.7	0.02	0.22	0.44	1.08 (0.88-1.33)	$2.51x10^{-7}$	1.23 (1.13-1.33)	75.6	$1.1x10^{-5}$
1	rs1360181	68248452	C	0.16	$8.4x10^{-5}$	1.25 (1.12-1.41)	0.17	0.008	1.30 (1.07-1.56)	$1.87x10^{-6}$	1.26 (1.14-1.41)	7.7	0.57	0.17	0.38	0.90 (0.72-1.14)	$1.09x10^{-5}$	1.22 (1.12-1.33)	32.2	0.57

The allele (A) and allele frequency (AF) for each of the variants is shown along with the p value for association, odds ratio (OR) and 95% confidence interval (95% CI). Q p values correspond to Cochran's Q p-values. The values shown are adjusted for age but similar results were obtained for unadjusted association tests. Position refers to Human Genome Assembly GRCh38.p11.

*Combined results showed the meta-analysis for discovery and replication stage.

**Total results showed the meta-analysis including the second replication in the UK Biobank cohort.

A second replication for the significant hit on chromosome 2 and suggestive SNPs on chromosomes 1, 11 and 15 was performed in 334 clinical vertebral fracture cases and 1,657 controls from UK Biobank. The top hit (rs10190845) on chromosome 2 was found nominally associated with clinical vertebral fractures (p=0.027, OR=1.66[1.060-2.600], MAF=0.049). No association was found for the suggestive SNPs in this cohort (Table 1).

Meta-analysis of the discovery and the two replication stages showed a combined p-value for rs10190845=$1.04x10^{-9}$ (OR=1.74[1.06-2.6]) with no evidence of heterogeneity between cohorts (I^2=0.0, p=0.48) (Table 1).

The SNPs rs7121756 on chromosome 11 and rs2290492 on chromosome 15 showed significant heterogeneity among cohorts (Cochrane's Q<0.05), and a random effect analysis was performed. rs7121756 remained suggestively associated with clinical vertebral fractures ($p=1.01x10^{-6}$), whilst rs2290492 showed a marginal association (p=0.004).

3.4.Functional evaluation of chromosome 2q13 locus

This analysis focused on a linkage disequilibrium block of approximately 700kb surrounding the top hit rs10190845. We identified a total of 936 SNPs within the region which were analysed in the GWAS (n=376) or which were in linkage disequilibrium (r^2 value of > 0.7) with rs10190845, or which showed suggestive association to clinical vertebral fractures ($p<5x10^{-3}$). We imputed the genotypes for the SNPs within the region of interest using the 1000 Genomes phase 3 panel as reference and tested the SNPs for association with clinical vertebral fractures. We removed 878 of the SNPs since they showed no association with clinical vertebral fractures in our dataset (p>0.05). The remaining 58 candidate SNPs were tested for association with the level of expression of genes within the candidate locus using a bone-derived gene expression dataset (eQTLs)[28] (Tables 2, 3 and Supplementary Figure 7). This resulted in the identification of nine SNPs which were eQTLs for genes within the region. In order to gain insight into the functional basis of the association at 2q13 we used SuRFR[29] which integrates functional annotation and prior biological knowledge to identify potentially causal genetic variants, to assess these 9 SNPs along with the top hit rs10190845 (Table 2 and Supplementary Figure 7).

Table 2. Functionality of SNPs in 2q13 region, ranked by SuRFR

SuRFR Rank	SNP ID	R^2 with rs10190845	A (AF)	GWAS p-value (Discovery cohort only)	OR (95% CI)	Location	GERP Value	DNase HS sit	DNase Foot	Ernst Score	Position Score	MAF Score	Enhancer score	TFBS score	Total score	eQTL	eQTL gene(s)	eQTL p
1	rs35586251	0.17	A (0.02)	2.09×10^{-4}	1.69 (1.28-2.24)	*Exon FBLN7*	4.47	0	0	7	5	0.02	0	0	9.89	Yes	*TTL*	6.6×10^{-6}
2	rs77172864	0.79	G (0.03)	4.96×10^{-5}	1.68 (1.31-2.17)	Intergenic	0.18	0	0	1	3	0.02	0	0	8.56	Yes	*SCL20A1*	0.0001
3	rs10190845	1	A (0.03)	2.4×10^{-5}	1.70 (1.33-2.17)	Intergenic	0	0	0	2	3	0.96	0	0	8.06	No	-	-
4	rs77996972	0.22	T (0.02)	2.11×10^{-4}	1.69 (1.28-2.23)	Intron *FBLN7*	1.77	313	0	7	1	0.02	0	0	7.61	Yes	*TTL* *SLC20A1*	3.8×10^{-6} 5.5×10^{-5}
5	rs75814334	0.22	T (0.02)	2.11×10^{-4}	1.69 (1.28-2.23)	Intron *FBLN7*	0.43	239	0	8	1	0.02	0	0	7.56	Yes	*TTL* *SLC20A1*	2.1×10^{-6} 6.6×10^{-5}
6	rs74792868	0.22	A (0.02)	2.1×10^{-4}	1.69 (1.28-2.24)	Intron *FBLN7*	0	0	0	9	1	0.02	0	0	7.5	Yes	*TTL* *SLC20A1*	2.0×10^{-5} 2.8×10^{-5}
6	rs72943913	0.29	G (0.03)	5.48×10^{-5}	1.67 (1.30-2.14)	Intron *ZC3H8*	0.15	0	0	3	1	0.02	0	0	6.46	Yes	*SLC20A1*	0.0001
7	rs112275607	0.22	A (0.02)	2.13×10^{-4}	1.69 (1.28-2.24)	Intron *FBLN7*	0	0	0	8	1	0.02	0	0	6.83	Yes	*TTL* *SLC20A1*	2.8×10^{-6} 6.2×10^{-5}
8	rs113085288	0.06	T (0.02)	1.79×10^{-4}	1.70 (1.29-2.24)	Intron *FBLN7*	0	0	0	7	1	0.02	0	0	6.08	Yes	*SLC20A1*	4.1×10^{-6}
9	rs113428223	0.29	T (0.03)	4.55×10^{-5}	1.70 (1.31-2.20)	Intron *ZC3H6*	0	0	0	2	1	0.02	0	0	5.61	Yes	*SCL20A1*	0.0001

A (AF): allele (allele frequency); GERP: Genomic evolutionary rate profiling; DNAase HS: DNase hypersensitivity; DNase foot: DNase footprint; Ernst score: classes of chromatin states (recurrent combinations of chromatin marks); MAF: minor allele frequency; TFBS: transcription factor binding site. Gene names: *FBLN7*: Fibulin 7; *ZC3H8*: Zinc Finger CCCH-Type Containing 8; *ZC3H6*: Zinc Finger CCCH-Type Containing 6.

Table 3. Correlation between genotypes for potentially functional SNP and bone-specific expression of genes in the candidate region

RANK	SNP	GENE	PROBE	A1	A2	FRQ	BETA	SE	P
1	rs35586251	*TTL*	224896_s_at	A	G	0.017	0.65	0.13	6.62×10^{-6}
2	rs77172864	*SLC20A1*	230494_at	G	A	0.013	-0.46	0.11	0.00011
4	rs77996972	*TTL*	224896_s_at	T	C	0.012	0.67	0.13	3.80×10^{-6}
		SLC20A1	230494_at	T	C	0.012	-0.49	0.11	5.50×10^{-5}
5	rs75814334	*TTL*	224896_s_at	T	C	0.013	0.67	0.13	2.10×10^{-6}
		SLC20A1	230494_at	T	C	0.013	-0.48	0.11	6.60×10^{-5}
6	rs74792868	*TTL*	224896_s_at	A	G	0.012	0.66	0.14	2.00×10^{-5}
		SLC20A1	230494_at	A	G	0.012	-0.53	0.12	2.80×10^{-5}
6	rs72943913	*SLC20A1*	230494_at	G	A	0.013	-0.46	0.11	0.00011
7	rs112275607	*TTL*	224896_s_at	A	G	0.013	0.67	0.13	2.80×10^{-6}
		SLC20A1	230494_at	A	G	0.013	-0.48	0.11	6.02×10^{-5}
8	rs113085288	*SLC20A1*	230494_at	T	A	0.008	-0.72	0.14	4.06×10^{-6}
9	rs113428223	*SLC20A1*	230494_at	T	C	0.013	-0.46	0.11	0.0001

The data shown are only for the associations which were significant after Bonferroni correction (p value for significance $\leq$0.0002). A1: allele 1, A2: Allele 2, FRQ: frequency of allele 1, BETA: effect size on regression analysis referred to A1 allele, SE: standard error of beta estimate, probe IDs obtained from the Affymetrix HG U133 2.0 plus array. Gene names: *TTL*: Tubulin Tyrosine Ligase; *SLC20A1*: Solute Carrier Family 20 Member 1 (also known as *PIT1*).

The top ranking variant identified by SuRFR, rs35586251, located within exon 3 of *FBLN7* is a non-synonymous substitution (p.Val119Met). However, analysis using various *in silico* software tools yielded inconsistent results with regard to functionality of this SNP at the protein level (Supplementary Table 6). The other 9 SNPs are associated with expression of *TTL*, *SCL20A* or both genes. The variant that ranked top by SuRFR, rs35586251, was associated with increased expression of *TTL* ($p=6.6x10^{-6}$). Four other variants were also associated with both increased expression of *TTL* and reduced expression of *SLC20A1* (p-values ranging from $2.1x10^{-6}$ to 10^{-5}). The second ranking variant, rs77172864, in strong LD with the GWAS top hit ($r^2=0.79$), was associated with reduced expression of *SLC20A1* ($p=10^{-4}$) (Tables 2 and 3).

The variants listed on Table 2 were tested in the UK Biobank cohort for further association with clinical vertebral fractures (Supplementary Table 7). Although none of them was significantly associated with the trait, a trend of significance was found for SNPs rs72943913, rs77172864, and rs113428223 (p=0.06, OR=1.66), and all of them identified as eQTLs for *SLC20A1* gene in bone. These variants showed a lower frequency (MAF=0.03) than the top hit (MAF=0.05), which could require a greater sample size to detect associations with the trait.

3.5. Association between clinical vertebral fractures and other osteoporosis related phenotypes

In order to determine if there is overlap between the SNPs identified as associated with lumbar spine BMD in previous GWAS with those associated with clinical vertebral fracture in this study, we evaluated 50 SNPs that have been associated with lumbar spine BMD at a genome-wide significant level in previous studies in our dataset.[10,11,13,30,31] Four variants were nominally associated with clinical vertebral fracture after Bonferroni correction (Table 4). We also analysed 15 variants previously associated with clinical fracture,[13] of which three were associated with clinical vertebral fractures in this study. We also analysed the SNPs identified by Nielson and colleagues[27] as genome-wide significant predictors of volumetric vertebral bone mineral density for association with clinical vertebral fractures in our dataset. Of the six genome-wide significant SNPs identified by Nielson et al, we found that one was significantly associated with clinical vertebral fractures after Bonferroni correction (rs12742784, $p=6.24x10^{-5}$). The BMD-increasing variants in Table 4 conferred a reduced risk of clinical vertebral fractures in our study, whilst the variants associated with appearance of clinical fractures in previous studies were also associated with a higher risk of developing a clinical vertebral fracture in our data.

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Table 4. Association between known genetic determinants of spine BMD and clinical vertebral fractures in the combined GWAS dataset.

Previous studies									**Present study**	
Study	SNP	Locus	Candidate gene	Phenotype	Method	Allele	Beta[1]	p	Beta[2]	p
Estrada	rs1346004	2q24.3	*GALNT3*	LS-BMD	DXA	A	-0.06	$3.87x10^{-30}$	+0.16	0.0002
Estrada	rs4727338	7q21.3	*SLC25A13*	LS-BMD	DXA	C	+0.07	$2.13x10^{-35}$	-0.15	0.0004
Estrada	rs6426749	1p36.12	*ZBTB40*	LS-BMD	DXA	C	+0.1	$1.86x10^{-44}$	-0.22	0.0003
Styrkarsdottir	rs7524102	1p36	*WNT4*	LS-BMD	DXA	A	-0.11	$9.2x10^{-9}$	+0.23	0.0002
Estrada	rs4727338	7q21.3	*SLC25A13*	Clinical fracture	Clinical records and X-rays	G	+0.08	$5.9x10^{-11}$	+0.14	0.0004
Estrada	rs6426749	1p36.12	*ZBTB40*	Clinical fracture	Clinical records and X-rays	G	+0.07	$3.6x10^{-6}$*	+0.22	0.0003
Estrada	rs6959212	7p14.1	*STARD3NL*	Clinical fracture	Clinical records and X-rays	T	+0.05	$7.2x10^{-5}$*	+0.15	0.001
Nielson	rs12742784	1p36.12	*ZBTB40*	Vertebral BMD	qCT imaging	T	+0.09	$1.05x10^{-10}$	-0.20	$6.24x10^{-5}$

The variants shown are those that were significant after Bonferroni correction for testing 56 BMD variants (p threshold for association 0.0009) and 16 fracture variants (p threshold for association 0.003). *SNP significantly associated with clinical fracture after Bonferroni correction (p threshold at Estrada et al $5x10^{-4}$).

Beta[1] showed the effect for the previous studies (LS-BMD, clinical fracture and vertebral BMD).

Beta[2] showed the effect for the present study on clinical vertebral fracture

Gene names: *GALNT3*: Polypeptide N-Acetylgalactosaminyltransferase 3); *SLC25A13*: Solute Carrier Family 25 Member 13; *ZBTB40*: Zinc Finger And BTB Domain Containing 40; *WNT4*: Wnt Family Member 4; *STARD3NL*: StAR Related Lipid Transfer Domain Containing 3 N-Terminal Like).

Method column shows the technique used to evaluate the BMD or assess the fracture (DXA: dual energy X-ray absorptiometry, CT: quantitative computerised tomography)

4. DISCUSSION

Many advances have been made in defining the genetic determinants of bone mineral density and fractures through large scale genome-wide association studies, genome sequencing studies and linkage studies in rare bone diseases.[32] For example, linkage studies have shown that loss-of-function and gain-of-function variants in *LRP5* cause early onset osteoporosis[33] and high bone mass[34] respectively, whereas loss of function mutations affecting *SOST* and *LRP4* have been identified as causes of high bone mass and osteosclerosis.[35,36] Genome-wide association studies and genome sequencing studies have also been successful in identifying multiple loci that regulate bone mineral density[9-11,30,37] and a smaller number that predispose to clinical fractures.[10,30]

Although vertebral fractures are one of the most common and important complications of osteoporosis, relatively little is known about the genetic determinants of this type of fracture.[38] In a previous study of 8,717 cases and 21,793 controls, Oei and colleagues failed to identify any locus with significant evidence of association with morphometric vertebral fractures.[21] In the present study however, we were successful in identifying one genome-wide significant variant that predisposed to clinical vertebral fractures, which was replicated in several populations. We also detected loci that might play a role in clinical vertebral fractures (showing suggestive association at the genome-wide level), but further studies need to be performed in further cohorts to confirm or refute these associations. A likely reason for the difference between our findings and those of Oei et al, is varying case definition. Here, we studied patients with clinical vertebral fractures as opposed to morphometric vertebral deformities, many of which may not be true fractures.[22] The genome-wide significant SNP identified in the present study, rs10190845, shows one of the largest effect size so far detected in the field of osteoporosis genetics (OR=1.75[1.45-2.12]). Most of the signals associated with BMD or fracture to date showed a very low effect (ORs between 0.90 and 1.10),[12,13] with a few exceptions.[20]

rs10190845 maps to chromosome 2q13, a region previously associated with low femoral neck bone density.[10] However, when conditioning on rs17040773, the previously reported top SNP at the locus,[10] the association with rs10190845 remained significant, indicating that rs10190845 represents a novel signal.

In order to determine if there was an overlap between the results of this study and those previously reported, we analysed 71 SNPs that have previously been associated with either spine BMD or clinical fractures and identified seven variants that were significantly associated with clinical vertebral fracture in this study, after Bonferroni correction (threshold

for significance 0.0009 for BMD and 0.003 for clinical fractures). However, the association for these variants did not reach genome-wide significance, therefore, they were not selected in the GWAS analysis. The SNPs associated with low BMD as well as increased risk of clinical fractures in previous studies were associated with an increased risk of clinical vertebral fractures in this study and those associated with an increased risk of clinical fractures in previous studies were associated with an increased risk of clinical vertebral fractures in this study.

Furthermore, when we analysed six SNPs that were significantly associated with vertebral bone mineral density on quantitative computerised tomography (qCT) analysis[27] one locus on chromosome 1p36, close to *ZBTB40*, was identified and significantly associated with clinical vertebral fracture in this study. These results support the importance of *ZBTB40* as a predictor of clinical fractures and suggest that the mechanism of association is most probably mediated by changes in BMD. The observations in this study, when taken together with the findings of Nielson and Estrada[10,27] indicate that there is a partial overlap between loci that regulate lumbar spine BMD, and clinical vertebral fractures. However, there are some genetic determinants of clinical vertebral fracture which are unique and which operate independently of BMD.

In order to identify the mechanisms by which 2q13 predisposes to vertebral fracture we conducted bioinformatics analyses to determine if rs10190845 or other SNPs nearby were likely to be functional variants. These studies identified several potentially functional SNPs in the same LD block as rs10190845, which might account for the association we observed. The top ranking SNP from SuRFR analysis was rs35586251, which was strongly associated with expression of the *TTL* gene within the candidate locus (Supplementary Figure 8). However, the second ranking SNP, rs77172864 (Supplementary Figure 9), in strong LD with the GWAS top hit, was significantly associated with the expression of *SLC20A1*. Several other SNPs were also significantly associated with expression of *TTL* and/or *SLC20A1*, raising the possibility that alterations in expression of one or both genes might account for the predisposition to clinical vertebral fractures. Association analysis performed using UK Biobank cohort for these SNPs showed a trend of association for markers regulating *SLC20A1* gene, which also showed some degree of linkage disequilibrium, with the GWAS top hit. The lack of significant association might be due to their low allele frequency (MAF=0.03), which means that a larger sample size may be required to detect a strong association. The Tubulin Tyrosine Ligase encoded by *TTL* is involved in regulation of the cytoskeleton. Previous studies have shown that *TTL* is involved in neuronal development[39]

and injury signalling,[40] raising the possibility that variants that regulate *TTL* might be involved in regulating pain perception, which could account for the fact that predisposing variants have not previously been associated with BMD. Other mechanisms might also be possible and further studies need to be performed in order to address the role of *TTL* in clinical vertebral fracture. The other main candidate gene, *SLC20A1*, encodes Pit1, which facilitates the entry of inorganic phosphate into the cytoplasm.[41] Previous studies have shown that *SLC20A1* is involved in mineralisation.[42-45] Altered expression of this gene could convey risk for vertebral fractures via an effect on bone mineralisation. Although *SLC20A1* presents as the candidate gene for association with clinical vertebral fractures in this study, it has not been identified previously as a predictor of BMD or fractures. This opens for alternative mechanisms, or that *TTL* rather than *SLC20A1* is the candidate gene within the 2q13 locus.

Limitations of the study include the fact that the total sample size was relatively small and the power to detect alleles of modest effect size was limited. It is possible that we may have missed associations between rare variants and clinical vertebral fractures since the imputation we performed was against HapMap reference panel rather than larger panels that increase imputation power particularly against low frequency variants. Although case definition was clinically based, there was no significant heterogeneity in the associations we observed across centres.

Strengths of the present study are that it has provided important new information on the genetic determinants of clinical vertebral fracture and that results, despite the sample size, have been validated in two independent replication stages.

4.1. Conclusion

Genome wide association analysis identified a significant association between a marker on chromosome 2 and clinical vertebral fractures in postmenopausal women, a finding validated in several independent populations.

It is of interest that the top hit and other suggestive hits identified acted independently of BMD, bringing to attention other bone microarchitectural modalities that determine fracture susceptibility. This suggests that the variants identified might be acting as markers for perception of pain or other factors that are associated with the clinical presentation of vertebral fractures. We also found that some of the variants previously identified as regulators of spine BMD were associated with clinical vertebral fractures, but with effects that were weaker than the top hit and other suggestive hits. Taken together, the data suggest that the genetic basis of clinical vertebral fracture is complex involving variants that act

independently of BMD as well as those that are associated with spine BMD. Further research is now warranted to fully investigate the mechanisms involved.

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Fig 1. Cohort specific association between rs10190845 and clinical vertebral fracture

The point estimates (squares) and 95% confidence intervals (horizontal lines) for individual studies are shown with the summary indicated by the diamond using a fixed effect model. Summaries are shown for meta-analysis with discovery cohorts only (Summary_discovery), with the first replication cohorts only (Summary_replication), and for the whole 3-stage meta-analysis (Summary_meta-analysis). "BRITISH-WTCCC" shows the results for the combined cohorts CAIFOS, AOGC, DOES, and EPIC, and the control cohort WTCCC2. "Scottish replication" corresponds to EDOS-ORCADES cohorts, "Italian_replication_1" study corresponds to Florence-InCHIANTI cohorts and "Italian_replication_2" study comprises the Turin and Siena cohorts. Cohort sizes are reflected by square dimensions.

Fig 2. Regional association plots of susceptibility locus for clinical vertebral fracture

The figure shows the results after imputation using 1000G v3 as reference panel. The SNPs are colour coded according to the extent of LD with the SNP showing the highest association signal from the combined analysis (represented as a purple diamond). The estimated recombination rates (cM/Mb) from HapMap CEU release 22 are shown as light blue lines, and the blue arrows represent known genes in the region. The red line shows the threshold for genome-wide significance ($p = 5 \times 10^{-8}$)