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Introduction
Loss of bone and muscle mass and strength (i.e., osteoporosis and sarcopenia) often occurs concomitantly with aging, thereby increasing the risk of fragility fractures (1–3). Whereas several drugs are approved for the treatment of osteoporosis, so far no therapy has been demonstrated to exert sufficiently positive effects on muscle to be approved for the treatment of sarcopenia (4). Hence there is a need to better understand the molecular pathways involved in the loss of muscle mass and function and their potential relationship with osteoporosis, to eventually identify novel molecular targets for the treatment of sarcopenia.

Increased expression of receptor activator of nuclear factor kappa-B ligand (RANKL) in postmenopausal women plays a central role in the development of osteoporosis (5). The binding of RANKL to its cognate receptor (RANK) leads to a cascade of signaling events triggering differentiation, activity, and survival of osteoclasts (6). Osteoprotegerin (OPG) is a soluble decoy receptor that binds to RANKL, preventing its interaction with RANK and thus restraining osteoclastogenesis and preventing bone loss (7, 8). In turn, a monoclonal antibody targeting RANKL, denosumab (Dmab), has been shown to reduce fracture risk and is broadly used to treat osteoporosis (9). Interestingly, the rate of falls was also lower in subjects receiving Dmab compared with placebo, but this observation remains without a pathophysiological explanation (10, 11).

RANK is also expressed in skeletal muscle and activation of the NF-κB pathway mainly inhibits myogenic differentiation, which leads to skeletal muscle dysfunction and loss (12, 13). In turn, OPG-Fc has been shown to reduce inflammation, restore the integrity, and improve the function of dystrophic muscles in a mouse model of Duchenne’s muscular dystrophy (mdx mice) (14, 15). In this model, RANK/RANKL/OPG controls calcium mobilization and the apoptotic and inflammatory processes (14, 15).

Finally, another key function of the RANK/RANKL/OPG pathway is the regulation of glucose homeostasis. Blocking RANK activity in mouse liver protects against diet-induced glucose intolerance. On the contrary, direct stimulation of NF-κB pathway in primary hepatocytes exposed to RANKL triggers an upregulation of proinflammatory genes and Kupfer cell activation, both known to generate hepatic insulin resistance and affect overall glucose homeostasis. In this context, 2 recent papers suggest that circulating levels of OPG could be markers not only of bone metabolism, but also of impaired glucose regulation (16, 17).

These observations led us to hypothesize that RANKL inhibitors could exert a positive influence on muscle mass and strength, particularly in conditions of osteoporosis and/or sarcopenia, and their effects mediated by glucose regulation in these cells. For this purpose we first examined lean mass changes in a group of postmenopausal women with osteoporosis treated with Dmab or bisphosphonates (BPs). Having observed that only Dmab pre-
vented the decline in lean mass and handgrip strength, we used transgenic mice expressing high copy numbers of human RANK that develop severe osteoporosis (18), as well as Pparb−/− mice that develop a combination of osteo/sarcopenia associated with an impairment of glucose homeostasis (19), to investigate the mechanisms by which the RANKL inhibitors Dmab and osteoprotegerin could improve muscle function.

Results

Denosumab improves muscle mass and strength in postmenopausal women with osteoporosis. As a proof-of-concept, we first analyzed the effects of Dmab in a group of postmenopausal women treated for osteoporosis for an average duration of 3 years, as compared with similar women without treatment or who received BPs. BPs include both alendronate and zoledrophosphonates (BPs, n = 20), denosumab (Dmab, n = 18). Statistical differences were assessed by a Kruskal-Wallis test. Bars show mean ± SD.

Dmab group but not in the other groups.

Effects of huRANKL overexpression on bone and muscle. We next investigated the effects of huRANKL overexpression on bone and muscle. In huRANKL transgenic mice, human RANKL expression levels were massively increased in bone and were approximately 5 times higher in the soleus compared with WT mice (Figure 2E).

As previously reported, huRANKL Tg+ mice of both sexes exhibited a severely decreased trabecular and cortical bone volume (Figure 3, A and B).

Lower maximal speed and limb force in huRANKL Tg+ compared with WT mice remained a trend only after normalization by gastrocnemius mass, arguing that decrease in functional parameters were mainly explained by muscle mass (Figure 3, C–G). At 4 months of age, the in vivo muscle volume in the limb was lower whereas fat infiltration between muscle groups was higher in huRANKL Tg+ compared with WT mice (Figure 3E). As previously reported, huRANKL Tg+ mice of both sexes exhibited a decreased muscle volume in the soleus (an oxidative muscle of predominantly type I fibers) than in gastrocnemius (a mix of type I and II fibers) (Figure 2, C and D).

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Figure 1. Bone mineral density, appendicular lean mass, and handgrip of postmenopausal osteoporotic women before and after 3 years of BP or Dmab treatment. (A) Delta lumbar spine bone mineral density (ΔL5 BMD). (B) Appendicular lean mass (ΔALN). (C) Delta handgrip. Control (n = 55), bisphosphonates (BPs, n = 20), denosumab (Dmab, n = 18). Statistical differences were assessed by a Kruskal-Wallis test. Bars show mean ± SD.
huRANKL Tg+ mice showed nonsignificant differences in the number and area of the islets as well as in insulin secretion (Supplemental Figure 2, F–H). At the muscular level, glucose uptake evaluated after 2-[14C] deoxyglucose administration was lower in the soleus of huRANKL Tg+ versus WT mice (Figure 3P). In contrast, glucose uptake was increased in the femur of huRANKL Tg+ mice versus WT mice, probably due to the high bone remodeling levels induced by RANKL.

Figure 2. Distribution of RANK and RANKL in tissue. (A and B) Relative mRNA gene expression of Rankl and Rank in 4-week-old mice (n = 12–18). Soleus, Sol; intestine, Int; white adipose tissue, WAT; gastrocnemius, Gas; brown adipose tissue, BAT. (C) Immunohistochemical staining of Dapi, RANK, and RANKL in gastrocnemius and soleus. Scale bars: 50 μm. (D) Western blot of RANK and RANKL in gastrocnemius and soleus. Bars show mean ± SEM. (E) Relative mRNA gene expression of human Rankl in WT (square) and huRANKL Tg+ (circle). **P < 0.01, ***P < 0.001 significant difference versus WT. Statistical differences were assessed by 1-way ANOVA.
Figure 3. Bone, muscle, and glucose phenotype of huRANKLTg+ mice. (A and B) Trabecular bone volume on tissue volume (BV/TV) at the distal femur and cortical bone volume (Ct.BV) at midshaft femur (n = 8 per group). (C) Absolute value of maximal speed evaluated on treadmill. (D) Maximal speed normalized by gastrocnemius mass. (E) Limb force evaluated by handgrip (n = 8 per group). (F) Limb force normalized by gastrocnemius mass. (G) Female skeletal muscle weight normalized by body weight (BW). (H–J) Skeletal muscle volume of the limb and fat infiltration evaluated by in vivo microCT. The red box in H indicates the region of interest, and the arrow points to the fat infiltration, which appears black in comparison to the surrounding muscle, which is grey. (K) Movement record in metabolic cages during 2 consecutive days and nights (n = 6 per group). Ambulatory, displacement activity; fine, activity without any ground displacement. (L) H&E and succinate dehydrogenase staining on sections of soleus. Arrows indicate mononucleated inflammatory cells and central necrosis of the myofibers which are indicators of necrosis (n = 6 per group with 2 sections per animal). Scale bar: 50 μm. (M) Relative mRNA gene expression in soleus (n = 4 per group). (N) Inflammatory cytokines in gastrocnemius and soleus muscle. (O) ITT AUC (n = 6 per group). (P) Tissue-specific 2-[14C] deoxyglucose (2DG-P) in brown adipose tissue (BAT), soleus (Sol), extensor digitorum longus (Edl), gastrocnemius (Gas), and inguinal WAT (Wati) of huRANKLTg+ mice (n = 6 per group). Statistical differences were assessed by 1-way ANOVA.*P < 0.05, **P < 0.01, ***P < 0.001 significant difference versus WT. Bars show mean ± SEM. Closed bars, huRANKLTg+; open bars, WT.
In summary, overexpression of RANKL decreased muscle mass, force, and glucose uptake associated with an upregulation of antimyogenic and inflammatory genes.

**RANKL induces insulin resistance in muscle cells through NF-kB signaling.** To further evaluate the mechanism by which RANKL could affect glucose utilization in muscle specifically, we measured insulin receptor (IR) and AKT phosphorylation, which have been widely used as measures of insulin action, in C2C12 myotubes chronically exposed to RANKL or insulin (model of insulin resistance).

Acute insulin exposure increased phosphorylation of AKTser473 (i.e., a key node in insulin signaling propagation) and phospho-IRS1 on Ser318, known to prevent insulin receptor 1 activation. Chronic exposure to RANKL did not change the AKTser473 response to insulin but increased phosphorylation of IRS1 on Ser318. OPG-Fc had the opposite effect, namely it decreased the phosphorylation of IRS1 on Ser318, known to prevent insulin receptor 1 activation - a key protein involved in NF-κB signaling represented by phospho-IRS1 on Ser318 in response to TNF-α (20), we tested if it was also true in response to RANKL. In cell cultures exposed to acute insulin, OPG-Fc reversed the effects of chronic RANKL by blocking NF-κB signaling represented by the decreased mRNA expression of Fos, Jun, NFAT, and Ptp-RG, without any effect on apoptotic markers (Casp 3, Bcl2) or calcium signaling (Syk; Figure 4B). Most importantly, chronic RANKL exposure increased glucose levels in the medium, and OPG-Fc reversed this effect (Figure 4C), consistent with a reactivation of the insulin signaling pathway by OPG.

In the gold standard model of insulin resistance (i.e., upon chronic insulin exposure), the expression of RANK-RANKL in C2C12 cells, as assessed by immunostaining, was increased (Supplemental Figure 3C). In turn, AKT Ser473 phosphorylation in response to an acute bolus of insulin was blunted (Figure 4D). OPG-Fc treatment in the last 2 days was sufficient to partially restore AKT phosphorylation in these conditions (Figure 4D and Supplemental Figure 3, D and E). In addition, in these conditions and similar to the observations above, OPG-Fc limited the phosphorylation of IR-Ser318, thereby improving insulin receptor activation. In accordance, after an acute exposure to insulin, chronic insulin exposure plus OPG-Fc increased Glut-1, Glut-4, and Fabp4 gene expression versus chronic insulin exposure alone. In addition, it decreased markers of inflammation and stress such Tnfα, Ccl5, and Fgf21, as well as Ptp-RG, a key protein involved in NF-κB signaling, which was overexpressed under chronic insulin treatment (Figure 4E). Last, as expected under chronic insulin exposure, glucose levels in the medium were higher than in the controls. Addition of OPG-Fc significantly decreased glucose levels (Figure 4F).

It is important to note that the effects of OPG-Fc were only observed upon chronic exposure to RANKL or insulin, and not in their absence. This observation indicates that a certain level of RANKL and/or insulin resistance is required in order to see a significant impact of OPG-Fc on insulin sensitivity.

**RANKL inhibitors restore muscle function and glucose utilization in huRANKL mice.** Having established that RANKL impairs muscle functions and glucose uptake, and that OPG improves insulin signaling in C2C12 myotubes, we further examined the effects of RANKL inhibitors on muscle functions in mice in vivo. As expected, OPG-Fc restored cortical bone volume by decreasing bone remodeling in huRANKL mice (Supplemental Figure 4, A and B). OPG-Fc increased gastrocnemius mass, maximal force of the limb, and maximal speed compared with huRANKLtg vehicle (increased by 9%, 21%, 44%, respectively, all \( P < 0.05 \); Figure 5A).

![Figure 4](https://example.com/figure4.png)

**Figure 4.** In C2C12 cell line, OPG-Fc decreased insulin resistant, inflammation, and glucose levels in the medium in a model of chronic RANKL and insulin. (A–C) C2C12 cell culture after differentiation into myotube and under a chronic exposure to RANKL with or without OPG-Fc and in response to an acute exposure to insulin. (A) Western blot \( n = 3 \). (B) Relative mRNA gene expression \( n = 6 \). (C) Glucose levels in medium \( n = 6 \). (D–F) C2C12 cell culture after differentiation into myotube and under a chronic exposure to insulin with or without OPG-Fc and in response to an acute exposure to insulin. (D) Western blot \( n = 6 \). (E) Relative mRNA gene expression \( n = 6 \). (F) Glucose levels in medium \( n = 6 \).
of the limb and maximal speed differences between OPG-Fc and controls were no more significant (Figure 5, B and C), arguing that the restoration of functional parameters was proportional to, and explained by, the improvement in muscle mass. Limb temperature of huRANKL Tg+ was improved by OPG-Fc, suggesting a rescue of muscle energy expenditure (Supplemental Figure 4C). In accordance, both in soleus and gastrocnemius, the uptake of 2-[14C] deoxyglucose was increased in response to OPG-Fc (Figure 5D) whereas no effect was seen in iWAT (Figure 5D). Gene expression analysis showed an increase in markers of fatty acid (FA) oxidation and muscle fiber type I and II, as indicated by an upregulation of Ppara, Myh1, and Myh2 and a decrease in myostatin and Ptp-RG in response to OPG-Fc, which is consistent with the changes observed in C2C12 in vitro (Supplemental Figure 4D).

Accordingly, circulating levels of myostatin were reduced upon OPG-Fc treatment (Supplemental Figure 4E), and insulin resistance evaluated by an ITT was abolished (Figure 5E). Again, most of the effects of OPG-Fc seen in huRANKLTg+ on bone structure and muscle function were not observed in WT mice, confirming that high levels of RANKL expression are both necessary and sufficient to induce muscle dysfunction.

Since OPG-Fc can have non-RANKL-mediated activities, such as antiapoptotic effects through Trail, we next treated the huRANKLTg+ mice with the selective RANKL antibody Dmab. As expected, Dmab increased trabecular and cortical bone volume in these mice and decreased bone remodeling (Supplemental Figure 4, F–H, and Supplemental Tables 2 and 3). Dmab increased gastrocnemius and soleus mass, maximal force of the limb, and

Figure 5. Muscle and glucose phenotype of huRANKLTg+ mice treated by OPG-Fc or Dmab. (A, F) Muscle mass normalized by body weight BW, n = 8 per group. (B, G) Limb force evaluated by handgrip normalized by gastrocnemius mass. (C, H) Maximal speed evaluated on treadmill normalized by gastrocnemius mass. (D, I) Tissue specific 2-[14C] deoxyglucose (2DG-P) in soleus (Sol), extensor digitorum longus (Edl), gastrocnemius (Gas), and inguinal white adipose tissue (Wati) (n = 6 per group). (E, J) ITT AUC (n = 8 per group). The differences in control values from panels A–E to respectively F–J are due to studies separated in time by 1 year. Statistical differences were assessed by 2-way ANOVA (genotype and treatment). †P < 0.05, ‡P < 0.01, §P < 0.001 significant difference between Tg and WT. Bars show mean ± SEM.
maximal speed compared with huRANKLTg+ vehicle (increased by 16%, 10%, 18%, and 33%, respectively, all P < 0.05; Figure 5F).

Dmab effects on maximal speed remained significant after adjustment by gastrocnemius mass (Figure 5, G and H), which would be consistent with an additional improvement in muscle metabolism (i.e., glucose uptake) independently of muscle mass. Spontaneous movement of the mice (more specifically, fine movement) was also increased in Dmab-treated mice (Supplemental Figure 4I). Moreover, as with OPG-Fc, Dmab abolished the systemic insulin resistance observed in huRANKLTg+ mice evaluated by ITT (Figure 5J).

Figure 6. Bone, muscle, and glucose phenotype of Pparb−/− mice treated by OPG-Fc. (A and B) Skeletal muscle volume of the limb and fat infiltration in muscle evaluated by in vivo microCT. (C) Maximal speed evaluated on treadmill normalized by gastrocnemius mass. (D) Limb force evaluated by handgrip normalized by gastrocnemius mass (n = 8 per group). (E) Body temperature evaluated by infrared camera (n = 8 per group). (F) Muscle fiber type, number, and area. Note the type I fibers in blue dark and type II fibers in light blue. (G) ITT AUC (n = 8 per group). (H) GTT. (I) Relative protein expression in the gastrocnemius. Hatch marks correspond to mice that have received an acute injection of insulin. (J) Relative mRNA expression in soleus. (K) Relative mRNA expression of Nfkb signaling in soleus (n = 6 per group). Statistical differences were assessed by 1-way ANOVA. †P < 0.05, ‡P < 0.01, §P < 0.001 significant difference versus WT. Bars show mean ± SEM.
Gastrocnemius and soleus weights were higher under Dmab versus vehicle (increased by 9.3% and 12%, respectively, P < 0.05; Figure 5H). 2-[¹⁴C] deoxyglucose administration showed a higher glucose uptake in huRANKLtg soleus and gastrocnemius treated by Dmab compared with vehicle (Figure 5I). Inversely, in the femur, the uptake was reduced by Dmab compared with vehicle, consistent with decreased bone remodeling. In accordance with the 2-[¹⁴C] muscle uptake, the drop in the temperature of the limb observed in huRANKLtg mice was rescued by Dmab (Supplemental Figure 4J). Western blot analysis indicated that the positive effects of Dmab on insulin signaling appear in the soleus but not in the gastrocnemius (Supplemental Figure 4, K and L). Last, in huRANKLtg mice, succinate dehydrogenases staining indicated that Dmab switched type II fibers to type I and increased the fiber area of both type I and II fibers to levels similar to WT mice (Supplemental Figure 5), without significant changes in the number of fibers per section of muscle. Distribution of type I and II fibers were confirmed by immunohistochemistry (Supplemental Figure 6).

OPG-Fc restores muscle dysfunction and insulin resistance in osteo-sarcopenic Pparb−/− mice. To determine whether the RANKL-RANK pathway could also be involved in sarcopenia, we took advantage of the Pparb−/− mice previously reported to develop bone fragility, muscle weakness, and insulin resistance (Supplemental Table 4).

At 5 months of age, Pparb−/− mice displayed reduced muscle volume and force normalized by gastrocnemius mass (reduced by 19% and 14%, respectively, vs WT; Figure 6, A–D, all P < 0.05), associated with a lower limb temperature (reduced by 1.6% vs WT; Figure 6E, P < 0.05). Succinate dehydrogenase staining indicated lower number and area of type I fibers (Figure 6F). ITT and glucose tolerance test (GTT) AUC were both higher in Pparb−/− mice, increased by 8% and 38%, respectively, versus WT mice (Figure 6, G and H, both P < 0.05). Western blot analysis confirmed an altered insulin response in muscles of Pparb−/− mice (Figure 6I). In the soleus, Glut1, Fabp4, Ccm1, CyclinD1, and Pdgfa gene expression were downregulated (reduced by 29%, 22%, 15%, 20%, and 7%, respectively, versus WT mice, all P < 0.05; Figure 6J), whereas markers of inflammation, myostatin / Fgf21, and Nfkb signaling, Jun/Nfat / Ptp-RG, were upregulated (increased by 33%, 172%, 30%, 14% and 19%, respectively, versus WT mice, all P < 0.05; Figure 6, J and K). OPG-Fc increased muscle volume (by 12% versus vehicle, P < 0.05) and tended to increase the force and temperature of the limb (by 6.7% and 1.8%, respectively, versus vehicle; Figure 6, A–E). OPG-Fc also decreased GTT and ITT AUC (by 36.7% and 22.3%, respectively, versus vehicle, P < 0.05; Figure 6, G–H), arguing for a restoration of systemic insulin sensitivity. Moreover, in soleus, gene expression of myosin I and II were increased whereas markers of inflammation myostatin and Fgf21 were decreased by OPG-Fc in association with a decreased in gene related to NF-κb signaling (Figure 6J).

Discussion

Bone and muscle loss leading to osteoporosis and sarcopenia, respectively, are common features of aging (2). Together, they contribute to frailty and the risk of fragility fractures. Although the central role of the RANK/RANKL/OPG system on bone metabolism has been elucidated (21), leading to the development of a monoclonal Ab against RANKL (Dmab) to treat osteoporosis (6), the concomitant reduction in falls (11) and potential influence of these molecules on muscle metabolism in the context of osteoporosis and/or sarcopenia remain unexplained. Although there were no significant differences on bone or muscle parameters in osteoporotic postmenopausal women treated with Dmab or BPs, only Dmab significantly improved muscle strength compared with no treatment. In mice, high levels of huRANKL expression not only induced bone loss but concomitantly impaired muscle structure, strength, and glucose uptake. These alterations are associated with increased expression of antmyogenic/inflammatory markers in muscle, namely myostatin and Ptp-RG. The latter has previously been reported to cause insulin resistance in relation to inflammation in the liver (22, 23). However, compared with some models of muscle dystrophy (24), inflammation is not severe and inflammatory cytokine expression is quite restricted in huRANKL mice, suggesting that it is not the main mechanism for muscle dysfunction in this model.

RANKL inhibitors such as OPG-Fc and Dmab corrected these abnormalities not only in huRANKL mice, but also in Pparb−/− osteo-sarcopenic mice, indicating that the RANKL-RANK system is ultimately involved in the development of muscle weakness irrespective of the triggering mechanism (i.e., whether directly mediated by increased RANKL or by deficiencies in more specific myogenic factors such as Pparb). Taken together with recent evidence that conditional knockout for RANK in muscle prevented denervation-induced muscle weakness (25), our data now establish that the RANK/RANKL/OPG system plays a key role in muscle metabolism and the development of sarcopenia.

The effects of RANKL inhibition on muscle are likely direct, since we confirmed that RANK and RANKL are expressed in skeletal muscles and particularly in oxidative muscles like the soleus (26). In WT and transgenic mice we showed that the soleus is the third tissue expressing the most RANKL and that high levels of RANKL expression are sufficient to induce muscular alterations and a lower glucose uptake in skeletal muscle. When we compared the effects of OPG-Fc (an inhibitor of both RANKL and TNF-related apoptosis-inducing ligand [TRAIL]) with Dmab (a selective RANKL inhibitor), both treatments rescued muscle weakness to similar levels, suggesting an action on muscle mainly mediated through RANK signaling rather than TRAIL.

Our findings somewhat contrast with a recent publication that shows the superiority of OPG-Fc treatment to monoclonal anti-RANKL, anti-TRAIL, or muscle RANK deletion in improving dystrophic muscle function (27). However, our models of muscle weakness differ from the mdx mouse in that muscles were neither dystrophic nor markedly inflammatory in huRANKLtg nor Pparb−/− mice. Consistent with our data, improving glucose entry into muscle through insulin sensitivity has been shown to improve muscle strength in 2 different mouse models of aging and type 2 diabetes (Db/Db) (28, 29).

To better understand the influence of RANKL-RANK signaling on muscle cell metabolism, we investigated insulin signaling in C2C12-differentiated myotubes expressing both RANK and RANKL (15, 30). In these cells RANKL increased, whereas OPG decreased, the level of IRS1 Ser318 phosphorylation, which is known to downregulate insulin receptor activity,
whereas opposite effects were observed on AKTser 473, which is a major activator of the IRS1. This was observed under both chronic RANKL and insulin exposure. Hence, these favorable effects of OPG on insulin receptor signaling were confirmed in vivo in both huRANKL+ and Pparb−/− mice as suggested by the better ITT curves (31). In fat, TNF-α-induced inflammation was previously shown to attenuate IRS1 ability to transduce insulin signals, by the activation of IkB kinase β/NF-κB pathway (20, 32). More recently, protein tyrosine phosphatase receptor gamma (PTP-RG) has been highlighted as an important link between inflammation and insulin resistance in the liver. Here, we show that this link is also true in muscle where Ptp-RG is increased by RANKL, respectively decreased by OPG-Fc in C2C12 myotubes, and similarly decreased by Dmab in the soleus of huRANKL+ mice (23). Hence, RANKL induces insulin signaling resistance, leading to poor glucose entry, and in parallel induces a limited expression of inflammatory markers (such as Ptp-RG and Tnfalpha) that could then contribute further to decreased glucose uptake and muscle dysfunction (20, 32). Changes in glucose uptake in skeletal muscle have been previously described (31) to lower contractile properties and muscle performance. In muscle-specific inducible Rac1 knockout mice for instance, 2-[3H] deoxyglucose uptake is blocked in soleus muscle and decreased by 80% and 60% in gastrocnemius and tibialis anterior muscles, respectively. One of the consequences is a significant reduction in maximal running speed (31).

In humans, beneficial effects of Dmab on skeletal muscle function have previously been suggested in rare cases of muscular dystrophy (33). We have now extended this observation to more common osteoporotic subjects with muscle weakness, in which Dmab prevented the decrease in appendicular lean mass and grip strength over 3 years. Of note, the improvement of muscle function with Dmab was tightly correlated with BMD gains, whereas no correlation was present with BPs. These observations, although preliminary, seem to indicate that the improvement in muscle function with RANKL inhibitors occurs in parallel, but is not a consequence of the decrease in bone turnover achieved with bone antiresorptives. This argues for a specific positive action of Dmab on muscles, which could contribute to the 21% reduction of falls previously observed in the FREEDOM trials (11).

There are limitations to our study. First, we used physiologically relevant and not muscle-specific transgenic mice overexpressing RANKL. Hence, we cannot exclude that the improvement of systemic glucose metabolism, notably through the liver (34), and neuronal or behavioral changes could also contribute to improved muscle function and particularly running speeds. However, the expression of RANK in C2C12 and the bulk of in vitro results indicating that OPG-Fc restores insulin receptor signaling, glucose uptake, and gene expression in these cells, argues for a direct impact of RANKL inhibitors on muscle cells. Second, the test used for evaluation of maximal speed on the treadmill exhibited a higher variability than the other test because fatigue of the mice was based on subjective operator appreciation, and fatigue depends of several environmental factors. However, these results remain in accordance with the variability of similar tests in humans (coefficient of variation = 25%) (35). Third, the number of human subjects treated by Dmab was limited, and these subjects were not recruited on the base of sarcopenia. Hence, a real prospective trial is necessary to definitely establish the potential efficacy of Dmab on muscle mass and function.

In summary, the RANK/RANKL/OPG system plays a key role not only in bone but also in muscle metabolism. Altogether, our data point to a potentially new mechanism relating RANKL expression to fracture risk, not only by decreasing bone, but also muscle strength. This work opens a whole new opportunity to further investigate the potential benefits of RANKL inhibitors in the treatment of sarcopenia and frailty.

Methods

In vivo experiment in mice. Osteoporotic huRANKL+ mice (Tg5519 lines) expressing huRANKL were previously described (18). For adult phenotype description, OPG-Fc (truncated OPG-Fc with RANKL domains only), and Dmab treatment experiments, see the Supplemental Material and Methods. Microcomputed tomography scans, hyperinsulinemic-euglycemic clamp, 2-[14C] deoxyglucose uptake, metabolic cage, positron emission tomography–computed tomography, histomorphometry, immunohistochemistry, multiplex ELISA, real-time PCR, Western blotting, and mechanical resistance of mouse femur were performed as described (36–38).

Cell culture. C2C12 myoblasts were cultured in growth medium (DMEM, 4.5 g/L glucose, 1% penicillin-streptomycin) supplemented with 10% FBS. Differentiation into myotubes was initiated by replacing growth medium by a differentiation medium (DMEM, 4.5 g/L glucose, 1% penicillin-streptomycin supplemented with 2% horse serum) when cells reached 80% confluence. For Western blot details, see the Supplemental Material and Methods.

Clinical investigation. Eighteen postmenopausal women (mean age 65.0 ± 1.5 years) treated for osteoporosis with Dmab and 20 women treated by BPs (alendronate n = 8, zoledronate n = 12; mean age 65.7 ± 0.9 years) were evaluated by DXA for body composition and for strength by handgrip before treatment and after 2.9 years (range 2.2–3.7 years) of follow-up as described (39–41). They were matched for analyses to 55 controls for age (mean age 65.0 ± 1.4 years), BMI, BMD, and fracture from the Geneva retired workers cohort (GERICO) (41).

Statistics. We tested the effects of genotype and treatment by a 1- or 2-way ANOVA. As appropriate, post hoc testing was performed using Fisher’s Protected Least Squares Difference (PLSD). The effects of treatment in postmenopausal women was analyzed by a Kruskal-Wallis test. Differences were considered significant at P < 0.05. Data are presented as mean ± SEM.

Study approval. All animal procedures were approved and carried out in strict accordance with the guidelines of the Institutional Animal Care and Use Committee and the canton of Geneva. Geneva Retirees Cohort protocol received the approval from the Geneva University Hospitals’ Ethics Committee (GERICO, http://www.isrctn.com/ISRCTN1186958), and all participants provided written informed consent.

Author contributions

NB and SF conceived the study and acquired funding. NB and LB created the study methodology. LB, EB, and NB conducted the formal analysis and investigation. NB prepared the original draft of the manuscript. NB, LB, EB, ED, and SF reviewed and edited the manuscript. NB, SF, ED contributed resources to the study. NB supervised the study.
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