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EDITORIAL

Hypotheses and Emerging Facts: the Vitamin D Receptor Capacitor, Rheumatoid Arthritis and Beyond

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ABSTRACT

As System-IN Failing, complex diseases such as autoimmune diseases (ADs) like rheumatic arthritis (RA), and the associated cancers remain as a challenge to thoroughly understand, though their common underlying mechanisms emerge. In this visionary article, we summarize some recent hypothesis-generating discussions on the Vitamin D and its receptor (VDR) capacitor for autoimmune diseases (ADs) and associated cancers, then update bioinformatics evidence along with latest progress in RA. We could conclude this may provide one unique angle to view the controversies surrounding the beneficial effects of Vitamin D supplementation.

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Key words: Rheumatoid arthritis; Autoimmune disaeses; Vitamin D receptor capacitor; Cancer; Prevention

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INTRODUCTION

Complex diseases such as autoimmune diseases (ADs) like rheumatoid arthritis (RA), ankylosing spondylitis (AS) and the associated cancers such as lung cancer and breast cancer are related to a reduction of mobility. Generally, RA is an autoimmune disease in which the body's own immune system mistakenly attacks patients' healthy tissue. This often causes pain, loss of joint shape and alignment, and consequently loss of movement. Currently, no single cause for RA has been assigned, but patients seem to be genetically predisposed to the disease. AS is a chronic, progressive inflammatory disease involving primarily the sacroiliac joints and the axial skeleton. Understanding the causes behind these diseases and then addressing them properly may allow patients to live a more active life.

Beyond bone health, basically, although we are still lacking convincing data [namely, if any, but very few facts and mainly bioinformatics dry evidence], in order to better understand their pathophysiology, the Vitamin D and its receptor (VDR) capacitor hypothesis for ADs and associated cancers has been developed. Vitamin D might only improve diseases status of patients with marginally insufficiency, for which high doses as 400-1,000 IU daily might be required. Beyond certain points, there would be not any beneficial effect with vitamin D supplementation. It does not mean that the vitamin D is sufficient in those individuals and/ or generally no beneficial effect for vitamin D supplementation. For decades, it remains debatable for beneficial effects and even definition of sufficiency of vitamin D. Rather than to resolve all these issues, this hypothesis may provide one viewpoint/interpretation for such controversy. Such capacitor (like the electronic device) has preventive effects and only slight side-effects at a rational range along with supplementation. Human beings are speculatively good at surviving the challenges of genetic variations and environmental factors, and rely on the robustness of complex genetic regulatory networks, possibly including the VDR as a capacitor, similar to its homologue DAF-12 in Caenorhabditis elegans. Besides, decoding the genetics of the complex diseases associated with the aging process with which that DAF-12 contribution was proven is critical in understanding the controversies surrounding the beneficial effects of Vitamin D supplementation. In this visionary article, we summarize some recent hypothesis-generating discussion as well as analyze latest bioinformatic indirect evidence from RA. In turn, this increased understanding has also heightened our awareness of current gaps in our knowledge. We conclude it by considering possible explanations, and suggesting future lines of experiments.

MAIN POINTS OF THE HYPOTHESIS

- (1) This hypothesis is distilled from the comparative advantages of different model systems, data from genome-wide association studies (GWAS), and chromatin immunoprecipitation (ChIP)-seq/ChIP-chip studies^[1-6] (Table 1).
- (2) It hypothesizes that the evolutionarily conserved roles of Vitamin D and the VDR may shed light on the important role of human VDR^[1-9].
- (3) Similar to DAF- 21/HSP90VDR may buffer disease-causing genetic mutations and/or variations, the diseased phenotype may occur with polygenic genetic mutations and/or variations plus a deficiency of Vitamin D and a lack of UVB. In these circumstances, mal-functional DAF-12/VDR loses of its buffering ability as a capacitor^[1-9].
- (4) Environmental factor-induced malfunctional DAF-12/VDR may be postulated to cause the dys-regulation of expression of an array of its target genes; supposedly, the citrullination of such dys-regulated genes might be tightly mediated by VDR-orchestrated processes and consequently end with autoimmunity^[4].
- (5) Human VDR studies^[1-4] show VDR binding loci to be enriched near AD-associated genes^[2,4] (Table 1) and to overlap many conserved targets of the homologous DAF-12/VDR in *C. elegans*^[5]. VDR ChIP-seq assays in primary CD4+ cells have related serum 25-hydroxyvitamin D levels to ADs^[6].
- (6) Regarding the signalling pathways, when VDR function is down-regulated due to genetic defects or by Vitamin D unavailability, it may remodel many different processes and make adjustments to multiple signal transducers, thereby simultaneously disturbing several developmental pathways. If DAF-12/VDR loses its buffering capability, ADs and associated cancers may arise in patients^[4].
- (7) At a systems biology level, the age-related genetic regulatory network (GRN) of VDR, the human homologue of DAF-12 in *C. elegans*, may play a central role as being the common basis preventing some ADs and associated cancers. In fact, the GRN of DAF-12/VDR combines microRNA regulations, autophagy, longevity and cellular reprogramming, and forward or feedback loops. Our recent ChIP-chip screening for DAF-12/VDR target genes^[5,7,8], along with NCBI Aceview, may reveal many translatable targets that overlap with validated homologues identified in human VDR studies that are significantly enriched near genes that are pathologically associated with ADs^[4,9], including phospholipase C-like 1 (PLCL1), B lymphoid tyrosine kinase (BLK) (i.e. *pll-1* and *src-1* respectively; Table 1). Vitamin D3 regulates matrix metallopeptidase (MMP3) in cultured human cells^[10].
- (8) Hypothesis: some of targets of vitamin D and VDR -associated "loci" identified by GWAS for ADs and associated cancers collectively have significance for gene function. Namely, some of them may contribute to producing self-antigens or the machinery of producing of autoantibodies; others may responsible for the quantity of either self-antigens, auto-antibodies and/or immune machinery capacitor^[1-9,19].
- (9) Different genetic backgrounds would create personalized Vitamin D insufficiencies and necessities of personalized Vitamin D supplementation.

(10). A Vitamin D deficiency status of a "system robustness failure" may lead to a "one-way" street and thus be irreversible for ADs, including RA. Vitamin D insufficiency might lead to a "system in failing".^[4].

EXPERIMENTAL AND/OR CLINICAL OBSER-VATIONS

One GWAS reveals that, strikingly, an allelic VDR variant may link to clinical autoimmune antibodies including the anti-p150 (TIF-1 γ)/p140 (TIF-1 α)^[11] and TIF-1 γ / α genes' *C. elegans* homologues, *flt-1* and *nhl-2*, which are also direct targets of DAF-12/VDR (Table 1)^[5].

One of our recent experiences is as follows: when the new key regulators for ADs were published online, we predicted that they would be putative target candidates of Vitamin D-VDR signalling (and DAF-12/VDR signalling); amazingly, for most, if not all, this turned out to be the case. For instance, the key regulator fibrillin-1/FBN1, which is responsible for fibrosis and autoimmunity in mouse models of scleroderma, turns out to be the homologue of *fbl-1* in *C. elegans*, the putative target of DAF-12/VDR^[12].

Another GWAS identified genetic variants for joint damage progression in autoantibody-positive RA[13], where three key genes (sperm-associated antigen 16 (SPAG16), and matrix metallopeptidase 1 and 3 (MMP1 and MMP3) are among human homologue candidates of DAF-12/ VDR target genes^[7,5,14-16]. Vitamin D regulates matrix MMP3 in cultured human cells[10] The latest case is POLR3A gene/ rpc-1, which is responsible for both scleroderma and cancer^[17]. Moreover, Miller FW et al^[18] reporting on a GWAS of dermatomyositis (DM), revealed a genetic overlap with other ADs, the first identification of genetic predispositions towards ADs shared with DM. Likely, a malfunction of VDR could affect the pathogenesis of RA and associated cancers [9,19,20] and expand to many other ADs, paraneoplastic neurological diseases and DM[18,21-23] (Table 1). Further patterns of genetic overlap across ADs have emerged^[18,24]. A malfunction in VDR could thus affect the pathogenesis of RA and possibly associated cancers^[9,19]. Importantly, MMP3 contributes to this process^[3,7,25]. In closing, the pathophysiology of ADs (or at least a subgroup of ADs) may share the common underlying mechanism of the GRN of VDR.

To seek for novel support of this emerging concept, we have extended these observations by looking into GWAS-identified AS (in preparation), such as *endoplasmic reticulum aminopeptidase* 1/ERAP-1 for AS mapping to the *pam-1*, one *C. elegans* DAF-12/VDR target genes), particularly RA risk loci as follows:

A recent study^[26] reported the discovery of 42 novel rheumatoid arthritis (RA) risk loci, providing insights into RA biology, contributing to drug discovery. Indeed, Vitamin D-VDR signalling (VITAMIN D-VDR) may act as a upstream master of the risk gene candidates found in RA and VITAMIN D-VDR studies over the last few decades^[1,2,4,5,25,27-31].

As VITAMIN D-VDR targets, some RA risk genes (*e.g. PTPN22*) may alter adaptive immunity and initiate abnormal responses. VITAMIN D-VDR studies relate 25-hydroxyvitamin D levels to ADs. Given that ~80% of the novel risk locus-associated candidate genes in Okada *et al*^[26] are VD3/VDR targets (Table 1) and one-third of them have homologous putative DAF-12/VDR targets^[5] (Table 1), about 80% (273/377, regardless of species^[1,4-5,7,27-31]) of 377 genes included in 101 loci^[26] (~½ (127/377) of their rat homologues^[27]) merge with VITAMIN D-VDR targets^[26] (Table 2), as do all (29/29) the highlighted RA drug target genes^[1,5,26,30,31]. This suggests that VITAMIN D-VDR may play a central role in RA pathogenesis^[2]. Further, multilayered regulatory networks benefit us in preventing RA

alongside using protein–protein interactions, including those applied for identifying RA drug target genes^[26] and complexes between VDR and its targets (e.g. MED1).

Innate immunity is important in RA pathogenesis. However, stating that there is no overlap in innate immunity^[26] may convey a biased message. Several innate immunity participants are actually among the latest highlighted 98 genes in a recent study^[26] (e.g. interleukin-1 receptor-associated kinase 1/IRAK1^[1], CD40^[4], colony stimulating factor 2 /CSF2[30], complement component 5/C5 and interferon regulatory factor 8/IRF8^[4]). Some drugs targeting innate immunity may be repurposed for RA. Since DAF-12/VDR and its targets are required for innate immunity in C. elegans, other innate immunity-related genes within 101 risk loci with a biological score of <2^[26] highlighted in that study^[26] but which overlap DAF-12/VDR targets (such as rpn-3/PSMD3 and MAK-2/MAPKAPK5^[5,32]) may be investigated for drug discovery. Indeed, GLPG0259, an inhibitor of MAPKAPK5, is a new target for treating RA that is undergoing trial^[33]. Lastly, half (34/66) of the VITAMIN D-VDR targets with a biological score of 1^[26] (e.g. rhotekin 2/RTKN2)^[34] may be possibly re-designated as risk genes because of their role in certain ADs.

As mentioned previously, the VITAMIN D-VDR capacitor is an extension from its homologous DAF-12/VDR development "capacitor", similar to the HSP90 capacitor^[35], likely masking minor genetic variations, mutations and environmental insults^[2,7]. If UVB and Vitamin D are insufficient or if mutations in VDR occur, this feature could become overtaxed, leading to RA^[2,4,35]. Many VITAMIN D-VDR (DAF-12/VDR) targets, such as *POLY3A/rpc-1*, may encode self-antigens that possibly elicit autoantibodies^[2,17] (Table 1).

Further investigation is needed for improving our understanding of RA, genetics and the role of Vitamin D. A fraction of ~1500 VITAMIN D-VDR targets^[4] may switch to context-dependent RA risk genes at certain points and democratically contribute to "system failure" RA. Vitamin D supplementation may prevent ADs by its buffering capability; outside these contexts, disease status becomes independent of it^[35], entering a "one-way street".

In closing, VITAMIN D-VDR regulation is critical for identifying RA risk genes and drug discovery. For healthcare, RA prevention with personalized Vitamin D optimization rather than disease reversal could be pursued, since therapies targeting a single RA risk gene may have a limited effect, e.g. RA therapy fails with the anti- TNF (a VITAMIN D-VDR target) alone^[25,26]; better inhibition of human Th17-mediated synovial inflammation is achieved by combining it with Vitamin D3^[25].

Therefore, we may draw the following conclusions. (1) The preventive effects of Vitamin D supplementation on such complex diseases may well need to be considered and we should avoid Vitamin D insufficiency in patients; (2) We predict that combination therapy with Vitamin D will likely benefit the treatment of ADs such as RA and AS.

METHODS

Analysis of Vitamin D/VDR context-dependent targets is based on data from several recent studies including microarray, ChIP-chip/ChIP-seq publications and some references therein [1,25,27,31,42]. NCBI Aceview is used to identify homologues of VDR downstream ADsrelated target gene candidates alongside published DAF-12/VDR binding sites [7]. For comprehensive identification of gene candidates, both sides of the DAF-12/VDR binding sites are considered, as some ADs-related gene homologues may be missed (the original online supplementary material may describe their neighbouring genes only). For BlastP, the $P < 10^{-04}$ is defined as the cut-off for the identification

of significant homologue candidates; otherwise, they are considered "exceptional".

"novel" RA risk		of the downstrea	am targets	of Vitamin D and its recep	tor VDR ir
ADs		Human/Mouse Genes	VD/VDR target	C. elegans DAF-12/VDR target	BlastP for C. elegans
Dermatomyositis	& RA	BLK	+ =	src-1	e=2 10 ⁻³⁴
Scleroderma (SSC)		FBN1	+ =	fbl-1	e=2 10 ⁻⁴⁷
SSC		TOP1	+ =	top1	$e=10^{-25}$
SSC & cancer		POLR3A	+	rpc-1	e=6 10 ⁻⁵¹
RA		SPAG16	N.D.	wdr-5.1	e=4 10 ⁻²⁶
RA		MMP3	+ =	H36L18.1	e=10 ⁻³⁸
RA II		ATG5	+	Atg-5	e=4 10 ⁻¹²
RA	Chr	Human genes	VD/VDR target	C. elegans DAF-12/VDR target	BlastP
rs227163	1	TNFRSF9	+	N.D.	
rs2105325	1 2	LOC100506023/ PRDX6	+		
rs10175798	2	LBH	+		
rs6732565	2	ACOXL	+		
rs6715284	2	CFLAR	+		
rs6715284	3	CASP8	+ √ =		
rs3806624	6	EOMES	+ √	N.D.	
rs9378815	6	IRF4	+		
rs2234067	6	ETV7	+		
rs9373594	7	PPIL4	+		
rs67250450 rs678347	8	JAZF1	+		
rs1516971	8	GRHL2 PVT1	+		
rs12413578	10 10	10p14	+		
rs726288	11	SFTPD	+	N.D.	
chr11:107967350	13	ATM	+ =		
rs9603616	14	COG6	+ =		
rs3783782	17	PRKCH	+ =		
rs72634030	17	C1QBP	+ =		
rs1877030	18	MED1	+		
rs2469434	19	CD226	+		
chr19:10771941 rs73194058	21	ILF3	+ = + =		
rs11089637	22 22	IFNGR2 UBE2L3	+ =		
rs11089637	22	YDJC	+		
rs909685	16	SYNGR1	+ 1		
chrX:78464616	10	P2RY10	+		
III					
RA			VD3/VDR target	C. elegans DAF-12/VDR	BlastP
rs28411352	1	MTF1	+ =	tra-1	e=3 10 ⁻²³
rs28411352	1	INPP5b	+	ocrl-1/C48B4.1 [*C48B4.3]	e=5 10 ⁻¹²
rs2664035	4	TEC	=	kin-22/src-2/ F49B2.5[*F49B2.6]	e=10 ⁻²⁵
rs4272	7	CDK6	+ =	cdk-5	e=9 10 ⁻⁶⁷
rs998731	8	TPD52	+ =	F13E6.1	e=3 10 ⁻⁹
rs793108	10	ZNF438	+	acd-3/C27C12.5[e=2 10 ⁻⁷
rs4452313	3	PLCL2	+ =	*egrh-1/C27C12.2] pll-1[*gei-4]	e=0.0
rs968567	11	FADS1	+ √ =	fat-3	e=10 ⁻¹¹
rs968567	11	FADS2	+	fat-4	e=3 10 ⁻²²
rs968567	11	FADS3	+	fat-3	e=10 ⁻⁹
rs73013527	11	ETS1	+ =	ets-5	e=9 10 ⁻³¹
rs773125	12	CDK2	+ =	cdk-1/ncc-1/ T05G5.3[*T05G5.5]	e=6 10 ⁻⁷⁰
rs10774624	12	SH2B3	+ =	csk-1/ Y48G1C.5[*Y48G1C.8]	e=7 10 ⁻⁶
rs10774624	12	PTPN11	=	anc-1/Zk973.6[*scpl-3/ Y47D9A.2]	e=3 10 ⁻⁴

Note: (1) adapted from table 1 in Okada *et al*¹²⁶; (2) +, $\sqrt{}$, =: yes; N.D.: not determined; further, +: Human; $\sqrt{}$: mouse; =: rat. Not exhaustive manual inspections. (3) *: listed in original table in the publication 5 .

+

RAD51B

16

TXNDC11

rs1950897

rs4780401

pdi-3/H06O01

 $e=2.10^{-22}$

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Table 2 Overlapping risk loci.	of VD-VDR targets and	Biologic	cal score	<u> </u>	s in the RA
RA risk SNP (cytoband)	Gene(VD-VDR target, yellow(human+/-rat); yellowish green for rat only)		Rat	Co-relate Autoimmune diseases	References
chr1:2523811 (1p36)	LOC115110	0			31
chr1:2523811 (1p36)	TNFRSF14	4	1		1,27,29,31
chr1:2523811 (1p36)	LOC100133445	0		1	26
chr1:2523811 (1p36) chr1:2523811 (1p36)	MMEL1 FAM213B	0		1	36
chr1:2523811 (1p36)	TTC34	0			
rs227163 (1p36)	TNFRSF9	2			30
rs2301888 (1p36)	PADI4	2			31
rs28411352 (1p34)	EPHA10	0			30
rs28411352 (1p34)	MANEAL	1 1			30,37
rs28411352 (1p34) rs28411352 (1p34)	YRDC C1orf122	0			30,37
rs28411352 (1p34)	MTF1	1	1		1,27
rs28411352 (1p34)	INPP5B	1	1		27,31
rs12140275 (1p34)	LOC339442	0			31
rs2476601 (1p13)	RSBN1	0			1
rs2476601 (1p13) rs624988 (1p13)	PTPN22 CD2	5			1 nd
rs2228145 (1p13)	IL6R	5	1		na 27
rs2228145 (1q21)	SHE	1			28
rs2228145 (1q21)	TDRD10	0			28
rs2317230 (1q23)	FCRL4	2			
rs2317230 (1q23)	FCRL3	3			20
rs2317230 (1q23)	FCRL2	1		1	38 38
rs2317230 (1q23) chr1:161644258 (1q23)	FCRL1 SLAMF7	1 2		1	31
rs4656942 (1q23)	LY9	3			31
rs4656942 (1q23)	CD244	1		1	1
rs4656942 (1q23)	ITLN1	0			31
chr1:161644258 (1q23)	ITLN2	0			31
chr1:161644258 (1q23)	F11R	0	1		27,31
chr1:161644258 (1q23) chr1:161644258 (1q23)	TSTD1 USF1	0	1		27
chr1:161644258 (1q23)	ARHGAP30	0	1		1
chr1:161644258 (1q23)	PVRL4	0			_
chr1:161644258 (1q23)	KLHDC9	1			31
chr1:161644258 (1q23)	PFDN2	0		_	
chr1:161644258 (1q23)	NIT1	0	1		27,30
chr1:161644258 (1q23) chr1:161644258 (1q23)	DEDD UFC1	0	1		27,30 27,31
chr1:161644258 (1q23)	USP21	0			1
chr1:161644258 (1q23)	PPOX	0			1
chr1:161644258 (1q23)	B4GALT3	0	1		27,31
chr1:161644258 (1q23)	ADAMTS4	0	1		27
chr1:161644258 (1q23)	NDUFS2	0			1.00
chr1:161644258 (1q23) chr1:161644258 (1q23)	FCER1G APOA2	2	1		1,30 27,31
chr1:161644258 (1q23)	TOMM40L	0	1		1
chr1:161644258 (1q23)	NR1I3	0			
chr1:161644258 (1q23)	MPZ	1		1	1,31
chr1:161644258 (1q23)	SDHC	1	1		27,30
chr1:161644258 (1q23)	C1orf192	0			1 20 21
rs72717009 (1q23) rs72717009 (1q23)	FCGR2A HSPA6	3 2			1,30,31 31
rs72717009 (1q23)	FCGR3A	1	1		27
chr1:161644258 (1q23)	FCGR3B	1		1	
chr1:161644258 (1q23)	FCGR2B	5	1		27,30
chr1:161644258 (1q23)	RPL31P11	0			
chr1:161644258 (1q23)	FCRLA	2			27
chr1:161644258 (1q23)	FCRLB	1		1	27 31
chr1:161644258 (1q23) chr1:161644258 (1q23)	DUSP12 ATF6	0	1		27,31 31
rs2105325 (1q25)	LOC100506023	0			Ü1
rs17668708 (1q31)	PTPRC	6	1		27,30
rs10175798 (2p23)	LBH	0			30
rs34695944 (2p16-p15)	FLJ16341	0			
rs34695944 (2p16-p15)	REL	4	1		27,31
rs34695944 (2p16-p15)	PEX13	0	1		1,27 30,31
rs34695944 (2p16-p15) rs34695944 (2p16-p15)	KIAA1841 LOC339803	0			50,51
rs34695944 (2p16-p15)		0			
(1 1 -)	,				

Table 2 Overlapping orisk loci.	of VD-VDR targets and	Biologic	cal score	s of the genes	s in the RA
RA risk SNP	Gene(VD-VDR target, yellow(human+/-rat);		Rat	Co-relate Autoimmune	References
(cytoband)	yellowish green for rat only)		rat	diseases	
rs34695944 (2p16-p15)	AHSA2	1	1		27,31
rs34695944 (2p16-p15)	USP34 SNORA70B	0			30,31
rs34695944 (2p16-p15) rs34695944 (2p16-p15)	XPO1	2	1		27,31
rs13385025 (2p15)	MIR5192	0	-		,-
rs13385025 (2p15)	B3GNT2	1		1	1,31
rs1858037 (2p14) rs9653442 (2q11)	SPRED2 AFF3	0 4	1		1,27,31,38 30
rs9653442 (2q11)	LONRF2	0			30
rs6732565 (2q13)	ACOXL	0			31,38
rs11889341 (2q32)	STAT4	3	1		27,31
rs6715284 (2q33) rs6715284 (2q33)	CFLAR CFLAR-AS1	3	1		27,30
rs6715284 (2q33)	CASP10	2			1,38
rs6715284 (2q33)	CASP8	2	1		27,30,31
rs6715284 (2q33)	ALS2CR12	1	1		27
rs6715284 (2q33) rs6715284 (2q33)	TRAK2 STRADB	0			1 30,31
rs6715284 (2q33)	ALS2CR11	0			00,01
rs1980422 (2q33)	CD28	4			31,38
rs3087243 (2q33)	CTLA4 PLCL2	4	1		27,31
rs4452313 (3p24) rs4452313 (3p24)	MIR3714	0	1		27,30,31
rs3806624 (3p24)	EOMES	1		1	30,31
rs73081554 (3p14)	FLNB	0	1		27,30
rs73081554 (3p14)	DNASE1L3 ABHD6	1 1	1	1	27,30,31
rs73081554 (3p14) rs73081554 (3p14)	RPP14	0	1 1		27,30 27,30,31
rs73081554 (3p14)	PXK	1	1		27,31
rs73081554 (3p14)	PDHB	0	1		27,31
rs73081554 (3p14)	KCTD6	0	1		27,31
rs9826828 (3q22) rs9826828 (3q22)	PCCB STAG1	1	1		27,30 27,30,31
rs9826828 (3q22)	SLC35G2	0			,,-
rs9826828 (3q22)	NCK1	1	1		27,30,31
rs9826828 (3q22) rs13142500 (4p16)	IL20RB CLNK	3	1		31 27
rs11933540 (4p15)	C4orf52	0			29
rs2664035 (4p12-p11)	TEĆ	2	1		27
rs10028001 (4q21)	ANXA3	1 0	1	1	27,30,31
rs10028001 (4q21) rs45475795 (4q26-q27)	LOC100505702 KIAA1109	0			31
	ADAD1	1		1	01
rs45475795 (4q26-q27)	IL2	5			29
rs45475795 (4q26-q27) rs7731626 (5q11)	IL21	3			31
rs2561477 (5q21)	ANKRD55 C5orf30	0			1,30
rs657075 (5q31)	CDC42SE2	0			1
rs657075 (5q31)	RAPGEF6	1			
rs657075 (5q31) rs657075 (5q31)	FNIP1 ACSL6	1 2			1,38 28,30,31
rs657075 (5q31)	IL3	4			31
rs657075 (5q31)	CSF2	4	1		27,31
rs657075 (5q31)	P4HA2	0	1		27
rs657075 (5q31) rs657075 (5q31)	PDLIM4 SLC22A4	0	1	1	27,28,31 30,37
rs657075 (5q31)	MIR3936	0		1	30,37
rs657075 (5q31)	LOC553103	0			
rs657075 (5q31)	SLC22A5	0	1		27,31
rs657075 (5q31) rs9378815 (6p25)	C5orf56 IRF4	3	1		29 1,27,31
chr6:14103212 (6p23)	CD83	3	1		27,31
rs2234067 (6p21)	ETV7	1			30,39
rs2234067 (6p21)	PXT1	0			1.20
rs2233424 (6p21) rs2233424 (6p21)	HSP90AB1 MIR4647	0			1,38
rs2233424 (6p21)	SLC35B2	0	1		27
rs2233424 (6p21)	NFKBIE	4			1
rs2233424 (6p21)	TMEM151B	0			20
rs2233424 (6p21) rs2233424 (6p21)	TCTE1 AARS2	2	1 1		30 27
(°P=1)			-		

Table 2 Overlapping	of VD-VDR targets and	Biologi	cal score	es of the ge <u>ne</u>	s in the RA
risk loci.		U			
RA risk SNP	Gene(VD-VDR target, yellow(human+/-rat);			Co-relate Autoimmune	
(cytoband)	yellowish green for rat only)		Rat	diseases	References
rs9372120 (6q21)	ATG5	1		1	1,30
rs17264332 (6q23)	LOC100130476	0		1	1,00
rs7752903 (6q23)	TNFAIP3	6			1,38
rs9373594 (6q25)	PPIL4	0			30
rs9373594 (6q25)	GINM1	0	_		
rs2451258 (6q25)	TAGAP	2			1,30
rs1571878 (6q27)	FGFR1OP	1 2	1	1	1,30 27
rs1571878 (6q27) rs67250450 (7p15)	CCR6 JAZF1	1	1	1	30
rs4272 (7q21)	FAM133B	0		1	30
rs4272 (7q21)	FAM133DP	0			
rs4272 (7q21)	CDK6	4	1		27,30,31,38
chr7:128580042 (7q32)	IRF5	4	1		27,30,38
chr7:128580042 (7q32)	TNPO3	1	1	1	27,31
rs2736337 (8p23)	FAM167A	0			
rs2736337 (8p23)	BLK	3			27,31
rs998731 (8q21)	TPD52	0	1		27,30,31
rs678347 (8q22)	GRHL2	0	1		29
rs1516971 (8q24) rs11574914 (9p13)	MIR1208 CCL19	0 2			29 31
rs11574914 (9p13)	CCL19 CCL21	2			30
rs11574914 (9p13)	FAM205A	0			30
rs10985070 (9q33)	LOC253039	0			
rs10985070 (9q33)	PHF19	1		1	1,30
rs10985070 (9q33)	TRAF1	4			30,31
rs10985070 (9q33)	C5	4			27,30,38
rs706778 (10p15)	IL2RA	5	1		27,31
rs947474 (10p15)	LOC399715	0	1		
rs3824660 (10p14)	GATA3-AS1	0			
rs3824660 (10p14)	GATA3	2			31
rs793108 (10p11)	ZNF438	0 2			1,30
rs2671692 (10q11)	WDFY4	0			30
rs2671692 (10q11) rs71508903 (10q21)	LRRC18 ARID5B	2			27,30,31
rs6479800 (10q21)	RTKN2	1	1		27,30,31
rs726288 (10q22)	MBL1P	1	1	1	30
rs726288 (10q22)	LOC100288974	0	_	*	
rs726288 (10q22)	SFTPD	2			31
rs331463 (11p12)	PRR5L	0			27,30,31
rs331463 (11p12)	TRAF6	4	1		27,31
rs331463 (11p12)	RAG1	4	1		27,31
rs331463 (11p12)	RAG2	3	1		31
rs331463 (11p12)	C11orf74	0			25.24
rs508970 (11q12)	CD5	4	1		27,31
rs508970 (11q12)	VPS37C	0			1,30
rs968567 (11q12) rs968567 (11q12)	MYRF TMEM258	0			
rs968567 (11q12)	MIR611	0			
rs968567 (11q12)	FEN1	1	1	1	30
rs968567 (11q12)	FADS1	3	1		27,30,31
rs968567 (11q12)	MIR1908	0			
rs968567 (11q12)	FADS2	3	1		27,30,31
rs11605042 (11q13)	ARAP1	0			30
rs4409785 (11q21)	FAM76B	0			
chr11:107967350 (11q22)	CUL5	1	1	1	27,30,31
chr11:107967350 (11q22)	ACAT1	0	1		27,31
chr11:107967350 (11q22)	NPAT	0	1		27,30,31
chr11:107967350 (11q22) chr11:107967350 (11q22)	ATM C11orf65	4	1		27,31
chr11:107967350 (11q22)	KDELC2	0			30
rs10790268 (11q23)	DDX6	1	1	1	27,31
rs10790268 (11q23)	CXCR5	2		1	30
rs73013527 (11q24)	ETS1	2	1		27,31
rs773125 (12q13)	CDK2	3	1		27,30,31
rs773125 (12q13)	RAB5B	0	1		27,31
rs773125 (12q13)	SUOX	2	1		27,30,31
rs773125 (12q13)	IKZF4	0			1
rs773125 (12q13)	RPS26	1	1		27,31
rs773125 (12q13)	ERBB3	2			40
rs1633360 (12q13-q14)	ARHGEF25	0			
rs1633360 (12q13-q14)	SLC26A10	U			

Table 2 Overlapping or risk loci.	of VD-VDR targets and	Biologic	cal score	es of the gene	s in the RA
D	Gene(VD-VDR target,			Co-relate	
RA risk SNP	yellow(human+/-rat);		Rat	Autoimmune	References
(cytoband)	yellowish green for rat only)			diseases	
rs1633360 (12q13-q14)	B4GALNT1	1	1		27
rs1633360 (12q13-q14)	OS9	0			30
rs1633360 (12q13-q14)	AGAP2	0			30
rs1633360 (12q13-q14)	LOC100130776 TSPAN31	0			26
rs1633360 (12q13-q14) rs1633360 (12q13-q14)	CDK4	3	1	1	36 27,30
rs1633360 (12q13-q14)	CYP27B1	2	1		30,31
rs1633360 (12q13-q14)	METTL1	0			1,30
rs1633360 (12q13-q14)	METTL21B	1		1	30
rs1633360 (12q13-q14)	TSFM	0			1
rs1633360 (12q13-q14)	AVIL	0	4		30
rs10774624 (12q24) rs10774624 (12q24)	CORO1C SSH1	0	1		27,30 1,30,38
rs10774624 (12q24)	DAO	0	1		27,31
rs10774624 (12q24)	SVOP	0	-		,-
rs10774624 (12q24)	USP30	0	1		27,31
rs10774624 (12q24)	USP30-AS1	0			
rs10774624 (12q24)	ALKBH2	0	1		27,31
rs10774624 (12q24) rs10774624 (12q24)	UNG ACACB	2	1		27,30,31 1,30
rs10774624 (12q24)	FOXN4	0			1,30
rs10774624 (12q24)	MYO1H	0			
rs10774624 (12q24)	KCTD10	0			1,31
rs10774624 (12q24)	MMAB	0			1
rs10774624 (12q24)	MVK	2			31
rs10774624 (12q24)	FAM222A	0			
rs10774624 (12q24) rs10774624 (12q24)	FAM222A-AS1 TRPV4	0	1	1	27
rs10774624 (12q24)	MIR4497	0	1	1	21
rs10774624 (12q24)	GLTP	0			1,30
rs10774624 (12q24)	ТСНР	0		_	
rs10774624 (12q24)	GIT2	1	1		27
rs10774624 (12q24)	ANKRD13A	0	1		27,30
rs10774624 (12q24) rs10774624 (12q24)	C12orf76 IFT81	0			30
rs10774624 (12q24)	ATP2A2	0	1		27,31
rs10774624 (12q24)	ANAPC7	0	1		27,31
rs10774624 (12q24)	ARPC3	0	1		27,31
rs10774624 (12q24)	GPN3	1			30,38
rs10774624 (12q24)	FAM216A	0			27.01
rs10774624 (12q24) rs10774624 (12q24)	VPS29 RAD9B	0	1		27,31 27,30,31
rs10774624 (12q24)	PPTC7	0	1		1
rs10774624 (12q24)	TCTN1	0			30
rs10774624 (12q24)	HVCN1	0			30
rs10774624 (12q24)	PPP1CC	0			31
rs10774624 (12q24)	CCDC63	1			
rs10774624 (12q24)	MYL2 LOC100131138	0			31
rs10774624 (12q24) rs10774624 (12q24)	CUX2	1			1
rs10774624 (12q24)	FAM109A	0			1,28
rs10774624 (12q24)	SH2B3	5			n.d.
rs10774624 (12q24)	ATXN2	0			1
rs10774624 (12q24)	BRAP	0			31
rs10774624 (12q24)	ACAD10	0			20
rs10774624 (12q24) rs10774624 (12q24)	ALDH2 Mapkapk5	1 1		1 1	30
rs10774624 (12q24)	MAPKAPK5-AS1	0		1	1
rs10774624 (12q24)	ADAM1A	0	1		27
rs10774624 (12q24)	TMEM116	0			
rs10774624 (12q24)	ERP29	0	1		27,30
rs10774624 (12q24)	NAA25	0			
rs10774624 (12q24)	TRAFD1	2			1
rs10774624 (12q24)	HECTD4 RPL6	0	1		27
rs10774624 (12q24) rs10774624 (12q24)	PTPN11	3	1 1		27
rs9603616 (13q14)	COG6	1	1	1	27
rs9603616 (13q14)	MIR4305	0			
rs3783782 (14q23)	PRKCH	2	1		27,28,30
rs1950897 (14q24)	RAD51B	0	1		27
rs2582532 (14q32)	PLD4	1		1	28,30

Gene(VD-VDR target, yellow(human+/-rat); yellowish green for rat only) AHNAK2		Rat	Co-relate Autoimmune	
yellowish green for rat only)		D-1	Autoimmuno	
only)				References
		rat	diseases	
ΛΙΙΙΝΛΙΚΔ	1			1,30
RASGRP1	2	1		27,31
LOC145837	0			31
SNN	0			1
TXNDC11 ZC3H7A	1			28,31
IRF8	3			1 30,36-38
				1
USP6	0	1		27,31
ZNF594	2			1
SCIMP	0			
				25.04
				27,31
				27,30,31 27,30,31
~		1		1
FBXL20	2	1		27,31
MED1	2			41
CDK12	0			1
NEUROD2	0			
PPP1R1B	1	1	1	27,31
STARD3	2			27,31
IKZF3	4			42
ZPBP2	2	1		27,31
GSDMB	2			1
OPMDI 2	2			1
UKWIDLS				1
LRRC3C	0			27,31
Eratese				27,01
GSDMA	1		1	nd
PSMD3	0	1		27,31
CODE				
CSF3	4	1		27
MED24	1			
		1		
		1		27,31,38
		- 4		27 20 21 20
		1		27,30,31,38 27,30,38
				27,30,30
				27,31
ZGLP1	0			
FDX1L	0			
RAVER1	0			31
ICAM3			_	43
		1		27,30,31
				31
				1,30
		1		27,31
		1		27,01
NCOA5	0			1
CD40	6			30
IFNGR2	6	1		1,27-31
TMEM50B	1			1
				1,30
		1	1	27,30
			T	1
				30
	5			30
DNMT3L	0	1		27,31
AIRE	4			30,31
UBE2L3	0	1		27,31
YDJC	1			1,37
	ZNF232 USP6 ZNF594 SCIMP LOC100130950 RABEP1 NUP88 C1QBP DHX33 FBXL20 MED1 CDK12 NEUROD2 PPP1R1B STARD3 IKZF3 ZPBP2 GSDMB ORMDL3 LRRC3C GSDMA PSMD3 CSF3 MED24 PTPN2 DOK6 CD226 ICAM1 ICAM4 ICAM5 ZGLP1 FDX1L RAVER1 ICAM3 TYK2 APIM2 SLC44A2 ILF3-AS1 ILF3 SLC12A5 NCOA5 CD40 IFNGR2 TMEM50B DNAJC28 GART RCAN1 LOC100506403 UBASH3A ICOSLG DNMT3L AIRE UBE2L3	ZNF232	ZNF232	ZNF232

Table 2 Overlapping risk loci.	of VD-VDR targets and	Biologic	al score	s of the gene	s in the RA
RA risk SNP (cytoband)	Gene(VD-VDR target, yellow(human+/-rat); yellowish green for rat only)		Rat	Co-relate Autoimmune diseases	References
rs11089637 (22q11)	SDF2L1	0	1		27,30,31
rs3218251 (22q12)	IL2RB	3			38
rs909685 (22q13)	RPL3	1	1	1	27
rs909685 (22q13)	SNORD83B	1			
rs909685 (22q13)	SNORD83A	1			
rs909685 (22q13)	RNU86	1			
rs909685 (22q13)	SNORD43	1			
rs909685 (22q13)	SYNGR1	1	1	1	27,31
chrX:78464616 (Xq21)	MIR4328	0			
chrX:78464616 (Xq21)	P2RY10	0			31
chrX:78464616 (Xq21)	GPR174	0			
rs5987194 (Xq28)	ARHGAP4	0			31
rs5987194 (Xq28)	NAA10	0			1
rs5987194 (Xq28)	RENBP	0	1		27,30,31
rs5987194 (Xq28)	HCFC1	0			1,28-30
rs5987194 (Xq28)	MIR3202-2	0			
rs5987194 (Xq28)	MIR3202-1	0			
rs5987194 (Xq28)	TMEM187	0			
rs5987194 (Xq28)	IRAK1	3			30,31
rs5987194 (Xq28)	MIR718	0			
rs5987194 (Xq28)	MECP2	0	1		27,30

Adapted from Supplementary Table 5^[26].

CONFLICT OF INTERESTS

There are no conflicts of interest with regard to the present study.

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