

Vitamin D Gene Pathway Polymorphisms and Risk of Colorectal, Breast, and Prostate Cancer

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Abstract

Higher vitamin D exposure is hypothesized to prevent several cancers, possibly through genomic effects modulated by the vitamin D receptor (VDR), and autocrine/paracrine metabolism of the VDR's ligand, $1\alpha,25-(\text{OH})_2$ -vitamin D. Herein we review the background and evidence to date on associations between polymorphisms in *VDR* and selected genes in the vitamin D pathway in relation to colorectal, breast, and prostate cancer. Although most studies to date have examined only a few *VDR* polymorphisms, more are beginning to comprehensively investigate polymorphisms in the *VDR* as well as in other vitamin D pathway genes, such as the vitamin D-binding protein gene (*Gc*) and *CYP27B1* and *CYP24A1*, which code for enzymes that, respectively, synthesize and degrade $1\alpha,25-(\text{OH})_2$ -vitamin D. Currently, there is no strong, consistent epidemiologic evidence for substantial influences of single variants in vitamin D pathway genes on risk for colorectal, breast, or prostate cancer, but promising leads are developing.

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INTRODUCTION

Overview

International incidence rates of colorectal, breast, and prostate cancer vary approximately 10-, 7-, and 40-fold, respectively, and immigrants from low-risk to high-risk countries acquire approximately the rates of their adopted countries within one to two generations, emphasizing the almost overwhelming influence of environment on the etiology of these diseases. In contrast, results from genome-wide association scan (GWAS) studies suggest that, aside from a few classic, high-penetrance, low-prevalence genetic variants (e.g., *BRCA1* or those resulting in familial adenomatous polyposis or hereditary nonpolyposis colon cancer), genetic variation in specific genes alone likely does not substantially contribute to risk for these cancers (64, 132, 146). On the other hand, it is clear that persons with certain ancestries appear to be at greater risk than those with

other ancestries when they adopt Western diets and lifestyles that vary from their ancestral ones (e.g., black-white differences in invasive prostate cancer in the United States). Taken together, these observations suggest that the primary influence of genetic variation on risk for these cancers is as modifiers of risk from environmental/lifestyle factors. It is also possible that cumulative risk from multiple variants of multiple genes may substantially affect risk for some individuals, either from these genetic profiles alone or in interaction with environmental/lifestyle factors.

Recently, vitamin D, long known to play an integral role in maintaining calcium homeostasis and skeletal health, has been linked to the prevention of several chronic diseases, including common cancers such as colorectal, breast, and prostate cancer (46). However, to date, most studies of vitamin D-related genes and risk for cancer have primarily investigated main effects of a few variants of these genes alone, and few have investigated these variants, alone or in combinations, as modifiers of associations of vitamin D exposure with cancer. Herein we review the background and evidence to date on associations between polymorphisms in *VDR* and selected genes in the vitamin D pathway in relation to colorectal, breast, and prostate cancer. Because of the strong biologic rationale for genotype-environment interaction, we also review published data on diet, particularly vitamin D status or intake, as a modifier of risk associated with these polymorphisms.

Vitamin D Metabolism

The primary hypothesized protective effects of vitamin D against cancer involve recently elucidated, autocrine/paracrine functions of vitamin D rather than its more well-known classical endocrine functions for calcium homeostasis and bone metabolism. The classical endocrine functions of vitamin D are reviewed extensively in standard texts, but since some of this background applies to the autocrine/paracrine functions of the vitamin, a brief summary is provided here. There are two precursors to

“vitamin D” (traditionally used as a collective term for vitamins D₂ and D₃), provitamin D₃ and provitamin D₂ (58) (**Figure 1**). Provitamin D₃ (7-dehydrocholesterol) is synthesized in the skin, where, when exposed to UVB radiation, it is converted to vitamin D₃. Vitamin D₃ is also found naturally in fatty fish and fish oil and, in many countries, including the United States, is added to milk and some cereals. Provitamin D₂ (ergosterol) is present only in plants. Vitamin D and multivitamin supplements can contain either or both forms. Vitamin D is transported by proteins (about 88% of which are a specific alpha₁ globulin, vitamin D-binding protein [VDBP or vitamin D-binding globulin], and about 11%–12% are albumin; about 0.03% is free) through the circulation to the liver, where it is hydroxylated at the 25 position to 25-OH-vitamin D [25(OH)D]. This reaction is catalyzed by one or more enzymes with 25-hydroxylase activity, including CYP27A1, CYP2D6, CYP2R1, CYP2C11, CYP3A4, CYP2D25, and CYP2J3. Vitamin D metabolites can also be taken up or sequestered and stored in adipose tissue (143). 25(OH)D can be stored in the liver or enter the circulation and be transported throughout the body. Since 25-hydroxylation is not tightly regulated, 25(OH)D levels reflect overall vitamin D status from combined dietary and sunlight sources. When serum calcium levels fall, parathyroid hormone (PTH) is released and, in the kidney, stimulates a CYP27B1-catalyzed second hydroxylation of 25(OH)D to 1 α ,25-(OH)₂-vitamin D [1,25(OH)₂D, which is 100- to 1000-fold more potent than 25(OH)D], which is then released into the circulation to increase calcium absorption from the gut, resorption from bone, and reabsorption from the kidneys through both passive and vitamin D receptor (VDR)-mediated mechanisms to restore blood calcium concentrations (**Figure 1**). The enzyme 24-hydroxylase [also known as 24(OH)ase or CYP24] initiates the degradation of 1,25(OH)₂D; in fact, the major inducer of 24(OH)ase is 1,25(OH)₂D, thus promoting its own inactivation and limiting its biologic effects.

More recently, autocrine/paracrine functions of vitamin D and their potential relevance to cancer prevention have become clearer via discoveries that (*a*) more than 36 cell types not involved with calcium metabolism are abundantly endowed with CYP27B1, CYP24, and the VDR, and produce, respond to, and degrade 1,25(OH)₂D [which is not released into the circulation because its synthesis is balanced with its degradation (41)]; and (*b*) there are vitamin D response elements (VDREs) on more than 200 genes that appear to be modulated, at least in part, by 1,25(OH)₂D, and to a lesser extent by 25(OH)D, influencing cell functions in a cell- and tissue-specific manner (34, 144). 1,25(OH)₂D is thought to act locally through genomic and nongenomic mechanisms (59, 79, 96, 110). Nongenomic effects, or rapid responses (59, 79, 96), may work through a plasma membrane receptor and second messengers involved in regulating various cell activities, including cell cycle control. Genomic effects are mediated via binding to the nuclear VDR (**Figure 2**). 1,25(OH)₂D, a relatively small, lipophilic molecule that easily penetrates the cell membrane, is taken up by the cell by simple diffusion, and binds to the VDR. The VDR then binds to target DNA sequences as a heterodimer with the retinoid X receptor (RXR), recruiting a series of coactivators resulting in the induction of target gene expression. As summarized in **Figure 2**, genomic autocrine/paracrine functions of vitamin D identified to date include roles in regulating cell proliferation, differentiation, apoptosis, growth factor signaling, and immunomodulation. Other potential functions include protection against oxidative stress, bile acid and xenobiotic metabolism, cell adhesion, DNA repair, and angiogenesis.

COMMON GENETIC POLYMORPHISMS IN THE VITAMIN D PATHWAY

Although the vitamin D “pathway” can be defined many ways, we include in our review polymorphisms associated with the *VDR* gene,

the vitamin D-binding protein gene (*Gc*), and genes that code for enzymes that initiate formation (*CYP27B1*) and degradation (*CYP24A1*) of 1,25(OH)₂D, the natural ligand for the VDR. Other genes, including the retinoic acid receptor (*RXR*), the multiple genes involved in synthesizing vitamin D in the skin or 25-hydroxylation in the liver, or genes involved in the synthesis of many other interrelated growth and risk factors involved in carcinogenesis, are not considered here.

The Vitamin D Receptor Gene (*VDR*)

By far the most well studied gene in the vitamin D pathway, *VDR*, encodes for the VDR, a nuclear transcription regulating factor that belongs to the steroid hormone superfamily of receptors. Nuclear receptors integrate hormonal, dietary, and other extracellular signals into cell-fate decisions via regulation of gene expression and repression of a host of common gene targets (133). The *VDR* gene, located on chromosome 12q13, spans over 100 kb (136) and contains six promoter regions, alternatively spliced untranslated exons 1a–1f, and eight protein-coding exons 2 to 9 (Figure 3) (116). The DNA-binding domain of the VDR peptide, encoded by exons 2 to 4, is responsible for high-affinity interaction with the VDRE in target genes. The ligand-binding domain encoded by exons 6 to 9 is responsible for 1,25(OH)₂D binding (116).

More than 470 single-nucleotide polymorphisms (SNPs) have been discovered on the

human *VDR* gene, but most have low allele frequencies. To date, only a few *VDR* SNPs have been extensively studied in relation to cancer (Table 1), and a limited number of studies have examined risk by linkage disequilibrium (LD) block (116). One commonly studied polymorphism, identified by the *FokI* restriction enzyme (*rs10735810*, also known as *rs2228570*), is in exon 2 of the promoter region of *VDR*. The presence of this site (“f”) allows protein translation to begin from the first initiation codon rather than from the second (“F”), resulting in a protein that is three amino acids longer. The longer protein (f allele) is a less active transcriptional activator (133, 137).

Three SNPs located near the 3′ region, historically identified by their restriction endonuclease cleavage sites (*TaqI*, *BsmI*, and *ApaI*), have been examined extensively in relation to bone disease (148) and cancer (133, 137). These polymorphisms include an intronic G→A replacement (*BsmI*, *rs1544410*, G = b), an intronic C→A replacement (*ApaI* *rs7975232*, C = a), both between exons 8 and 9, and a T→C replacement in exon 9 (*TaqI* *rs731236*, T = T) that results in a synonymous change at codon 352 (isoleucine). Although not functional, these SNPs are strongly linked with a poly(A) microsatellite repeat in the 3′ untranslated region. The poly(A) microsatellite repeat contains a variable number of 12 or more alleles; because the population distribution of the number of these alleles is bimodal, individuals can be classified as having short (A13–A17) or long (A18–A24) nucleotides. The poly(A) sequence

Table 1 Common *VDR* SNPs, gene positions, and putative risk alleles

SNP name	Position on <i>VDR</i>	DbSNP reference	Gene position	Major allele	Putative risk allele ^a
<i>FokI</i>	Exon 2	<i>rs10735810</i> (aka <i>rs2228570</i>)	C/T 30875	C (F)	f
<i>Cdx2</i>	Block C2	<i>rs11568820</i>	G/A 1229	G	G
<i>BsmI</i> ^b	Block B	<i>rs1544410</i>	G/A 64922	G (b)	b
<i>ApaI</i>	Block B	<i>rs7975232</i>	C/A 63935	A (A)	a
<i>TaqI</i>	Block B	<i>rs731236</i>	T/C 65013	T (T)	T
<i>Poly(A)</i> ^b	3′ UTR	<i>rs17878969</i>	Microsatellite repeat	A ₁₈ –A ₂₄	L

^aPutative risk haplotype: bL, baTL.

^bD′ *BsmI* and *Poly(A)*: Whites, 0.96; African Americans, 0.53; Hispanics, 0.77; Japanese Americans, 0.90; Chinese, 0.77 (67).

in the 3' UTR region of genes is thought to be important in post-transcriptional control of gene expression (32), either by altering mRNA stability or the interaction of the mRNA with the translational apparatus, with the long genotype resulting in greater mRNA instability.

One of the earliest studies to examine the distribution of *VDR* polymorphisms by race/ethnicity (67) described the haplotype frequencies of the *BsmI* and *Poly(A)* genotypes as follows: Among African Americans all four haplotypes (*bS*, *BS*, *bL*, *BL*) were expressed, among non-Hispanic Caucasian individuals only haplotypes *BS* and *bL* ("risk" haplotype) were commonly expressed, and among Asians only the *bL* haplotype was commonly expressed. The *BS* and *bL* haplotypes were most commonly found among their sample of Hispanics. The authors proposed that all four haplotypes were originally present, but only a subset of African alleles persisted after the races diverged (67). LD in the *BsmI* and *Poly(A)* markers is not complete; thus, two markers are probably not interchangeable for evaluating putative disease loci in association studies (67, 137). **Table 1** provides information on LD for these two SNPs. Others have extended the linkage analysis to include *Apa1* and *Taq1* SNPs to identify *baTL* and *BaTS* haplotypes (127), with the former being the putative high-risk haplotype.

Cdx2. Situated in exon 1e, *Cdx-2* modulates specific transcription of *VDR* gene expression. The *Cdx2 A* allele results in increased binding of the *Cdx-2* protein in vitro and increased transcriptional activity of *VDR* in Caco-2 colon cancer cell lines (39). In another study, the *Cdx-2* binding element with the *G* allele was associated with significantly lower transcriptional activity and somewhat lower bone mineral density than that of the *A* allele (10). The *Cdx2* SNP is in linkage with a *GATA3* SNP, which is a G to A substitution further in the promoter region upstream of the exon 1a transcription start site (54). A base change in this polymorphism leads to a change in protein-DNA complex formation (116).

VDR blocks. Nejentsev et al. (94) developed high-resolution SNP, haplotype, and LD maps of the *VDR* gene region in five population samples and identified three extensive LD blocks, termed A, B, and C (see **Figure 3**), with identical patterns in all four European groups examined. The LD blocks identified demonstrate intrablock but little interblock LD. In an African population, two additional LD-breaking spots were apparent. The variable LD observed among European and Gambian populations potentially explains some of the variation in rates of vitamin D-related cancers by race/ethnicity (94).

1,α-Hydroxylase (*CYP27B1*)

CYP27B1 encodes for 1,α (OH)ase, which resides in the inner mitochondrial membrane where it hydroxylates 25(OH)D at the 1α position to form 1,25-(OH)₂D, the natural VDR ligand. *CYP27B1* is located on chromosome 12q13.1-q13.3, spans 4.8 kb, and contains nine exons. Although four nonsynonymous SNPs have been identified, all are uncommon. Holick et al. (57) evaluated tag SNPs from *CYP27B1* with $r^2 \geq 0.8$ with common genetic variants [minor allele frequency >5% in Caucasians (57)] and identified three tag SNPs. An earlier study that sequenced the gene also identified three noncoding SNPs (55). To date, there is limited evidence as to whether polymorphisms of *CYP27B1* affect gene function.

24-Hydroxylase (*CYP24A1*)

24(OH)ase, a member of the cytochrome P450 superfamily of enzymes, is encoded by the *CYP24A1* gene, located on chromosome 20q13. The gene is 20.5 kb long and contains 12 exons. It contains four nonsynonymous SNPs, all with low allele frequency. Using HapMap data and the criteria of $r^2 \geq 0.8$ with common genetic variants (minor allele frequency >5% in Caucasians), 20 tag SNPs were selected by Holick et al. (57). Whether any of the identified SNPs have functional effects is unclear. Roff & Wilson (112) describe a functional

SNP in the *CYP24A1* promoter that results in lower expression of CYP24A1 protein. This mitochondrial enzyme initiates the degradation of 1,25(OH)₂D, the physiologically active form of vitamin D, by hydroxylation of the side chain. By regulating the level of active vitamin D, this enzyme plays a role in calcium homeostasis. Presumably, because of its important role in vitamin D metabolism and blood calcium homeostasis, major alterations in vitamin D hydroxylation activity would lead to serious illness and may have been selected against through evolution. However, if certain genotypes influence primarily autocrine/paracrine vitamin D metabolism, alterations may still occur that have minimal influence on circulating calcium levels. Because 24(OH)ase may lead to abrogation of the growth control mediated by 1,25(OH)₂D, *CYP24*, the gene that produces this enzyme, is considered a candidate oncogene (6, 90, 103).

Vitamin D–Binding Protein (*Gc*)

The protein encoded by the *Gc* gene belongs to the albumin family, together with human serum albumin and alpha-fetoprotein. Located on chromosome 4q11-q13, the *Gc* gene is 42.5 kb long and contains 13 exons and at least six nonsynonymous SNPs, two with relatively common frequency (*rs7041* and *rs4588*). The vitamin D–binding protein (DBP) greatly facilitates vitamin D actions by carrying vitamin D metabolites to various sites of action, and polymorphic DBP proteins differ in their affinity for 1,25(OH)₂D (102). The DBP may also have a role in inflammation and the immune system (76). Ezura et al. (38) characterized a C/T polymorphism at position –39 in the *Gc* promoter region that was strongly linked to bone mineral density. Kidd et al. (73) identified two of three SNPs in the *Gc* promoter region with functional effects on transcription factor binding sites. Recent studies have shown that allelic variation in the *Gc* gene is associated with DBP and serum 25(OH)D concentrations as well as higher affinity of the DBP to vitamin D metabolites (37, 77).

VITAMIN D GENE PATHWAY SINGLE-NUCLEOTIDE POLYMORPHISMS AND CANCER RISK

Colorectal Cancer

Background. Colorectal cancer is the third most commonly diagnosed cancer and the third leading cause of cancer death among both men and women in the United States (7). Although colorectal cancer screening can detect and remove adenomatous polyps, and therefore prevent most cancers, fewer than 50% of men and women in the United States age 50 and older are screened annually (8). Prevention of the disease through lifestyle modification, including engaging in regular physical activity, avoiding tobacco, and making changes in diet, can reduce the risk of colorectal cancer (108). A diet pattern low in red and processed meat and high in fruits and vegetables (and their components, such as fiber, and carotenoids) has been associated with lower risk of the disease (142). Higher circulating 25(OH)D concentrations have been fairly consistently associated with a lower risk of colorectal cancer (49), and calcium supplementation reduces adenoma recurrence (11, 17), especially among individuals with better 25(OH)D status (50). Calcium and vitamin D have antiproliferative and prodifferentiation effects in vitro, and some evidence suggests that the two nutrients act together to control colon epithelial cell proliferation (30).

Vitamin D, acting at least in part through binding with the VDR, is thought to protect against colorectal cancer via several distinct and complementary mechanisms. It reduces mutation and promotes safer patterns of cell cycle events in colon crypt cells, and it improves expression of various genes regulating the normal structure and function of the colon crypt. These effects are likely modulated through colon tissue autocrine/paracrine synthesis of 1,25-(OH)₂D. In addition, the secondary bile acid, lithocholic acid (LCA), can also activate the VDR, inducing expression in vivo of CYP3A4, a cytochrome P450 enzyme

that detoxifies LCA in the intestine and liver (85). Such increased bile acid detoxification leads to reduced colonocyte DNA mutation, cell damage, compensatory hyperproliferation, and inflammation.

VDR genotypes and colorectal cancer risk.

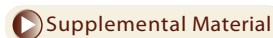
To date, approximately a dozen studies have examined selected *VDR* SNPs in relation to risk of colorectal cancer (40, 72, 93, 100, 104, 124–127, 129, 131, 141). The largest studies to date include several publications from a combined case-control dataset from the state of Utah, the Kaiser Permanente Medical Care Program of northern California, the Twin Cities metropolitan area of Minnesota (93, 124–127, 129), and a recently published large case-control study in Scotland (131) (**Supplemental Table 1**; for all **Supplemental Material**, follow the **Supplemental Material link** from the Annual Reviews home page at <http://www.annualreviews.org>). Several studies investigated potential interactions between *VDR* SNPs and calcium and vitamin D intakes or status.

The most commonly examined *VDR* SNPs were *FokI* and *BsmI* from the 5' promoter region and 3' flanking region, respectively. Out of eight studies that examined variants in the *FokI* SNP in relation to colorectal cancer (93, 100, 104, 126, 127, 129, 131, 141), two observed a significant inverse association with the *FokI* *ff* genotype and colorectal cancer risk (93, 104), one observed a significant increase in risk associated with the *FokI* *FF* genotype (100), and in another study (129), two haplotypes that included the *FokI* *F* allele were associated with significantly increased risk. Thus, four of the seven studies observed a similar association with the *FokI* SNP.

Specifically, in two analyses of data from all three participating states from the aforementioned combined case-control study, the *FokI* *Ff* genotype was associated with a 10% nonsignificant reduction in colorectal cancer risk [odds ratio (OR) 0.90, 95% CI 0.80–1.02], whereas the *ff* genotype was associated with a somewhat more pronounced decreased risk

(OR 0.81, 95% CI 0.68–0.96) (93). The common haplotype *bLF*, containing the *BsmI* *b*, *Poly(A)* long (*L*) and *FokI* *F* alleles, was associated with a slightly increased risk of colon cancer (OR 1.13, 95% CI 1.01–1.26) as was the rare *BLF* haplotype (OR 2.26, 95% CI 1.36–3.78) (129). In a population-based study of *VDR* genotypes and colorectal cancer conducted in South Korea (104), colorectal cancer patients (*n* = 190) who underwent surgical treatment for colorectal cancer at a large medical center in Seoul were compared to 318 healthy controls with no history of colorectal cancer. Colorectal cancer risk was significantly lower among those with the *FokI* *ff* genotype (compared to *FF*) (OR 0.35, 95% CI 0.19–0.65). In a case-control study conducted in Kentucky, Ochs-Balcom et al. (100) observed an increased risk associated with having the *FokI* *FF* genotype (OR = 1.87, 95% CI 1.03–3.38) and haplotypes associated with this genotype. In contrast, in a nested case-control study (*n* = 217 cases, 890 controls) in a cohort of Singapore Chinese, *VDR FokI Ff* and *ff* polymorphisms were associated with moderately higher colorectal cancer risk: ORs 1.51 (95% CI 1.00–2.29) and 1.84 (95% CI 1.15–2.94), respectively (141). This positive association was stronger among individuals with lower dietary calcium intake (*p* interaction = 0.07) (141). However, a large Scottish case-control study observed the opposite: the overall association with the *ff* genotype was null, but it was slightly positive (but not statistically significant) among individuals with higher dietary calcium intake (*p* interaction = 0.006) or vitamin D intake (*p* interaction = 0.06).

Polymorphisms in the 3' end of the *VDR* gene were not associated with colorectal cancer in the studies that examined SNPs in this region (40, 72, 100, 104, 126, 127, 129, 131). The exception is that the *Apa* *aa* allele was associated with a more than twofold increased colorectal cancer risk in a population-based case-control study in Korea (104), but not in a hospital-based case-control study in Russia (40) or a case-control study in Scotland (131), the only other studies to examine the *ApaI* SNP.



Despite the absence of associations of colorectal cancer with individual SNPs located in the *VDR* 3' region, analyses from the large multicenter U.S. case-control study support a possible lower risk of colorectal cancer associated with the *SS* genotype of the *Poly(A)* repeat and haplotypes associated with this genotype (126, 127, 129). In an analysis that included the Utah and California sites, the *Poly(A)* *SS* genotype and the *BsmI* or *Poly(A)* (*SSBB*) diplotypes were moderately inversely associated with risk [ORs 0.79 (95% CI 0.56–0.96) and 0.82 (95% CI 0.69–0.98), respectively], although the results for *BsmI* alone were null (126). There was also some evidence of an interaction between calcium intake and *BsmI*/*Poly(A)* diplotypes for rectal but not colon cancer (126). The common haplotype *bLF*, containing the *BsmI* *b*, *Poly(A)* *L*, and *FokI* *F* alleles, was associated with a slightly increased risk of colon cancer (OR = 1.13, 95% CI 1.01–1.26) as was the rare *BLF* haplotype (OR 2.26, 95% CI 1.36–3.78) (129). Therefore, there is some indication that the *Poly(A)* variants may influence risk of colorectal cancer, but that individual 3' SNPs may not predict risk when not included in haplotypes. In addition, these genotypes and haplotypes may interact with dietary calcium or vitamin D to influence risk for colorectal cancer, but the limited studies to date do not paint a clear picture.

Recently, Slattery et al. (124) found no association between the *Cdx2* polymorphism and risk of colon or rectal cancer in a large, combined case-control study. However, inclusion of the putative high-risk *Cdx2* (*A*) allele with the *bLF* haplotype was associated with a greater increased risk of colon (OR = 2.45, 95% CI 1.38–4.38) but not rectal cancer (124). Although the *bLFA* haplotype was relatively uncommon in white (6.5%) and Hispanic (6%) participants, it was much more common in African Americans (41%) and Asians (33%), raising questions about ethnic-specific genetic risk factors (124). Unfortunately, this study was too small for meaningful analyses stratified by racial/ethnic groups. A population-based case-control study of 250 cases and 246 controls from Kentucky also observed a greater than twofold increased

risk of colorectal cancer among individuals with the *Cdx2* *AA* vs. *GG* genotype (100). In the only study to examine interactions between diet and the *Cdx2* polymorphism, Slattery et al. (124) observed no interaction between dietary calcium or vitamin D and the *Cdx2* polymorphism.

***VDR* genotypes and colorectal adenoma risk.** None of the eight studies that examined associations between *VDR* polymorphisms and risk of colorectal adenoma observed a statistically significant association with colorectal adenoma risk (18, 48, 50, 63, 69, 74, 105, 106). Most included more than 200 cases (63, 69, 74, 105, 106). An advantage of the adenoma studies was that they were endoscopy based (18, 48, 50, 69, 74, 106). In one colonoscopy-based case-control study of incident, sporadic, colorectal adenoma in North Carolina, the *VDR* *Tru9I* polymorphism variant *u* allele was associated with a modest but not statistically significant decreased risk for adenoma: ORs were 0.88 (95% CI 0.17–4.55) and 0.69 (95% CI 0.40–1.25) for the *Uu* and *uu* genotypes, respectively (48). In the same population, there was no evidence for an association with the *VDR* *BsmI* polymorphism (18). Two similarly designed case-control studies found weak, nonsignificant lower colorectal adenoma risk among participants with *VDR* *FokI* *Ff* or *ff* genotypes (69, 106). In another similarly designed case-control study (74), relative to the *VDR* *BsmI* *bb* genotype, neither the *Bb* nor the *BB* genotype was strongly associated with risk of colorectal adenomas. A case-control study of colorectal adenoma nested within the Prostate, Lung, Colorectal, and Ovarian Cancer Screening Trial (*n* = 239 cases, 228 controls) found no evidence for associations with *VDR* *TaqI* genotypes (105). In a cohort analysis of the Calcium Polyp Prevention Study, there was no evidence for an association of *VDR* *TaqI* or *FokI* genotypes with adenoma recurrence (50).

These adenoma studies, although decidedly null overall for genotype associations, observed some interactions with dietary intake of vitamin D, calcium, or dairy products. In one study, participants in the lowest tertile of vitamin D

intake who had the *BB* genotype were at lower risk (OR 0.24, 95% CI 0.08–0.76) of colorectal adenoma than those in the highest tertile of vitamin D intake who had the *bb* genotype ($p_{\text{interaction}} = 0.09$) (74). A similar, non-significant association was observed for calcium intake. In the U.K. Colorectal Adenoma Prevention Trial (63), risk of recurrent adenoma was significantly lower with higher intake of dairy products, but that risk did not differ by *Cdx2*, *Fok1*, *Bsm1*, or *Taq 1* genotype. However, a significant interaction ($p = 0.02$) between the *Apa1 aA* or *AA* genotype and dairy intake was noted, suggesting that there was lower risk of recurrence among individuals with a higher-dairy diet who also had the *Apa1 aA* or *AA* genotype (63). However, the findings from the five other studies that examined interactions between dietary calcium, vitamin D, and *VDR* SNPs were null (18, 48, 50, 69, 106).

Summary. The available human studies of *VDR* and colorectal cancer do not suggest that *VDR* polymorphisms strongly, independently influence colorectal cancer risk. Although four of seven studies suggest lower colorectal cancer risk associated with the *VDR Fok1 ff* genotype, findings across studies and study designs are inconclusive for the *Fok1* SNP. The preponderance of published studies used a retrospective case-control design, possibly because of smaller numbers of incident colorectal cancer cases relative to breast and prostate cancers in the reported prospective cohort studies. Interestingly, the evidence for a role of vitamin D and calcium (as main exposures) in carcinogenesis appears to be strongest for colorectal compared to other cancers. Thus, one might expect associations with *VDR* SNPs to emerge with colorectal cancer, if they exist. It may be that polymorphisms of *VDR* (and other genes in the vitamin D pathway) modify risk related to vitamin D or calcium exposure. Although some studies reviewed suggest such an interaction, data are insufficient to draw any conclusions on gene-diet interactions and colorectal cancer. In summary, there have been no reported epidemiologic studies of polymorphisms of *CYP27B1*,

CYP24A1, or *Gc* in relation to risk for colorectal neoplasms, and currently there is neither strong nor consistent evidence that genetic variation in *VDR* plays a role in colorectal carcinogenesis, overall or in interaction with vitamin D or other exposures.

Breast Cancer

Background. Although breast cancer death rates have declined in recent years, breast cancer remains the most common cancer diagnosed, and it is the second cause of cancer deaths in women (7). Risk factors include positive family history, high breast tissue density, long menstrual history (menstrual periods that begin early and end late in life), reproductive factors (e.g., nulliparity, late age at first birth), hormone replacement therapy, regular alcohol consumption, low physical activity, and high BMI and weight gain during adulthood (for postmenopausal breast cancer). Apart from energy imbalance, few dietary risk factors have been consistently associated with risk of the disease (142).

Breast cancer rates are higher in areas of the United States with lower overall UVB exposure, raising the possibility that vitamin D may play a role in breast cancer etiology (44). In support of this hypothesis, epidemiologic studies have observed lower breast cancer risk with greater self-reported (75) and measured (71) sun exposure. The association between dietary and supplemental sources of vitamin D with breast cancer risk has been inconsistent (113), potentially because the typical doses of vitamin D intake have comparatively less impact on 25(OH)D concentrations compared to sun exposure. Circulating 25(OH)D reflects integrated input of vitamin D from sun exposure and diet over several weeks, and thus represents a better measure of vitamin D status. In some (1, 14, 43, 81) but not all (42) studies, greater circulating 25(OH)D concentrations were associated with lower breast cancer risk. This metabolite is thought to be relevant because 25(OH)D provides substrate for tissue-specific synthesis of the *VDR* ligand (97).

There is biologic support for a role of vitamin D and the VDR in breast cancer prevention. The VDR is present in all major cell types of mouse mammary gland and is upregulated during puberty, pregnancy, lactation, and involution (reviewed in 139). MMTV-neu mice lacking *VDR* exhibit abnormal mammary ductal morphology characterized by dilated, distended ducts containing dysplastic epithelial cells (147). *VDR* gene dosage also appears to influence age-related changes in ductal morphology and oncogene-induced tumorigenesis of the mammary gland in vivo. Results from animal models of breast cancer show that treatment of tumor-bearing animals with vitamin D analogues can lead to inhibition of tumor progression or regression of established tumors (reviewed in 80). 1,25(OH)₂D transcriptionally downregulates the estrogen receptor, further desensitizing cells to estrogen-driven proliferation. Dysregulation of vitamin D signaling [due to lack of 1,25(OH)₂D, mutations in the VDR, or disruption of VDR target genes] would lead to unopposed proliferation of undifferentiated cells, which may predispose to transformation (139).

Vitamin D pathway genotypes and breast cancer. The polymorphic *VDR* was first observed in human breast cancer cells 30 years ago (36). To date, at least 18 studies have evaluated associations between polymorphisms in *VDR* and other vitamin D pathway genes; most examined *VDR* 5' *FokI* and 3' *BsmI* polymorphisms (Supplemental Table 2).

The *FokI* genotype, which results in a longer, less transcriptionally active *VDR*, has been examined in at least nine studies (3, 19, 23, 31, 52, 66, 71, 86, 87), with two observing increased risk associated with the *ff* genotype (23, 87). In a nested case-control study of Caucasian women, the *FokI ff* genotype was associated with a 34% higher breast cancer risk in 1234 cases and 1676 controls (23). However, such an association has not been reported in other, mostly smaller studies of Caucasian women (3, 19, 31, 52, 71, 86), Latina women (66), or African American women (71). However, in a large, pooled anal-

ysis from six cohorts (including two previously analyzed populations; 23, 86), a statistically significant 16% increased breast cancer risk was observed for women with the *ff* (*vs FF*) genotype (87). When the previously published study that reported a positive association (23) was excluded from the pooled analysis, the risk was still increased but no longer statistically significant (87). In this large pooled analysis, associations with the *FokI* SNP were slightly stronger for localized invasive cases (OR = 1.23, 95% CI 1.08–1.41) and did not vary by ER/PR tumor type or menopausal status (Figure 4). No interactions between dietary vitamin D intake (86) or blood levels of 25(OH)D (1, 14, 52) and *FokI* genotypes have been observed. The large pooled analysis found a borderline interaction between dietary calcium intake, *FokI*, and breast cancer risk using data collected from six international cohorts. However, subanalyses may lead to chance findings and should be interpreted cautiously. Although calcium is well recognized to influence endocrine vitamin D metabolism (117), and dietary calcium may protect against local 1,25(OH)₂D degradation through direct intestinal mucosal contact (30), the regulation of vitamin D metabolizing enzymes is likely tissue specific and may not pertain to breast carcinogenesis (92).

Ten studies have examined the *BsmI* SNP in the 3' end of the *VDR* gene in relation to breast cancer risk (19, 20, 23, 52, 60, 66, 81, 86, 87, 134). The *BsmI bb* genotype is linked with a longer *Poly(A)* microsatellite repeat, which may produce more unstable *VDR* mRNA. Initial case-control studies of the *BsmI* polymorphism (*rs1544410*) suggested that variation at this site may play an important role in breast cancer risk (19, 52, 81, 114) (Supplemental Table 2). However, several other individual studies observed no association with the *BsmI* SNP (20, 23, 60, 66, 86). In a study of pre- and postmenopausal Caucasian and African American women, Trabert et al. (134) observed a higher breast cancer risk for the *BsmI bb* genotype only among postmenopausal Caucasian women. A recent pooled analysis of data from six cohorts

with more than 5000 cases observed no overall association between the *BsmI* *bb* SNP and breast cancer, regardless of race or menopausal status (87), indicating little support for an association of this SNP with breast cancer. However, consistent with several of the earlier, smaller case-control studies of the *BsmI* *bb* genotype in which a higher risk of advanced or metastatic breast cancer was observed (19, 52, 81), the pooled analysis found a lower risk of advanced breast cancer with the *BsmI* *BB* SNP in all races combined (OR = 0.74, 95% CI 0.60–0.92, *p* trend = 0.015) (87) (**Figure 4**). Although the results remained significant when limited to Caucasians (OR = 0.77, 95% CI 0.61–0.97, *p* trend = 0.045), confounding by population stratification is still a potential concern, particularly since there may be racial/ethnic differences in breast cancer survival (25, 109). Case-series studies have also suggested that the *BsmI* *bb* genotype is associated with poorer prognosis (114, 118). In animal models, hypothesized mechanisms for better prognosis with more favorable vitamin D status involve modulation of cell cycle progression, apoptosis, and cell signaling leading to reduced tumor invasiveness and angiogenesis (28).

Results from studies that explored interactions between the *BsmI* SNP and vitamin D intake or status and breast cancer risk have been mixed. Dietary or total vitamin D intake did not modify the association between vitamin D pathway genotype and breast cancer risk in one U.S. study (86). In a British case-control study in which blood was drawn after diagnosis, the higher risk of breast cancer associated with the *bb* genotype was more pronounced among those with a low level of circulating 25(OH)D (81); the OR for having a *bb* genotype and being in the lowest quartile of plasma 25(OH)D was 6.82 (2.57–17.1), whereas the main effect ORs were, for the *bb* genotype alone, 2.02 (1.03–3.97), and for being in the lowest quartile of 25(OH)D alone, 5.83 (2.31–14.7) (81). However, an interaction was not observed in a U.S.-based nested case-control study (23). Calcium intake modified associations between *BsmI* and other 3' *VDR* SNPs and breast cancer risk in

one study (86), but this was not replicated in the larger pooled analysis (87).

The 3' polymorphisms are hypothesized to be linked to a functional SNP, such as the *Poly(A)* *L* variant. The *Poly(A)* *LL* genotype was associated with a higher risk of breast cancer in three (19, 52, 66) of six (19, 52, 66, 86, 134, 138) studies. Generally, breast cancer associations with the *b* allele corresponded to associations with the *Poly(A)* *L* allele, when both were measured within a study (19, 52, 86, 134). One exception was in a study of Latinas, where the *BB* genotype was associated with increased risk of breast cancer, and the *Poly(A)* *LL* genotype was also positively associated with higher risk (66). As previously noted, linkage disequilibrium between the *BsmI* and *Poly(A)* genotypes varies by ethnicity, which underscores the point that examination of single SNPs will not reflect similar LD across populations studied and may explain heterogeneous findings in the literature (94, 116, 137).

The *ApaI* and *TaqI* SNPs, as previously noted, are in variable LD with the *BsmI* and *Poly(A)* genotypes. Four studies of *ApaI* (31, 60, 86, 122) and nine studies of the *TaqI* SNP (3, 20, 33, 60, 71, 82, 86, 95, 122) yielded inconsistent associations with breast cancer. In a small Australian study (31), the *a* allele and the *aT* haplotype were associated with higher breast cancer risk, a finding that was consistent with the higher risk hypothesized for the *baTL* haplotype. In contrast, a Finnish study reported a significant inverse association with the *a* allele, which was stronger among women with a positive family history of breast cancer (OR = 0.73) (122). In a case-series of 183 women with breast cancer, Schoendorf et al. (118) reported a higher risk of metastases to the bone in those with the *ApaI* *AA* or *TaqI* *tt* genotype. These discordant findings may be due to different influences of *VDR* SNPs on different stages of breast carcinogenesis, or they may be due to chance.

Relatively few studies have examined *VDR* genotype–breast cancer associations by ethnicity. In analyses within the racial/ethnic subgroups in the multiethnic cohort (87), the

FokI *ff* genotype was associated with highest risk among Japanese American women (OR = 1.63, 95% CI 1.07–2.49); however, the *p* for heterogeneity across racial/ethnic subgroups was not statistically significant (*p* = 0.31) (87). Japanese American women with the *BsmI* *B* allele were at comparatively lower breast cancer risk, although numbers of cases were small and the *p* for heterogeneity across racial/ethnic groups was borderline (*p* = 0.08). Neither *BsmI* nor *FokI* SNPs were associated with risk for breast cancer in African American women in either of the two studies that reported results for this racial group (87, 134).

Of other *VDR* SNPs examined, the *BglI* *BB* genotype, which lies 303 base pairs downstream of the stop codon, was associated with a 63% lower risk of advanced breast cancer (OR = 0.37, 95% CI 0.18–0.76) in a subgroup of women with medium pigmentation (71). It is unclear why this subgroup would be singled out, but the group with constitutive medium pigmentation comprised 25% of the Caucasian and 68% of the Hispanic women studied. No other studies of breast cancer have reported on this SNP. In another study, the *Cdx2* SNP was not associated with breast cancer risk (3).

Other genes in the vitamin D pathway. Two common vitamin D-binding protein gene (*Gc*) exon 11 nonsynonymous SNPs, *rs4588* and *rs7041*, were recently examined in relation to 25(OH)D and 1,25(OH)₂D concentrations (37, 77) and breast cancer risk (2, 86). The *rs4588* SNP *C* allele was associated with higher circulating levels of both metabolites in three study centers that examined Hispanic and African American populations in the United States, whereas the *rs7041* SNP *T* allele was associated with lower levels of 25(OH)D (37). However, neither SNP was associated with postmenopausal breast cancer risk in one study (86), nor was an interaction with vitamin D or calcium intake observed in that study. Another study described differences in vitamin D metabolites according to three alleles in the

vitamin D-binding protein gene (*Gc*), *Gc1s*, *Gc1f*, and *Gc2*, that produce known, common phenotypes (77). The phenotypes that result from combinations of the two nonsynonymous single-nucleotide polymorphisms, *rs4588* and *rs7041*, on the *Gc* gene were examined in relation to breast cancer risk (2). Abbas et al. (2) observed a lower breast cancer risk associated with the *Gc2*–2 allele, which corresponded to the *rs7041* *TT* and *rs4588* *AA* genotypes (versus the *rs7041* *GG* and *rs4588* *CC* genotypes). Adjustment or stratification by 25(OH)D status did not change the results. Although the *Gc2*–2 allele is associated with lower circulating levels of 25(OH)D, the *Gc2* protein is converted to GcMAF by deglycosylation. GcMAF is a potent activator of macrophages, which may have antitumorigenic properties (2). Given the functional effects of these common SNPs and their potential importance in carcinogenesis, additional studies involving these SNPs and their associated proteins are needed.

Other than SNPs in the *Gc* gene, one study examined the association between a SNP in the *CYP24A1* gene (86), a synonymous A→G SNP in exon 4 (*rs2296241*). No main effect or interaction with dietary calcium or vitamin D intake was observed (86).

Summary. The small but statistically significant associations between *FokI* and *BsmI* and breast cancer in the largest studies to date suggest that vitamin D and its receptor may impact breast cancer risk in humans. However, these associations were not strong, and those for *BsmI* were limited to advanced tumors. Furthermore, associations appear to vary by ethnic subgroups, but this has been understudied. New evidence on functional polymorphisms in the vitamin D-binding protein gene will likely lead to more research into the potential importance of vitamin D binding in relation to carcinogenesis. Additional research on the association between genotypes and tumor progression, and the roles of genotypes and gene-environment interactions among various racial-ethnic groups, is warranted.

Prostate Cancer

Background. Prostate cancer is the leading cancer diagnosed among men, accounting for 25% of incident cancers annually (7). Following death from lung cancer, it is the second cause of cancer death among men (7). Few risk factors for prostate cancer have been identified and include age, race/ethnicity, and family history of prostate cancer. African American men and Jamaican men of African descent have the highest prostate cancer incidence rates in the world. Dietary factors associated with lower risk include foods containing lycopene and selenium (142). In addition, some studies suggest that death from prostate cancer increases with obesity (111). Ecological studies show a latitudinal gradient in prostate cancer occurrence, supporting a hypothesis relating the disease to vitamin D status (119). However, findings from epidemiologic studies of dietary vitamin D and blood 25(OH)D in relation to prostate cancer risk do not suggest that high levels are necessarily associated with lower risk (5, 84, 89, 107, 135). On the contrary, higher circulating plasma 25(OH)D may be associated with greater risk of aggressive prostate cancer (5, 89).

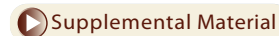
Vitamin D metabolizing enzymes are present in prostate tissue (121). In a study using prostate epithelial cells, local synthesis of 1,25(OH)₂D was found to be independent of PTH and calcium (145), indicating that endocrine regulation of 1,25(OH)₂D and local synthesis are independent. With prostate cancer progression, local 1 α -hydroxylase activity is reduced and eventually becomes nonexistent (22, 61, 140). Because prostate cancer cells lose hydroxylation capabilities but retain the VDR, circulating 1,25(OH)₂D and exogenous administration may play a more important role in inhibiting prostate tumor progression (89, 120).

High dietary calcium and dairy product intake was associated with a higher risk of prostate cancer (4, 47), especially aggressive prostate cancer, in some (47) but not all (4) observational studies that have investigated the possible association. A proposed mechanism is the downregulation of 1,25(OH)₂D by higher

levels of dietary calcium or dairy products (45). This hypothesis is supported by a recent study relating higher serum calcium [which would also suppress circulating 1,25(OH)₂D synthesis] to increased risk of fatal prostate cancer (123). However, studies in animal models found that calcium and suppression of circulating 1,25(OH)₂D did not affect prostate tumor development or growth (92). Although a secondary analysis from a randomized, double-blind, placebo-controlled clinical trial of supplemental calcium and colorectal adenoma recurrence found no evidence for higher risk of overall prostate cancer (12), the number of cases was small and the study could not examine aggressive prostate cancer.

Vitamin D pathway genotypes and prostate cancer.

Approximately 30 studies have reported on associations between vitamin D pathway genotypes and risk of prostate cancer (9, 13, 15, 16, 21, 24, 26, 27, 29, 51, 53, 56, 57, 62, 65, 68, 70, 73, 78, 83, 84, 88, 89, 91, 98, 99, 101, 115, 128, 130) (**Supplemental Table 3**). A meta-analysis of 14 studies published by Ntais et al. (98) in 2003 concluded that four common polymorphisms (*BsmI*, *TaqI*, *Poly(A)* repeat, and *FokI*) in *VDR* are unlikely to be major determinants of prostate cancer susceptibility on a population-wide basis. Associations were null regardless of whether individuals were of European, Asian, or African descent, and whether genotypes were treated as recessive (including heterozygotes) or dominant (by allele) (98). The meta-analysis did not examine whether these polymorphisms were related to clinicopathological attributes. A subsequent meta-analysis in 2006 by Berndt et al. (13) included 10 studies that were published after the initial meta-analysis of Ntais et al. (98). The results of the second meta-analysis concurred with the first (and in addition reviewed the *Apal* SNP) and found no associations with these *VDR* polymorphisms in codominant, recessive, or dominant models (13). Subsequent studies of *VDR* polymorphisms and prostate cancer risk have found generally similar null results overall



(56, 57, 70, 78, 89). Finally, recently available GWAS data do not link prostate cancer risk with the 12q12-q14 chromosomal region that encompasses the *VDR* gene (35, 132).

Interactions between *VDR* genotypes and vitamin D status. More studies have evaluated potential interactions between vitamin D status and vitamin D–pathway genotypes and risk for prostate cancer than for the other cancers reviewed; therefore, additional attention is given here to findings in this area. Studies that reported interactions of genotype or haplotype with vitamin D assessed vitamin D exposure using estimated UV exposure (16, 70, 115) or circulating levels of vitamin D metabolites (78, 89). A U.K. case-control study found no association overall for three *VDR* SNPs; however, among men who reported a greater number of hours/year of UVR exposure, the homozygote variant genotype for the *Cdx2* (*AA*) and *FokI* (*ff*) SNPs were associated with higher prostate cancer risk (16). John et al. (70) reported statistically significant, approximately 50% reduced risk of advanced prostate cancer among those with the high-activity allele genotypes, *FokI* *FF* or *Ff*, *TaqI* *tt*, and *BglI* *BB*, and nonsignificant lower risk among those with *Cdx2* *AG* or *AA* genotypes, but only in the presence of high sun exposure. The authors speculated that low vitamin D status might mask the relative importance of these genotypes in relation to prostate cancer risk. Rukin et al. (115) found a nonsignificant lower risk of prostate cancer only among men with the *FokI* *C* (*F*) allele who also had very low UV exposure. These investigators also found statistically significant lower risk among men with Block C SNPs in the 5' end of the *VDR* gene who also had a history of very low estimated UV exposure during adulthood.

In a nested case-control study from the Physicians' Health Study, Li et al. (78) found that neither the *FokI* SNP nor plasma 25(OH)D were independently associated with overall or aggressive prostate cancer risk. However, men with low plasma 25(OH)D combined with the *FokI* *ff* genotype had a 2.5-fold increased prostate cancer risk compared with those who

had greater than the median plasma 25(OH)D levels and the *FokI* *F* allele. Another study of male health professionals observed no main effect associations of *FokI*, *BsmI*, or *Cdx2* *VDR* SNPs or their related haplotypes with overall prostate cancer risk; however, two haplotypes (*Afb* and *AFB*) relative to *AFb* were associated with a significantly lower risk of aggressive prostate cancer (89). These authors also observed interactions between the *Cdx2* *A* allele and both 25(OH)D and 1,25(OH)₂D status, such that the *A* allele was associated with lower risk of poorly differentiated prostate cancer in a low 25(OH)D environment, but higher risk in a low 1,25(OH)₂D environment. The authors speculated that low 1,25(OH)₂D may be more relevant for prostate cancer (89). Additional studies will be needed to tease apart whether circulating levels of vitamin D metabolites interact with *VDR* genotypes to affect risk for prostate cancer.

Polymorphisms in other vitamin D pathway genes. Several studies examined whether polymorphisms in other genes in the vitamin D pathway are associated with prostate cancer risk. Hawkins et al. (55) sequenced the *CYP27B1* gene in 32 case and control samples and found six common SNPs, three of which were examined in relation to prostate cancer risk in 245 cases and 434 controls; no associations were observed. All of the identified SNPs were found to be in the noncoding regions of the gene, suggesting that *CYP27B1* sequence variants are unlikely to be strongly related to prostate cancer risk. In addition, no associations were observed when cases were stratified by a Gleason score ≤ 6 or ≥ 7 (55). Kidd et al. (73) observed no association with two novel SNPs in the vitamin D-binding protein gene (*Gc*). In a comprehensive analysis of the *VDR*, *CYP27B1*, and *CYP24A1* genes, Holick et al. (57) found that tag SNPs in the *CYP27B1* and *CYP24A1* genes were not associated with prostate cancer risk in a case-control study that included 630 cases and 565 controls. The null findings from these studies are consistent with the findings from the GWAS, which found no significant

associations for the *CYP27B1* or *CYP24A1* genes (35, 132).

Summary. Common polymorphisms of genes in the vitamin D pathway do not appear to be related to prostate cancer risk in the studies published to date. However, studies that quantified and stratified on UVR exposure or circulating vitamin D metabolite concentrations found associations in various subgroups. The stratified analyses are difficult to interpret because genotype associations either appear enhanced or muted in the presence of low or high UVR exposure or 1,25(OH)₂D or 25(OH)D concentrations. Because stratified analyses increase the potential for type 1 error, these findings should be considered hypothesis generating and need to be replicated in studies with larger sample sizes. In addition, a greater understanding of the relationship between circulating and tissue-specific vitamin D metabolites is needed.

FUTURE DIRECTIONS

Fine mapping of the genes involved in vitamin D metabolism and their surrounding areas of the human genome may yet uncover important gene variants that independently influence the risk of colorectal, breast, prostate, and other cancers. Future studies may also identify important phenotypic variations resulting from polymorphisms in these genes, using in vitro, animal, and proteomic or metabolomic approaches. Future epidemiologic studies must also carefully examine linked polymorphisms in a way that will not obscure potential associations between genotype and phenotype. More emphasis is needed on evaluating polymorphisms, alone or in combinations, as modifiers of risk from relevant environmental/lifestyle exposures. Much larger studies using more powerful statistical approaches and software will be required to examine the multitude of potential gene-gene and gene-exposure interactions (many which may realistically involve greater than two-way interactions). In large pooled analyses, extra attention should be given to the collection and harmonization of covariate and

dietary data across these studies to minimize between-study heterogeneity and potential for measurement error.

SUMMARY

Studies of common polymorphisms in *VDR* and other genes in the vitamin D pathway do not provide evidence for substantial influences of single variants on risk of colorectal, breast, or prostate cancer. These findings are generally consistent with available GWAS data on these cancers. Furthermore, with some exceptions, functionality of genetic variation in this pathway is not well understood. The changing rates of colorectal, breast, and prostate cancer observed in migrant studies, in addition to recent GWAS study data, suggest that if vitamin D pathway gene variants influence risk, they may act largely as modifiers of risk from environmental/lifestyle factors. It is possible that associations with *VDR* genotypes may only be observed in the presence of low or high vitamin D status and may be more apparent or relevant in the setting of other environmental or dietary extremes. Most studies of vitamin D-related genes and cancer risk have primarily investigated main effects of a few variants of these genes alone. Few studies have investigated vitamin D-related gene variants, either alone or in combination, as modifiers of associations of vitamin D exposure and status on cancer risk; for those that have, results have been inconsistent.

Some "signals" did appear in our review of this literature that are worth noting. The largest studies to date suggest that the *FokI* *ff* genotype may be associated with lower risk for colorectal cancer but increased risk for breast cancer; however, these associations were neither strong nor entirely consistent. The *BsmI* *bb* genotype may be associated with higher risk of advanced breast cancer, but replication of these findings in additional human studies of various designs is needed. The variable linkage disequilibrium of common polymorphisms in *VDR* by ethnicity underscores the need to examine linked tag SNPs or haplotypes with disease risk among different racial/ethnic groups. The evidence for a

role of genetic variation in other genes in the vitamin D pathway (e.g., *CYP27B1*, *CYP24A1*, *Gc*) is limited, but the recent discovery of functional *Gc* gene variants holds promise for future research in this area. In conclusion, very large

studies with carefully collected data on vitamin D status and other environmental factors are needed to fully understand the role of genetic variation in the vitamin D pathway on cancer risk.

DISCLOSURE STATEMENT

For the past three years, Roberd Bostick has been a principal investigator and a co-investigator of NCI-funded grants related to vitamin D as a possible chemopreventive agent against colorectal neoplasms.

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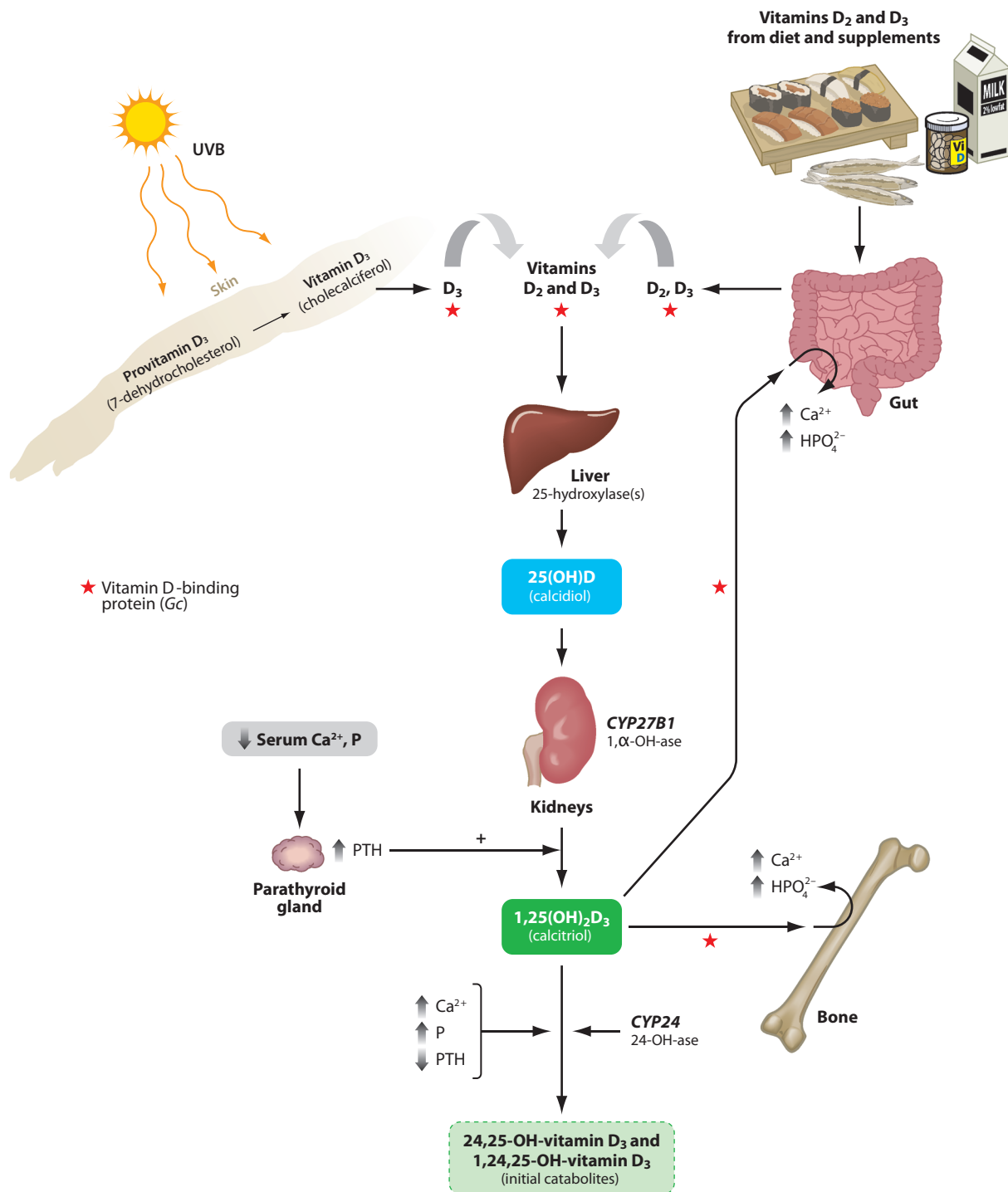


Figure 1

“Classical” role of vitamin D in calcium homeostasis. Vitamin D is synthesized in the skin from provitamin D₃ (7-dehydrocholesterol) and is also obtained through dietary and supplemental sources (vitamins D₂ and D₃). Vitamin D is transported through the circulation bound to vitamin D-binding protein (DBP) to the liver, where it is hydroxylated at the 25 position to 25-OH-vitamin D [25(OH)D], the major circulating form. This reaction is catalyzed by one or more cytochrome P₄₅₀ enzymes with 25-hydroxylase activity. Alternatively, vitamin D metabolites can be stored in adipose tissue. During periods of calcium deprivation, serum ionized calcium (Ca²⁺) levels decline, and parathyroid hormone (PTH) or low phosphorus (P) stimulates a second hydroxylation of 25(OH)D catalyzed by 1 α (OH)ase to form 1,25(OH)₂D. 1,25(OH)₂D produced in the kidneys increases calcium absorption from the gut, calcium resorption from bone and tubular reabsorption from the kidneys, through both passive and vitamin D receptor (VDR)-mediated mechanisms, to restore blood calcium concentrations. When Ca²⁺, P, and parathyroid hormone levels stabilize, 1,25(OH)₂D is degraded by 24-OH-ase to initial catabolites through a feedback loop. Genes are italicized adjacent to relevant proteins.

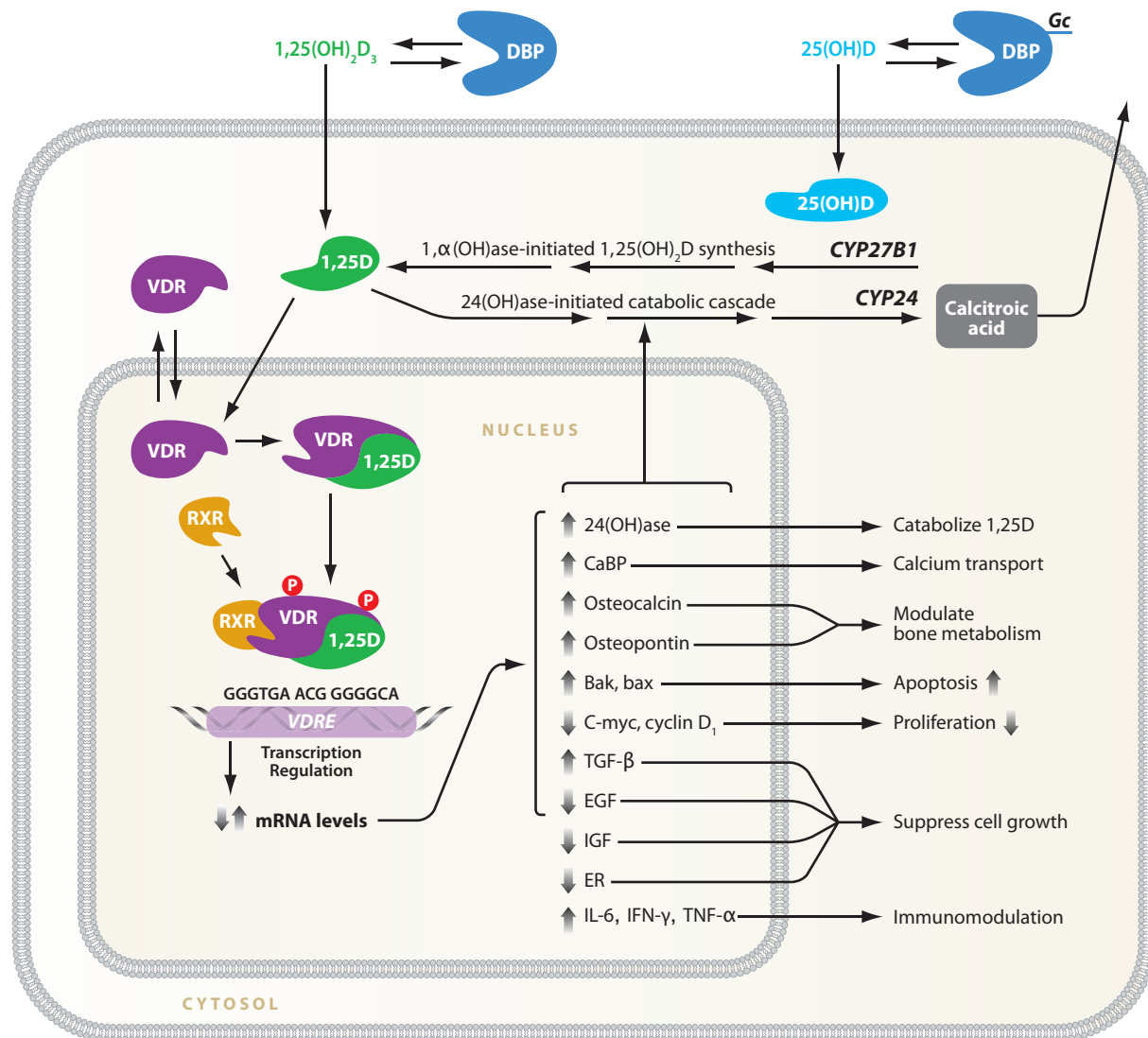


Figure 2

Proposed mechanism of action of vitamin D receptor (VDR) and 1,25(OH)₂D in target cells. 1,25-(OH)₂D is a relatively small, lipophilic molecule that easily penetrates the cell membrane, is taken up by the cell by simple diffusion, and binds to the VDR. Because many nonendocrine tissues possess 1α(OH)ase and 24(OH)ase, local synthesis and degradation of 1,25(OH)₂D is also thought to occur in an autocrine/paracrine manner. 25(OH)D can also bind to the VDR, but with 100- to 1000-fold lower magnitude. The VDR complex then binds to target DNA sequences as a heterodimer with the retinoid X receptor (RXR), recruiting a series of coactivators, resulting in the induction of target gene expression. More than 200 genes contain vitamin D response elements (VDREs) and influence a wide array of functions. Examples of genes with VDREs related to carcinogenesis include those involved in regulating cell proliferation, differentiation, apoptosis, and modulation of growth and inflammatory factors. Genes are italicized adjacent to relevant proteins. Modified from Holick (58).

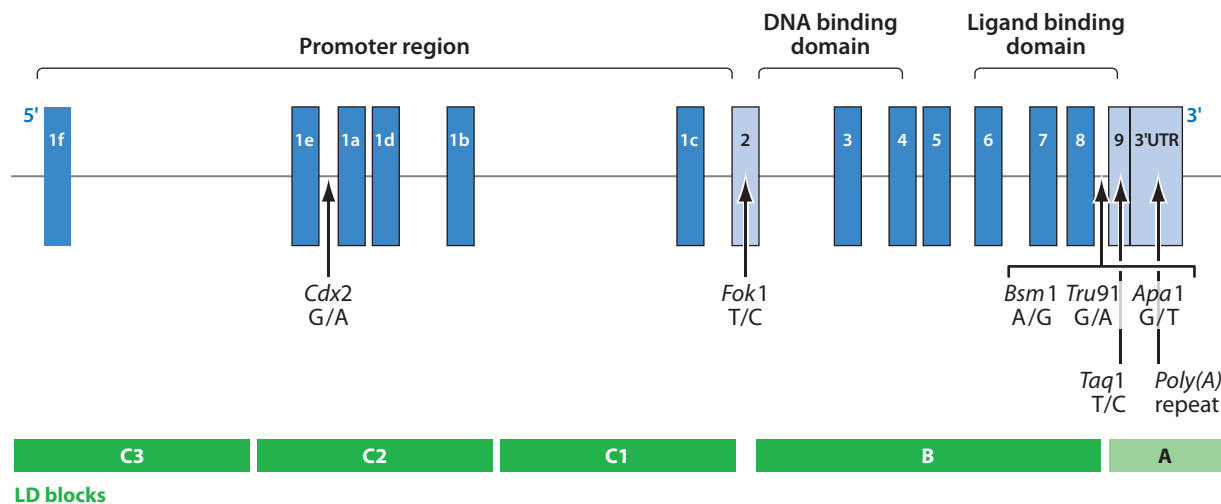


Figure 3

Vitamin D receptor gene (*VDR*). The gene is located on chromosome 12q13 and is <100 Kb long. It contains eight protein-coding exons 2–9, six untranslated exons 1a–1f, and several promoter regions. The most commonly examined single-nucleotide polymorphisms to date are identified above, most in the 3' end of the gene. Linkage disequilibrium (LD) is strong within LD blocks, but there is little LD between blocks (94). Modified from Rukin et al. (116).

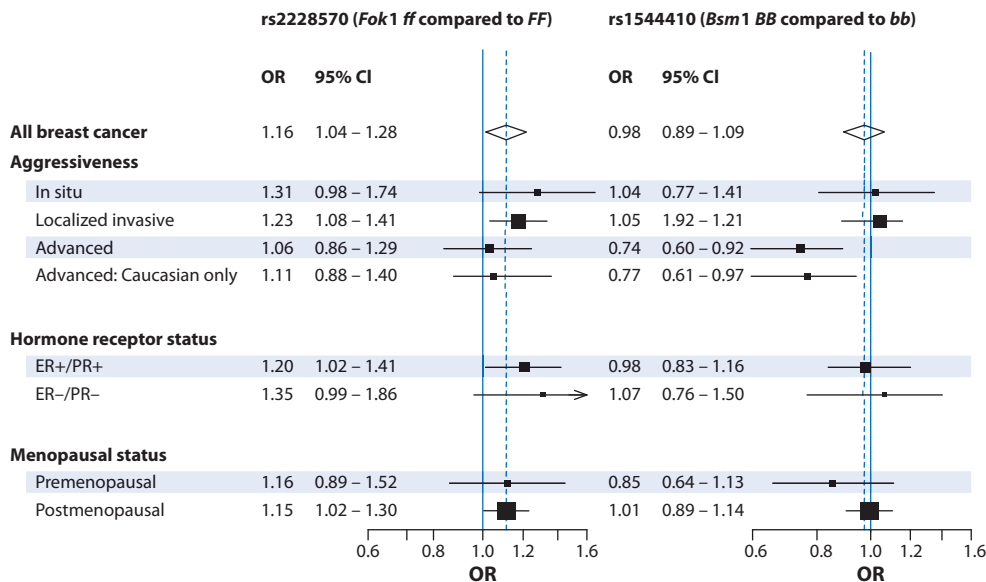


Figure 4

Risk of breast cancer by tumor characteristics and menopausal status for rs2228570 (*Fok1*) and rs1544410 (*Bsm1*). Odds ratios (OR) and 95% confidence intervals (CI) were calculated by conditional logistic regression and compared subjects homozygous for the less common variant (*ff* and *BB*, respectively) to subjects homozygous for the more common variant (*FF* and *bb*, respectively). The overall OR is represented by the diamond and the dashed line.



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Errata

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