#### **Review**

# RANKL, RANK, osteoprotegerin: key partners of osteoimmunology and vascular diseases

M. Baud'huin<sup>a, b</sup>, F. Lamoureux<sup>a, b</sup>, L. Duplomb<sup>a, b</sup>, F. Rédini<sup>a, b</sup> and D. Heymann<sup>a, b, c, \*</sup>

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Abstract. 1997 saw the identification of a novel set of proteins within the tumor necrosis factor (TNF)/TNF receptor families that are required for the control of bone remodeling. Therefore, these receptors, receptor activator of nuclear factor kappa B (RANK), osteoprotegerin (OPG) and their ligand RANK ligand (RANKL) became the critical molecular triad controlling osteoclastogenesis and pathophysiologic bone remodeling. However, the establishment of the corresponding knock-out and transgenic mice revealed unexpected results, most particularly, the involvement of these factors in the vascular system and immunity.

Thus, the OPG/RANK/RANKL molecular triad appears to be associated with vascular calcifications and plays a pivotal function in the development of the immune system through dendritic cells. OPG/RANK/RANKL thus constitute a molecular bridge spanning bone metabolism, vascular biology and immunity. This review summarizes recent knowledge of OPG/RANK/RANKL interactions and activities as well as the current evidence for their participation in osteoimmunology and vascular diseases. *In fine*, the targeting of the OPG/RANK/RANKL axis as novel therapeutic approaches will be discussed.

**Keywords.** RANKL, osteoprotegerin, bone remodeling, osteoclast, osteolysis, osteoimmunology, cardiovascular disease.

#### Introduction

Genomic and proteomic research over the past decade has identified a large number of cytokines, growth factors, transcriptional factors and enzymes controlling cell metabolism and/or participating in the establishment of the molecular network in each cell, into all tissues and between all organs. Such systems allow the coordination of cell differentiation during embryogenesis and coordinated cell activities throughout life [1], and a molecular cross-talk in bone between osteoblasts and osteoclasts to maintain bone mass. Thus, osteoclasts originating from hematopoietic multinucleated cells are specialized in calcified matrix resorption [2, 3], whereas osteoblasts derived from bone marrow mesenchymal stem cells are responsible for new bone formation [4]. It has been estimated that around 10% of total bone mass is renewed per year, participating in calcium and phosphorus homeostasis [5]. The communication networks between osteoclasts and osteoblasts are mainly com-

<sup>&</sup>lt;sup>a</sup> Université de Nantes, Nantes Atlantique Universités, Laboratoire de Physiopathologie de la Résorption Osseuse et Thérapie des Tumeurs Osseuses Primitives, EA3822, F-44035 Nantes (France), Fax: +33 240 412 845, e-mail: dominique.heymann@univ-nantes.fr

<sup>&</sup>lt;sup>b</sup> INSERM, ERI 7, F-44035 Nantes (France)

<sup>&</sup>lt;sup>c</sup> CHU de Nantes, F-44035 Nantes (France)

<sup>\*</sup> Corresponding author.

prised of soluble cytokines and growth factors which modulate the expression of a wide range of genes through specific receptors and numerous transcription factors. However, it has been established that osteoblast-osteoclast contacts are required for the differentiation of osteoclast progenitors, thus demonstrating the pivotal role played by the membrane form of growth factors [6, 7]. These observations led the international scientific community to identify the soluble and membrane factors involved in osteoblast-osteoclast interactions.

Parathyroid hormone (PTH) [8], vitamin D3  $[1,\alpha(OH)_2D_3]$  [9] and calcitonin [10] have been considered for a long time as the principal regulators of calcium homeostasis in terrestrial vertebrates. Similarly, macrophage colony-stimulating factor (M-CSF) is a critical cytokine involved in osteoclastogenesis. M-CSF participates in the proliferation of osteoclast progenitors, maintaining a pool of progenitors in bone marrow, and it cooperates with receptor activator of nuclear factor kappa B (RANK) ligand (RANKL) to induce the fusion of osteoclast progenitors (pre-osteoclasts) into osteoclasts which will be secondarily activated into mature osteoclasts by RANKL (see below) [11, 12]. In contrast, interferons (IFNs), which play crucial roles in the regulation of a wide variety of innate and adaptive immune responses, interfere with RANKL-induced osteoclastogenesis and thus represent a critical mechanism for the suppression of pathological bone resorption associated with inflammation [13]. However, recent investigations in bone biology clearly identified a novel set of cytokines/cytokine receptors within the tumor necrosis factor (TNF) family that are required for the control of bone remodeling [14-18]. These molecules - RANKL and its receptors RANK and osteprotegerin (OPG) – appear as the final effectors of most of the osteotropic factors already identified [19]. RANKL is considered to be a powerful stimulator of bone resorption, while OPG is a soluble bone protector. In this context, pathologies characterized by deregulated bone remodeling are often associated with an imbalance between OPG and RANKL [18–21]. Furthermore, recent studies demonstrated that the OPG/RANK/RANKL molecular triad is also strongly implicated in the control of immune [22] and vascular [23] systems. Thus these three molecules constitute a molecular cross-talk between bone, vessels and immune cells, providing new strategies for the prevention and/or treatment of corresponding

The present review summarizes recent knowledge of OPG, RANK and RANKL interactions and roles in the pathophysiology of bone, vessels and immunity.

## RANKL and its receptors OPG and RANK regulate bone metabolism: prognostic markers and therapeutic agents

Cytokines and growth factors can exist as different forms: expressed at the cell membrane, associated with the extracellular matrix, or in soluble forms, interacting with their membrane and soluble receptor to modulate cellular activities. *In fine*, the effects of a cytokine result in the balance between its own activities and the biological influence of its soluble receptors which act as agonist or antagonist agents. As the molecular partners OPG/RANK/RANKL thus include the RANKL cytokine, its membrane or soluble receptors, respectively RANK and OPG, it is necessary to take into consideration the potential duality of both receptors to determine RANKL activities.

#### **OPG/RANK/RANKL:** molecular and functional characteristics

Osteoclast activities are related to the bone resorption process in physiological as well as in pathological conditions. For many years, mesenchymal-derived stem cells including osteoblasts have been well known to modulate osteoclast differentiation and bone degradation [24-26]. However, the major inhibitor of osteoclastogenesis was only identified in 1997–1998 simultaneously by Tsudas group [27, 28] and Amgen Company [29]. They respectively named this novel negative regulator of osteoclast differentiation 'osteoclatogenesis inhibitory factor' (OCIF) and 'osteoprotegerin.' Its international name according to the TNF nomenclature is TNFRSF11B. The role of OPG has been clearly demonstrated by the development of transgenic and knock-out mice. Indeed, OPG knockout mice exhibit a strong decrease in total bone density and bone volume and suffer from osteoporosis associated with a high incidence of fractures and vertebral deformities [30, 31]. Furthermore, this induced osteoporosis was totally reversed by intravenous injection of recombinant OPG [32]. In contrast, OPG transgenic mice suffer from a marked osteopetrosis characterized by a high bone turnover and an inhibition of osteoclastogenesis [29]. These data demonstrated that the presence of OPG is absolutely required to maintain bone mass in physiological situations. In vitro experiments confirmed the observations in the animal models and provided an explanation for the phenotype exhibited by the mice. Immediately after the identification of OPG, both laboratories identified within the TNF cytokine family, the ligand which bound OPG with high affinity, and called this molecular effector OPG ligand (OPGL) [33, 34]. OPGL was RANKL or the TNF ligand superfamily member 11, TNFSF11, already known for its activity on the immune system. Indeed, RANKL is considered to be a dendritic cell-stimulating agent and acts as a survival factor for dendritic cells and for mature T cells, therefore regulating their proliferation [35–37]. These activities are associated with the activation of the nuclear factor kappa B (NF-κB) transcription factor after the binding of RANKL to its membrane receptor RANK (TNFRSF11A) [38, 39].

To determine the involvement of RANKL in bone metabolism, similar approaches based on genetically modified mice have been used by both research groups. In contrast to OPG-modified mice, RANKL transgenic mice exhibit a marked osteoporosis [33] and mice disrupted for RANKL are strongly osteopetrotic with a total absence of mature osteoclasts [40, 41]. Furthermore, severe bone loss and hypercalcemia are the main phenotypic characteristics of mice treated with recombinant RANKL. Overall, these data demonstrated that RANKL is a pro-resorptive factor while OPG is a powerful osteoprotective agent. In vitro experiments supported in vivo observations. Indeed, using a primary culture of osteoclast progenitors from bone marrow or a precursor cell line such as the murine monocytic cell line RAW264.7, RANKL induces osteoclast differentiation whereas OPG abolishes this phenomenon [16, 32-44]. Figure 1a illustrates RANKL/OPG activities in the RAW264.7 cells. After 4 days of culture in the presence of RANKL, RAW264.7 cells differentiate into large and multinucleated cells expressing osteoclastic markers (calcitonin receptor, cathepsin K, TRAP). When the cells are treated simultaneously with OPG and RANKL, osteoclast formation is abolished. RANKL is also able to activate mature osteoclasts, as determined by the stimulation of MMP and cathepsin K activities and the bone resorption capability of these cells [43, 44].

RANKL and OPG activities/functions were demonstrated in the years after their identification (Fig. 1b). In normal bone, RANKL is preferentially expressed on committed pre-osteoblastic cells, whereas its specific receptor RANK is expressed on osteoclast progenitors. In this system, RANKL is required for osteoclast differentiation and acts as a survival factor for osteoclast precursors [15–17]. OPG is a soluble factor produced by osteoblastic cells, and thus is considered as a decoy receptor for RANKL as confirmed by molecular binding experiments [45]. Indeed, OPG blocks the interaction between RANKL and RANK, inhibits the terminal stage of osteoclastic differentiation and then inhibits bone resorption (Figs. 1b, 2a) [15–18]. Furthermore, the inhibitory effect of OPG on bone resorption can be explained not only as a decoy receptor function but also as a modulator of the RANKL half-life [46]. Studies of OPG/RANKL in the serum of RANKL-/- and OPG-/- mice are in agreement with a potential role for OPG in the shedding of RANKL [47]. In turn, RANKL controls the bioavailability of OPG and its internalization and degradation [46]. In pathophysiological situations, OPG and RANKL must be considered as a molecular balance and be evaluated separately. OPG and RANKL expression are not restricted to bone tissue, as both factors can be produced by numerous cell types. OPG is a soluble factor, produced by a large number of cells, including immune cells, endothelial cells and osteoblasts [see review in ref. 18]. RANKL is expressed on the cell membrane and is also produced as a soluble factor by the same cells [40] (Fig. 2a). Three isoforms of RANKL have been identified in human and rodent, the first encoding a transmembrane form, the second, a soluble cytokine and the third, a cytoplasmic molecule [48, 49]. The soluble form of RANKL can also be produced by enzymatic shedding by the metalloprotease-disintegrin TNF-alpha convertase (TACE, also named a disintegrin and metalloproteinase, ADAM17) [50, 51], ADAM10 [52], ADAM19 [53], MMP-3 [54], MMP7 [54] and MMP-14 [52]. The exact function of each RANKL isoform must be clarified, but the literature clearly revealed the major relevance of the balance in RANKL-expressing cells between these three RANKL forms in osteoclastogenesis [55]. The third protagonist of the molecular triad is RANK. Like OPG and RANKL, transmembrane RANK is ubiquitously expressed, but in contrast to OPG/ RANKL, it is considered to be an osteoclastic marker in physiological bone tissue [56] (Fig. 2a). Like the other members of the TNF receptor superfamily, RANK assembles into functional trimeric receptors after binding with RANKL [57]. This trimerization appears to be required to generate mature and functional osteoclasts. Indeed, RANK dimerization allows the formation of multinuclear TRAP-positive cells but without any osteoclastic markers and unable to induce pit resorption [57]. Similarly, using X-ray crystallographic analysis, Ito et al. [58] showed the ability of the RANKL ectodomain to constitute a trimer complex [58] and then confirmed that the formation of a 3:3 RANK-RANKL binary complex is necessary to generate optimal osteoclastogenesis (Fig. 1b). Although RANKL binding to RANK induced RANK trimerization, RANK is also able to self-assemble [59], similarly to other TNF receptors [60]. Thus, Kanazawa and Kudo [59] demonstrated that RANK is self-assembled through a restricted cytoplasmic domain (amino acid residues 534-539). Interestingly, overexpression of full-length RANK results in activation of NF-κB and osteoclastogenesis,

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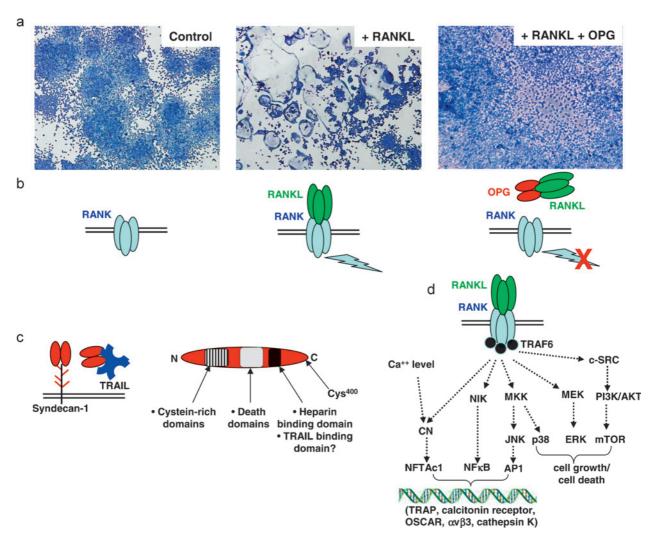
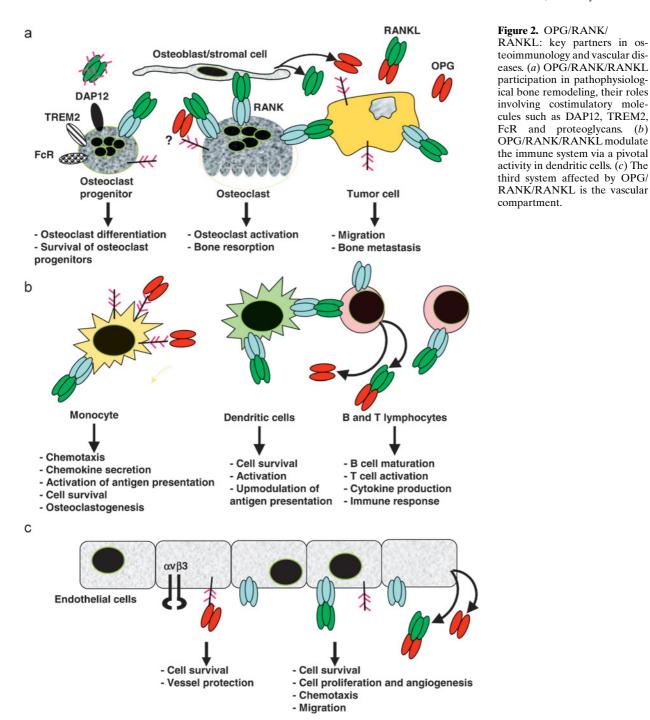


Figure 1. Characteristics of OPG/RANK/RANKL interactions. (a) After 96 h in the presence of 100 ng/ml human RANKL, the murine RAW264.7 monocytic cell line differentiates into osteoclasts while 100 ng/ml human OPG totally abolishes RANKL effects. (b) RANK is expressed on the osteoclast membrane and binds RANKL produced by osteoblast/bone marrow stromal cells. OPG acts as a decoy receptor and blocks the interaction between RANKL and RANK. (c) OPG possesses a heparin binding domain and interacts with two other ligands, TRAIL and syndecan-1; (d) RANKL binding to RANK transduces specific signals in osteoclasts corresponding to novel therapeutic targets of bone diseases; CN, calcineurin.

even in the absence of RANKL. It was earlier demonstrated that TNF receptor (TNFR)-I and II also selfassembled through a specific extracellular domain named the pre-ligand binding assembly domain (PLAD), thus avoiding the formation of mixed receptors TNFR-I and TNFR-II [60]. Overall, these data indicate that such a RANK domain could also be useful to allow the formation of specific receptoractivating signal transduction pathways (see below) and to avoid the formation of hybrid receptors.

OPG, belonging to the TNFR superfamily, is able to self-dimerize through a disulfide bond using Cys<sup>400</sup> at the C-terminal portions [61, 62]. Indeed, the most active form of OPG is a homodimer that possesses higher affinity for the RANKL ectodomain compared to OPG monomer [63]. OPG contains seven domains: four cysteine-rich N-terminal domains (domains 1–4), two death domain-homologous regions (domains 5 and 6) and a C-terminal heparin-binding domain (domain 7) (Fig. 1c). Domains 1-4 are structurally related to the TNF receptor family and are sufficient to abolish osteoclast differentiation. Domains 5 and 6 can mediate a cytotoxic signal when they are included in a chimeric protein OPG-Fas [61], but their physiological functions remain to be elucidated. Domain 7 is composed of a heparin-binding domain and a Cys<sup>400</sup> at its C-terminal portion (Fig. 1c). Although the affinity for heparin does not correlate with OPG inhibitory potential, this domain plays numerous key functions not all of which have been determined. Thus, OPG through its binding to syndecan-1 exerts a chemotaxis activity in human peripheral blood monocytes [64]. In



turn, syndecan-1 controls OPG bio-availability and is associated with an increase in local RANKL concentration and osteolysis in myeloma cells which over-express this proteoglycan [65]. Furthermore, shedding of TNF-α proteoglycans and glycosaminoglycans strongly modulates OPG/RANK/RANKL interactions. Indeed, recent data demonstrated that RANK, RANKL, OPG and proteoglycans could form a very large complex 3:3:2:1 related to specific activities in osteoclasts such as MMP9 activities [66]. Such a very

large complex involving protegoclycans can be compared to the cooperative dimerization of fibroblast growth factor (FGF)-1 upon a single heparin saccharide that may drive the formation of a 2:2:1 FGF1-FGFR2c-heparin ternary complex [67]. In this case, proteoglycans act as coreceptors for growth factors. Furthermore, depending on the bone remodeling step, OPG could be released from the bone matrix and thus modulate bone remodeling in a fashion similar to  $TGF-\beta$  [68]. In bone tissue, proteoglycans thus appear

critical for maintaining an appropriate number of osteoblasts and osteoclasts by modulating their proliferation and/or differentiation. OPG activities could involve the ras/MAPK pathways [45] but also PKC and PI3K/Akt [64].

Similarly to OPG/ RANK/RANKL, heparan sulfate proteoglycans appear crucial for other members of the TNF/TNFR superfamilies. While glycosaminoglycans mainly modulate OPG-RANKL interactions, dermatan sulfate also interacts with RANKL [69]. Indeed, Shinmyouzu et al. [69] showed that dermatan sulfate reduced the RANKL-induced levels of phosphorylation of p38 and ERK in osteoclast progenitors, thus abolishing osteoclastogenesis. Very recently, Bishof et al. [70] identified syndecan-2 as a new binding partner of the transactivator and calcium modulator and cyclophilin ligand interactor (TACI), a member of the TNFR family [71]. Similarly, heparin sulfate proteoglycan serves as a receptor for A proliferation-inducing ligand (APRIL), a member of the TNF family, promoting tumor cell proliferation [72]. OPG also has a third ligand, TNF-related apoptosis-inducing ligand (TRAIL; Fig. 1c) [73]. OPG binding to TRAIL results in the abolition of TRAIL apoptotic activity [74-82]. This cross-regulation has a strong impact in cancer biology. Indeed, these observations suggest that OPG is deleterious, acting as a survival factor in several cancer pathologies by the inhibition of TRAIL, a natural inducer of tumor cell apoptosis [76–82].

Recent data reveal that several membrane proteins cooperate with the RANK/RANKL complex to control bone remodeling. The signaling adapter protein DNAX-activating protein-12 (DAP12) is a homodimeric transmembrane molecule modulating cellular activation and maturation in myeloid lineage cells in association with the DAP12-associated receptors (DARs) which include triggering receptor expressed on myeloid cells (TREM), DAP12-associated lectin (MDL)-1 and NKG2D. In 2003, Kaifu et al. [83] showed that mice deficient for DAP12 exhibit a marked osteopetrosis owing to impaired osteoclastogenesis through a blockade of progenitor multinucleation. They also determined the molecular motif associated with this bone phenotype and provided evidence for the function of the immunoreceptor tyrosine-based activation motif (ITAM) in the regulation of osteoclastogenesis [84]: mice lacking ITAMharboring adaptors such as Fc receptor common gamma subunit (FcRy) and DAP12 are osteopetrotic [84, 85]. Similarly, Humphrey et al. [86] recently demonstrated the involvement of TREM2 in the regulation of osteoclast multinucleation, resorption and migration. In fact, DARs such as TREM2 associate with DAP12 or FcRy and transduce costimulatory signals (especially calcium signaling through phospholipase Cγ) which cooperate with RANKL signaling during osteoclast differentiation (Fig. 2a) [87, 88]. In this context, any disturbance in the DAR-DAP12 signaling complex contributes to the development of bone diseases.

This section has described the main molecular and functional characteristics of OPG/RANK/RANKL. Overall, the abundant literature demonstrates that RANKL and OPG appear as final effectors of osteoclastogenesis and bone resorption.

#### **OPG/RANK/RANKL** and bone pathologies

Osteolytic processes are the main skeletal-related events in patients suffering from bone metastases and are associated with major sequelae and high levels of individual incapacity. In this context and according to the pivotal role of the OPG/RANK/ RANKL triad in osteoclastogenesis, blocking osteoclastogenesis and osteoclast activities via RANKL pathway inhibition constitutes a potential novel approach to maintain skeletal integrity. It has been suggested that high levels of bone degradation could enhance cancer cell establishment and growth in bone tissue through biological factors such as growth factors sequestrated in bone extracellular matrix. Indeed, cancer cells express soluble or membrane factors promoting osteoclastogenesis and accentuating bone resorption. Thus, a vicious cycle is generated between bone and cancer cells [89]. The expression of RANKL has been demonstrated in a wide range of benign and malignant tumor cells [18, 20, 75, 89, 90] (Fig. 2a). Although RANKL released in the bone microenvironnement affects osteoclast activities, RANKL can also directly modulate the behavior of cancer cells. Indeed, very recently, several papers have reported the expression of functional RANK in human breast cancer cells, human prostate cancer and mouse melanoma cell lines [91-93]. These studies show that RANKL triggers RANK-positive cancer cell migration and growth in bone tissue. However, the development of bone metastases is probably not limited to the action of RANKL on cancer cells and cannot exclude the pivotal role of osteoclasts [94, 95]. We indicated above that several proteases produced in the bone microenvironment modulate the shedding of RANKL and then bone resorption. The following theory has been proposed: osteoclastogenesis and activation of immature osteoclasts could be mediated by a direct interaction with RANKL-expressing osteoblasts or/and by the protease-solubilized RANKL which can also participate in the recruitment of osteoclast progenitors [54]. Although the expression of RANKL by cancer cells is controversial (especially for breast carcinoma cells), it is now hypothesized that the metastatic cells might express RANKL in an osseous context in contrast to the primary tumors [96]. Their migration to bone tissue is linked to the expression of membrane RANK and the chemoattractive function of RANKL. Based on these observations, current studies have disclosed that blocking RANKL-RANK interaction prevents the progression of prostate cancer in bone [97–100]. However, RANK expression is not restricted to nonbone cancer cells, because we recently showed that functional RANK is expressed at the surface of mouse [101] and human [102] osteosarcoma cell lines without modulation of cancer migration. RANK is also detected in more than 50% of human osteosarcoma specimens studied, with a preferential expression on osteosarcoma developed in pathological bone and bad responders to chemotherapy [102] (Fig. 2a). Thus RANKL may act as a 'soil' factor in primary and secondary bone cancer development dependently or independently of its direct effects on cancer cells. This fact is supported by several groups that have shown that inhibition of bone resorption using RANK-Fc or OPG-Fc blocks growth of tumor cells such as myeloma cells that do not express RANK [103, 104]. However, a wide range of benign and malignant tumor cells express OPG simultaneously with RANKL [18, 20, 75, 89, 90, 105] (Fig. 2a). Such an observation has led to evaluation of the clinical interest in measuring the RANKL/OPG ratio in bone pathologies. Thus, the RANKL/OPG balance is disturbed in severe osteolytic pathologies in favor of RANKL [106–108]. In such cases, the tumor microenvironment releases high levels of OPG to counterbalance the high concentration of RANKL. OPG may reflect a protective mechanism of the skeleton to compensate for increased bone resorption. This hypothesis is strengthened by the effect of bisphosphonate treatment which results in a decrease in the OPG level in contrast to RANKL which is not modified [109, 110]. In fine, as the RANKL/ OPG ratio is significantly higher in patients with severe malignant osteolytic pathologies [106, 111— 113], it could predict survival as demonstrated in multiple myeloma [114]. Moreover, the RANKL/ OPG ratio may be used as a prognostic biological marker in non-malignant pathologies such as osteoporosis [108, 115], ankylosing spondylitis [116], rheumatoid arthritis [117], benign bone tumors, osteolysis associated with hip prosthetic loosening [106, 118, 119] or bone fractures [120]. For example, elderly women with hip fractures exhibit an increased RANKL/OPG mRNA content in iliac bone which is associated with increased fracture susceptibility. This ratio can also be considered as an

important index for the evaluation of new drugs against bone diseases or as therapies for bone pathologies [121–129].

### **OPG/RANK/RANKL:** the crossroads of immunity and bone metabolism

The immune phenotype of OPG transgenic mice demonstrated for the first time the relationship between the OPG/RANK/RANKL triad and the immune system [30]. OPG transgenic mice exhibit impaired thymocyte development. Consistent with these findings, mice with a disrupted RANKL gene show a lack of all lymph node organogenesis, normal splenic and Peyer's patches organization, and impaired thymocyte development [40, 41]. Moreover, RANK knock-out mice also lacked lymph nodes and produced defective B and T lymphocyte maturation while they exhibited normal thymic development [130]. RANKL expressed by thymic epithelial cells may be responsible for the development and maturation of RANK-positive lymphocytes [131]. In this context, the OPG/RANK/RANKL molecular triad constitutes a cross-talk between bone metabolism and the immune response, which has been labeled osteoimmunology [18, 132]. The OPG/RANK/RANKL triad exerts its activities on the different cell types involved in immunity. Thus, RANKL behaves as a chemotactic factor for monocytic cells through its binding to membrane RANK [133, 134], similar to its effect observed on osteoclasts [135], emphasizing the cross-talk between bone and immune systems (Fig. 2b). The RANKL-induced migration involved phosphatidylinositol 3-kinase, phosphodiesterase, and Src kinase signaling pathways. OPG also modulates the migration of monocytes via its binding to syndecan-1 and signaling involving protein kinase C, phosphatidylinositol 3-kinase/Akt and tyrosine kinase [64]. However, further experiments are needed to define the functional importance of the OPG/ RANKL balance in the monocyte migration.

Complementary to their role in cell migration described above, recent data implicate the OPG/RANK/RANKL triad in inflammatory processes. A large number of cytokines are known to regulate many of the bone responses in inflammatory conditions [136]. Several cytokines are modulated by RANKL, thus affecting cell behavior [18, 137]. Thus, RANKL induced CCL22 (macrophage-derived chemokine) [138], monocyte chemotactic protein 1 (MCP-1) [139] and interleukin-8 [140]. In turn, the chemokine increased RANKL expression [18] leading to the establishment of a vicious cycle exacerbating the inflammatory process and the associated pathologies [141, 142]. Similarly, RANKL has been found to upregulate RANK expression on monocytes, to activate

their capacity for antigen presentation through upregulation of costimulatory molecule expression and to promote cell survival [143, 144]. Thus, RANKL enhanced the survival of macrophages and up-regulated the expression of CD86, and RANKL-treated macrophages show increased allogeneic T cell activation and phagocytic activity compared to control cells [144]. In a model of lipopolysaccharide (LPS)-induced endotoxic shock, administration of soluble RANK-Fc protects mice from death induced by sepsis, and in a model of inflammation-mediated arthritis, RANK-Fc ameliorates disease development and attenuates bone destruction [143]. Although lymphocytes are probably the major source of RANKL in inflammatory processes, mast cells [145], endothelial cells and platelets [146] also represent a potential origin of RANKL. Blockade of RANKL may allow treatment of human inflammatory disorders in which RANKL is overexpressed, such as periodontal diseases, rheumatoid arthritis or wear debris prosthesis [147–150]. However, very recently Maruyama et al. [151] found that a RANKL pre-treatment suppressed production of inflammatory cytokines in macrophages in response to LPS. In this model, prior administration of RANKL protects mice from LPS-induced death [151]. These data and those published by Seshasayee et al. [143] appear contradictory. In fact, RANKL may be produced to counterbalance the inflammatory process maintained by inflammatory cytokines. Unfortunately, when the inflammation is initiated, RANKL appears unable to block this process and may even contribute to maintain the pathology.

The RANKL/OPG molecular duo is also strongly associated with the biology of dendritic cells expressing RANK. Indeed, RANKL dramatically inhibits the apoptosis of dendritic cells via increased Bcl-xL expression [35] and induces T lymphocyte proliferation [36] (Fig. 2b). However, the core function of RANKL in dendritic cell biology is still not well understood. RANKL has been reported to activate intestinal dendritic cells, increase their survival in vivo, and inhibition of the RANK/RANKL axis by OPG-Fc results in reduced colitis [152]. On the other hand, in an inflammation-mediated transgenic mice model for type I diabetes, RANK-Fc treatment decreases the numbers of CD4+CD25+ regulatory T lymphocytes in pancreas-associated tissue that can exacerbate disease [153]. More recently, Loser et al. [154] reported that RANKL is expressed in keratinocytes of the inflamed skin and that RANKL can modify dendritic cell functions to maintain the number of peripheral CD4+CD25+ regulatory T lymphocytes. OPG might contribute to this control since it is expressed in dendritic cells and its expression is increased with their maturation [155]. Moreover, dendritic cells from homozygous OPG-deficient mice potentiate the mixed leukocyte reaction despite CD86, MHCII, and antigen presentation levels which are similar to heterozygous OPG-deficient mice [156]. Overall, these data demonstrated that RANKL is a key regulator of T lymphocyte-dendritic cell communication, modulating immunity and bone remodeling through dendritic cells [157].

## **OPG/RANKL** and endothelial cells: a close functional relationship in vascular biology

The first clue that the OPG/RANK/RANKL triad might be the molecular system linking bone metabolism and vessel biology was provided by the vascular phenotype of OPG-deficient mice [30]. OPG-deficient mice exhibited medial calcification of the aorta and renal arteries but not of smaller vessels, suggesting that OPG and its molecular partners may play a role in the long-term observed association between osteoporosis and vascular calcification [30]. The lesions observed resemble human atherosclerotic lesions (RANKL and RANK expression, presence of osteoclast-like cells adjacent to the RANKL-expressing cells). OPG administration prevents calcification induced by warfarin or high doses of vitamin D in rat [158] but could not reverse this phenomenon once the mineralization process had occurred [32]. Moreover, OPG physically associated with the von Willebrand factor is localized in the Weibel-Palade bodies of endothelial cells and is rapidly secreted in response to inflammatory stimuli [158]. This observation definitively supports the notion that OPG/RANK/RANKL constitute a molecular bridge spanning skeletal disorders, vascular injury, inflammation and hemostasis [159, 160].

RANKL and OPG are differentially expressed in calcific aortic stenosis [161]. Indeed, while RANKL was not expressed at relevant levels in controls but detectable in aortic stenosis, OPG expression was marked in controls but significantly lower in this pathology. Furthermore, RANKL promotes matrix calcification and induces the expression of osteoblastassociated genes in cultured human aortic valve myofibroblasts, revealing a transition towards an osteogenic phenotype [161]. Microvascular endothelial cells produce an adapted microenvironment favorable to calcified tissue formation and thus stimulate the adhesion and transendothelial migration of monocytes that can differentiate into osteoclasts in the presence of RANKL [162]. These results suggest that the RANKL/OPG pathway may regulate valvular calcification in calcific aortic stenosis. Furthermore, Olesen et al. [163] suggested that OPG may play a special role in arterial disease in diabetes, since increased levels of OPG found in aortic tunica media

from diabetic patients are associated with calcification of human vascular smooth muscle cells [164]. In agreement with these findings, Anand *et al.* [165] revealed that among inflammatory biomarkers, only OPG predicted both subclinical disease and near-term cardiovascular events and may then be considered as a simple test for identifying high-risk type 2 diabetic patients. Similarly, Vik *et al.* [166] and Ziegler *et al.* [167] demonstrated the relationship between OPG serum levels and severity of artery disease.

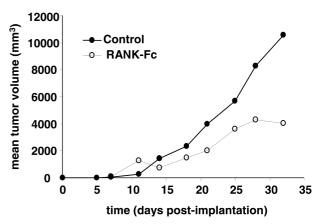
The RANKL/OPG system exerts its activities simultaneously on endothelial cells and vascular smooth muscle-related cells. Thus, OPG promotes endothelial cell survival through neutralizing pro-apoptotic TRAIL [73, 168] and must be considered as an ανβ3-induced and NF-κB-dependent survival factor for endothelial cells whose survival depends on OPG induction by NF-kB [169, 170] (Fig. 2c). The OPG survival effect has also been demonstrated in pathological conditions such as periodontitis [171]. Indeed, OPG produced by microvascular endothelial cells controls endothelial cell survival and bone remodeling during this pathology [172]. Cross et al. [173] also reported a pro-angiogenic effect of OPG and correlated OPG expression by tumor endothelial cells with clinical data in human tumors. However, while the role of OPG in vascular pathogenesis is not fully understood, OPG may reflect a protective mechanism of endothelial cells and bone during aggressive inflammation. RANKL has also been implicated in endothelial cell metabolism, as it induces angiogenesis in vitro and in vivo, acts as a chemotactic factor for endothelial cells and induces their migration [174, 175]. RANKL also promotes endothelial proliferation and survival [175, 176], suggesting a potential implication in tumor development and increased vascular permeability [177] (Fig. 2c). OPG and RANKL activities in endothelial cells are tightly regulated by cytokines and growth factors present in the microenvironment of endothelial cells [18, 178, 179].

### RANK signal transduction pathway as a potential therapeutic target

RANKL has been named for its ability to activate NF-kB which constitutes one of the early molecular events induced by the binding of RANKL to RANK [26, 180, 181] (Fig. 1d). Similar to the other TNFR family members, RANK activation first recruits the TNR receptor-associated factor (TRAF) adaptor proteins associated with the intracytoplasmic domain of RANK and implicated in its oligomerization. Furthermore, TRAF6 acts as a pivotal adaptor leading to specific gene expression regulating osteoclast differentiation and activation. The downstream targets of

TRAF6 include transcription factors such NF-κB, activator protein-1 (AP-1) and nuclear factor of activated T cells (NFAT), the cascades of mitogenactivated protein kinases (MAPKs) such as p38 stress kinase, c-Jun N-terminal kinase (JNK), ERK and the PI3K/AKT pathways which involve the mammalian target of rapamycin (mTOR) [18, 181].

The OPG/RANK/RANKL molecular triad constitutes a strategic therapeutic target for bone diseases and associated disorders. Thus, several approaches based on recombinant molecules (OPG-Fc, RANK-Fc) or specific antibodies against RANKL have been successfully reported in benign and malignant pathologies [89, 182-184] (Fig. 3). Recently, Cheng et al. [186] envisaged another strategy based on an OPGlike peptidomimetic. This peptide has been designed to avoid its binding to TRAIL and showed an effective activity in preventing myeloma bone disease [187]. Peptidomimetics selectively inhibiting RANKL but not TRAIL activity thus constitute novel therapeutic approaches to treat tumor-associated osteolysis. Similarly, TNFR loop peptides have been developed and abolish RANKL-induced signaling, bone resorption and bone loss [188]. Such peptidomimetics that mimic either cytokine receptors such as TNFR [188] or a 'decoy receptor' such as OPG [184, 187] may present various advantages, mainly a reduced immunogenicity, a more targeted effect and multiple applications in which these molecules are implicated (e.g. inhibition of bone resorption and inflammation) [189].



**Figure 3.** OPG/RANK/RANKL molecular pathway as a potential target for bone diseases. Sprague-Dawley rats with transplanted osteosarcoma [185] were treated or not with recombinant RANK-Fc (750 μg, once a week during 3 weeks). Representative mean tumor volumes of rats treated by RANK-Fc compared to the untreated control.

As another strategy to treat osteolysis relates to the blockade of specific signaling pathways currently activated by bone resorption effectors, the RANK signaling pathway has been identified as one of the best approaches [190]. NF-κB plays a key role in RANK signaling and appears critical for osteoclastogenesis. This transcription factor is not necessary for the formation of osteoclast progenitors but is absolutely required for the differentiation steps of these progenitors [191, 192]. Furthermore, NF-κB bridges inflammation and bone homeostasis [193]. Indeed, NF-κB controls bone mass as demonstrated by the bone phenotype of knock-out mice [194] and contributes to the onset and progression of arthritis [195-198]. A role of NF-kB in osteolytic bone metastasis through granulocyte/macrophage colony-stimulating factor (GM-CSF) induction has also been very recently identified [199]. The authors identified the gene encoding GM-CSF as a target of NF-κB and showed that GM-CSF mediates osteolysis bone metastasis of breast cancer by stimulating osteoclastogenesis. In this respect, as NF-κB represents a potential target for the treatment of osteolysis of benign and malignant origin, therapeutic strategies based on inhibition of this transcription factor have recently emerged. Thus, Clohisy et al. [200] demonstrated that NF-kB signaling blockade abolished implant particle-induced osteoclastogenesis in vitro. They also demonstrated a significant decrease in bone erosion associated with inflammatory arthritis using dominant-negative IkB or mutated IkB proteins [201]. Similarly, synthetic double-stranded oligodeoxynucleotides demonstrated their efficacy in a mice model of intestinal carcinoma, acting as 'decoy' cis elements that block the binding of nuclear factors to promoter regions of targeted genes, resulting in the inhibition of gene transactivation in vivo as well as in vitro [202]. Penolazzi et al. [203, 204] developed peptide nucleic acid-DNA decoy chimeras targeting NF-κB which strongly induced osteoclast apoptosis and inhibited their differentiation. Umezawa's group chose the development of a synthetic NF-κB inhibitor [205] which abolishes osteoclast differentiation through down-regulation of NFATc1 [206], thus suggesting cross-talk between NFATc1 and NF-κB in RANKL-dependent osteoclastogenesis (Fig. 1d). TRAF6 actively participates in the signal transduction induced by the TNFR superfamily [18, 39] (Fig. 1) and thus represents a strategic therapeutic target of osteolytic pathologies. In this context, therapeutic use of antagonist peptides of RANK-TRAF6 interactions has been also envisaged [207].

Therapeutic targeting of OPG/RANK/RANKL interactions and signaling holds great promise for the treatment of malignant osteolysis (primary bone tumors, bone metastasis) and in inflammation-associated bone diseases (e.g. rheumatoid arthritis, prosthesis loosening). In the near future, additional studies

are required to validate these therapies in pre-clinical models and to determine their clinical safety and efficacy.

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