The vitamin D receptor: biological and molecular properties

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Summary

Vitamin D/Vitamin D Receptor (VDR) endocrine system plays an essential role in regulation of calcium homeostasis and bone metabolism together with other calciotropic hormones. However recent studies evidenced further unexpected roles for this complex system ranging from control of cell proliferation and differentiation to modulation of the immune system. Similarly to other proteins, belonging to the family of nuclear hormone receptors, VDR shows different molecular mechanisms supporting the wide range of its biological actions. Among them the regulation of transcription of vitamin D-dependent genes is the most important one. This paper is a comprehensive review of the biological actions of VDR but for each of them an attempt to give details of the molecular mechanism has been made. Special attention has been paid in evidencing the important role of genomic and proteomic approaches in the study of such a complex system where different signal pathways are involved.

The second part of the paper is dedicated to polymorphic variants of VDR gene with special care for functional implications, thus functional studies rather then genetics ones have been reviewed in this section.

KEY WORDS: vitamin D receptor, functionality, genetics, polymorphisms.

Introduction

Vitamin D receptor (VDR) (1) is the responsible of much of the vitamin D $[1,25-(OH)_2D_3]$ signalling. It is a direct regulator of gene transcription, belonging to the nuclear receptor family. Within this family, it has sequence and structure resemblance with the subfamily that includes retinoic acid, thyroid hormone and peroxisome proliferator activator receptor (PPAR) receptors (2).

VDR is a protein of 427 amino acids, with a molecular mass of approximately 48 kDa. Similarly to the other nuclear receptors VDR consists of several distinct functional domains, namely the NH2 terminus A/B domain whose function is still unclear, a DNA binding domain (DBD), termed C domain, spanning from amino acid 20 to 90, a hinge or D domain (amino acids 90 to 130) and the ligand binding domain (LBD), or E domain, spanning from amino acid 130 to 423 (3). The last one is the most complex domain of the protein as it is responsible for the specific binding of VDR ligands, for heterodimerization with retinoid X receptor (RXR) and for interactions with transcription factors (Figure 1) (2).

VDR cDNA was firstly cloned from chicken (4) and shortly thereafter from human (1). Genomic organization of the human VDR gene, which locates on chromosome 12q13-14, is similar to other nuclear receptor genes. The gene is made up of 11 exons spanning approximately 75 kb (Figure 2). The non coding 5' end of the gene includes several exon 1 isoforms (from 1A to 1E) while exons 2-9 encode the structural portion of the VDR gene product. Alternative splicing of exon 1 provides at least five different VDR mRNA transcripts, while the presence of a polymorphic sequence in exon 2 determines the presence or absence of an alternative start translation site (5). Most of the promoter sequence is upstream exon 1 and has high GC content but does not contain an apparent TATA box. The promoter



Figure 1 - Schematized linear amino acid sequence illustration of VDR protein showing the functional domains of protein that mediate ligand and DNA binding, nuclear localization, heterodimerization with retinoid X receptor (RXR) and transactivation. COOH-terminal ligand activation funtion 2 (AF2) is shown in anthracite-grey.



Figure 2 - Schematic view of the genomic sequence of VDR gene containing Exon (Ex.) – Intron structure and position of known polymorphic variants.

is capable to generate multiple tissue-specific transcripts (6) and is positioned just downstream from collagen type II alpha 1 gene (7, 8). A unique feature for this gene is the presence of an additional exon that is not found in other nuclear hormone receptors family members. It encodes for an insertion peptide of about 40 amino acid that locates in the LBD of the receptor (5).

VDR binds its physiological ligand 1,25-(OH)₂D₃ with high affinity (about 10^{-10} M) (9, 10) and both hydroxyl groups seem to be relevant in determining it as the absence of either results in approximately a 500-fold decrease in affinity (11).

Although widely expressed, VDR protein levels are usually low and reach relatively high values only in targets tissues such as bone, kidney and intestine (3,000-6,000 fmol/mg protein) (12).

In contrast to other nuclear receptors which are usually bound to cytoplasmic proteins before hormone binding (13), VDR is predominantly nuclear (14).

Similarly to other nuclear receptors VDR is active as a heterodimer with members of the RXR family of receptors and the binding with RXR LBD stabilizes both heterodimerization and high affinity interaction with DNA (15). VDR regulates target genes transcription in part by binding specific DNA sequences known as vitamin D responsive elements (VDREs), located in the 5'-flanking region of target genes and composed of tandem hexameric motifs with the consensus PuG(G/T)TCA which are often arranged as direct repeats separated by 3 bp (DR3-type) but that occur also as inverted repeats separated by 6 or 9 bp (16-19).

VDR regulates gene transcription by ligand-dependent recruitment of coregulators such as SRC family proteins (20-23) and transcriptional "integrators" like Calcium binding protein (CBP) and p300 which, in addition to other functions, have been demonstrated to act as histone acetylases (24-26). This series of events leads to DNA structure remodelling through acetylation of histones and their subsequent release from DNA and consequently to the opening of the promoter to the transcriptional machinery with the final event of an increased rate of transcription of that gene. Although not speculative, the proposed mechanism is far from being well characterized, a number of details and the exact sequence of events remaining unclear at this point.

Vitamin D signalling has numerous biological effects affecting the physiology of a broad range of human tissues (3, 27). First of all it controls calcium transport in the intestinal epithelia affecting the physiology of bone metabolism; in several studies vitamin D effects on cellular proliferation and differentiation have been demonstrated, as well as an antiproliferative action on several kinds of cancer such as myeloid leukaemia, melanoma and different carcinomas (reviewed in 3). Moreover vitamin D analogues have proved to have chemopreventive action in animal models of colon, hamster check pouch, hepatocellular, gastrointestinal and skin carcinogenesis (28). Consistently with the broad expression of VDR in cells of the immune system and with its effect on cell differentiation, an important role as modulator of the immune response has been demonstrated (29).

Polymorphic sequence variations in VDR gene occur frequently in the population, but they are less analysed and their effects on gene function are poorly understood. Most of them consist of anonymous variations that do not modify the coding region with unknown functional effects. Several studies using candidate gene approach demonstrate that supplementation of 1,25-(OH)₂D₃ increases bone mineral density (BMD) and decreases the risk of osteoporotic fracture (30, 31). Thus, to understand the mechanisms underlying these associations we need to analyze genomic organisation of *VDR* locus (polymorphisms, linkage disequilibrium and haplotypes). Literature regarding *VDR* polymorphisms in relation to bone metabolism diseases, and osteoporosis in particular, is well represented, while studies on *VDR* polymorphisms and other cancer and immune response diseases are restricted and started later on.

Transcriptional regulation by VDR

Ligand binding, involving the AF2 domain, imparts a conformational change in the secondary structure of the VDR which triggers the recruitment of motor proteins (32) responsible for cytoplasmic VDR transition to the nucleus along microtubules (33). VDR heterodimerization with its protein partner RXR confers a conformational structure to the receptor which is critical for transactivation function (34) by high affinity interaction with VDREs in the promoter region of vitamin D-responsive genes (Figure 3). During VDR-RXR interaction with the most common VDRE type, DR3, RXR binds the 5' half-site and the VDR occupies the 3' one (35). According to mutagenesis experiments in the VDRE of avian parathyroid hormone (PTH) gene promoter, the switch between VDR-RXR-activated or -repressed gene transcription depends on the polarity of the VDR/RXR-VDRE complex (35). However recent experimental evidences regarding VDR interactions with nuclear coregulator molecules and their action on VDR-mediated regulation of gene transcription have provided further complexity to the entire mechanism. In fact RXR heterodimerization and AF2 domains are both involved in interactions with nuclear proteins which serves as VDR-coregulators (36). In details the ligand-induced conformational change in AF2 domain is critical for the receptor to interact with components of the transcription initiation complex, RNA polymerase II and nuclear transcription coactivators which promote chromatin remodelling necessary to gene transcription. Some of them in fact, such as SRC-1 and CBP/p300 are histone acetylases which determines the recruitment of a second complement of transcription coactivators, the DRIP-TRAP complex. This is a 15 proteins-complex which facilitates the assembly of the preinitiation complex thus strengthening VDR-induced gene transcription. Binding of VDR-RXR complex



Figure 3 - Proposed model for the control of VDR-mediated transactivation. Vitamin D (represented by black triangle) - VDR complex heterodimerizes with RXR. The resultant heterodimer binds specific sequences in the promoter region of target genes. The DNA - bound heterodimer recruits components of the RNA polymerase II (Pol II) preinitiation complex and nuclear transcription regulators, thereby altering the rate of gene transcription.

to a negative VDRE promotes recruitment of corepressors which have histone deacetylase activity and then inhibit binding of proteins promoting the assembly of the transcription machinery (37, 38). The situation is further complicated by comodulator proteins, such as NCoA62/Skip which can act as corepressor or coactivator depending on the specific cell context of coregulator molecules (39). The NH₂-terminal region of Skip protein is targeted by both nuclear corepressors, such as NCoR, and coactivators, like CBP/p300, and more importantly some of them are under VDR-mediated transcriptional regulation (39, 40). Recently an ATP-dependent chromatin remodelling complex has been demonstrated to amplify VDR activation and repression of transcription (41).

Calcium homeostasis

Vitamin D metabolism is a classic endocrine system that responds to changes in serum calcium concentrations. A decrease in serum calcium concentration, due to low dietary calcium intake, causes an increased production and release of PTH which, among many other functions, stimulates renal 1a-hydroxylase activity and leads to increased conversion of 25-hydroxyvitamin D₃ [25(OH)D₃] to its active metabolite 1,25(OH)₂D₃. Increased level of serum 1,25(OH)₂D₃ activates VDR in a tissue specific manner and stimulates the expression of vitamin D-responsive genes in districts that control calcium homeostasis, for example TRPV6 and calbindin D9k in intestine, osteocalcin and RANKL in bone, TRPV5 and calbindin D28k in kidney (42).

The traditional reductionist approach used in the past decades, to understand biological processes, has been undoubtedly useful for the elucidation of signal transduction pathways and will certainly continue to be so but it has the fault to deal only with proteins and functions we already know, testing single hypothesis of their involvement in the biological process, while the newly born genomic and proteomic approach let us gather the global changing (at the mRNA or protein levels) accompanying a biological process.

Calcium is critical for a number of life's essential functions and probably its employment in so important biological process (neural transmission, muscle contraction and relaxation, exocrine secretion, blood clotting and cell adhesion) occurs because of the constancy and abundance of calcium in seawater which is the medium where higher animals arose (Figure 4). The high abundance of calcium in the seawater also explains its use in the construction of structural elements such as the skeleton. The important calcium involvement in the biology of higher animals is the reason for being one of the most tightly regulated substance in their plasma (43) and make it reasonable that the evolution of the calcium homeostatic system took place as animals emerged from the sea into fresh water and further onto land. This is a very complex system that involves many hormones with the vitamin D endocrine system being the basic one in managing plasmatic calcium levels, with equally important roles for PTH and calcitonin (3).

Calciotropic hormones

Role of PTH

The parathyroid gland is the calcium-sensing organ in the body (43, 44) and in a few seconds it responds to even slight hypocalcaemia by secreting the 84-amino acid peptide hormone PTH (45). Its receptor is expressed in the nephron and in osteoblasts but not in intestine and osteoclasts for example (46). In the kidney PTH acts as a phosphate antireabsorptive agent causing a phosphate diuresis (47), activates 25-hydroxyvitamin D-1 α -hydroxylase and inhibits 24-hydroxyvitamin D-1 α -hydoxylases



Figure 4 - Biological actions of vitamin D in calcium and phosphorus homeostasis in mammals. Vitamin D is mostly synthesized in the dermis under UV B radiation from its precursor (7-dehydrocholesterol). It is hydroxylated to 25(OH)D in the liver and then activated to $1,25(OH)_2D_3$ (calcitriol) in the kidneys. Calcitriol induces intestinal absorption, controls bone remodelling, suppresses parathyroid function, and renal calcium reabsorption to maintain calcium on limit levels for normal cell physiology and skeletal integrity. Renal vitamin D production also serves autocrine and paracrine functions.

through cAMP increase (48) thus causing an increment in plasma levels of active $1,25(OH)_2D_3$ (49) (Figure 4).

Role of vitamin D

Vitamin D initiates an active intestinal calcium transport in the small intestine (50). This action has the longer lifetime, measurable in days, while the other actions are shorter (51). The results of the action of PTH and 1,25(OH)₂D₃ is the mobilization of calcium by the skeleton into the plasma compartment and this is obtained by either osteoclast stimulation to resorb bone and to reverse calcium transport from bone fluid compartment to plasma (52-54) (Figure 4). Even in the distal renal tubule PTH and 1,25(OH)₂D₃ act synergistically to reabsorb the last 1% of the filtered load of calcium into the plasma compartment (55, 56). Interestingly, through the study of animal models, defective for either 1,25(OH)₂D₃ or PTH, it has become evident that the presence of both hormones is required for this system to operate in vivo although the precise mechanism of the interaction between them is still poorly understood (57). Finally the rise in serum calcium level resets the sensing point of the calcium receptor and shuts down the secretion of PTH (3).

Role of calcitonin

To guard against the calcification effects of hypercalcaemia (dangerous for kidney, heart, aorta and intestine) there is also the response of parafollicular and C cells of the thyroid which respond to hypercalcaemia with calcitonin secretion, a 34-amino acid peptide hormone that causes lowering in serum calcium level by its action on the skeleton through inhibition of osteoclasts and osteocytes activities (58). There have been reports of calcitonin effects on kidney and intestine but these are derisive respect to those on the skeleton (3) and a sort of regulation on $1,25(OH)_2D_3$ metabolism has been described but this has been shown to be largely secondary to changes in parathyroid secretion (59, 60).

Physiological action of VDR

Effects on intestinal calcium

The role of vitamin D in intestinal absorption of calcium is well known and the vitamin D endocrine system has been finally identified as the agent that stimulates intestinal calcium absorption to meet the needs of the skeleton (61) (Figure 4). Epithelial calcium channel TRPV6 (CaT1 or EcaC2) is necessary for calcium uptake together with TRPV5 (EcaC1). Then calbindin D shuttles the ion across the cell and finally the plasma membrane Ca²⁺ ATPase (PMCA1b), and the Na⁺/Ca²⁺ exchanger (NCX1) deliver it into the bloodstream (62). TRPV5 and TRPV6 expression levels depend on VDR regulation as demonstrated by their reduction in VDR-null mice and their induction by calcitriol supplementation in wild-type mice (62-64). These two channels confer high Ca2+ selectivity and negative feedback regulation to intestinal Ca2+ influx, strictly resembling that in native distal renal cells (65). Vitamin D has a clear role even in stimulating intestinal absorption of phosphate which is another active calcium transport mechanism but which appears to be completely independent from the direct one (66-68). VDR-mediated mechanism to maintain the Ca-PO₄ ion product seems to primary involve induction of phosphate translocating proteins in kidney and perhaps in intestine. Indeed the renal sodium-phosphate cotransporter-2 (NPT2) is a likely vitamin Dinduced protein containing a VDRE in the promoter region (69, 70). Another role of VDR in phosphate homeostasis is due to

1,25(OH)₂D₃ induction of PEX gene expression. PEX gene, which harbours a VDRE in its promoter region (71), is a phosphate-regulating gene, showing high homologies to endopeptidases located on the X-chromosome and postulated to be the proteolytic agent for inactivation of phosphatonins (72) which in turn have phosphaturic action through potent inhibitory effects on NPT2 and 1 α -hydroxylase (73, 74). From a mechanicistic point of view, intestinal active phosphate transport is stimulated by a vitamin D-induced increase of Na- PO₄ cotransporter and plasma membrane fluidity of enterocytes (75, 76). On the contrary the mechanism that mediates phosphate transport through basolateral membrane is still unknown.

Effects on bone calcium mobilization

A vitamin D deficient animal on a zero-calcium diet will adjust serum calcium level at the expense of skeleton when given $1,25(OH)_2D_3$ in the presence of PTH (57). A clear stimulatory effect on osteoclastic bone resorption has been widely demonstrated for vitamin D (77, 78) although there is no expression of PTH receptor nor of VDR in osteoclast (79). On the contrary PTH and vitamin D interact with osteoblast arising a paracrine signal which facilitates osteoclast differentiation (80-82) and calcium mobilization from bone fluid compartment to the plasma one (83). Stimulation of osteoclastic bone resorption is, however, rarely finalized to provide calcium for plasma but more likely it is coupled to formation in completing the bone-remodelling process. Thus $1,25(OH)_2D_3$ results to be involved in important processes which strengthen bone and repair microfractures (78, 84).

From a molecular point of view vitamin D/VDR system permits a regular coupling in bone turnover by controlling the interaction between receptor activator of NF-kB ligand (RANKL) and receptor activator of NF-kB (RANK). In fact RANKL, expressed on osteoblast surface, can bind either RANK, inducing a signalling cascade leading to differentiation and maturation of osteoclasts, or to an osteoblast-produced decoy receptor, osteoprotegerin (OPG), which in turn blocks this signalling (85, 86). Vitamin D, PTH and prostaglandins stimulate RANKL expression but the first one also inhibits OPG synthesis (87,88) (Figure 5).



Figure 5 - Schematized representation of Vitamin D-regulated osteoclastogenesis. Vitamin D regulates this process by transcriptional control of both receptor activator of NF-kB (RANK) ligand (RANKL) and osteoprotegerin (OPG). Vitamin D – VDR complex increases the expression of RANKL on the surfaces of osteoblast, where it interacts with RANK promoting maturation of osteoclast progenitor cells to mature osteoclasts. Vitamin D – VDR complex also represses the expression of OPG (a bait receptor that binds RANKL and prevents RANK-mediated osteoclastogenesis).

Moreover data obtained from VDR-null mice together with the ability of a lactose-, calcium-and phosphate-rich diet to reverse their bone abnormalities, stress the concept that vitamin D plays its important physiologic effects on intestinal absorption of calcium and phosphate although some calcium regulating devices, such as depressed renal calbindin D_{9k} mRNA expression in kidney, are not restored under the above diet (89). A VDRE has in fact been demonstrated to be present in the calbindin D_{9k} promoter in mammals (90), thus accounting for a direct effect of VDR on its expression.

Effects on parathyroid glands

Vitamin D acts in parathyroid tissue through its binding to VDR and consequent regulation of gene transcription (91, 92) and a VDRE was demonstrated in the promoter region of the PTH gene (93, 94). Thus 1,25(OH)₂D₃ exerts a negative feedback on PTH production in response to PTH-dependent activation of calcium mobilization from kidney and bone, through a VDR-mediated silencing of PTH gene transcription (95-97). Moreover 1,25(OH)₂D₃ regulates parathyroid level of VDR and its response to calcium. The first effect is due to an increase in VDR mRNA level, possibly secondary to serum calcium increase (98), as well as to a ligand-dependent VDR protection from proteosomal degradation (99). The second one directly involves VDR-mediated regulation of calcium sensing receptor (CaSR) gene transcription as evoked by the presence of two VDREs in its promoter region (98, 100). The other important effect of 1,25(OH)₂D₃ on parathyroid glands involves cell growth regulation and is described in other chapter.

Effects on the kidney

One of the major effect of vitamin D in the kidney is its own homeostasis through inhibition of 1 α -hydroxylase and stimulation of 24-hydroxylase expression as well as through induction of megalin expression in the proximal tubule (101). Moreover it stimulates renal calcium reabsorption and enhances calbindin expression, accelerating PTH-dependent calcium transport in the distal tubule (102) (Figure 4). Finally vitamin D/VDR acts on TRPV5 promoter to increase its mRNA and protein levels which is an important actor in vitamin D-mediated calcium reabsorption (103).

Regulation of cell proliferation/differentiation and chemopreventive actions of vitamin D

Vitamin D has been shown to have pro-differentiation action on preadipocyte cell lines (104), on immature basal layer skin cells into keratinocytes (105) and on haematopoietic cell lines along the macrophage/monocyte pathway (106-108). Finally a potential use of $1,25(OH)_2D_3$ in the treatment of leukaemia and other myeloproliferative disorders is suggested by observations on vitamin D ability to inhibit clonal proliferation and promote a more differentiated and less aggressive phenotype in a variety of human leukaemia cell lines (109) (Figure 4).

Suppression of cell growth

A common aspect to different mechanisms through which vitamin D suppresses cell growth is the arrest at G_1 - G_0 transition. 1) Vitamin D induces gene transcription of p21, a cyclin-dependent kinases inhibitor, inducing growth arrest and promoting cell differentiation of monocyte-macrophage lineage (110). 2)

Vitamin D induces p27 synthesis through VDR-Sp1 interaction at the p27 promoter and inhibits p27 degradation rate through reduction of CDK2 activity and Skip2 protein level (111). 3) In TGF-a/EGFR-driven tumorigenesis vitamin D sequesters ligand-activated EGFR thus reducing growth signal at the cell membrane and EGFR-mediated activation of cyclin D1 gene transcription (112). Vitamin D efficacy in inhibiting mitogenic signals from the TGF- α /EGFR growth loop is also fundamental in mediating its efficacy in treating psoriasis and scleroderma. 4) Vitamin D is also able to induce C/EBPβ expression with the consequent suppression of the oncogenic-cyclin D1 signature in human epithelial tumours (113). Moreover the dominant negative isoform of C/EBPB, LIP, lacking the transactivation domain, strengthens cyclin D1 induction of cell growth and the ratio C/EBPβ:LIP has been indicated as a major mechanism for EGFR-induced proliferative action (114). Vitamin D-mediated induction of C/EBPß expression should contribute to higher C/EBP_β:LIP ratio and, consequently, to reduce proliferation rates (115).

Regulation of apoptosis

Vitamin D exerts proapoptotic as well as antiapoptotic effects which affect both normal tissues growth and function and cancerous as well as noncancerous hyperproliferative tissues. Evidences regarding certain VDR alleles association with cancerprone phenotypes suggest the involving of VDR in these effects (116, 117). For instance, in breast cancer cells vitamin D induces apoptosis through reciprocal modulation of Bcl2 and Bax content (118). Moreover it causes the calcium-dependent proapoptotic proteases microcalpain and caspase 12 activation through intracellular calcium increase (119, 120). Vitamin D proapoptotic actions have been demonstrated even in glioma (121) and in melanoma (117), while they are absent in normal astrocytes, melanocytes and mammary cells (122). Rather, vitamin D protects keratinocytes from UV radiation- or chemotherapy-initiated apoptosis (123) and melanocytes from TNF- α - and UV irradiation-dependent apoptosis through induction of sphingosine 1-phosphate (122). Other mechanisms through which vitamin D affects apoptosis seem to be tissue specific: for instance in colorectal cancer VDR expression is negatively influenced by transcription factor Snail, which is recruited to the VDR promoter, with the consequent lowering of E-cadherin expression which in turn influences cell fate during colon cancer progression. This mainly influences the efficacy of vitamin D adjuvant therapy in colon cancer (124). On the other hand, in prostate cancer, defective nuclear vitamin D localization and SMRT corepressor altered expression levels, but not reduced VDR levels, are responsible for resistance to vitamin D therapy (125).

Regulation of the immune response

Vitamin D endocrine system positively affects infection, autoimmune diseases, tolerance in transplantation and this mainly derives from prodifferentiating effects on monocytemacrophages, antigen-presenting cells, dendritic cells (DC) and lymphocytes (126) as evidenced from *in vivo* and *in vitro* studies (Figure 4).

One of the mechanisms mediating vitamin D function in resistance to infections is the already mentioned induction of C/EBP β which enhances monocyte differentiation to macrophage, immune function, host defence against bacterial infection and tumour cell growth and production of IL-12, the cytokine inducing Th1 response (115, 127). On the other hand γ -interferon is a potent inducer of 1 α -hydroxylase in macrophage thus increasing vitamin D local production through a C/EBP_β-mediated mechanism (128). Local macrophage-produced vitamin D is also an inducer of T cell response to cutaneous antigens in vivo, including CD4-Th2 cell-mediated and mucosal antibody responses (129). In contrast to these stimulatory effects on monocyte-macrophages, vitamin D is an immunosuppressor for lymphocytes (130). This effect is due to a vitamin D/VDR-mediated inhibition of expression of cytokines involved in T cell functions, including IL-2 (131), Vitamin D plays also an important role in the establishment and maintenance of immunological self-tolerance as observed in studies on animal models demonstrating a vitamin D-induced inhibition of disease induction in experimental autoimmune encephalomyelitis, thyroiditis, insulin-dependent diabetes mellitus, inflammatory bowel disease, systemic lupus erythematosus and both collagen-induced arthritis and Lime arthritis (129, 132). Finally vitamin D inhibits rejection of transplanted tissue probably through a VDR-mediated mechanism involving TGFβ/Smad3 interactions (133). In conclusion vitamin D seems to be a modulator of the immune response mainly acting through a paracrine loop which may block inflammation and/or modulate the differentiation of activated CD4 T cells as well as the suppressor T cell function (126).

VDR polymorphisms and VDR function

VDR gene polymorphisms are one of the more intriguing and controversial questions, in terms of genetics and functional understanding about genetics of bone. Nevertheless, in the last years the interest about these polymorphisms on other diseases, such as breast, prostate, colon cancer and immune response, is growing. The majority of *VDR* polymorphisms are in the regulatory areas, such as 5' promoter and 3'UTR regions, rather than in coding exons. The reason for this hot-spot location is that the variation in the protein sequence could result in drastic functional effects, such as alterations on ligand and DNA binding. Therefore, polymorphic variation, that can explain population variance, exist in areas of gene that mainly affect VDR expression level.

Genetics of VDR polymorphisms

Several polymorphisms have been identified in human *VDR* gene locus using various approaches that include the following: a) screening with different restriction enzymes for polymorphic banding patterns in Southern blot hybridisation experiments (RFLPs); b) *VDR* sequencing in a number of different individuals; and c) in silico polymorphism identification through bio-informatics approaches (Figure 2). Among numerous osteporosis candidate genes that harbour polymorphic sites, the gene encoding for VDR was the first to be described (134) and, according to its functional role, it was proposed as a major locus for genetic effect on osteoporosis (135-137).

The restriction endonucleases *Taql*, *Apal*, *Bsml* and *Eco*RV allow to recognise the allelic variants due to single nucleotide polymorphisms (SNPs) at the 3' region of human *VDR* gene. Another polymorphic variant, recognized by *Fokl* endonuclease, is located in a putative initiation transcription codon of exon 2. The alleles are named T-t, A-a, B-b, E-e and F-f respectively, where the lowercase letter means presence of restriction site and the uppercase letter indicates absence of restriction site. PolyA variable number of tandem repeats (VNTR) is present in the 3' UTR (138). This polymorphism determines at least 12 different alleles, with a bimodal distribution. Subjects can be classified as short or long PolyA carriers. Finally, caudal-related homeodomain (Cdx2) polymorphism was found through sequence analysis (139). This new *VDR* polymorphism

(G to A) is located in Cdx2 binding site at 5' $V\!D\!R$ promoter area.

VDR polymorphisms and association studies

Morrison and co-workers analysed an Australian population sample and evidenced the presence of association between allelic variants in the 3' region (for B allele) and osteocalcin bone turnover marker levels in serum (135). Since 1992, several studies about correlation of VDR polymorphisms with BMD and bone turnover markers have been published, generating conflicting data (140-163). In order to elucidate these pitfalls, a more recent meta-analysis study confirmed the contribution of Bsml allelic variants on variation of BMD values, even if this analysis showed weaker association than originally claimed (165). This observation is also supported by another metaanalysis study, where allele B significant association with spine BMD was demonstrated, following a supposed recessive model of transmission, with the BB genotype having lower BMD than Bb and bb genotypes at the baseline (166). Consequently, BMD resulted to be associated to VDR gene polymorphisms with high levels of confidence. Moreover, it is not possible to completely exclude a presence of linkage disequilibrium between VDR polymorphisms and other important genes for bone metabolism, such as $ER\alpha$. In fact $ER\alpha$ exerts a modulation effect on VDR in BMD determination, suggesting the existence of gene-gene interaction (167, 168).

Several studies on population of Mexican-American (169), Japanese (170), North American (171) and Italian (172) postmenopausal women, showed an association between low lumbar BMD and *ff* genotype, while no significant association was found in French (173) and Swiss women (143). These contrasting results may be due to ethnic and age differences. Moreover environmental factors, such as calcium intake, may conceal *Fokl* genotype effects on BMD. A recent study on a Finnish population indicates that the *Ff* genotype is associated with higher forearm BMD and calcaneal ultrasound values in adolescent boys (174).

Cdx2 polymorphism may modulate BMD in postmenopausal Japanese women (139). In fact, Japanese women who carry the A allele have higher BMD. Nevertheless, this result was not confirmed for Caucasian women where this allele resulted to be associated only with a decrease of fracture risk (175).

It is largely demonstrated that VDR polymorphisms may influence bone metabolism. Nevertheless, some recent isolated studies showed the association between VDR polymorphisms and other diseases risk. It was found a role for VDR polymorphisms (Apal and Tagl) increasing the risk of developing multiple sclerosis (176). Variants of Bsml VDR polymorphism were associated with increased risk of developing hypercalcemia in peritoneal dialysis patients (177). Lower VDR mRNA levels associated with b, a, and T alleles may affect the calcitriol-mediated control of parathyroid function and thereby contribute to the development of sporadic primary hyperparathyroidism (178). Fokl VDR polymorphism may influence parathyroid response in chronic renal failure (179). Fokl C allele was also found to be associated to high risk for colorectal cancer (180). Another study found sun exposure and VDR polymorphisms act synergistically in the aetiology of prostate cancer (181). And finally, Bsml VDR genotypes in combination with low Vitamin D circulating levels, may increase risk of breast cancer in Caucasian population (182). However, these observations need to be confirmed by further independent studies.

VDR polymorphisms and haplotyping

Linkage disequilibrium measures the association of alleles of adjacent polymorphisms (183). Besides, many studies have

addressed on the relationship between multiple individual polymorphisms in *VDR* gene and bone health, but only few have analysed *VDR* gene data in terms of haplotypes. Haplotypes are blocks of linked alleles of neighbour polymorphisms, whereby the length of such a block coincides with the strength of linkage disequilibrium across the area. When a haplotype is identified as the risk allele it is possible to determinate which variants on that haplotype allele truly causes this effect.

A meta-analysis study with data on 3' *VDR* gene polymorphisms was performed in order to estimate haplotype frequencies, determine linkage disequilibrium and estimate the magnitude of the association between haplotypes and osteoporosis/ BMD (184). Results show that the most common haplotype for *VDR* gene, regardless of ethnicity, is the *baT*, followed by *BAt* and *bAT* in Caucasians, and *bAT* followed by *BAt* and *bAT* in Caucasians, and *bAT* followed by *BaT* in Asians, indicating strong linkage disequilibrium between *BsmI* and *TaqI* polymorphisms. These observations demonstrate a gain in the power considering the haplotypes rather than single polymorphism. In fact, in this study, *VDR* gene polymorphisms were not significantly associated with osteoporosis risk on their own, but *Bat* and *BAt* haplotypes were significantly associated.

PolyA polymorphism showed strong linkage with BsmI polymorphism (142), where *b* allele was associated with long PolyA allele and *B* allele with the short one. Combining the results the following can be deduced: baT haplotype is linked to long PolyA allele and BAt haplotype to short one.

VDR polymorphisms and its ethnic distribution

Similarly to other genes polymorphisms, significant differences exist in VDR polymorphisms distribution among different ethnic groups. A possible explanation to polymorphism generation phenomena is DNA damage events in an ancient small population that grow up in frequency becoming polymorphisms in modern populations. VDR haplotypes distribution reflects out-of-Africa evolution theory that describe human populations origin and dispersion around the world, where gene-environment interactions favours the survival of some allelic variants. Old polymorphisms might show large population/ethnic variability (Fokl), while new ones are likely characterized by small population variability (Cdx2). Assuming that a polymorphism should have the same functional effect in different ethnic groups, different allele frequencies across these groups may explain differences in the incidence of pathologies and variability on drug response among them (i.e. Asians seem to be more vitamin D-sensitive while Caucasians appear more oestrogen-sensitive than other ethnic groups). In the case of non-functional polymorphisms, frequencies of these markers are very different among ethnic groups. It is also difficult to understand consequences of ethnic allele variation in this case, because of environmental factors interference, such as diet and physical exercise. This emphasises that an haplotypes map of VDR polymorphisms in different ethnic groups is necessary (116).

Functionality of VDR polymorphisms

Functional studies are needed to determinate the way certain haplotypes in a candidate gene affects protein function. Compared to the larger number of genetic association studies, there has been little published on the mechanism through which *VDR* gene polymorphisms might influence VDR receptor functionality.

Functional studies include *in vitro* cell biological and molecular studies and *in vivo* measurements of biological markers, and response to treatments (vitamin D, calcium, hormone replace-

ment therapy and bisphosphonates). Whereas the functionality cf *Cdx2* and *Fokl* alleles are well known, there are less certainty and some controversies regarding 3' region RFLPs and VN-TR polymorphisms effects. As these ones do not involve amino acid substitutions in the protein, these allelic variants may be related to regulative differences. The 3'UTR of genes is known to be involved in regulation of expression and in mRNA stability. Some studies show that the 3'UTR *VDR* gene polymorphisms do not affect abundance of VDR mRNA, nor its stability (185-189). These findings suggest that these polymorphisms do not affect VDR function, but rather may be a marker for a nearby gene that is responsible for the genotype associated variation.

The case of *Fokl* polymorphic variant (ATG/ACG) of VDR gene (169) is something different. It generates a length difference of 3 amino acids in the protein. *In vitro* studies on HeLa cells showed that *FF* genotype (short form) gave an approximately 1.7-fold increase in transcription activation (170). Whereas, no difference was found using GMK-Cos7 and human fibroblasts (190). More recent data confirmed Arai results using Cos7, HeLa and ROS 2/3 cell lines (191), and peripheral mononuclear cells (192). Jurutka et al. demonstrated the short form interacts more efficiently with transcription factor TFIIB, and Col-in found that it also had a lower dose effect and thus determined a more active VDR molecule in inhibiting the (Phytohemagglutin-stimulating) cell growth. In conclusion this polymorphism seems to be functional in terms of VDR transactivation function.

Functional studies showed that Cdx2 polymorphism affects VDR expression in the small intestine (139). As intestine is the predominant area for calcium absorption, it is possible that Cdx2 influences vitamin D-mediated regulation of calcium absorption. The allele A, which shows a more efficient binding to Cdx2 transcription factor, is thought to cause increased VDR expression in intestine with a consequent increase in the transcription of calcium transporting proteins. This process can enhance calcium absorption resulting in higher BMD values. However, this increase was only demonstrated for Japanese women (139), and was not found in Caucasian ones (174), where A allele correlate with lower fracture risk independently of BMD values. Despite this controversial results, the functionality of this polymorphism has been demonstrated but this last issue (fracture risk) requires further studies. In fact, a recent study (193) regarding haplotype alleles of the 5' promoter region and of the 3' UTR region, strongly associated with increased fracture risk, was performed. This study demonstrates lower VDR mRNA levels in an osteoblast cell line harbouring the fracture risk haplotype. Low VDR mRNA levels impact on vitamin D signalling efficiency and might contribute to the increased fracture risk observed for these risk haplotype alleles.

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