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## **Genetic Diseases Related with Osteoporosis**

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Additional information is available at the end of the chapter

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### **1. Introduction**

Osteoporosis is a disease entity characterized by the progressive loss of bone mineral density (BMD) and the deterioration of bone microarchitecture, leading to the development of fractures. Its classification encompasses two large groups, primary and secondary osteoporosis [1].

Primary osteoporosis is the disease's most common form and results from the progressive loss of bone mass related to aging and unassociated with other illness, a natural process in adult life; its etiology is considered multifactorial and polygenic. This form currently represents a growing worldwide health problem due in part, to the contemporary environmental conditions of modern civilization. Risk factors that are considered as "modifiable" also play an important role and include physical activity, dietary habits and eating disorders. Furthermore, there is another group of associated risk factors that are considered "non-modifiable", including gender, age, race, a personal and/or family history of fractures that in turn, indirectly reflect the degree of genetic susceptibility to this disease [2-4]. Secondary osteoporosis encompasses a large heterogeneous group of primary conditions favoring osteoporosis development. Table 1 summarizes some of the disease entities associated to primary and secondary osteoporosis.

#### **1.1. Genetic aspects of primary osteoporosis**

This form of osteoporosis results from the interaction of several environmental and genetic factors, leading to difficulties in its study. It is not easy to define the magnitude of the effect of genetic susceptibility since it is a trait determined by multiple genes whose products affect the bone phenotype; moreover, the environmental factors compromising bone mineral density are also difficult to analyze. However, in spite of these barriers, research suggests that inherited factors affect BMD in ranges between 40 – 70% in the spine, 70 – 85% in the hip and 50 – 60%

| Type of osteoporosis | Causes   |
|----------------------|--|
| Primary              | Multifactorial, polygenic. Senile/Involutional   |
| Secondary            | <p>Drugs compromising bone quality: anticonvulsants, antidepressants, anticoagulants, antacids with aluminum, aromatase inhibitors, barbiturates, cimetidine, corticosteroids, glucocorticoids, birth control pills, cancer drugs, gonadotropin releasing hormone (GnRH), loop diuretics, methotrexate, phenobarbital, phenothiazines, among others.</p> <p>Other entities: nephropathies, malabsorption syndromes, neoplasias, rheumatoid arthritis, ankylosing spondylitis, multiple sclerosis, any process leading to decreased mobility or prolonged immobility.</p> <p>Metabolic diseases: diabetes, hyperthyroidism, hyperparathyroidism.</p> <p>Hypogonadism: Turner and Klinefelter syndromes.</p> <p>Behavioral disorders: anorexia nervosa, depression, prolonged physical inactivity, malnutrition, high caffeine intake, smoking and/or chronic alcoholism.</p> <p>Monogenic diseases: osteogenesis imperfecta, glioma syndrome, osteoporosis.</p> |

**Table 1.** Osteoporosis classification.

in the wrist. Bone density studies in monozygotic (MZ) and dizygotic (DZ) twins suggest that spinal and femoral neck BMD concordance is higher (6-8:1) in MZ versus DZ twins. Other studies have estimated that fracture predisposition heritability per se ranges between 25 – 35% and up to 40% of patients with osteoporotic fractures have a positive family history of fractures, thus reflecting the great influence of genetic factors in this disease. On the other hand, the geometry and length of the femoral neck, the bone's properties on ultrasound, growth speed and bone remodeling variations are also dependent on genetic factors. The genes associated with the bone phenotype are distributed throughout the human genome and located in practically all chromosomes; their products fulfill specific functions and contribute in different manners to the genetic control of the bone tissue phenotype [5-12]. Some of these genes and their products are presented in Table 2 [13-23].

It is important to mention that the mechanisms conditioning the hereditary susceptibility to osteoporosis are determined, among other factors, by the presence of mutations or genetic polymorphisms (natural genomic variations) in one or several genes involved in bone phenotype genetic control. These polymorphisms follow a well-defined inheritance pattern and their distribution is different among racial groups and populations. There are several reports in the world literature, of associations between specific genetic variants and

osteoporosis development or the risk of fractures; these risks may vary according to the fractures' anatomic location [3, 4, 24-30]

| Product Function                           | Genes  |
|--|--|
| Matrix components                          | COL1A1, COL1A2, OPN  |
| Hormones and their receptors               | ESR1, ESR2, AR, VDR, PTHR1, CASR, PTH, CYP1A1, PRL, LEP, LEPR, INS, INSR |
| Participants in osteoblastogenic processes | ALOX12, ALOX15, BMP4, BMP7, IGF-1, LRP5, LRP6, SOST                      |
| Participants in osteoclastogenic processes | P53, RANK, RANK-L  |
| Citokines and their receptors              | IL1 $\alpha$ , IL1 $\beta$ , IL6, TNF, TNFR2                             |
| Other                                      | MTHFR, APOE  |

**Table 2.** Genes involved in bone metabolism.

## 2. Mendelian diseases and osteoporosis

The description in the literature of some genetic diseases of monogenic inheritance and whose phenotype includes the loss or increase in bone mineral density and even fractures, has suggested and even proved that bone phenotype has an important genetic component. These diseases include idiopathic osteoporosis, osteogenesis imperfecta in all its variants, osteopetrosis, pycnodysostosis and the osteoporosis syndrome associated to pseudoglioma, among others. In some cases of severe osteoporosis, mutations in the estrogen and even the androgen receptor genes have been detected.

### 2.1. Idiopathic juvenile osteoporosis

This is an unusual variety of osteoporosis whose frequency has not been precisely determined. This disease may develop in females and males, usually around 7 – 10 years of age; children present difficulty in gait, pain in the lower extremities, ankles, knees, occasionally in the hip and fractures tend to develop particularly in long bones. Radiologically, it is characterized by diffuse osteopenia, metaphyseal fractures – especially of the femur -, and vertebral collapse that may lead to severe kyphoscoliosis or collapse of the thoracic cage. This disease is considered potentially reversible whereby in most cases, there is almost complete recovery of the bone tissue; growth, however, may be compromised.

In these patients, it is important to exclude other disease entities or conditions manifesting secondarily as osteoporosis. A differential diagnosis must be made with other genetic diseases, particularly the different variants of osteogenesis imperfecta; this is relatively easy

due to its clinical characteristics, lacking in idiopathic osteoporosis. The genetic basis of this disease has of yet, not been established but it is possible that genetic mutations with preferential tissue expression in bone and with great impact on the tissue's phenotype, may explain some of these cases [31, 32].

## 2.2. Osteogenesis imperfecta

Osteogenesis imperfecta, also known as "brittle bone disease", has an estimated incidence of approximately 1 in 20 000 births. It has great phenotypic variability, different patterns of inheritance and a wide clinical spectrum ranging from very mild forms of the disease to severe cases with an unfavorable prognosis. It is caused by the defective synthesis of one of the two alpha chains of type I collagen (COL1A1 and COL1A2), leading to anomalies in these protein's structure; it is normally constituted by 3 coiled sub-units, two  $\alpha$ 1 chains and one  $\alpha$ 2 chain. This type of collagen is considered the most abundant component of structural protein in bone as well as in ligaments, tendons, sclerae and skin. Quantitative or qualitative defects in this protein lead to bone fragility and hence, to an increased risk of fractures.

The genes encoding the  $\alpha$ 1 and  $\alpha$ 2 chains are located in the 17q21.31-q22 and 7q22.1 chromosomes, respectively. Aside from brittle bones, these patients may also present long bones with no curvatures, severe deformities preventing appropriate gait and even standing, conductive deafness due to malformations of the auditory canal, dentinogenesis imperfecta, joint hyperlaxity and intervertebral disc herniation. Patients with severe forms of the disease have a long history of fractures on mild impact and variable bone deformities. The most severe variants may even lead to fractures in utero and pre or perinatal death. Tables 3 and 4 shows different forms of the disease [33-35].

## 2.3. Osteoporosis – Pseudoglioma Syndrome (OPPG)

This syndrome is an autosomal recessive disease characterized by bone and visual abnormalities including short stature, osteoporosis development during infancy, spontaneous fractures, scoliosis, platyspondyly and long bone deformities. A crucial associated finding is the presence of pseudoglioma that may be associated to microcephaly, blindness during childhood, cataracts and iris atrophy. Occasionally, some patients present interventricular septal defects and mental retardation. This disease is conditioned by mutations of the LRP5 gene, located on chromosome 11q13.4 and that encodes the low-density lipoprotein receptor-related protein 5 (LRP5). It was initially believed that this entity was another variant of osteogenesis imperfecta (OI) but the study of collagen in patients with OPPG established that this protein was normal and the hypothesis was discarded; however, this is still the most relevant differential diagnosis [36-41].

## 2.4. Neuromuscular disorders

Muscular dystrophies, peripheral neuropathies and muscle atrophies of hereditary origin, represent broad groups of diseases that aside from their characteristic clinical stigmata, can be associated with osteoporosis as one of their complications. As the disease progresses in these

patients, there is increased difficulty and limitation in walking and periods of immobility become progressively more prolonged leading to the gradual loss of the mechanical stimuli that bone needs to maintain its strength and hence, favoring the development of osteoporosis. As all Mendelian diseases, these neuromuscular abnormalities follow different inheritance patterns and present phenotypic variability [42-44].

## 2.5. Inborn errors of metabolism

This group of genetic diseases encompasses a great number of inborn defects with repercussions in several aspects of carbohydrate, amino acid, protein, vitamin, mineral, complex molecule, neurotransmitter and energy metabolism. The genetic basis of most of these entities hinges on gene mutations encoding proteins, particularly enzymes, leading to partial or complete blockade of one or several metabolic processes. In these diseases, symptoms arise for different reasons, including: a deficit of the products generated by the compromised enzymatic reaction, accumulation of the precursor immediate to the defect, an increase in alternative products due to increased activation of alternate metabolic pathways or inhibition of these alternate pathways due to the accumulated substrate. In most cases, inheritance of these diseases is autosomal recessive and less frequently, X-linked recessive.

In cases of metabolic errors, osteoporosis tends to develop for different reasons: in some cases, it is secondary to nutritional deficiencies, progressive neurologic or muscular impairment or as a consequence of the therapeutic measures taken in the management of the primary disease: their secondary effects directly compromise bone quality (steroids, antiseizure drugs, etc.). The number of monogenic diseases whose phenotype may include osteoporosis is large and are shown in Tables 3-5, according to their Mendelian inheritance pattern [45-56].

| Disease                                    | Gene   | Product                            | Genomic Location | Reference |
|--|--------|------------------------------------|------------------|-----------|
| Hutchinson-Gilford progeria syndrome; HGPS | LMNA   | Prelamin-A/C precursor (LMNA)      | 1q22             | 57, 58    |
| Osteogenesis imperfecta, Type I; OI1       | COL1A1 | Collagen, type I, alpha 1 (COL1A1) | 17q21.33         | 33, 34    |
| Osteogenesis imperfecta, Type II; OI2      | COL1A1 | Collagen, type I, alpha 1 (COL1A1) | 17q21.33         | 33, 59    |
|  | COL1A2 | Collagen, type I, alpha 2 (COL1A2) | 7q21.3           |           |
| Osteogenesis imperfecta, Type III; OI3     | COL1A1 | Collagen, type I, alpha 1 (COL1A1) | 17q21.33         | 33, 60    |
|  | COL1A2 | Collagen, type I, alpha 2 (COL1A2) | 7q21.3           |           |
| Marfan syndrome; MFS                       | FBN1   | Fibrillin 1 (FBN1)                 | 15q21.1          | 61, 62    |

| <b>Disease</b>                           | <b>Gene</b>     | <b>Product</b>   | <b>Genomic Location</b> | <b>Reference</b> |
|--|-----------------|--|-------------------------|------------------|
| Loeys-Dietz syndrome, Type 1A; LDS1A     | TGFBR1          | Transforming growth factor-beta receptor, Type I (TGFBR1)      | 9q22.33                 | 63, 64           |
| Loeys-Dietz syndrome, Type 1B; LDS1B     | TGFBR2          | Transforming growth factor-beta receptor, Type II (TGFBR2)     | 3p24.1                  | 65, 66           |
| Loeys-Dietz syndrome, Type 2B; LDS2B     | TGFBR2          | Transforming growth factor-beta receptor, Type II (TGFBR2)     | 3p24.1                  | 63, 65           |
| Loeys-Dietz syndrome, Type 3; LDS3       | MADH3/<br>SMAD3 | Mothers against decapentaplegic homolog 3 (Drosophila) (SMAD3) | 15q22.33                | 67, 68           |
| Ehlers-Danlos syndrome, Type I           | COL5A2          | Collagen, type V, alpha 2 (COL5A2)                             | 2q32.2                  | 69, 70           |
|  | COL5A1          | Collagen, type V, alpha 1 (COL5A1)                             | 9q34.3                  |                  |
|  | COL1A1          | Collagen, type I, alpha 1 (COL1A1)                             | 17q21.33                |                  |
| Ehlers-Danlos syndrome, Type II          | COL5A1          | Collagen, type V, alpha 1 (COL5A1)                             | 9q34.3                  | 70, 71           |
|  | COL5A2          | Collagen, type V, alpha 2 (COL5A2)                             | 2q32.2                  |                  |
| Pseudohypoparathyroidism, Type IA; PHP1A | GNAS            | GNAS complex locus (GNAS)<br>[Gs, alpha subunit, included]     | 20q13.32                | 72, 73           |
| Pseudohypoparathyroidism, Type IC; PHP1C | GNAS            | GNAS complex locus (GNAS)<br>[Gs, alpha subunit, included]     | 20q13.32                | 73, 74           |
| Pseudopseudohypoparathyroidism; PPHP     | GNAS            | GNAS complex locus (GNAS)<br>[Gs, alpha subunit, included]     | 20q13.32                | 73, 75           |
| Epiphyseal dysplasia, multiple, 1; EDM1  | COMP            | Cartilage oligomeric matrix protein (COMP)                     | 19p13.11                | 76, 77           |



| Disease  | Gene               | Product  | Genomic Location   | Reference |
|--|--------------------|--|--------------------|-----------|
| Prader-Willi syndrome; PWS   | NDN<br>SNRPN /PWCR | Necdin homolog<br>(mouse) (NDN)<br>Small nuclear<br>ribonucleoprotein-<br>associated protein N<br>(SNRPN/PWCR) | 15q11.2<br>15q11.2 | 78, 79    |
| Hajdu-Cheney syndrome; HJCYS   | NOTCH2             | Neurogenic locus<br>Notch homolog<br>protein 2 (NOTCH2)  | 1p12-p11           | 80, 81    |
| Nephrolithiasis/osteoporosis,<br>hypophosphatemic, 1; NPHLOP1                          | SLC34A1            | Sodium-dependent<br>phosphate transport<br>protein 2A<br>(SLC34A1/ .NPT2A)                                     | 5q35.3             | 82, 83    |
| Nephrolithiasis/osteoporosis,<br>hypophosphatemic, 2; NPHLOP2                          | SLC9A3R1/<br>NHERF | Na(+)/H(+) exchange<br>regulatory cofactor<br>NHE-RF1 (SLC9A3R1/<br>NHERF)                                     | 17q25.1            | 84-86     |
| Cardiomyopathy, dilated, with<br>hypergonadotropic hypogonadism                        | LMNA               | Prelamin-A/C<br>precursor (LMNA)   | 1q22               | 87, 88    |
| Dyskeratosis congenita, autosomal<br>dominant, 1; DKCA1                                | TERC               | Telomerase RNA<br>component (TERC)<br>(RNA)  | 3q26.2             | 87, 88    |
| Dyskeratosis congenita, autosomal<br>dominant, 2; DKCA2                                | TERT               | Telomerase reverse<br>transcriptase (TERT)   | 5p15.33            | 89, 90    |
| Dyskeratosis congenita, autosomal<br>dominant, 3; DKCA3                                | TINF2              | TERF1-interacting<br>nuclear factor 2<br>(TINF2)   | 14q12              | 91, 92    |
| Pigmented nodular adrenocortical<br>disease, primary, 1; PPNAD1                        | PRKAR1A            | cAMP-dependent<br>protein kinase type I-<br>alpha regulatory<br>subunit (PRKAR1A/<br>TSE1)                     | 17q24.2            | 93, 94    |
| Pigmented nodular adrenocortical<br>disease, primary, 2; PPNAD2                        | PDE11A             | Dual 3',5'-cyclic-AMP<br>and -GMP<br>phosphodiesterase<br>11A (PDE11A)   | 2q31.2             | 95, 96    |
| Hyperostosis corticalis generalisata,<br>benign form of worth, with torus<br>palatinus | LRP5               | Low density<br>lipoprotein receptor-   | 11q13.2            | 97, 98    |



| Disease  | Gene   | Product  | Genomic Location | Reference |
|--|--------|--|------------------|-----------|
|  |        | related protein 5 (LRP5)   |                  |           |
| Van Buchem disease, Type 2; HVB2   | LRP5   | Low density lipoprotein receptor-related protein 5 (LRP5)  | 11q13.3          | 99, 100   |
| Osteopetrosis, autosomal dominant 1; OPTA1                                     | LRP5   | Low density lipoprotein receptor-related protein 5 (LRP5)  | 11q13.3          | 101, 102  |
| Osteopetrosis, autosomal dominant 2; OPTA2                                     | CLCN7  | H(+)/Cl(-) exchange transporter 7 (CLCN7)  | 16p13.3          | 103, 104  |
| ACTH-independent macronodular adrenal hyperplasia; AIMAH                       | GNAS   | GNAS complex locus (GNAS) [Gs, alpha subunit, included]  | 20q13.32         | 105, 106  |
| Hyper-IgE recurrent infection syndrome, autosomal dominant                     | STAT3  | Signal transducer and activator of transcription 3 (STAT3)   | 17q21.2          | 107, 108  |
| Coronary artery disease, autosomal dominant 2; ADCAD2 or CADO                  | LRP6   | Low density lipoprotein receptor-related protein 6 (LRP6)  | 12p13.2          | 109, 110  |
| Avascular necrosis of femoral head, primary; ANFH                              | COL2A1 | Collagen, type II, alpha 1 (COL2A1)  | 12q13.11         | 111, 112  |
| Spondyloepimetaphyseal dysplasia with joint laxity Type 2; SEMDJL2             | KIF22  | Kinesin-like protein KIF22 (KIF22)   | 16p11.2          | 113, 114  |
| Spondyloepiphyseal dysplasia, Maroteaux type (pseudo-Morquio syndrome, Type 2) | TRPV4  | Transient receptor potential cation channel, subfamily V, member 4 (TRPV4)                         | 12q24.11         | 115, 116  |
| Hypophosphatasia, adult  | ALPL   | Alkaline phosphatase, liver/bone/kidney or alkaline phosphatase, tissue-nonspecific isozyme (ALPL) | 1p36.12          | 117, 118  |

| Disease                                       | Gene  | Product  | Genomic Location | Reference |
|---|-------|--|------------------|-----------|
| Cleidocranial dysostosis; CLCD                | RUNX2 | Runt-related transcription factor 2 (RUNX2)    | 6p21.1           | 119, 120  |
| Trichorhinophalangeal syndrome, type I; TRPS1 | TRPS1 | Zinc finger transcription factor Trps1 (TRPS1) | 8q23.3           | 121, 122  |

**Table 3.** Autosomal dominant diseases with bone mineral density loss.

| Disease  | Gene   | Product   | Genomic location | Reference |
|--|--|---|------------------|-----------|
| Vitamin D hydroxylation-deficient rickets, Type 1A; VDDR1A   | CYP27B1                                      | 25-hydroxy-vitamin D-1 alpha hydroxylase, mitochondrial (CYP27B1) | 12q13            | 123, 124  |
| Hemochromatosis; HFE   | HFE (C282Y y H63D)                           | Hereditary hemochromatosis protein (HFE)                          | 6p22.2           | 125, 126  |
|  | BMP2 [HFE hemochromatosis, modifier of]      | Bone morphogenetic protein 2 (BMP2)                               | 20p12.3          |           |
| Beta-Thalassemia   | beta-Thalassemia:HBB                         | Hemoglobin subunit beta (HBB)                                     | 11p15.4          | 47, 48    |
|  | Thalassemia, Hispanic gamma-delta-beta: LCRB | Locus control region, beta (LCRB)                                 | 11p15.5          |           |
| Osteoporosis-pseudoglioma syndrome; OPPG                     | LRP5   | Low density lipoprotein receptor-related protein 5 (LRP5)         | 11q13.2          | 127, 128  |
| Homocystinuria due to cystathionine beta-synthase deficiency | CBS/HIP4                                     | Cystathionine beta-synthase (CBS)                                 | 21q22.3          | 45, 46    |
| Homocysteinemia  | MTHFR (C677T)                                | Methylenetetrahydrofolate reductase (MTHFR)                       | 1p36.6           | 129, 130  |
|  | CBS  | Cystathionine beta-synthase (CBS)                                 | 21q22.3          |           |
|  | MS/MTR                                       | Methionine synthase (MTR/METH)                                    | 1q23             |           |

| <b>Disease</b>   | <b>Gene</b>   | <b>Product</b>   | <b>Genomic location</b> | <b>Reference</b> |
|--|---------------|--|-------------------------|------------------|
| Homocysteinemia  | MTHFR (C677T) | Methylenetetrahydrofolate reductase (MTHFR)                        | 1p36.6                  | 33, 131, 132     |
|  | CBS           | Cystathionine beta-synthase (CBS)                                  | 21q22.3                 |                  |
|  | MS/MTR        | Methionine synthase (MTR/METH)                                     | 1q23                    |                  |
| Osteogenesis imperfecta, Type IX; OI9<br>[Osteogenesis imperfecta type II-B, III or IV PPIB related] | PPIB          | Peptidyl-prolyl cis-trans isomerase B (PPIB)                       | 15q22.31                | 35, 133          |
| Propionic acidemia   | PCCA          | Propionyl-CoA carboxylase alpha chain, mitochondrial (PCCA)        | 13q32.3                 | 134, 135         |
|  | PCCB          | Propionyl-CoA carboxylase beta chain, mitochondrial (PCCB)         | 3q22.3                  |                  |
| Ehlers-Danlos syndrome, type VI; EDS6  | PLOD1         | Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 (PLOD1)          | 1p36.22                 | 69, 136          |
| Hypertrophic osteoarthropathy, primary, autosomal recessive, 1; PHOAR1                               | HPGD          | 15-hydroxy-prostaglandin dehydrogenase [NAD+]<br>(HPGD)            | 4q34.1                  | 137, 138         |
| Pituitary adenoma, ACTH-secreting; CUDP  | AIP           | AH receptor-interacting protein (AIP)                              | 11q13.2                 | 139, 140         |
| Gaucher disease, Type I; GDI   | GBA           | Glucosylceramidase (GLCM/GBA)                                      | 1q22                    | 49, 50           |
| Paget disease, juvenile; JPD   | TNFRSF11B     | Tumor necrosis factor receptor superfamily, member 11b (TNFRSF11B) | 8q24.12                 | 141, 142         |
| Pycnodysostosis; PKND  | CTSK          | Cathepsin K  | 1q21.3                  | 143, 144         |
| Lipodystrophy, congenital generalized, type 4; CGL4  | PTRF          | Polymerase I and transcript release factor (PTRF)                  | 17q21.2                 | 145, 146         |

| <b>Disease</b>  | <b>Gene</b> | <b>Product</b>  | <b>Genomic location</b> | <b>Reference</b> |
|---|-------------|---|-------------------------|------------------|
| Niemann-Pick disease, Type A  | SMPD1       | Sphingomyelin phosphodiesterase 1, acid lysosomal (SMPD1/ASM) | 11p15.4                 | 147, 148         |
| Niemann-Pick disease, Type B  | SMPD1       | Sphingomyelin phosphodiesterase 1, acid lysosomal (SMPD1/ASM) | 11p15.4                 | 147, 149         |
| Lathosterolosis   | SC5DL       | Lathosterol oxidase (SC5DL)                                   | 11q23.3                 | 150, 151         |
| Mucopolysaccharidosis Type IVA (Morquio syndrome A)                 | GALNS       | N-acetyl-galactosamine-6-sulfatase (GALNS)                    | 16q24.3                 | 152-154          |
| Mucopolysaccharidosis Type IVB (Morquio syndrome B)                 | GLB1        | Beta-galactosidase1 (BGAL)                                    | 3p22.3                  |                  |
| Fibromatosis, juvenile hyaline; JHF                                 | ANTXR2      | Anthrax toxin receptor 2 (ANTXR2)                             | 4q21                    | 155, 156         |
| Aromatase deficiency  | CYP19A1     | Cytochrome P450 19A1 (CYP19A1)                                | 15q21.2                 | 157, 158         |
| Diastrophic dysplasia   | SLC26A2     | Sulfate transporter 2 (S26A2)                                 | 5q32                    | 159, 160         |
| Desbuquois dysplasia; DBQD  | CANT1       | Soluble calcium-activated nucleotidase 1 (CANT1)              | 17q25.3                 | 161, 162         |
| Torg-winchester syndrome  | MMP2        | 72 kDa type IV collagenase (MMP2)                             | 16q12.2                 | 163, 164         |
| Geroderma osteodysplasticum; GO                                     | GORAB       | RAB6-interacting golgin (GORAB)                               | 1q24.2                  | 165, 166         |
| Lysinuric protein intolerance; LPI                                  | SLC7A7      | Y+L amino acid transporter 1 (YLAT1)                          | 14q11.2                 | 167, 168         |
| Cerebroretinal microangiopathy with calcifications and cysts; CRMCC | CTC1        | CST complex subunit CTC1                                      | 17p13.1                 | 169, 170         |
| Exudative vitreoretinopathy 4; EVR4                                 | LRP5        | Low density lipoprotein receptor-related protein 5 (LRP5)     | 11q13.2                 | 171, 172         |
| Nestor-Guillermo progeria syndrome; NGPS                            | BANF1       | Barrier to autointegration factor 1 (BANF1)                   | 11q13.1                 | 173, 174         |

| <b>Disease</b>   | <b>Gene</b>   | <b>Product</b>   | <b>Genomic location</b> | <b>Reference</b> |
|--|---------------|--|-------------------------|------------------|
| Dyskeratosis congenita, autosomal recessive, 1; DKCB1  | NOLA3 / NOP10 | H/ACA ribonucleoprotein complex subunit 3 (NOP10/ NOLA3)                     | 15q14                   | 175, 176         |
| Macrocephaly, alopecia, cutis laxa, and scoliosis  | RIN2          | Ras and Rab interactor 2 (RIN2)  | 20p11.23                | 177, 178         |
| Hypertrophic osteoarthropathy, primary, autosomal recessive, 1; PHOAR1                             | HPGD          | 15-hydroxyprostaglandin dehydrogenase [NAD+] (PGDH)                          | 4q34.1                  | 137, 179         |
| Multiple joint dislocations, short stature, craniofacial dysmorphism, and congenital heart defects | B3GAT3        | Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3 (B3GAT3) | 11q12.3                 | 180, 181         |
| Hyalinosis, infantile systemic; ISH  | ANTXR2        | Anthrax toxin receptor 2 (ANTXR2)  | 4q21.21                 | 182, 183         |
| Ovarian dysgenesis 1; ODG1   | FSHR          | Follicle stimulating hormone receptor (FSHR)                                 | 2p16.3                  | 184, 185         |
| Epiphyseal dysplasia, multiple, with early-onset diabetes mellitus                                 | EIF2AK3       | Eukaryotic translation initiation factor 2 alpha kinase 3 (EIF2AK3)          | 2p11.2                  | 186, 187         |
| Cerebrooculofacioskeletal syndrome 1; COFS1  | ERCC6         | DNA excision repair protein ERCC-6   | 10q11.23                | 188, 189         |
| Wilson disease; WND  | ATP7B         | Copper-transporting ATPase 2 (ATP7B)   | 13q14.3                 | 190, 191         |
| Werner syndrome; WRN   | WRN/RECQL2    | Werner syndrome ATP-dependent helicase (WRN / RECQL2)                        | 8p12                    | 192, 193         |
| Rothmund-thomson syndrome; RTS   | RECQL4        | ATP-dependent DNA helicase Q4 (RECQL4)                                       | 8q24.3                  | 194, 195         |
| Schwartz-Jampel syndrome, Type 1; SJS1   | HSPG2         | Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG2) | 1p36.12                 | 196, 197         |

| <b>Disease</b>  | <b>Gene</b> | <b>Product</b>   | <b>Genomic location</b> | <b>Reference</b> |
|---|-------------|--|-------------------------|------------------|
| Perrault syndrome; prlts                                      | HSD17B4     | Peroxisomal multifunctional enzyme type 2 (HSD17B4)              | 5q23.1                  | 198, 199         |
| Glycogen storage disease Ia; GSD1A                            | G6PC        | Glucose-6-phosphatase, catalytic subunit (G6PC)                  | 17q21.31                | 200, 201         |
| Glycogen storage disease Ib; GSD1B                            | SLC37A4     | Glucose-6-phosphate translocase (SLC37A4)                        | 11q23.3                 | 200, 201         |
| Cranioectodermal dysplasia 1; CED1                            | IFT122      | Intraflagellar transport protein 122 homolog (IFT122)            | 3q21.3                  | 202, 203         |
| Cerebrotendinous xanthomatosis; CTX                           | CYP27A1     | Sterol 26-hydroxylase, mitochondrial (CYP27A1/CP27A)             | 2q35                    | 204, 205         |
| Arthropathy, progressive pseudorheumatoid, of childhood; PPAC | WISP3       | WNT1-inducible-signaling pathway protein 3 (WISP3)               | 6q21                    | 206, 207         |
| Genitopatellar syndrome; GTPTS                                | KAT6B       | Histone acetyltransferase KAT6B                                  | 10q22.2                 | 208, 209         |
| Congenital disorder of glycosylation, Type IIk; CDG2K         | TMEM165     | Transmembrane protein 165 (TMEM165/TM165)                        | 4q12                    | 210, 211         |
| Cutis laxa, autosomal recessive, Type IA; ARCL1A              | FBLN5       | Fibulin-5 (FBLN5)  | 14q32.12                | 212, 213         |
| Cutis laxa, autosomal recessive, Type IIB; ARCL2B             | PYCR1       | Pyrroline-5-carboxylate reductase 1, mitochondrial (PYCR1/P5CR1) | 17q25.3                 | 166, 214         |
| Cutis laxa, autosomal recessive, Type IIIB; ARCL3B            | PYCR1       | Pyrroline-5-carboxylate reductase 1, mitochondrial (PYCR1/P5CR1) | 17q25.3                 | 212, 215         |
| Niemann-Pick disease, Type B                                  | SMPD1       | Sphingomyelin phosphodiesterase (SMPD1)                          | 11p15.4                 | 149, 216         |
| Trichothiodystrophy, photosensitive; TTDP                     | ERCC3       | TFIIH basal transcription factor                                 | 2q14.3                  | 217, 218         |

| Disease  | Gene     | Product   | Genomic location | Reference |
|--|----------|---|------------------|-----------|
|  |          | complex helicase XPB subunit (ERCC3)  |                  |           |
|  | GTF2H5   | General transcription factor IIH, subunit 5 (GTF2H5)  | 6q25.3           |           |
|  | ERCC2    | TFIIH basal transcription factor complex helicase XPD subunit (ERCC2)                                     | 19q13.32         |           |
| Cerebral autosomal recessive arteriopathy with subcortical infarcts and leukoencephalopathy; CARASIL | HTRA1    | Serine protease HTRA1   | 10q26.13         | 219, 220  |
| Weill-Marchesani syndrome 1; WMS1  | ADAMTS10 | A disintegrin and metalloproteinase with thrombospondin motifs 10 (ADAMTS10/ATS10)                        | 19p13.2          | 221, 222  |
| Laron syndrome   | GHR      | Growth hormone receptor (GHR)   | 5p13-p12         | 223, 224  |
| Mandibuloacral dysplasia with type A lipodystrophy; MADA   | LMNA     | Prelamin-A/C precursor (LMNA)   | 1q22             | 225, 226  |
| Keutel syndrome  | MGP      | Matrix Gla protein (MGP)  | 12p12.3          | 227, 228  |
| Hypophosphatasia, childhood  | ALPL     | Alkaline phosphatase, liver/bone/kidney or alkaline phosphatase, tissue-nonspecific isozyme (ALPL / PPBT) | 1p36.12          | 229, 230  |
| Fanconi-Sickel syndrome; FBS   | SLC2A2   | Solute carrier family 2, facilitated glucose transporter member 2 (SLC2A2 / GTR2)                         | 3q26.2           | 231, 232  |
| Lactose intolerance, adult type  | MCM6     | DNA replication licensing factor MCM6   | 2q21.3           | 233, 234  |
| Trichohepatoenteric syndrome 1; THES1  | TTC37    | Tetratricopeptide repeat domain 37 (TTC37)  | 5q15             | 235, 236  |
| Costello syndrome  | HRAS     | GTPase HRas (HRAS / RASH) (HRAS / RASH)   | 11p15.5          | 237, 238  |



| Disease   | Gene    | Product                          | Genomic location | Reference |
|---|---------|----------------------------------|------------------|-----------|
| Adrenal hyperplasia, congenital, due to 21-hydroxylase deficiency | CYP21A2 | Steroid 21-hydroxylase (CYP21A2) | 6p21.33          | 239, 240  |

**Table 4.** Autosomal recessive diseases with bone mineral density loss.

| Disease  | Gene             | Product   | Genomic location | Reference |
|--|------------------|---|------------------|-----------|
| Hypophosphatemic rickets, X-linked dominant; XLHR or HYP | PHEX             | Phosphate-regulating neutral endopeptidase (PHEX/PEX) | Xp22.11          | 241, 242  |
| Androgen insensitivity syndrome; AIS                     | AR               | Androgen receptor (AR)                                | Xq12             | 243, 244  |
| Fragile X mental retardation syndrome                    | FMR1             | Fragile X mental retardation protein 1 (FMR1)         | Xq27.3           | 245, 246  |
| Fabry disease  | GLA              | Galactosidase, alpha (AGAL)                           | Xq22.1           | 51, 52    |
| Occipital horn syndrome; OHS                             | ATP7A            | Copper-transporting ATPase 1 (ATP7A)                  | Xq21.1           | 247, 248  |
| Menkes disease   | ATP7A            | Copper-transporting ATPase 1 (ATP7A)                  | Xq21.1           | 249, 250  |
| Dyskeratosis congenita, X-linked; DKCX                   | DKC1             | H/ACA ribonucleoprotein complex subunit 4 (DKC1)      | Xq28             | 251, 252  |
| Hyperglycerolemia (glycerol kinase deficiency; GKD)      | GK               | Glycerol kinase (GK)                                  | Xp21.2           | 253, 254  |
| Premature ovarian failure 2B; POF2B                      | FLJ22792 / POF1B | Protein POF1B   | Xq21.1-q21.2     | 255, 256  |
| Terminal osseous dysplasia; TOD or ODPF                  | FLNA             | Filamin-A (FLNA)                                      | Xq28             | 257, 258  |

**Table 5.** X-linked recessive diseases with bone mineral density loss.

## 2.6. Genetic diseases of chromosomal origin and osteoporosis

Within the different categories of genetic diseases, we can include numeric or structural chromosomal abnormalities. Two of the most common chromosomal diseases are Turner's syndrome and Klinefelter's syndrome, both associated to X chromosome aneuploidy; in the first case, there is complete or partial absence of an X chromosome and less frequently, it can be caused by structural anomalies in the short arms of the X chromosome. In Klinefelter's syndrome, there is an additional X chromosome and occasionally, there may be more than one

extra X chromosome. In both syndromes, the phenotypic spectrum includes gonadal dysgenesis, in Turner's syndrome there are fibrous bands instead of ovaries and in Klinefelter's, the testicles are hypoplastic, leading in both cases to hypogonadism and a partial or complete deficit in the sex hormones that would normally be produced by the ovaries and testicles. Due to their lack, the development of normal secondary sexual characteristics is stunted and the various metabolic processes dependent on the hormones are also compromised. One of these metabolic processes occurs in bone [259-262].

Undoubtedly, bone metabolism is complex and the processes of osteoblastogenesis, osteoclastogenesis and remodeling must occur in a balanced manner; it is important to mention that the entire family of steroid hormone receptors (estrogen, androgen, vitamin D and retinoids), are expressed in bone, both in osteoblasts and osteoclasts as well as in chondrocytes. Within this microenvironment, the action of these hormones on their receptors is key to appropriate skeletal development; as a matter of fact, individuals with genetic mutations encoding any of these receptors develop, among other manifestations, bad quality bone mass. These hormones and their receptors play a pivotal role in female and male bone growth and may also favor epiphyseal closure at the end of the growth period. It is known that one of effects of steroid hormones on bone metabolism is resorption inhibition since they promote osteoclast apoptosis and decrease the frequency of remodeling unit activation. Therefore, the integral treatment of both entities includes hormone replacement that to a certain extent, will improve bone mass and will prevent or delay the development of osteoporosis [263, 264].

### 3. Conclusion

Bone metabolism and the large amount of processes that it involves, such as osteoblastogenesis, osteoclastogenesis and bone remodeling, must be kept in constant balance. Each one of these aspects of the physiology of bone shows a particular gene expression patterns, which may even differ according to conditions and tissue needs. As previously mentioned the number of genes involved is very large and sometimes their expression might be modified by multiple environmental conditions. It is important to mention that the expression of these genes is ubiquitous and is not restricted to the bone tissue, which explains why the phenotypic characteristics of a large number of monogenic and some polygenic entities include alterations on bone mineral density and on the microarchitecture of this tissue; this includes several degrees of osteopenia, osteoporosis or increased bone mineral density. Even a good number of these genes have been identified through the study of human disease whose phenotype includes altered bone mineral density. Without a doubt, the investigation of several processes that regulate bone metabolism will continue generating new knowledge that will allow better understanding of bone physiology and physiopathology of multiple diseases and possibly new therapeutic options in diseases which compromise the quality and function of the bone.

## Nomenclature

OPN-Osteopontin

ESR1-Estrogen Receptor Alpha

ESR2-Estrogen Receptor Beta

AR-Androgen Receptor

VDR-Vitamin D Receptor

PTHr1-Parathormone Receptor

PTH-Parathormone

CASR-Calcium Sensing Receptor

CYP1A1-Cytochrome P450, Subfamily A, Polypeptide 1

PRL-Prolactin

LEP-Leptin

LEPR-Leptin Receptor

INS-Insulin

INSR-Insulin Receptor

ALOX12-Arachidonate 12-Lipoxygenase

ALOX15-Arachidonate 15-Lipoxygenase

BMP4-Bone Morphogenetic Protein 4

BMP7-Bone Morphogenetic Protein 7

IGF-1-Insulin-Like Growth Factor 1 (Somatomedin C)

SOST-Sclerostin

P53-Protein 53

RANK-Receptor Activator Of Nf-Kb2

RANK-L.-Receptor Activator Of Nf-Kb2 Ligand

IL1 $\beta$ -Interleucin 1 Beta

IL6-Interleucin 6

TNF-Tumor Necrosis Factor

TNFR2-Tumor Necrosis Factor Receptor

APOE-Apolipoprotein E

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