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Review Article

Pharmacogenomics of osteonecrosis of the jaw

Guang Yang[a], Sonal Singh[a], Yiqing Chen[a], Issam S. Hamadeh[b], Taimour Langaee[a], Caitrin W. McDonough[a], L. Shannon Holliday[c], Jatinder K. Lamba[a,d], Jan S. Moreb[e], Joseph Katz[f], Yan Gong[a,d,*]

[a] Department of Pharmacotherapy and Translational Research, Center for Pharmacogenomics and Precision Medicine, College of Pharmacy, University of Florida, Gainesville, FL, USA
[b] Cancer Pharmacology Department, Levine Cancer Institute, Charlotte, NC, USA
[c] Department of Orthodontics, College of Dentistry, University of Florida, Gainesville, FL, USA
[d] UF Health Cancer Center, Gainesville, FL, USA
[e] Novant Health Forsyth Medical Center, Hematology, Transplantation and Cellular Therapy Division, Winston-Salem, NC, USA
[f] Department of Oral Medicine, College of Dentistry, University of Florida, Gainesville, FL, USA

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ABSTRACT

Osteonecrosis of the jaw (ONJ) is a rare but serious drug induced adverse event, mainly associated with the use of antiresorptive medications, such as intravenous (IV) bisphosphonates (BPs) in cancer patients. In this review, we evaluated all the pharmacogenomic association studies for ONJ published up to December 2018. To date, two SNPs (*CYP2C8* rs1934951 and *RBMS3* rs17024608) were identified to be associated with ONJ by two genome-wide association studies (GWAS). However, all six subsequent candidate gene studies failed to replicate these results. In addition, six discovery candidate gene studies tried to identify the genetic markers in several genes associated with bone remodeling, bone mineral density, or osteoporosis. After evaluating the results of these 6 studies, none of the SNPs was significantly associated with ONJ. Recently, two whole-exome sequencing (WES) analysis (including one from our group) were performed to identify variants associated with ONJ. So far, only our study successfully replicated discovery result indicating *SIRT1* SNP rs7896005 to be associated with ONJ. However, this SNP also did not reach genome-wide significance. The major limitations of these studies include lack of replication phases and limited sample sizes. Even though some studies had larger sample sizes, they recruited healthy individuals as controls, not subjects treated with BPs. We conclude that a GWAS with a larger sample size followed by replication phase will be needed to fully investigate the pharmacogenomic markers of ONJ.

1. Introduction

Pharmacogenomics, or the genetic/genomic determinants of drug response and adverse effects, is a tool that has been useful in individualizing medication therapy in order to improve drug efficacy and minimize adverse effects [1,2]. Osteonecrosis of the jaw (ONJ) is a rare but severe drug induced adverse event, which is defined as the exposure of jaw bone (mandible, maxilla, or both) with slow healing for > 8 weeks, or even no healing [3]. ONJ was first reported in 2003 among cancer patients treated with high doses of intravenous (IV) bisphosphonates (BPs) (pamidronate and zoledronate) [4]. Hence, the term "Bisphosphonates Related Osteonecrosis of the Jaw" (BRONJ) was initially used by the American Association of Oral and Maxillofacial Surgeons (AAOMS) to describe this drug induced complication. In 2009, the term BRONJ was replaced with "Antiresorptive Related Osteonecrosis of the Jaw" (ARONJ) because another class of antiresorptive agents, receptor activator of nuclear factor kappa-B ligand (RANKL) inhibitor, denosumab (Prolia®, Xgeva®) was found to be associated with ONJ [5]. Later in 2014, the term "Medication Related Osteonecrosis of the Jaw" (MRONJ) was introduced in light of the fact that antiangiogenic therapies were also linked to this complication [6]. For simplicity, we will use the term 'ONJ' in this review.

* Corresponding author at: Department of Pharmacotherapy and Translational Research, University of Florida, PO Box 100486, 1345 Center Drive, Gainesville, FL 32610-0486, USA.
E-mail address: gong@cop.ufl.edu (Y. Gong).

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2. Potential mechanisms of ONJ

Although many risk factors of ONJ have been identified, the mechanisms of ONJ is still not clear. Based on the different potential mechanisms of ONJ development, three main hypotheses have been proposed [6]. The first hypothesis involves bone remodeling inhibition *i.e.* disruption of bone formation and bone resorption induced by osteoblasts and osteoclasts, respectively. Both BPs and RANKL inhibitor (denosumab) are antiresorptive agents which interfere with the bone resorption process. The second hypothesis is angiogenesis inhibition which results in bone necrosis secondary to prevention of the formation of new blood vessels in the bone. Bevacizumab, an angiogenesis inhibitor, has been reported to be associated with ONJ [7]. The third hypothesis is inflammation and infection. Studies showed that most ONJ patients had record of tooth extraction (~50%) [8–10]. Lots of bacteria live in human mouth with gum disease and they likely induce inflammation/infection after tooth extraction and lead to ONJ.

Even though increasing numbers of medication classes have been reported to be associated with ONJ, antiresorptive agents still show the highest risk for ONJ. Studies have shown that the average incidence of ONJ was around 1.8% and 1.3% for denosumab and BPs, respectively, but the difference was not significant [11,12]. The risk of ONJ in cancer patients treated with IV BPs is ~10 times higher than that in osteoporosis patients based on the higher doses or more frequent administration in cancer patients. The incidence rates of ONJ range from 0.8% to 18% depends on oral or IV route of administration [12–14]. For this review, we will focus on ONJ related to BPs since all the pharmacogenomic association studies for the ONJ phenotype were for BPs-related ONJ.

BPs, as stable analogue of pyrophosphate, contain two phosphonate groups with a central carbon. The chemical structure also contains one short side chain (R1) and one long side chain (R2), which determine the chemical properties of BPs. The BP structure creates high affinity for hydroxyapatite binding sites on the bone surface [15]. BPs are incorporated into osteoclasts cells when the bone mineral is resorbed by osteoclasts through bone remodeling [16–18]. After embedding into the osteoclasts, BPs induce osteoclasts apoptosis that leads to inhibition of bone resorption. Based on the difference in the structure of the R2 side chain, BPs are divided into two classes: nitrogen containing BPs and non-nitrogen containing BPs. These two classes of BPs inhibit osteoclasts differentiation and induce osteoclasts apoptosis [19–21] through different mechanisms. Nitrogen containing BPs, such as zoledronate and pamidronate, inhibit bone resorption by binding and inhibiting farnesyl pyrophosphate synthase (FPPS) in the HMGA-CoA reductase pathway also known as mevalonate pathway [15,22]. This results in the disruption of osteoclasts cytomembrane ruffles that lead to osteoclasts apoptosis. On the other hand, non-nitrogen containing BPs, such as etidronate and clodronate are metabolized in the cells to compounds that replace the pyrophosphate moiety from ATP to form a non-functional molecule. The accumulation of non-functional molecules (toxic analog of ATP) leads to inhibition of protein synthesis through competition with ATP in mitochondria [23], which then induces apoptosis in osteoclasts. Based on the effect on osteoclasts, BPs are used as antiresorptive agents for treatment and prevention of osteoporosis. Studies have shown that BPs significantly decrease the risk of fractures and increase bone mass density (BMD) in osteoporosis patients [12,24–26]. Given their non-proliferative action, BPs are important and effective medications for preventing bone loss in cancer patients [15,21,27] especially used for patients with multiple myeloma (MM) and other cancers which metastasize to the bone, to prevent skeletal related events (SREs) [28].

Metastasis is one of the main properties of cancer cell [29]. Most cancers with metastases have high morbidity and mortality. Bone is the third common site for the metastasis that is observed in MM and many other solid cancers, such as breast, lung, and prostate cancers [30]. Previous studies have shown that cancer cells from breast and prostate are most likely to migrate to bone during late-stage of these diseases [31,32]. Based on the data from National Cancer Institute, almost 50% of the breast and prostate cancer patients die due to bone metastases. Bone metastasis occurring commonly in breast and prostate cancer results in the increase of osteoclasts cell growth and differentiation [33,34]. The increasing osteoclastic activity leads to SREs, such as bone pathological fractures and severe bone pain, which decreases the quality of life of cancer patients.

The incidences of ONJ reported by European Association for Cranio-Maxillo-Facial Surgery (EACMFS) and AAOMS are higher than those reported in Japan [6,35,36]. MM shows a higher incidence in African-American individuals, but ONJ cases in MM patients mostly occur in those of European ancestry. Based on these, genetic factors likely contribute to the development of ONJ. So far, multiple studies that have been performed to assess the genetic determinants for ONJ [37–50]. This review evaluated all articles identifying genetic factors for ONJ and recapitulated the current evidence on pharmacogenomics of ONJ.

3. Search strategy

Online literature searches were performed using PubMed databases to retrieve the published studies. The search strategy was based on the combination of the following **separate** terms: "genetic ONJ", "pharmacogenetics ONJ", "pharmacogenomics ONJ", "polymorphisms ONJ", "SNPs ONJ", "GWAS ONJ", "genome ONJ", "exome ONJ" or "genome wide ONJ". These terms were serached again replacing "ONJ" with "osteonecrosis of the jaw".

4. Eligibility criteria

Literature was reviewed by two authors (GY, YC) independently. Studies matching the following items were included: (1) Articles focusing on investigating the risk of ONJ; (2) Case control ONJ studies or clinical studies comprising of baseline data; (3) Studies that included genetic or SNPs analysis. Exclusion criteria were: (1) reviews or letters about ONJ; (2) Studies that included ONJ but not genes or SNPs research.

Based on the eligibility criteria, fifteen publications were included in the review consisting of two genome-wide association study (GWAS) [37,38], two whole exome sequencing analyses [39,40], and eleven candidate gene studies [41–48,50–52] (Fig. 1).

5. Discovery candidate gene studies on ONJ

A total of six discovery candidate gene studies were published between 2010 and 2018 [43,46,47,50–52] (Table 1). These studies investigated the effects of variants in several genes, which had been selected based on a potential role in BPs metabolism and/or ONJ pathogenesis (*e.g.* bone turnover). Most of these studies genotyped only a small number of variants and had small cohorts and are therefore susceptible to limitations such as inadequate power. None of the single-nucleotide polymorphisms (SNPs) tested in these studies reached significance level after accounting for multiple comparisons.

The study by Di Martino et al [43] used Affymetrix DMET™ plus platform [53], which genotyped a total of 1936 SNPs in 225 drug target genes, to identify 8 SNPs with p-value < 0.05 located in 4 different genes that are associated with development of ONJ (Table 1). This case-control study comprised of 19 MM patient samples including 9 cases suffering from ONJ induced by zoledronate and the other 10 MM patients were controls, who did not develop ONJ after treatment with zoledronate. However, although this study genotyped total 1936 SNPs which makes the Bonferroni corrected alpha as $2.5*10^{-5}$, none of 8 SNPs reached this alpha level. The top SNP rs1152003 was located on *PPARG* (peroxisome proliferator-activated receptor gamma) gene with the strongest p-value of 0.0064. *PPARG* is a compelling candidate gene that is associated with bone remodeling [54–57], and is involved in

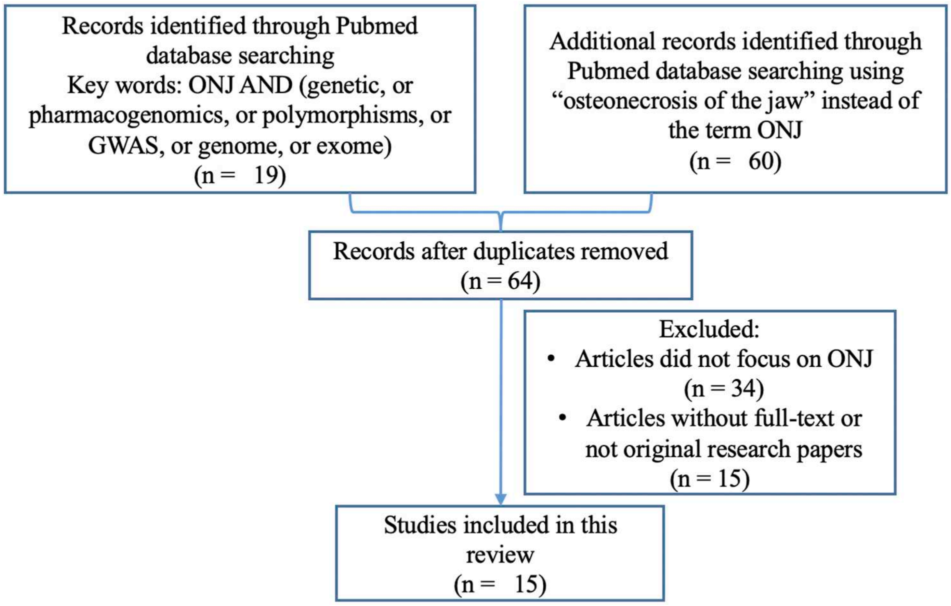

Fig. 1. Flow diagram for the article selection process.

decreasing osteoblasts and increasing osteoclasts differentiation. Even though this gene is a strong candidate for bone remodeling, the SNP located at *PPARG* needs to be further replicated in other independent studies.

The study by Arduino et al [50] included 30 breast cancer or MM female patients with ONJ as cases, 30 breast cancer or MM women without ONJ as controls. All these 60 patients were treated with zoledronate (mean of duration therapy: 17.1(cases) and 11.4 (controls) months, respectively). This study also included 125 unrelated healthy volunteers as healthy controls. Because BPs have the ability to inhibit angiogenesis [58], the investigators hypothesized that vascular endothelial growth factor (*VEGF*) may play an important role in development of ONJ. Previous studies have identified 3 common functional SNPs in *VEGF* (rs2010963, rs3025039, and rs699947) [59–61]. The aim of this study was to test the effect of these 3 SNPs in *VEGF* gene on ONJ. This study compared ONJ cases with BPs tolerant control or healthy controls, respectively. Upon analysis, none of these three SNPs was associated with ONJ development. However, the haplotype AC determined by two SNPs rs2010963 and rs699947 was significantly associated with ONJ (corrected p-value = 0.024).

Studies have shown that estrogen plays an important role in bone remodeling by inhibiting osteoclasts formation and differentiation [62]. Estrogen also increases the inhibitory activity of BPs on osteoclasts [63], thereby inducing osteoclasts apoptosis. Based on these findings, La Ferla, et al postulated that estrogen may be associated with development of ONJ [52]. To test this hypothesis, they genotyped two estrogen SNPs (rs2234693 and rs9340799) and one aromatase SNP (rs10046) using Taqman genotyping assay. Aromatase, also named estrogen sythetase, play a key role in the biosynthesis of estrogen. This study included 20 ONJ cases and 53 controls. All samples were MM or patients with metastatic cancer and treated with zoledronate. Results showed that the aromatase SNP, rs10046, was significantly associated with development of ONJ (p = 0.0439, OR = 2.83).

Marini F, et al showed that the *FDPS* intronic region SNP rs2297480 C allele showed lower response to serum osteocalcin by amino-bisphosphonate therapy [64]. *FDPS* is farnesyl diphosphate synthase gene, which encodes a key enzyme of the mevalonate pathway. Studies have shown that *FDPS* plays a vital role in the mechanism by which BPs affect osteoclasts survival [21,65,66]. They thus tested rs2297480 SNP in the *FDPS* gene in 68 Caucasian MM or metastatic cancer patients who received zoledronate treatment (34 ONJ cases and 34 non-ONJ controls) [51]. This study showed *FDPS* intronic region SNP, rs2297480, was significantly associated with ONJ with a p-value of 0.03.

Katz et al [46] investigated 10 SNPs in 7 candidate genes (*CYP2C8, COL1A1, RANK, OPN, MMP2, OPG and TNF*) in total 78 MM patients treated with zoledronate and/or pamidronate, including 12 ONJ cases and 66 non-ONJ controls. All 7 genes were selected because they were associated with bone remodeling, BMD, or osteoporosis. Upon analysis, none of these SNPs were associated with ONJ (all p-values > 0.05). However, this study constructed genotype scores for 5 candidate gene (*OPG, COL1A1, RANK, MMP2,* and *OPN*) to study the potential combined effect of all five SNPs located in these genes. Genotype score is a method to estimate multiple SNPs or genes effects on complex diseases [67,68]. For this study, the combined genotype of *OPG, COL1A1, RANK, MMP2,* and *OPN* was significantly associated with ONJ development with p-value = 0.0097 (OR: 11.2; 95% confidence interval (CI): 1.8–69.9).

Several clinical studies and animal studies have demonstrated that inflammation/infection is associated with ONJ development [69–72]. Major histocompatibility complex (MHC) class II molecules are important in immune responses, and one study has shown that mice with MHC class II deficiency were more susceptible to infection [73]. The study of Stockmann et al [47] conducted so far the largest discovery candidate gene study to investigate the effect of the SNPs of MHC class II on ONJ development. Total 204 MM or malignant cancer participants treated with BPs were recruited, including 94 ONJ cases and 110 non-ONJ controls. After Bonferroni correction, HLA haplotype DRB*15-DQB1*06:02 (p-value = 0.032, OR 2.5, 95% CI 1.3–5.0), was significantly associated with ONJ development. Moreover, DRB1*01H and/or DRB1*15H (p-value = 0.0003, OR 3, 95% CI 1.7–5.5) were even more significantly associated with ONJ.

6. Genome-wide association studies (GWAS) on ONJ

GWAS is a method for researchers to identify genetic variants associated with risk of disease or drug response to medications. GWAS evaluate the entire genome for genetic polymorphisms and sequence SNPs based on the linkage disequilibrium (LD). As of the time of writing of this review, only two GWASs of ONJ have been published [37,38] (Table 2). The study of Sarasquete et al [37] was the first GWAS on the phenotype of ONJ. This study included 87 MM patients (22 cases and

Table 1
Summary of discovery candidate gene studies for ONJ.

Authors	Population	Disease	BPS	Cases/ control (N)	SNPS	Genes	P-value	OR (95% CI)	Function
Di Martino MT, et al. (2011) PMID: 21517810	Not reported	Multiple myeloma	Zoledronate	9/10	rs1152003 rs10893 rs4725373 rs1049793 rs2463437 rs903247 rs2468110 rs2097937	*PPARG ABP1 ABP1* *ABP1 CHST11 CHST11 CHST11* *CROT*	0.0064 0.0327 0.0327 0.0327 0.0434 0.0205 0.1008 0.0381	NA NA NA NA NA NA NA NA	5′-upstream Synonymous NA Missense 3'-UTR 3'-UTR 3'-UTR Intergenic
Katz J, et al. (2011) PMID: 21396799	White African American Hispanic Other	Multiple myeloma	Zoledronate Pamidronate	12/66	rs1934951 rs1934980 rs1800012 rs12458117 rs243865 rs2073618 rs3102735 rs11730582 rs28357094 rs1800629	*CYP2C8 CYP2C8 COL1A1* *RANK MMP2 OPG OPG OPN* *OPN* *TNF*	0.63 0.66 0.55 0.38 0.11 0.38 0.75 0.21 0.41 0.67	0.68 (0.14–3.22) 0.70 (0.15–3.36) 1.69 (0.30–9.70) 2.14 (0.39–11.71) 3.49 (0.75–16.18) 2.16 (0.38–12.23) 0.79 (0.19–3.34) 2.97 (0.53–16.55) 0.51 (0.10–2.59) 0.68 (0.12–3.95)	Intronic Intronic Intronic Intronic Intronic Missense Intergenic Intergenic Intergenic intergenic
Marini F, et al. (2011) PMID: 21196316	Not reported	Multiple myeloma Mammary cancer Prostate cancer	Zoledronate	34/34	rs2297480	*FDPS*	0.033	NA	Intronic
Arduino PG, et al. (2011) PMID: 21251073	Caucasian	Multiple myeloma Breast cancer	Zoledronate	30/155	rs2010963 rs3025039 rs699947	*VEGF* *VEGF* *VEGF*	0.117	2.76 (1.09–4.94)	5'-UTR 3'-UTR Intergenic
La Ferla F, et al. (2012) PMID: 22448795	White	Multiple myeloma Breast cancer Prostate cancer Other cancers	Zoledronate	30/53	rs2234693 rs9340799 rs10046	*ESR1* *ESR1 CYP19A1*	> 0.05 > 0.05 0.0439	NA NA 2.83	Intronic Intronic 3'-UTR
Stockmann P, et al. (2012) PMID: 23218978	White	Malignant cancer	Zoledronate Pamidronate	94/110	rs3135388 rs10988217	*HLA-DRB1* *HLA-DQB1*	0.014 0.014	2.3 (1.2–4.4) 2.3 (1.2–4.6)	Intergenic Intronic

BPs: bisphosphonates; OR: odds ratio; 95% CI: confidence interval.

Table 2
Summary of genome-wide association studies for ONJ.

Authors	Population	Disease	BPS	Cases/controls (N)	SNPS	Genes	P-value	OR (95% CI)	Function	Replication
Sarasquete ME, et al. (2008) PMID:18594024	European (Spanish)	Multiple myeloma	Pamidronate Zoledronate	22/65	rs1934951 rs19934980 rs1341162 rs17110453	*CYP2C8* *CYP2C8* *CYP2C8* *CYP2C8*	1.07 *10–6 4.231*10–6 6.22*10–6 2.15*10–6	12.75 (3.7–43.5) 13.88 (4.0–46.7) 13.27 (3.5–49.9) 10.2 (3.2–32.1)	Intronic Intronic Intronic 5′ of CYP2C8	No
Nicoletti P, et al. (2012) PMID: 22267851	European	Breast cancer Osteoporosis	Zoledronate	30/1743	rs17024608	*RBMS3*	7.47*10–8	5.8 (3.0–11.0)	Intronic	No

BPs: bisphosphonates; OR: odds ratio; 95% CI: confidence interval.

65 controls) treated with pamidronate or zoledronate. This study identified 4 *CYP2C8* SNPs (rs1934951, rs19934980, rs1341162 and rs17110453) to be associated with ONJ. However, only one SNP, rs1934951, showed a significant association with ONJ development after the Bonferroni correction (corrected p-value = 0.02). T allele of this SNP showed a higher risk of ONJ development with OR of 12.75 (95% CI: 3.7–43.5). CYP2C8 enzyme plays an important role in drug metabolism and synthesis of cholesterol, steroids and other lipids [74]. So far, the underlying mechanism of the association of *CYP2C8* with the development of ONJ is still not clear.

Another GWAS was published in 2012 by Nicoletti et al [38]. This study included 30 breast cancer patients who developed ONJ after treatment with zoledronate as cases, and 17 breast cancer patients who did not develop ONJ after treatment with BPs, as the control group. In addition, this study included 1726 healthy population controls to increase the power. A *RBMS3* gene SNP, rs17024608, was identified to be significantly associated with ONJ (p-value: $7.47*10^{-8}$, OR = 5.8, 95% CI: [3.0–11.0]). This study further showed that there was an interaction between *RBMS3* and *ZNF516* which affects bone mineral density [75]. *RBMS3* encodes an RNA-binding protein, which is associated with up-regulation of collagen type I [76], which an important component of the bone matrix.

Lack of replication was the biggest limitation of both these studies. Moreover, both of these studies had limited sample sizes and the p-value for GWAS did not reach genome-wide significance level of $5*10^{-8}$.

7. Replication studies

So far, five candidate gene studies have attempted to replicate the results of GWAS of Sarasquete ME, et al [41,42,45,46,48] (Table 3). These studies investigated the effect of *CYP2C8* SNP, rs1934951, on the development of ONJ in other independent cohorts. All five studies failed to demonstrate significant association between SNP rs1934951 and ONJ development (p-value > 0.05). Balla B, et al investigated the effect of *CYP2C8* rs1934951 on ONJ development in 270 Hungarian subjects, including 46 ONJ cases and 224 healthy unrelated Hungarian controls. Their study showed SNP rs1934951 to be significantly associated with the localization of ONJ among the affected patients (p-value < 0.05). Heterozygous genotype A/G of this SNP had the higher risk for mandibular ONJ as compared to the maxilla or both locations together. Homozygote G/G showed no significant difference ONJ localization. However, this study did not show association between this SNP and ONJ development. Kastritis et al [45] genotyped *CYP2C8* SNP rs1934951 in 140 subjects treated with zoledronate, including 36 ONJ cases and 104 controls. This study showed no significant difference between ONJ cases and non-ONJ controls for the allele frequency this SNP. However, this study found that the dose of zoledronate was associated with ONJ development. Higher dose of zoledronate was associated with higher risk of ONJ development. Longer use of zoledronate was associated with higher risk for ONJ development. This study also attempted to replicate the result of Di Martino et al [43] by genotyping the *PPARG* gene SNP rs1152003. This SNP also showed no significant association with ONJ. The study of Katz et al [46] failed to show that *CYP2C8* SNP rs1934951 was associated with ONJ development in 78 MM patients (p-value = 0.63). English et al [41] failed to replicate the result of first GWAS performed by Sarasquete ME, et al. in prostate cancer patients with p-value > 0.47 (OR = 0.63, 95% CI: 0.165–2.42). Such et al [42] tried to use similar samples and medication conditions as the study by Sarasquete ME, et al to replicate the effect of *CYP2C8* SNP rs1934951 on ONJ development, but they also failed to replicate this association.

Another replication candidate gene study focused on *VEGF* gene was published by Choi H, et al in 2015 [44]. This study genotyped *VEGF* SNPs rs699947, rs2010963, and rs3025039 in a total of 45 patients (26 cases and 19 controls). The results showed that rs699947 and

Table 3
Summary of replication candidate gene studies for ONJ.

Authors	Population	Disease	BPS	Cases/ controls (N)	SNPS	Genes	P-value	OR (95% CI)	Function
English BC et al. (2010) PMID: 21151627	Caucasian African American Hispanic Asian	Prostate cancer	Zoledronate	17/83	rs1934951	*CYP2C8*	> 0.05	0.63 (0.165–2.42)	Intronic
Such E, et al. (2011) PMID: 21685474	European	Multiple myeloma	Zoledronate	42/37	rs1934951	*CYP2C8*	0.13	NA	Intronic
Katz J, et al. (2011) PMID: 21396799	White African American Hispanic Other	Multiple myeloma	Zoledronate Pamidronate	12/66	rs1934951	*CYP2C8*	0.63	0.68 (0.14–3.22)	Intronic
					rs1934980	*CYP2C8*	0.66	0.70 (0.15–3.36)	Intronic
					rs1800012	*COL1A1*	0.55	1.69 (0.30–9.70)	Intronic
					rs12458117	*RANK*	0.38	2.14 (0.39–11.71)	Intronic
					rs243865	*MMP2*	0.11	3.49 (0.75–16.18)	Intronic
					rs2073618	*OPG*	0.38	2.16 (0.38–12.23)	Missense
					rs3102735	*OPG*	0.75	0.79 (0.19–3.34)	Intergenic
					rs11730582	*OPN*	0.21	2.97 (0.53–16.55)	Intergenic
					rs28357094	*OPN*	0.41	0.51 (0.10–2.59)	Intergenic
					rs1800629	*TNF*	0.67	0.68 (0.12–3.95)	Intergenic
Balla B, et al. (2012) PMID: 22339777	Hungarian	Osteoporosis Multiple myeloma Breast cancer Cervix cancer Prostate cancer Renal cancer	Alendronate Pamidronate Zoledronate Ibandronate Risedronate Clodronate	46/224	rs1934951	*CYP2C8*	0.015	NA	Intronic
Choi H, et al. (2015) PMID: 26086871	Korean	Surgical intervention	Alendronate Ibandronate	26/19	rs2010963 rs3025039	*VEGF*	0.04 0.03	17.66 (1.17–267.25) 0.17 (0.04–0.81)	5'-UTR 3'-UTR
Kastritis E, et al. (2017) PMID: 28604257	European	Multiple myeloma	Zoledronate	36/104	rs1152003 rs1934951	*PPARG* *CYP2C8*	< 0.05	NA	Intergenic Intronic

BPs: bisphosphonates; OR: odds ratio; 95% CI: confidence interval.

rs2010963 were nominally associated with ONJ development ($p = 0.04$, $p = 0.03$, respectively). However the haplotype AC determined by two SNPs rs2010963 and rs699947 was not significantly associated with ONJ ($p = 0.126$), even though these two SNPs have high LD ($r^2 = 0.96$).

There are some potential reasons for the failure of the replication efforts. Firstly, there were differences in the population that was used for replication in the candidate gene studies. The first GWAS by Sarasquete ME, et al was conducted in individuals of Spanish ancestry whereas none of other replication efforts used subjects of Spanish ancestry, even though some studies used European patients. Secondly, the GWAS was conducted in MM patients treated with zoledronate and/or pamidronate. However, only two of the replication studies focused on MM patients. Moreover, subjects in these two studies were treated with zoledronate only.

The discovery candidate gene study for *VEGF* used patients of European ancestry, but replication effort for this gene was undertaken using patients of Korean ancestry. HaploReg v4.1 [77] shows that the LD (r^2) for SNP rs699947 and rs2010963 is 0.45 in Europeans, but 0.96 in Asians.

8. Whole-exome sequencing analysis

Whole-exome sequencing (WES) determines the sequence of all protein-coding genes in human genome. This method covers < 2% of human genome, but contain > 85% of known disease-related variants [78]. Based on above mentioned, WES is a cost-effective alternative to whole-genome sequencing.

So far, two WES studies have been published [39,40] (Table 4). Kim et al [40] identified four genes (*ARSD, SLC25A5, CCNYL2,* and *PGYM*) associated with ONJ with the lowest *p*-value (p-value < 0.05) using WES and Gene set enrichment analysis (GSEA) methods. GSEA is a computational method that investigates genetic variants in a group of genes to elucidate the gene differences between cases and controls. This was the first study that combined WES and GSEA methods to investigate the function of SNPs between ONJ patients and non-ONJ participants.

The WES from our group [39] was the first study that performed both discovery and replication followed by meta-analysis so far. Moreover, our study included not only MM but also other metastatic solid cancers as cases and controls. The meta-analysis identified *SIRT1* SNP rs7896005 and *HERC4* SNP rs3758392 to be associated with ONJ with the lowest *p*-value ($3.9*10^{-7}$) approaching genome-wide significance. The *HERC4* SNP rs3758392 had the same p-value as rs7896005 because of high LD ($r^2 = 0.88$). These two SNPs were both expression quantitative loci (eQTLs) for *SIRT1*. *SIRT1* was a very compelling candidate gene of bone remodeling. Studies had shown that *SIRT1* plays a vital role in bone remodeling by affecting the Wnt signaling pathway [79–82] and RANK/RANKL/OPG pathway [83,84].

9. Conclusion

ONJ is a rare but serious drug induced adverse event, which critically increases discomfort and reduces quality of life in patients. Studies have shown that the risk of ONJ development is higher in patients of European ancestry than other populations [12,14,85]. Investigators believe that genetic factors play an important role in ONJ development. Candidate gene studies have focused on investigating the association between genetic variations within certain genes of interest and ONJ. However, the selection of candidate genes is limited by priori knowledge. WES approach identifies potentially functional genetic variations through sequencing protein-code region of genes in the human genome.

Table 4
Summary of Whole-exome sequencing studies for ONJ.

Authors	Population	Disease	BPS	Cases/controls (N)	SNPS	Genes	P-value	OR (95% CI)	Function	Replication
Kim JH, et al. (2015) PMID: 25668207	Oriental	Tooth extraction Implant surgery	Alendronate Zoledronate Risedronate	16/126	Not reported	*ARSD* *SLC25A5* *CCNYL2* *PYGM*	< 0.05	Not reported		No
Yang G, et al. (2018) PMID: 28856724	European ancestry	Multiple myeloma Breast cancer Cervix cancer Prostate cancer Renal cancer	Zoledronate Pamidronate	39/22	rs7896005 rs3758392	*SIRT1* *HERC4*	3.9*10–7 3.9*10–7	0.07 (0.01–0.46) 0.07 (0.01–0.46)	Intronic Intronic	Yes

BPs: bisphosphonates; OR: odds ratio; 95% CI: confidence interval.

However, since it only cover < 3% of human genome, WES may also miss the important genetic markers that are potentially associated with ONJ. Even though GWAS surveys the entire genome, it requires larger sample sizes and replication phase. So far, none of the genetic polymorphisms reported in the ONJ GWAS studies have been replicated, largely due to limited sample size and lack of validation. In summary, after reviewing the ONJ Pharmacogenomics literature, no genetic markers for ONJ have been replicated or functionally validated. We conclude that a GWAS with larger sample size followed by replication and functional validation will be needed to fully investigate the pharmacogenomics of ONJ.

Contributions

All authors contributed to the conception, drafting, and critical review of the manuscript and provided final approval.

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Conflict of interest

The authors report no relationships that could be construed as a conflict of interest.

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