

## The bad relationship, osteo-decay and diabetes type 2 searching for a link: a literature review

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The diabetes and osteoporotic metabolic diseases are characterized by a wide prevalence of the population worldwide and correlated to alteration of the bone tissues. Several cofactors could influence the clinical course and the biochemistry of the pathologies such as human microbiome, nutrition characteristics, gut microbiota activity and interactions with vitamin K and D across IGF/GH and TP53 signaling pathways and the glucose/energy as mechanism for bone tissue health. Moreover, also the calories and sugar consumption seem to be correlated to an increased inflammatory state with several consequences for hematopoiesis and host tissues response. The aim of the present literature review was to highlight the role of osteoporotic diseases and diabetes type 2 link for the bone metabolism. The literature cases showed that a correlation between bone-gut-kidney-heart-CNS-Immunity crosstalk seems to be linked with bone metabolism and health regulation. Moreover, also the aging process could represent a valuable co-factor for the sustaining of the metabolic disorders upon a multi-systemic level.

Diabetes complications and osteoporotic fractures are two of the most important causes of morbidity and mortality in elderly patients and share many features including genetic susceptibility, molecular mechanisms, and environmental factors (1). Type 2 diabetes mellitus (DM2) compromises bone microarchitecture by inducing abnormal bone cell function and matrix structure, with increased osteoblast apoptosis, diminished osteoblast differentiation, and enhanced osteoclast-mediated bone resorption (2). The relation between these two metabolic types of disease has to be found within

three areas, the micro-molecular compartment of gut microbiota, at the energy regulatory level of intracellular compartment, at the mesenchymal stem cell (MSCs) differentiation apparatus to osteoblasts and, at the neuro-endocrine regulatory compartment of hormones and immune responses (4-6). Both glycemic and bone homeostasis mechanisms share the same regulatory factors and interface with the same signaling pathways. Despite the rapid progress in understanding the role of the different signaling pathways that links the skeleton homeostasis and diabetes insurgence doubts remain. For instance, it

*Key words: Diabetes type 1-2; metabolic syndrome; enteric nervous system; central nervous system; mesenchymal stem cells; bone marrow; mTOR; IGF-1-2 PT53; Wnt; Rank-l; receptor activator NF kappa B ligand (NFκB-RANK); osteoblasts; mitochondria; ATP; ROS; telomere/telomerase; ageing*

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is still unclear the signal inputs within the mTOR pathways and the corresponding mechanisms for activating mTORC1 versus mTORC2 and the effective role of PT53, secondly how this defection may compromise the regenerative mechanism which involves the activation of MSCs from BM.

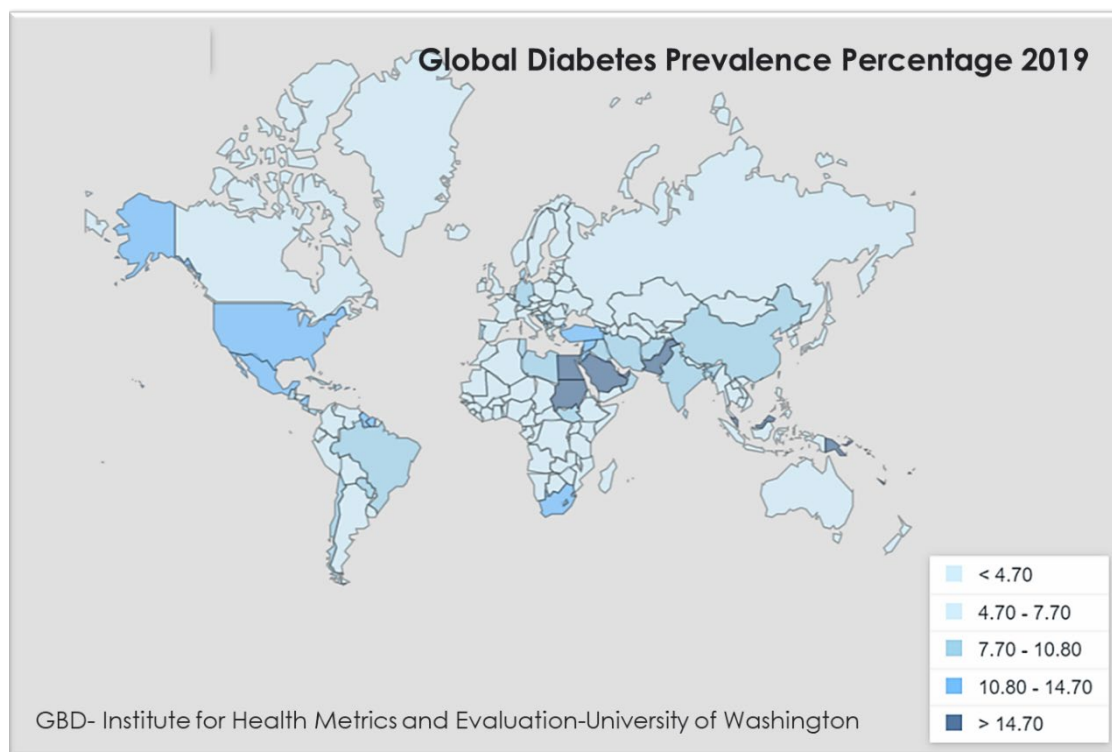
Current outcomes have confirmed the co-expression of multiple growth factors, proteins and hormones including Wnt, IGF1-2, and Bmp that may definitively play a role along the whole axis that links together gut, skeleton, and metabolism. Any disturbance of this mechanism may trigger a cascade that will negatively affect bone homeostasis, bone cell differentiation and bone remodeling process. The types of dysfunction may include changes in intracellular pH balance, the over-expression of ROS, the increase of pro-inflammatory signaling pathways, the accumulation of CO<sub>2</sub> and toxins within intracellular space and in tissue. The side-

effects may be also seen to affects the immune-endocrine-metabolic system at the level of central nervous system (CNS) and the enteric nervous system (ENS) of the gut. This small review's aim is to briefly explore the systemic impact of endocrine-metabolic dysfunctions in bone homeostasis decay and the gradual uprising of DM2, elucidating the key role of skeleton system in preserving health and regenerative process.

## DISCUSSION

### *Nutrition, human microbiome and metabolic syndrome*

During last few decades, in both Western and Eastern countries it has been experienced an exponential increase of non-communicable diseases, such as allergies, autoimmune disorders, and inflammatory conditions. The incidence of Diabetes for instance has reached an alarming



**Fig. 1.** The prevalence of diabetes worldwide in the 2019. The data were obtained by the Global Health Data electronic database (GBD Institute for Health Metrics and Evaluation-University of Washington) (3).

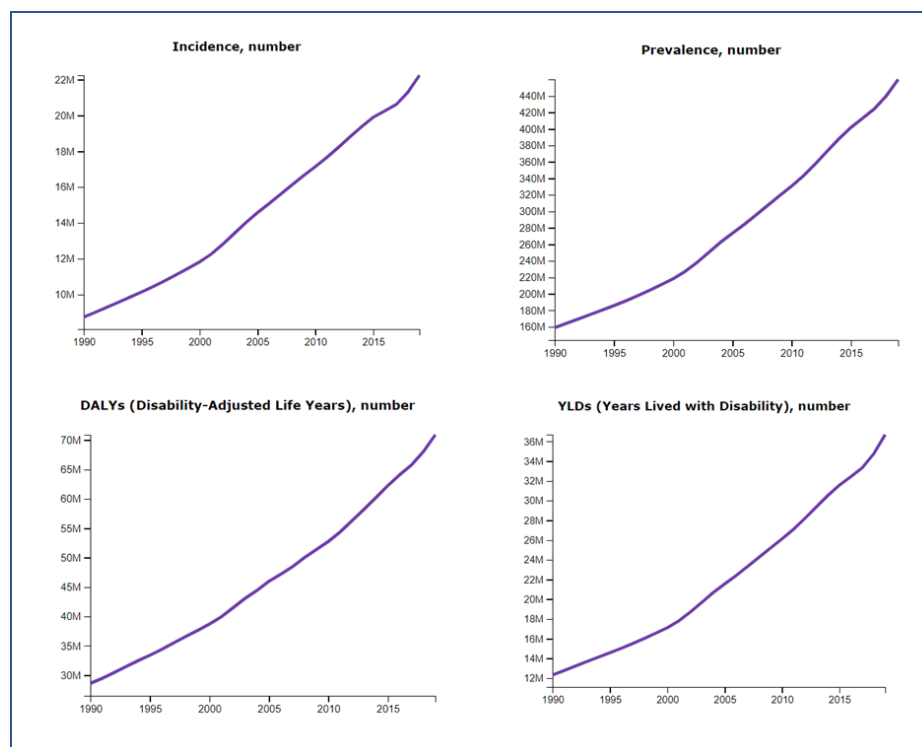
level and has become a major lifestyle metabolic disorder globally, in developing Asian countries it contributes to more than 60% of the world's diabetic population (Fig.1, 2) (7, 8).

Important data, mainly from nutrition science, stressed out the protecting effects of a balanced and uncontaminated diet versus the consequences of the ageing process inducing more regenerative responses. Findings have indicated that ageing and physiological decay are strictly correlated with weakening of the adult stem cell regeneration process as consequence of high industrial processed food intake (9).

Metabolic syndrome (MSy) is a consequence of the modern industrialized fatty/sugar food production that includes severe clinical complications such as dyslipidemia, hypertension, diabetes and dementia that share underlying common pathophysiological mechanisms. Unhealthy fat and toxins buildup predispose individuals to MSy, the long term presence

accumulation of adipose tissue may negatively affect the correct functionality of pituitary/hypothalamus system indirectly interfering with the normal relation within organs (10-14) resulting in clinical conditions such as metabolic syndrome, early atherosclerosis, dyslipidemia, hypertension and type 2 diabetes (T2D).

The core momentum has to be searched within the gut system. Simple chain refined carbohydrates and sugars are fermented by specific gut bacteria and are broken down into short-chain fatty acids (SCFAs), primarily acetate, propionate, and butyrate. The importance of SCFAs is based on their role in modulating the use of energy derived from the diet through the interaction G protein-coupled receptor 41-43 (GPR41-43) with special entero-endocrine cells that are in charge of inducing the secretion of peptide YY (PYY) that in turn enables food transit in the intestines. The special commitment of GPR43 is characterized by the activation of the glucagon-like peptide 1 (GLP-1) essential in the constant insulin



**Fig. 2.** The incidence, prevalence, DALYs (disability-adjusted life years) and YLDs (Years Lived with disability) of diabetes worldwide in the 2019. The data were obtained by the Global Health Data electronic database (GBD Institute for Health Metrics and Evaluation-University of Washington) (3).

sensitivity. The gut microbiota work based on a finely coordination between leptin, insulin hypothalamus hormone axis and, by this way can regulate the fasting-induced adipose factor (Fiaf) expression in the ileum, a key factor in blocking the lipoprotein lipase (LPL) for fat storage in white adipose tissue to prevent excessive fat accumulation. The SCFAs also activate the intestinal gluconeogenesis (IGN mechanism) via the ENS pathway improving the glucose metabolism decisive in the satiety level mechanism (15-20).

*Stem cells/osteoblast disrupted differentiation pathway in DM II: the role of dysbiosis*

The dysfunction of gut microbiome generates an event known as dysbiosis, a condition characterized by the abnormal balance between all different constituents of the gut micro-flora which predisposes an over accumulation of humus of indigested starches and sugars in the intestinal epithelium (21) dental stem cells from apical papilla (SCAPs). In the medium, long term, this accumulation leads to the intensification of methane, hydrogen, and nitrogen gases with a consequent inhibitory effect on the local compensatory/regulatory mechanism. The main relevant end-point is seen with the upsurge of both fermenting bacteria and the increase of pH acid level that favor uncontrolled auto-immune responses and the uprising of a systemic chronic inflammatory state (15-19).

Though apparently may seem incongruous, the connection diabetes/bone degeneration should be seen in the gut subverted environment otherwise known as “diabetic stem cell mobilopathy” and “diabetes induced bone marrow micro-angiopathy”, conditions which indicate impairments of the stem cell differentiation and mobilization mechanisms (22-26) and their cell surface marker profiles change during the process of mobilization and maturation. Hence, a generally accepted marker combination and a standardized protocol for the quantification of EPCs remain to be established. To determine the EPC subsets that are affected by diabetes, we comprehensively analyzed 32 surface marker combinations of mouse peripheral blood (PB). The reduced availability of circulating stem cells and downregulation of both osteoblast and endothelial progenitor cells (EPCs) caused by hyperglycemia and the oxidative stress together with consistent acidic

pH microenvironment are among the several causes accountable for the occurrence of endothelial dysfunction in cardiovascular disease and bone decay in diabetic patients (25, 27-29) and their cell surface marker profiles change during the process of mobilization and maturation. Hence, a generally accepted marker combination and a standardized protocol for the quantification of EPCs remain to be established. To determine the EPC subsets that are affected by diabetes, we comprehensively analyzed 32 surface marker combinations of mouse peripheral blood (PB).

More specific, chronic gut dysbiosis is characterized by local physiological alteration due to uncontrolled increase of different types of bacteria such as the Firmicutes, Staphylococcus, Enterobacteriaceae and E coli, changes that are clinically confirmed in patients diagnosed with gut inflammatory disease like Crohn's disease and ulcerative colitis who also are affected by osteoporosis and osteopenia (30, 31).

*Hormones, bones and diabetes*

Molecularly, one of the mechanisms involved may be related to deficits incurred in the RANKL (receptor activator NF kappa B ligand NFκB-RANK), osteocalcin (OCN), osteoprotegerin (OPG) and, the immunoreceptor tyrosine-based activation motif (ITAM) system. Noteworthy, the RANKL, OPG and ITAM are members of the TNF super-family and share the same signaling pathway of androgen hormones (32).

The activation in mononuclear cells of NFκB which coordinates the transcription of IL-1, IL-6, IL-8, and other peptides increase important inflammatory responses up-regulating viciously the expression of pro-inflammatory genes such as TNF-α, adhesion molecules, and different chemokines generating a consistent and perturbing inflammatory state typical of metabolic related disorders (33-35).

A further co-related effect linked to these disturbances is the inhibitory effect on the hypothalamus/pituitary/adrenal axis with a further and progressive decay of testosterone, estrogen and progesterone and the augmentation of pro-inflammatory factors such as TNFα. However, deficits in testosterone levels are common in men with Type

2 diabetes. Such men are characterized by normal gonadotropin responses to gonadotropin-releasing hormone stimulation (24-26).

It is interesting to note how the frequency of androgen deficiency in male patients with MSy and DM2 has been seen more than a simple coincidence, the outcomes showed how this association is in real much higher than that in the normal population. Data found that the prevalence low testosterone levels in DM2 reached almost 40% either Europe or China (36-38).

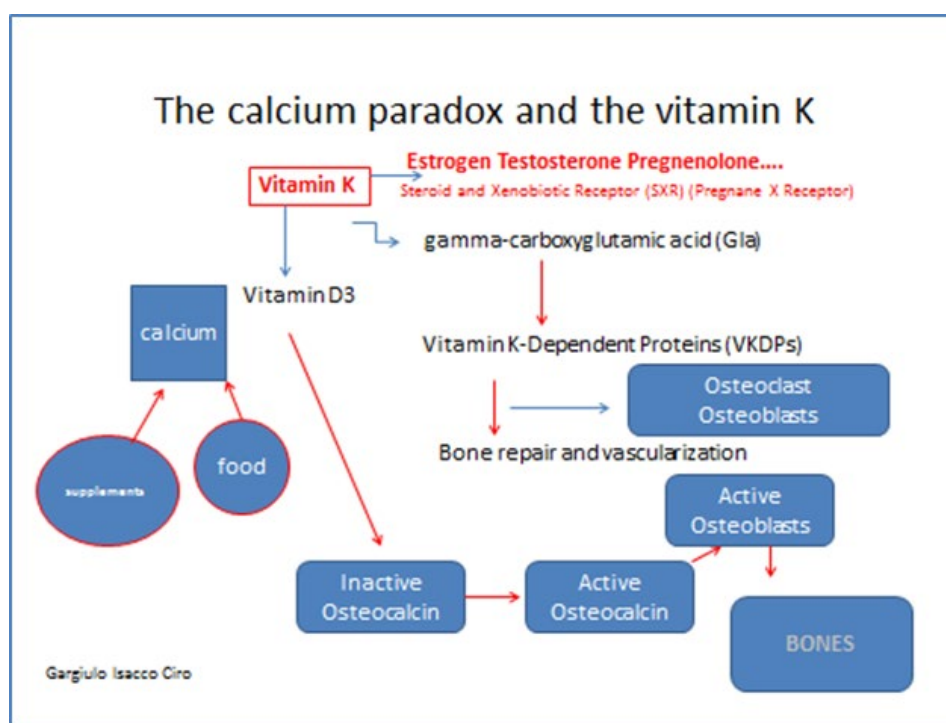
Granim and colleagues recently showed that following testosterone treatment it was noted a substantial increase in serum OCN concentrations, they endpoint showed the change from baseline in OCN at week 23 of the study group significantly higher than the placebo group [mean change (95% CI), 3.52 [0.45, 6.59],  $P = 0.008$ ] (37).

Of note in this situation the OPG is concomitantly down regulated that in turn induces an uncontrolled osteoclast hyper-activity. The OPG which main activity is the modulatory activity of the osteoclastogenesis via RANK pathway is expressed primarily by BM stromal

MSCs whilst can be activated in B lymphocytes, follicular DCs, and could be regulated positively by TGF- $\beta$ , IL-1, TNF, estrogen, Wnt ligands and negatively regulated by prostaglandin E2 (PGE2) and glucocorticoids. At this point it is essential to remark that the progressive decrease of testosterone, estrogen and progesterone witnessed in diabetic individuals reveals a complex situation. A scenario characterized by a compromised regenerative process of MSCs within the BM niches concomitant to an elevated systemic inflammatory state on one hand and, a skeleton system steady decay related to the decline of both OPG and OCN functionality, on the other hand (39-41).

#### *Gut microbiota, calcium absorption and the role of vitamin K and D*

Diabetes type 2, vascular calcification and osteoporosis involve the same degenerative mechanisms all related to gut dysbiosis in which the synthesis of important molecules such as the vitamin K provokes deep homeostatic deteriorations. The vitamin K deficiency triggers the so called “calcium



**Fig 3.** The important role of Vitamin K in formation of bone and osteoblasts activation and regulating bone homeostasis (Gargiulo Isacco Ciro).

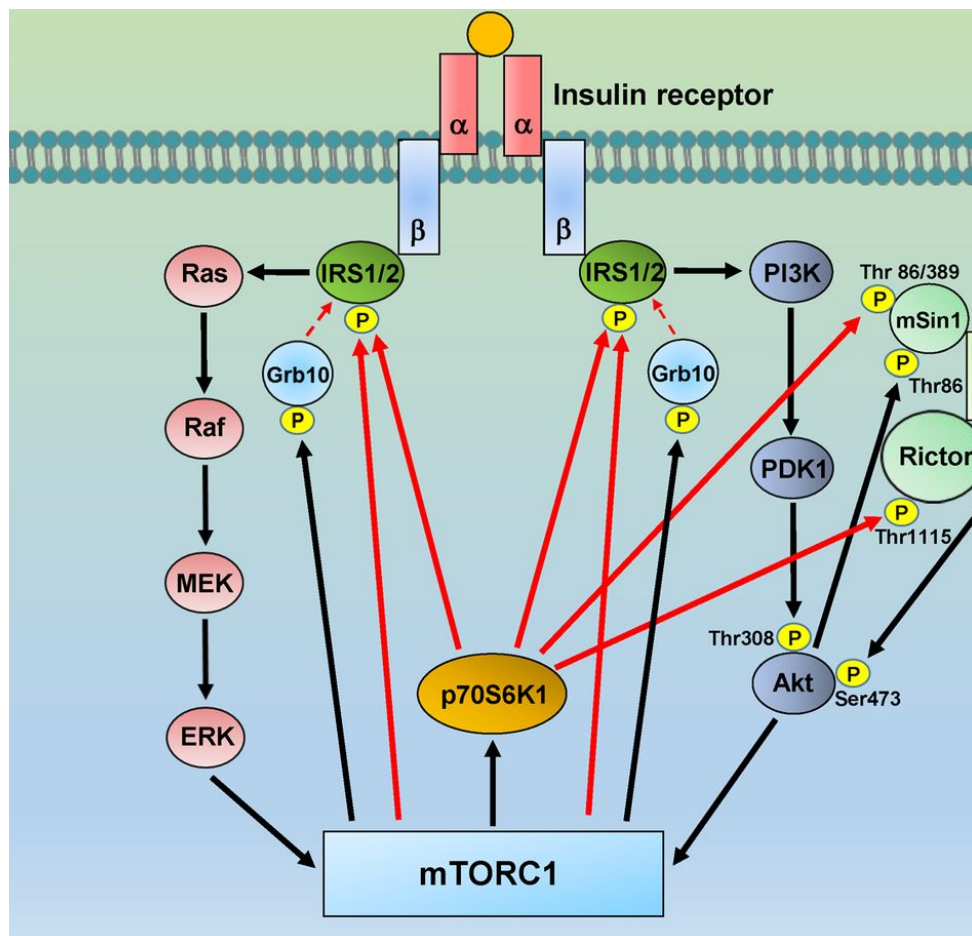


paradox", that is contradistinguished by the lack of calcium in the bone and its ectopic deposit in different location other the skeleton such as, the vessel walls, bone surfaces (osteophytes) and joints (42-49).

The role of vitamin K in bone formation and bone homeostasis has been for long time neglected, Vitamin K participates as coenzyme for the gamma-Glutamyl Carboxylase (GGCX) enzyme formation inside the endoplasmic reticulum that catalyzes the carboxylation of glutamic acid residues (Glu), which in turns once converted into gamma-carboxyglutamic acid (Gla) enhances the activity of Vitamin K-Dependent Proteins (VKDPs). The importance of VKDPs is their involvement in the vascular and bone tissue repair mainly thanks to the activity of the bone Gla protein and osteocalcin (50,51).

Of note, the Warfarin anti-coagulant use in patients with cardio vascular diseases (CVD) acts as a Vitamin K antagonist in preventing vitamin K activity by inhibiting two vitamin K correlate enzymes, the epoxide reductase (VKOR) and vitamin K quinone reductase; the long term usage of Warfarin showed evident decay of bone tissue and of note, the VKOR subunit 1(VKORC1) has been also used as a marker for bone degenerative condition (52-55).

The strategic function of VKORC1 as main oxidoreductase enzyme is to allow the absorption of vitamin K quinone by dietary uptake reducing it into the hydroquinone (KH<sub>2</sub>) form, allowing the entry of vitamin K into the whole vitamin K cycle (55,56). The following steps lead to oxidation of vitamin K hydroquinone to vitamin K 2,3-epoxide (K<sub>2</sub>O) mechanism that takes



**Fig. 4.** The inhibition of IRS under hyper-activation of mTORC1 due to high energy diet such as sugars and refined carbs. The p70S6K plays a pivotal role in inhibiting the IRS that loses its capability of glucose transporters transferring to the cell surface (69).

place in the post-translational activation of vitamin K-dependent (VKD) phase where are involved proteins in charge of the enzymatic conversion of Glu residues into  $\gamma$ -carboxyglutamate (Gla) residues. The VKORC1 is in charge conclude the cycle by reducing the K<sup>+</sup>O to K and KH<sub>2</sub>, to ensure the efficient reuptake of vitamin to lead the necessary following sequences of  $\gamma$ -glutamyl carboxylation (57,58).

Vitamin K may act as ligand of the nuclear receptor for Steroid and Xenobiotic Receptor (SXR) (Pregnane X Receptor, PXR, murine homolog). Kato and colleagues showed that SXR/PXRs are expressed in osteoblasts and it is activated by vitamin K that in turns up-regulate gene expression such as tsukushi (Tsk), matrilin-2 (Matn2) and CD14 involved in bone morphogenetic and formation (Fig. 3).

The Tsk gene was showed to be important in collagen-accumulating mechanism, the Matn2 is involved in formation of extracellular matrix like collagen, whereas CD14 controls both osteoblast and osteoclast producing mode through B lymphocyte differentiation mechanism, indicating the SXR/PXR-vitamin K mechanism as key regulator of bone homeostasis (56,59,60).

In addition, vitamin K, and specifically K<sub>2</sub> in its form of menaquinone 4 and 7 (MK 4-7) were confirmed to inhibit osteoclastic bone resorption, by suppression of RANKL expression (61-67).

#### *The pathway of cell energy consumption, the metabolic role of mTORC1 in insulin resistance*

The bone system in mammalian plays a crucial role regulating the whole homeostasis of the body and maintains the pH alkaline/acid of organs, tissues and cells. As mentioned above, in diabetic individuals the bone regenerative mechanism and homeostasis is generally compromised following a chronic accumulation of toxic oxidative derivatives within the intracellular compartment such as the advanced glycation end-products [AGEs] that contribute to bone fragility and tissue deterioration. This activity is mainly based on two molecules, the mTORC1 and 2 (mammalian target of rapamycin complex 1 and 2) which are protein complex in charge of osteoblast growth and proliferation and act as cell sensors playing an active part in the control for the cellular

energy mechanism. The mTORC1 has been specifically linked with insurgence of both DM1 and DM2 due to the blockage of the insulin receptor substrate (IRS), the high carbs-sugar prolonged diet interferes to the IRS mechanism through the activity of class 1 P13-kinases (p70S6K) crucial for pancreatic  $\beta$ -cells insulin regulation. The high presence of p70S6K inhibits IRS to transfer the glucose transporters on to cells surface let glucose molecules free within systemic circulation; in response to this event the brain/liver/adipose axis force the lipoprotein lipases to decrease and triggering the triglycerides increase (67-86) (Fig 4).

The mTORC1-2 is the key in regulating multiple aspects of bone and cartilage development with mineral addition via specific inhibition exerted on MSCs differentiation mechanism. Either hyper-expression or deletion of mTORC1 via diet mice showed a reduced size of limb bud cells and impaired chondrogenesis from the MSC progenitors (85,86). Evidence is quite clear in showing the involvement of mTORC1-2 within a wider mechanism constituted by a complexity of hormones, growth factors, proteins and immune signaling pathways. The crosstalk takes place at several level and within different modalities, the relation of androgen-receptor and mTOR is mediated by testosterone availability; the IGF-1 activates mTORC1-2 signaling to stimulate osteoblast differentiation of bone marrow MSCs, mTORC1 systematically mediates the Wnt osteogenic activity through the activity on glutamin catabolism and IRS 1 and 2 which sequentially promote the expression of protein anabolism gene essential in MSCs differentiation to osteoblasts (Fig. 5-6). Of note the bone morphogenetic protein 2 (Bmp2) a protein extremely important in bone formation is partly activated in mTORC1-dependent manner, whereas significant is the involvement of the mTORC2 in bone formation by promoting osteoclastogenesis that takes place by modulating the expression of Rankl (87-99).

Additionally, the mTOR's crosstalk with hormones like the GLP 1-2 also play a crucial position. The GLP 1-2 belongs to the incretin hormone axis released in response to food intake by the L cells through the proglucagon processing in the upper part of intestines (93). Food intake, peptide and CNS involvement through vagal nerve innervation control the GLP-

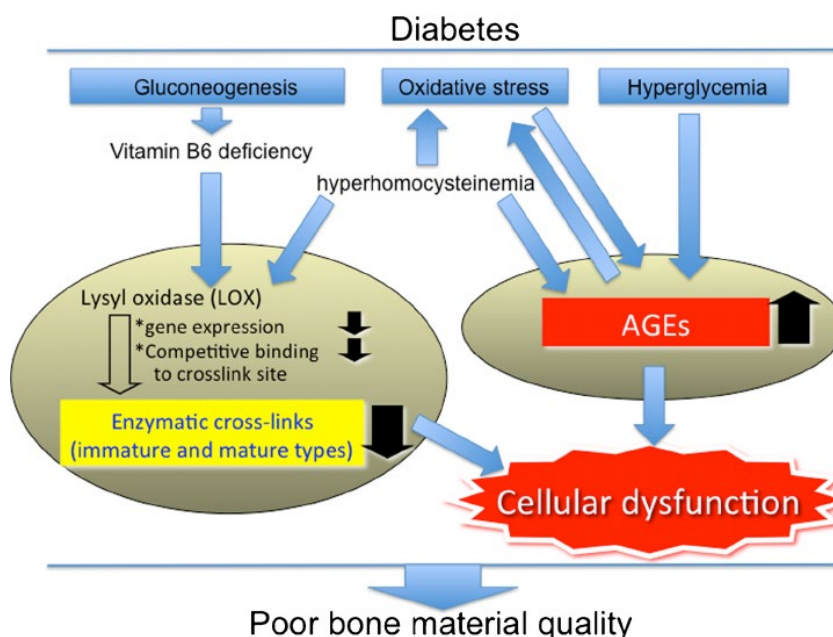
1 secretion. The intracellular signaling pathway by which all this process takes place and is synchronized still remaining unclear, however we may suppose that L cells may respond in coordination with GLP-1 through mTOR and the presence of the complex net of different hormones like leptin, ghrelin, insulin, androgen hormones and estrogen. In fact, gastric mTOR changes affect negatively the expression and secretion of ghrelin and nesfatin-1/nucleobindin 2 the latter well known as cancer cell migration factors, compromising glucose homeostasis and food intake (93, 100-102).

*The IGF/GH and TP53 signaling pathways converge upon the glucose/energy mechanism, a possible key to understand bone health and longevity?*

Those invertebrate species that has maintained insulin and insulin-like growth factor (IGF) signaling (IIS) pathway during their evolutionary process manifest a better control of their longevity. However, mammals have a more complicated system that is different one to another that makes even more

difficult to correctly understand the mechanism. One of the issues is mainly related to the different biology of mammals and humans which show the insulin, IGF-1 and IGF-2 in different tissues and molecular signaling pathways. Mutated mice for instance like the FIRKO mice, in which the insulin receptor was ablated in fat tissue, showed to live longer. FIRKO mice reduced fat mass and lessened age were concomitant factors related to loss of insulin sensitivity. It should be noted that the expenditure/need of calories and energy supply in rodents and small mammals with fast metabolic rate is extremely high, traits that are extremely different from those in humans (104-110).

In humans, any deficiencies in the insulin signaling pathway lead to insulin resistance and diabetes (111, 112). However, in the Laron syndrome where there are specific defects in the growth hormone-GH/IGF-1 signaling mechanism associated with high risk of cardiovascular disease and obesity, the patients do not develop DM2, condition which seem to have a sort of protection against cancer and show quite



**Fig. 5.** The diabetes effects on bone. The glucose and insulin metabolism indirectly alter skeletal muscle signaling, which in turns induce accumulation of AGEs subverting the collagen cross-linking with the impairment on bone remodeling. The glucose/insulin metabolic impairment to the bone is also weakened as the microenvironment signaling pathways are engulfed or mismatching. The changes in bone microenvironment directly impact on MSCs differentiation path to osteoblast resulting in decreased bone formation with higher bone resorption rate with an increased risk of fractures (103).



a significant longevity (113, 114). Intriguingly, the presence of single nucleotide polymorphism (SNP) was detected in the IIS genes and this was a common pattern of longevity across diverse cohorts. In a group of centenarians in Italy it was seen a common pattern contradistinguished by a low level of IGF-1 in plasma and linked with a specific genotype combination at IGF-IR and PI3KCB gene level (14, 114-116). The most interesting findings come from Dato et al, the team was able to detect repair mechanism shared by specific genes, the TP53-DNA repair pathway/ TXNRD1-pro-antioxidant pathway and TP53-DNA repair pathway/ERCC2-DNA repair pathway (92, 117). The TP53 is a very well-known protein that plays a key role in DNA damage response safeguarding tissues, organs in a conservative/regenerative mode by keeping stem cells pool in stand-by position whilst exerting a powerful anticancer in mediating the DNA repair through the pro-antioxidant pathway or by inducing apoptosis (117).

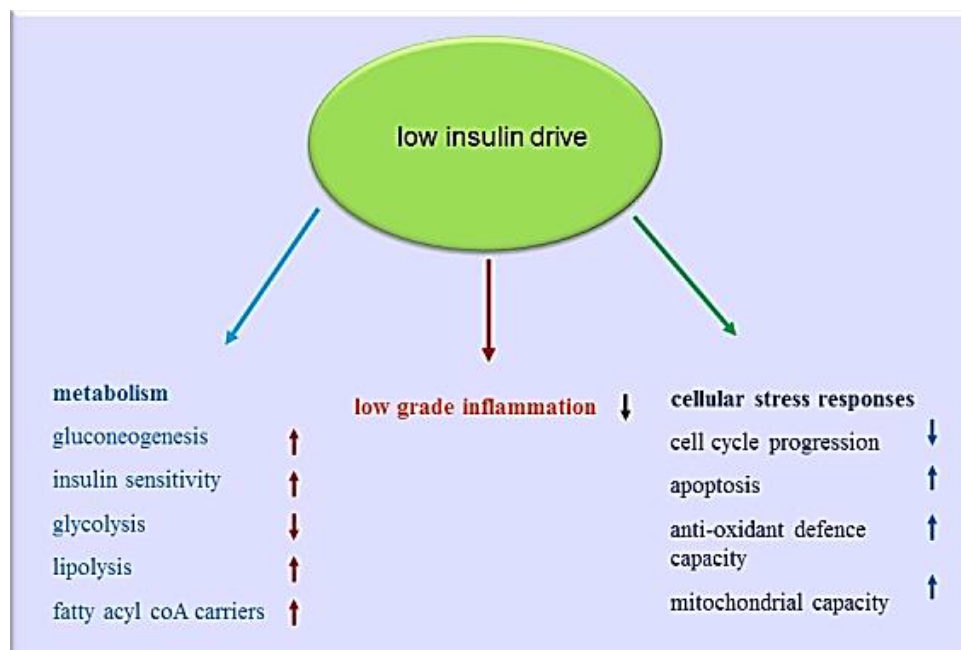
The interesting fact is that mTOR, TP53, IGF1-2, GLP-1, testosterone, estrogen, progesterone all seems to share some sort of mitochondrial relation. Whereas any impairments on this relation definitely contribute to insulin metabolic dysfunction that also

may suggest a clear low expression of specific genes involved in mitochondrial ATP regulation it definitely confirms the strict association between DM2 and healthy bone homeostasis. In fact, mitochondrion serves as energetic control unit of many catabolic and anabolic pathways essential in cell maintenance, activity, proliferation and signal transduction through ROS generation (119-123).

Mitochondria due to their deep involvement into the energy-metabolic activity like ATP production consume the highest amount of cellular oxygen and, of this a consistent part is used for the production of ROS as a by-product of oxidative phosphorylation. In humans and in mammals in general, low calorie consumption showed to reduce the energy outflow with a sensitive saving of oxidative stress and less ROS which in turns improves body energy efficiency use and muscle mitochondrial function (122-126) (Fig. 6).

*Telomere/telomerase, energy consumption, inflammation and immune responses towards infectious diseases like COVID-19, HVB and HIV*

Saeed and colleagues were able to confirm that telomerase over-expression enhanced BM-MSC differentiation to osteoblasts either in vitro or in



**Fig. 6.** A low insulin drive may be associated with metabolic rate, low grade inflammation and cellular stress responses (118).

vivo. However, telomere and telomerase activity are very susceptible to inflammatory process typical of metabolic disorder due to fat accumulation and insulin resistance seen in DM 1 and 2, CVD and Kidney disorders. The telomere and telomerase are therefore highly sensitive to chronic hyperglycemia and nutritional overload (126-128).

Different are the pro-inflammatory mediators that play a ground role in this condition, for instance the transcription factor NF- $\kappa$ B that is strictly connected with pattern recognition receptor (PRR) signaling and inflammation and patients with DM2 showed a high level of NF- $\kappa$ B, that in turns was identified as key player in the telomere complex (128, 129).

This abnormal condition is a constitutive part of reaction loop contradistinguished by high level of oxidative stress, an over-expression of the protein kinase C pathway (which negatively impact on mitochondria) and, a high ROS expression that keep constantly active pro-inflammatory cytokines. The close relation of DM and telomere shortness, the high presence of inflammatory agents, the subversion of mitochondria activity and the high expression of ROS are intricate portions of a unique interrelated signaling mechanism that eventually led to the inhibition of the regenerative capacity within the BM, in which the MSCs are completely blocked to differentiate to osteoblasts (127-129).

Therefore, shorter telomeres could be seen as indicators of serious degenerative patterns contradistinguished by faster cell senescence and tissue decay, but what about long telomeres? Could the long length telomeres indicate an ongoing disease as well? For instance, increased level of IL-6 and TNF- $\alpha$  which are usually correlated with high levels of CRP have seen reliable forecaster in severe and dangerous inflammatory and age-related disorders they also intensify telomerase activity through the NF- $\kappa$ B, STAT1, and STAT2 activation (130-132). The telomere length may be suggestive of something highly fluctuating contingent to current health status of the patient, in which telomere length maintenance mechanism and the immune system reciprocally affect via telomerase constant adjustments (130, 133-135). Furthermore, carcinogenic-malignant changing cells like melanoma may show high telomerase activity

(hTERT) that amplifies telomeric DNA repeats, allowing the cells to escape from apoptosis. The authors suggested it may occur during the very first stage of cancer development in which carcinogenic mutation take place in precursor somatic cells with long telomeres, cells that are constantly target of pro-inflammatory cytokines and NF- $\kappa$ B. In addition, long telomeres provide affected neo-cancerous cells enough replicative potential to avoid any-checkpoint that may inhibit the re-activation of telomerase (136) [111]. It follows that telomere length is not always linked to cell senescence and telomerase activity, telomeres steady shorten during the lifetime but the length is also subject to persistent fluctuations of reductions and repairs, suggestive of an individual's present condition during daily life.

These observations provide support for the hypothesis of a potential metabolic effect of many diseases that are of great threat nowadays, such as COVID-19, HIV or HBV, far beyond the well-recognized stress response associated with severe illness. However, whether the alterations of glucose metabolism and immune responses that may occur with a sudden onset in severe COVID-19 for instance may persist or remit when the infection resolves is unclear. Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), this virus is able to bind to angiotensin-converting enzyme 2 (ACE2) receptors, which are expressed in different metabolic organs and tissues, including pancreatic beta cells, adipose tissue, the small intestine, bone and the kidneys. It follows that is plausible that SARS-CoV-2 may trigger multiple alterations in glucose metabolism that could complicate the pathophysiology of preexisting metabolic diseases or lead to new degenerative mechanisms in multiple sites brain, lungs, heart, vessels and bones.

How frequent is the phenomenon of new-onset diabetes, osteo-decay and immunity unbalance it may refer to definitive telomere length reduction or uncontrolled telomerase? Do these patients remain at higher risk for any other type of infection and metabolic disorders? In patients with preexisting metabolic comorbidities such as hypertension, CVD and DM, do Covid-19, HBV or HIV change the underlying pathophysiology and the natural history

of the disease? We need to answer these questions in order to assess wider clinical picture to better understand and monitoring the affected patients (135-141) the derepressed expression of the catalytic subunit of telomerase, human telomerase reverse transcriptase (hTERT).

### Conclusion

The biological and molecular scheme that links together subverted immune responses, osteoblast decay and metabolic disorders must be investigated through the vigil eyes of the Regenerative Medicine. The regenerative methodology well explains the entire loop of domino effects that links together troubled gut metabolism, immune/inflammatory responses, mitochondria instability, the deactivated bone marrow MSCs/SCs differentiation mechanism and telomere shortening. In this perspective the initial issues seem to arise from metabolic/catabolic cellular mitochondrial disturbances, the center that regulates the whole energy functions vital to cells, tissues and organs. It follows that any clinical and therapeutic strategy requires a wider and deeper diagnostic evaluation on past and present condition of the patient. Patients with elusive metabolic/immune disorders such as the DM2, CVD and Kidney failure all manifest impairment in regenerative stem cell pathway and more specifically in MSCs differentiation process towards osteoblast phenotype.

Thus, it can be firmly listed that senescence that has not be confused with biological clock ageing, is the final phase long interconnected molecular processes. Despite intensive research over the last two decades and a deeper understanding of the features of immune/metabolic ageing, the whole bunch of molecular mediators that are involved in this chain of events and the extent to which they interact still need a clearer definition. In addition, though the association of telomere length with cellular senescence and decay has been widely researched, the precise relationship between telomere/telomerase activity and the entire sequences of signaling pathways involved in cells and tissue homeostasis still a matter of big debate. A better definition of this crosstalk will be essential to understanding the influence of sugar and calorie overload and the inflammatory reaction on human

hematopoiesis and cell/tissue regeneration. The recently identified ability of a hypocaloric diet on stem cells regeneration mechanism to control mitochondria consumption of extra-energy and ROS overload may lead to significant progress in developing strategies of treating degenerative immune/metabolic senescence in a wide range of human diseases like DM and bone decay. Together, these outcomes emphasize the importance of detecting earlier inflammatory responses that could take place in the gut microbiome which led to dysbiosis as a major driver of immune deterioration and senescence advancement as optimal condition for pathogen up rising. These outcomes have also clearly confirmed the presence of a bone-gut-kidney-heart-CNS-Immunity crosstalk, suggesting that the ageing process is a multi-factorial mechanism in which each single component regulates whilst is being regulated.

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