

Research Article

Identification of Genotypes and Allelic Prevalence of the Vitamin D Nuclear Receptor Gene in People Living with Human Immunodeficiency Virus in Côte d'Ivoire

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Abstract

Introduction: Studies conducted in Côte d'Ivoire with HIV patients have revealed disorders in phosphorus/calcium metabolism and 25-hydroxyvitamin D₃ status. Due to the important role played by VDR-1,25 (OH)₂ D₃ in the biological activity of 25-hydroxyvitamin D₃, it has become necessary to describe the polymorphism of 4 fragments (Fok-1, Bsm-1, Apa-1, Taq-1) of the nuclear receptor gene Vitamin D₃ (VDR) in PLHIV. **Methods:** The study collected blood samples from 50 individuals, including 32 HIV positive patients and 18 HIV negative as a control. The extraction of genomic DNA from peripheral blood mononuclear cells (PBMC) was done using the QIAamp kit (QIAGEN). After amplification, the PCR products obtained were purified using the "High Pure PCR product purification kit" and sequenced at Eurofilms MWG operon. **Results:** The prevalence of the Fok-1 mutant C allele was 87.5% (28/32) in PLHIV against 77.8% (14/18) in controls. The single mutant genotype Thr1Met4 was 62.5% in PLHIV versus 55.6% in controls. The prevalence of the mutant allele A (g.63510 A) of Bsm-1 (rs 1544410) was 28% in HIV-infected against 66.7% (12/18) in controls. The mutant GG genotype was more prevalent in 34.4% of PLHIV. Two types of mutant alleles A (g.65023 A) and C (g.65024 C) and the AC mutant genotype of Apa-1 (rs 7975232) were more observed in 28% of those infected with HIV versus 0% in controls. No significant difference was observed between the frequencies of wild T (g.65058 T) allele and mutant C or A (g.65058 C or A) of Taq-1 (rs 731236) (p = 0.47). The wild genotype Ile352 was the most common regarding the Taq-1 polymorphism. Ten PLHIV and controls have the combination Fok-1 + Bsm-1 in common. The combinations Fok-1 + Bsm-1 + Apa-1 and Fok-1 + Apa-1 were specific to PLHIV. **Conclusion:** The blood sample of PLHIV subjects is characterized by polymorphisms affecting Fok-1, Bsm-1, and Apa-1. In addition, the combination of Fok-1 and Bsm-1 was observed in both PLHIV patients and controls.

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Keywords

Polymorphism, VDR Gene, HIV Positive Patients, C ôte d'Ivoire

1. Introduction

Human immunodeficiency virus (HIV) infection is a pandemic disease [1]. In C ôte d'Ivoire, the prevalence rate was 1.82% in 2024 [2]. During HIV infection, the virus uses micronutrients from the body for replication [3]. These micronutrients, including vitamins are essential to the proper functioning of the body. Vitamins exist in two forms: water-soluble vitamins (group of vitamin B and vitamin C) [4] and fat-soluble vitamins (vitamins A, D, E and K) [5]. Unlike other fat-soluble vitamins that have a dietary source, the main source of vitamin D (Calciferol) is the sun [6]. Vitamin D₃ ensures its biological activities through its nuclear receptor or VDR [7]. VDRs are present in more than thirty (30) tissues, including those of the intestine, kidneys, bones, brain, stomach, heart, pancreas, skin, colon, kidney ovary, breast and prostate. They are also found in peripheral blood mononuclear cells [8, 9] such as monocytes, dendritic cells, macrophages, activated T cells and B [10, 11]. As a result, VDR is an important therapeutic target in the treatment of various ailments [12]. The existence of a genetic polymorphism of the VDR would therefore be an important factor of individual susceptibility to the biological effects of vitamin D₃ [13]. Indeed, analysis of the VDR coding gene in coding or non-coding regions has shown that there may be a base substitution by a nucleotide called Single Nucleotide Polymorphism (SNP). Several polymorphisms of the VDR gene have been identified that can influence serum vitamin D₃ concentrations [14, 15].

The main polymorphisms of the VDR gene are: Bsm-I, Apa-I, and Taq-I, which are found in the untranslated region 3' (UTR); Cdx2 and A-1012G in the regulatory region 5', and Fok-I in the coding region. The Bsm-I or rs1544410 polymorphism is characterized by an adenine-guanine (A/G) substitution and consists of the B and b alleles, while the Apa-I or 7975232 polymorphism is created by a guanine-thymine (G/T) substitution and consists of the A and a alleles. It is important to note that the polymorphism in the 3'UTR region of the VDR gene is associated with the stability of VDR mRNA, which is involved in VDR expression, and that other VDR polymorphisms also modulate the activity of the vitamin D-VDR complex [16]. VDR gene polymorphisms have been associated to susceptibility and progression of HIV/AIDS, since they may alter gene function and compromise the role of 1,25[OH]₂D and could influence the risk of HIV-1 infection [10].

The most frequently analyzed polymorphisms of VDR correspond to the Apa-1 and Bsm-1 endonuclease cleavage sites in intron 8, Fok-1 in exon 2, and Taq-1 in exon 9 [16].

Studies have shown that vitamin D₃ deficiency in HIV positive patients [17] may be related to mutations in the vitamin D nuclear receptor (VDR) [18]. The polymorphisms of the VDR gene would contribute to the progression of the disease in HIV-1 patients [8].

In C ôte d'Ivoire, studies conducted in the people living with HIV (PLHIV) showed disorder in calcium/phosphorus metabolism [19] and in 25-hydroxyvitamin D₃ (25 (OH) D₃) status [20]. In view of the important role of the VDR-1,25 (OH)₂ D₃ signaling complex in the biological activity of vitamin D₃ [21] and since no molecular studies have been performed on the gene of the vitamin D₃ receptor (VDR) in the people living with HIV (PLHIV) in C ôte d'Ivoire, it becomes necessary to investigate this gene.

The aim of this work was, therefore to describe the polymorphism on the basis of the 4 regions of the nuclear receptor gene of vitamin D₃ [Fok-1 (rs2228570) in exon 2, Bsm-1 (rs1544410) and Apa-1 (rs7975232) in intron 8 and Taq-1 (rs731236) in exon 9] in the blood samples of people living with HIV (PLHIV).

2. Material and Methods

2.1. Study Population

The study was conducted from November 2015 to December 2016 in the Department of Clinical and Fundamental Biochemistry of the Institut Pasteur of C ôte d'Ivoire (IPCI). It involved 50 blood samples taken from people including 32 PLHIV and 18 HIV-negative (control) aged between 18 and 49 years. The blood samples of pregnant women and children under 15 were not included in the study.

2.2. Collection of Blood Samples and Performance of Serological Tests

Blood was collected from the elbow, in tubes without anticoagulant (dry tube) for serological test and in tubes containing EDTA for the extraction of peripheral blood mononuclear cells (PBMC).

Two rapid serological tests allowed the detection of anti-HIV antibodies: the Alere Determine™ HIV-1/2 immunochromatographic kit, the principle of which is based on the formation of an antigen-antibody complex revealed after staining [22] and the SD Bioline HIV-1/2 3.0 immuno-

zymatic confirmation test based on the detection of anti-HIV1 and anti-HIV2 antibodies directed specifically against antigens [23].

2.3. Extraction of Genomic DNA from Peripheral Blood Mononuclear Cells

Genomic DNA was extracted from the PBMC using the QIAamp QIAGEN Kit following the manufacturer instruction.

A 200 μ L volume of suspension of PBMC (5.10^6 cells) was put in a lysis tube (LT) before addition of 200 μ L of lysis buffer (AL). After homogenization (15 sec), 20 μ L of proteinase K (QP) were added. The whole was incubated (10 min at 56 °C.) after homogenization (15 sec). The lysate obtained was gently transferred to a Qiagen column. Then, 200 μ L of ethanol 96 °C was introduced into the Qiagen column and centrifuged at 8000 rpm (1 min). The column was then placed in a new washing tube (WT). Then, a volume of 500 μ L Wash Buffer 1 (AW1) was added to the column. After centrifugation at 8000 rpm (1 min), the column was then placed in a new washing tube (WT), and 500 μ L of wash buffer 2 (AW 2) was introduced into the column and centrifuged at 14,000 rpm (3 min). The column was then placed in a new washing tube (WT) and centrifuged at 14,000 rpm (3 min) to dry the membrane. To remove the DNA, the column was placed in a new elution tube (ET) and 200 μ L of elution buffer (AE) was dropped. The whole was incubated (1 min) at room temperature (15-25 °C) and centrifuged at 8000 rpm (1 min).

The quantity and purity of the genomic DNA was determined by measuring the absorbance at 260/280 nm according to the method of Fan and Margaret [24]. The genomic DNA extract obtained was conserved at 4 °C until PCR was performed.

2.4. Amplification of VDR Genes

The genes VDR Fok-1 (Exon 2, rs2228570), Bsm-1 (Intron 8, rs1544410), Apa-1 (Intron 8, rs7975232) and Taq-1 (Exon 9, rs731236) were amplified by PCR using a specific pair of primers and DNA polymerase kit, 5X FIREPol Blend Master Mix with 2.5 mM $MgCl_2$. This kit is a pre-mix (for the reaction mixture) ready to use composed of DNA polymerase (FIREPol® DNA polymerase), buffer (5 x Blend Master Mix Buffer), $MgCl_2$ (7.5 mM $MgCl_2$) and dNTPs (2 mM dNTPs of each). The PCR of these genes were carried out in a reaction volume of 25 μ L containing: 0.625 μ L of each primer (10 μ M), 3 μ L of genomic DNA of PBMC, 5 μ L of Taq DNA polymerase and 15.75 μ L of milliQ water. The mixture was then put into a thermocycler type Applied Biosystems (2720 ThermalCyber, Singapore), programmed as follows: Initial denaturation at 95 °C for 5 min followed by 35 denaturation cycles at 94 °C for 30 sec, hybridization at 51 °C (Fok-1), 53 °C (Bsm-1 and Apa-1), 69 °C (Taq-1), respectively for 30 sec and extension at 72 °C for 1 min. Finally, a terminal extension at

72 °C for 7 min.

The primer pairs used for the amplification of 267, 822, 195 and 745 bp of Fok-1, Bsm-1, Apa-1 and Taq-1 respectively, consisted of Fok-1F/Fok-1R (5'AGCTGGCCCTGGCACTGACTCTGCTCT/5'ATGGAAACACCTTGCTTCTTCTCCCTC);

Bsm-1F/Bsm-1R (5'CAACCAAGACTACAAGTACCGCGTCAGTGA/5'AACCAGCGGGAAGAGGTCAAGGG);

Apa-1F/Apa-1R (5'GTGGGATTGAGCAGTGAG/5'ATCATCTTGGCATAGAG);

Taq-1F/Taq-1R (5'CAGAGCATGGACAGGGAGCAA/5'GCAACTCCTCATGGCTGAGGTCTC) [25, 26].

2.5. Detection and Analysis of PCR Products

The amplification products were migrated on a 2% agarose gel containing SYBR® green I. After migration, the gel was recovered and then observed under a UV lamp using the UV transilluminator (Gel Doc™ EZ Imager). The presence or absence of bands made it possible to judge the effectiveness of the PCR.

The DNA size fragments were determined by using the SmartLadder- Eurogentec of 100 bp (molecular marker of weight).

2.6. Sequencing Amplification

The amplified DNA fragments of Fok-1, Bsm-1, Apa-1 and Taq-1 gene were sequenced according to the Sanger method by the company Eurofins MWG operon (Cochin sequencing platform). Samples were dropped to the platform in a microplate (Greiner Bio-one-652270B) along with a deposit slip that was sent to the platform's email address.

A reaction medium was prepared for the PCR sense primer (sequencing primer) from the amplification products. In each well of the microplate, a volume of 15 μ L of amplification product was added to 2 μ L of sequencing primer at 10 μ M. Wells containing the sequencing reaction medium were sealed with cap strips (4titude-044737) before covering the entire surface of the microplate with an adhesive film (AmpliSeal, Greiner Bio-one-676040). This microplate containing the samples was sent to the platform for sequencing.

After the sequencing reaction, the received DNA sequences were recovered as fasta. The use of the software BioEdit made it possible to analyze the sequences to search for possible mutations.

2.7. Statistical Analysis of Data

The XLSTAT 2017.7.48969 software was used to analyze the qualitative data of the sequencing results. Software R was used for the statistical analysis of proportions by the Chi-2 test; thus, a value of $p < 0.05$ is considered statistically significant.

3. Results

3.1. Allelic and Genotypic Prevalence of Fok-1 (rs 2228570) in Exon 2 of the VDR Gene

The analysis of the Fok-1 polymorphism (rs 2228570) in

exon 2 revealed the presence of mutation at start codon ATG into ACG at sites g.30920 and g.30929. They are 87.5% (g.30920) and 25% (g.30929) respectively in the DNA fragments of the PLHIV subjects. The prevalence of the mutant allele C was 87.5% in the DNA fragments of the PLHIV subjects against 77.8% in the HIV negative controls (Table 1).

Table 1. Distribution of alleles and Fok-1 mutations of the VDR gene.

Fragment analysed	Position analysed	Sample PLHIV n (%)	Sample Control n (%)	P value
Fok-1 Exon2	Alleles			
	g.30920 T	4 (12.5)	4 (22.2)	0.62
	g.30920 C	28 (87.5)	14 (77.8)	0.62
	g.30929 T	24 (75)	14 (77.8)	0.86
	g.30929 C	8 (25)	4 (22.2)	1
	Genotypes			
	Met1Met4 (Wild)	4 (12.5)	4 (22.2)	0.62
	Thr1Met4 (Simple mutant)	20 (62.5)	10 (55.6)	0.86
	Thr1Thr4 (Double mutant)	8 (25)	4 (22.2)	1

allele T (thymine) = wild; allele C (cytosine) = mutant; genotypes Met1Met4 (methionine1 methionine4), Thr1Met4 (threonine1methionine4) and Thr1Thr4 (threonine1 threonine4); Met1Met4= (1 et 4) codon position ATG translated into Met on VDR protein

3.2. Allelic and Genotypic Prevalence of Bsm-1 (rs 1544410) in Intron 8 of the VDR Gene

Analysis of the Bsm-1 polymorphism (rs 1544410) in intron 8 of the VDR gene in the study population revealed three types of mutation, G → A of g.63510, A → G and A → C of g.63905 (Table 2). The prevalence of the wild-type G allele (g.63510 G) at the first mutation site was 71.9% (23/32) in the DNA fragments of PLHIV compared to 33.3% (6/18) among those of

HIV negative controls (p = 0.02). However, the prevalence of the mutant allele A (g.63510 A) in the DNA fragments of control was higher, 66.7% (12/18) (p = 0.02). As for the other two mutations [A (g.63905 A); C (g.63905 C)], their prevalence among PLHIV is insignificant compared to controls (p > 0.05).

In addition, the prevalence of the mutant genotype GG was 34.4% (11/32) in PLHIV and 5.6% (1/18) in the control subject with a significant difference (p = 0.05) (Table 2).

Table 2. Distribution of allelic and genotype Bsm-1 (rs 1544410) in intron 8 of the VDR gene.

Fragment analysed	Position analysed	Sample PLHIV n (%)	Sample Control n (%)	p value
Bsm-1 in intron 8	Alleles			
	g.63510 G	23 (71.9)	6 (33.3)	0.02
	g.63510 A	9 (28.1)	12 (66.7)	0.02
	g.63905 A	12 (37.5)	6 (33.3)	1
	g.63905 G	17 (53.1)	8 (44.4)	0.77
	g.63905 C	3 (9.4)	4 (22.2)	0.4

Fragment analysed	Position analysed	Sample PLHIV n (%)	Sample Control n (%)	p value
<i>Genotypes</i>				
	GA	11 (34.4)	4 (22.2)	0.56
	GG	11 (34.4)	1 (5.6)	0.05
	AG	6 (18.7)	7 (38.9)	0.22
	AC	2 (6.2)	3 (16.7)	1
	AA	1 (3.1)	2 (11.1)	0.6
	GC	1 (3.1)	1 (5.6)	1

alleles G (guanine) and A (adenine) = wild; alleles G (guanine) and C (cytosine) = mutants; genotype GA = wild, genotypes AG, AA, GC, AC and GG = mutants

3.3. Allelic and Genotype Prevalence of Apa-1 (rs 7975232) in Intron 8 of the VDR Gene

Analysis of the Apa-1 polymorphism (rs 7975232) in intron 8 of the VDR gene showed that two mutants A (g.65023 A)

and C (g.65024 C) mutant alleles were found in 28.1% (9/32) of the HIV-infected DNA fragments. In addition, the AC mutant genotype was the most common in 28.1% (9/32) of HIV positive DNA fragments against 0% (0/18) in controls with a significant difference ($p = 0.03$) (Table 3).

Table 3. Allelic and genotypic distribution of Apa-1 (rs 7975232) in intron 8 of the VDR gene.

Fragment analysed	Position analysed	Sample PLHIV n (%)	Sample Control n (%)	p value
<i>Alleles</i>				
Apa-1 in intron 8	g.65023 C	23 (71.9)	18 (100)	0.03
	g.65023 A	9 (28.1)	0 (0)	0.03
	g.65024 A	23 (71.9)	18 (100)	0.03
	g.65024 C	9 (28.1)	0 (0)	0.03
	<i>Genotypes</i>			
	CA	23 (71.9)	18 (100)	0.03
	AC	9 (28.1)	0 (0)	0.03

alleles C (cytosine) and A (adenine) = Wild, alleles A (adenine) and C (cytosine) = mutants; genotype CA = wild, genotype AC = mutant

3.4. Allelic and Genotype Prevalence of Taq-1 (rs 731236) in Exon 9 (codon 352) of the VDR Gene

Analysis of Taq-1 polymorphism (rs 731236) in exon 9 (codon 352) revealed the presence of mutation in the codon ATT into ATA or ATC and TTA at site g.65058. In addition,

the prevalence of the mutant allele A was 40.6% in the DNA fragments of the PLHIV subjects against 55.6% in the control HIV negative ($p = 0.47$).

Also, genotype prevalence of wild-type mutant Ile352 93.7% (30/32) and genotype single-mutant Leu352 6.2% (2/32) in PLHIV are not-significant ($p = 1$) when compared to HIV negative controls 94.4% (17/18) and 5.6% (1/18) respectively (Table 4).

Table 4. Allelic distribution and mutations of Taq-1 (rs 731236) in exon 9 (codon 352) of the VDR gene.

Fragment analysed	Position analysed	Sample PLHIV n (%)	Sample Control n (%)	P value
Taq-1 in exon 9	Alleles			
	g.65058 T	19 (59.4)	6 (33.3)	0.14
	g.65058 A	13 (40.6)	10 (55.6)	0.47
	g.65058 C	0 (0)	2 (11.1)	0.24
	Genotypes			
	Ile352 (Wild)	30 (93.7)	17 (94.4)	1
	Leu352 (Simple mutant)	2 (6.2)	1 (5.6)	1

allele T (thymine) = wild; alleles A (adénine) and C (cytosine) = mutants; genotype Ile352 (Isoleucine352); genotype Leu352 (Leucine352); Ile 352= (352) position of the codon ATT translated in Ile on VDR proteins

3.5. Polymorphism of the VDR Gene Through Fok-1, Bsm-1, Apa-1 and Taq-1

The results showed that the DNA fragments most affected by the polymorphisms of the VDR are found more in the blood specimen of the PLHIV subjects. Thus, for example, 8 (25%), 5 (15.6%) and 3 (9.3%) PLHIV samples had the Fok1 polymorphism and the combinations Fok-1 + Bsm-1 + Apa-1, and Fok-1 + Apa-1, respectively (Figure 1). However, the Fok-1 + Bsm-1 combination was the most observed in this study: 10 (31.25%) among the 32 PLHIV against 10 (55.5%) among the 18 controls (Figure 1).

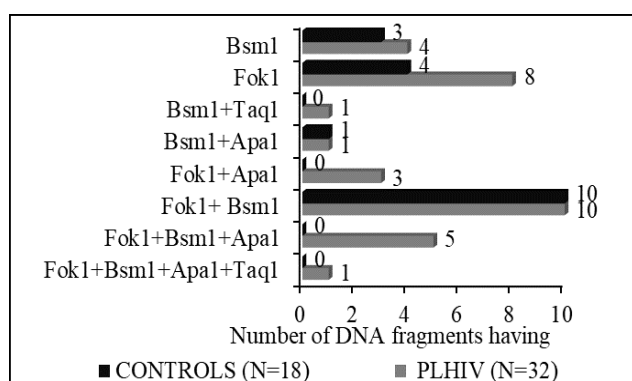


Figure 1. Distribution of the number of DNA fragments having mutation according to the type of combination of the SNP of the VDR gene.

4. Discussion

More than 470 polymorphisms of the VDR gene have been reported; however, the most studied fragments are Fok-1 (rs 2228570) in exon 2, Bsm-1 (rs 1544410) and Apa-1 (rs 7975232) in intron 8 and Taq-1 (rs 731236) in exon 9 [15, 27].

In this study, analysis of the Fok-1 polymorphism revealed the presence of two start codons (ATG) at sites g.30920 T and g.30929 T, similar to the work of O'Neill et al. [28]. The mutant C allele of the Fok-1 fragment was the most common in the study population. This polymorphism occurs near the 5'-UTR region of the gene in the DNA binding domain and plays a critical role in message stability and in post-transcriptional processes [29]. Indeed, it produces a shortened VDR protein of 3 amino acids [30] and is more efficient in the transactivation of the target gene regulating vitamin D₃ [31]. The high prevalence of the "single mutant" genotype Thr1Met4 in both HIV-positive (62.5%) and HIV-negative (55.6%) controls shows that more than half of the study population would have VDR protein with greater transcriptional activation of the target gene in common. Moreover, this single mutation is not linked to HIV infection. However, Nieto et al. [7] have shown that this polymorphism has been associated with a rapid progression of HIV infection. In addition, Suneetha et al. [32] reported an association between Bsm-1, Apa-1 and Taq-1 polymorphisms, and the stability of VDR messenger RNA (mRNA). Indeed, the polymorphisms in intron 8 and exon 9 of the VDR directly control the expression of its protein [33]. The polymorphisms of the VDR gene have functional significance for mRNA stability and efficiency of VDR protein translation. As a result, they are thought to be responsible for the reduced level of VDR protein [13].

The polymorphism of Bsm-1 is localized in the 3' non-transcribed region of the VDR. It would not affect the amino acid sequence of the VDR, but would intervene in the regulation of the stability of the VDR mRNA [34]. In this study, the prevalence of the Bsm-1 mutant A (g.63510 A) allele was lower (28%) in HIV-positive people than in HIV-negative controls (67%). That of the GG mutant genotype was 34% in PLHIV and 5% in HIV negative controls. All these mutations are therefore linked to HIV infection. These results corroborate with those of de la Torre et al. [10] and Alagarasu et al. [35] who found that Bsm-1 polymorphism was associated with

increased susceptibility to HIV infection and a high rate of HIV infection progression among Caucasian adults.

As for Apa-1, the AC mutant genotype was the most common among HIV-infected people. This same result was reported by McNamara et al. [36] in the study of African population with or without HIV showing differences in the polymorphism of the Apa-1 fragment. In addition, the average frequency of allele A in Asians population is 29%, 53% in the whites and 67% in African-Americans [37].

The Bsm-1 and Apa-1 polymorphisms are located in the 3' region of the VDR gene with a strong binding imbalance. Their polymorphisms are considered as single nucleotide polymorphisms (SNPs). Therefore, they do not modify the sequence of coding amino acids like polymorphisms of the Fok-1 fragment. Both Bsm-1 and Apa-1 polymorphisms would have influences on mRNA stability. However, different polymorphisms of Bsm-1 and Apa-1 could lead to different biological functions of VDR [34] like polymorphisms of the Taq-1 fragment also [38].

Unlike the polymorphism of the Bsm-1 fragment, it has been shown that the Taq-1 fragment polymorphism affects the stability of mRNA, resulting in alteration of protein levels and biological functions of vitamin D [34]. In this study, no significant difference was observed between the frequencies of the wild-type T (g.65058 T) and mutant C or A (g.65058 C or A) of Taq-1 (rs 731236) alleles between DNA fragments of the PLHIV and control subject. The same is true for the "wild" genotypic frequencies Isoleucine between infected (93.7%) and controls (83.3%). This Taq-1 polymorphism is located in the 3' region untranslated involved in the regulation of gene expression, in particular by regulating the stability of the VDR mRNA, thus affecting the level of circulating 25-hydroxyvitamin D₃ [39]. According to studies, the frequencies of different Taq-1 genotypes vary considerably among different populations, probably due to different evolutionary processes [14].

In this study, the Fok-1 + Bsm-1 combination was the most observed in PLHIV and controls. The Bsm-1 and Fok-1 polymorphisms have been described as being associated with the concentrations of 25 (OH) D₃ and also with the activity of the VDR [40, 41]. These VDR polymorphisms may explain why some populations are more at risk to vitamin D deficiency or vitamin D-dependent pathologies than others. Similarly, a difference in the frequency of certain VDR polymorphisms has been demonstrated in Caucasians, African-Americans and Asians [42].

5. Conclusion

This study found that the Fok-1 fragment had the most common polymorphism among both HIV-positive and HIV-negative controls. In addition, the combination Fok-1 + Bsm-1 was observed in both PLHIV (more than a third of them) and HIV negative controls (more than half); on the other hand, the polymorphism affecting Fok-1, Bsm-1 and Apa-1 was more common among PLHIV. It would be inter-

esting to further examine the distribution of these allelic and genotypic prevalence of the vitamin D nuclear receptor gene in these PLHIV in relation to their vitamin D status.

Abbreviations

VDR	Vitamin D nuclear Receptor
PLHIV	People Living with HIV
PBMC	Peripheral Blood Mononuclear Cells
SNP	Single Nucleotide Polymorphism

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Djaman Allico Joseph: Conceptualization, Project administration

Ethical Statement

This study was conducted in accordance with the Helsinki 2000 Declaration on HIV and AIDS Research in Poor Countries and in accordance with local legislation on the National Program for the Care of People Living with HIV / AIDS (Decree No. 411 of 23 December 2001). In addition, in this study, informed consent was obtained from participants for the use of their blood samples taken during biological monitoring.

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Data Availability Statement

The data is available from the corresponding author upon reasonable request.

Conflicts of Interest

The authors declared that there is no conflict of interest.

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Research Field

Aké Aya Jeanne Armande: Biochemistry, Molecular Biology, Immunology, Hematology, Infectiology, Immunogenetics

Séri Kipr é Laurent: Biochemistry, Functional and molecular Biology, Functional nutrition, Toxicology, Pharmacology, Proteomics, Metabolomics

Boyvin Lydie: Biochemistry, Molecular Biology, Microbiology, hematology, Pharmacology

Koui Toss é St éphane: Genetic, Molecular Biology, Biology, Immunogenetics

Siransy Kouabla Liliane: Immunology, Allergology, Biochemistry, Molecular Biology, Histocompatibility, Immunogenetics

N'guessan Kouassi Raymond: Molecular Biology, Microbiology, Tuberculosis

Yapo Adou Francis: Biochemistry, Hematology, Pharmacology

S ékongo Yassongui Mamadou: Hematology, Immunology, Blood transfusion, Hemoglobinopathies

Djaman Allico Joseph: Biochemistry, Parasitology, Molecular Biology, Microbiology, Hematology, Pharmacology