

Supplementary Online Content

Burns EM, Guroji P, Ahmad I, et al. Association of vitamin D receptor polymorphisms with the risk of nonmelanoma skin cancer in adults. *JAMA Dermatol*. Published online August 23, 2017.
doi:10.1001/jamadermatol.2017.1976

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This supplementary material has been provided by the authors to give readers additional information about their work.

eTable 1. VDR Polymorphism Primer Details

Primer	Sequence (5' – 3')	T_m (°C)
<i>Apal</i>	F: GCAAAGATAGCAGAGCAGAGTTCC	57
	R: AGGTTGGACAGGAGAGAGAATGG	
<i>BsmI</i>	F: GGGGAGTATGAAGGACAAAGAC	54
	R: TTCTCACCTCTAACCAGCGG	
<i>TaqI</i>	F: CAGAGCATGGACAGGGAGCAAG	65
	R: GCAACTCCTCATGGCTGAGGTCTC	

eTable 2. Genotype and Allele Frequencies of the *VDR* Polymorphisms in Men

		Cases		Controls		p-value	Odds Ratios and 95% Confidence Intervals			
		N	(%)	N	(%)		Crude OR	95% CI	Adj OR*	95% CI
<i>Apal</i>						0.1684 [†]				
	AA	14	21.2	11	23.9		1.0	Ref	1.0	Ref
	Aa	22	33.3	22	47.8		0.79	0.29 – 2.11	0.90	0.27 – 2.96
	aa	30	45.5	13	28.3		1.81	0.65 – 5.04	2.10	0.61 – 7.20
	AA + Aa	36	54.5	24	64.9	0.0679 [‡]	2.12	0.95 – 4.73	2.25	0.83 – 6.07
	A allele freq	0.412		0.466						
<i>BsmI</i>						0.5535 [†]				
	bb	18	26.5	10	21.7		1.0	Ref	1.0	Ref
	Bb	30	44.1	18	39.1		0.93	0.35 – 2.44	0.95	0.28 – 3.23
	BB	20	29.4	18	39.1		0.62	0.23 – 1.68	0.60	0.17 – 2.18
	Bb + bb	48	70.6	28	60.9	0.5653 [‡]	1.30	0.54 – 3.14	1.29	0.41 – 4.01
	b allele freq	0.463		0.375						
<i>TaqI</i>						0.4840 [†]				
	TT	22	32.4	20	43.5		1.0	Ref	1.0	Ref
	Tt	30	44.1	17	37		1.60	0.69 – 3.75	1.84	0.64 – 5.25
	tt	16	23.5	9	19.6		1.62	0.59 – 4.47	1.62	0.44 – 6.05
	Tt + tt	52	76.5	37	80.4	0.6162 [‡]	1.27	0.51 – 3.17	1.18	0.36 – 3.88
	t allele freq	0.434		0.375						

* Adjusted for other factors (skin, age, sun, tan) in a logistic model

[†] Distribution of 3 genotypes

[‡] Distribution of combined genotypes

eTable 3. Genotype and Allele Frequencies of the *VDR* Polymorphisms in Women

		Cases		Controls		p-value	Odds Ratios and 95% Confidence Intervals			
		N	(%)	N	(%)		Crude OR	95% CI	Adj OR*	95% CI
<i>Apal</i>						0.5237 [†]				
	AA	7	24.1	13	24.1		1.0	Ref	1.0	Ref
	Aa	13	44.8	30	55.6		0.81	0.26 – 2.55	0.65	0.17 – 2.51
	aa	9	31.0	11	20.4		1.44	0.39 – 5.26	1.61	0.35 – 7.47
	AA + Aa	20	69.0	43	79.6	0.2817 [‡]	1.76	0.63 – 4.92	2.14	0.61 – 7.54
	A allele freq	0.414		0.519						
<i>BsmI</i>						0.2489 [†]				
	bb	3	10.3	5	9.3		1.0	Ref	1.0	Ref
	Bb	18	62.1	24	44.4		1.25	0.26 – 5.93	0.52	0.08 – 3.24
	BB	8	27.6	25	46.3		0.53	0.10 – 2.74	0.26	0.04 – 1.79
	Bb + bb	21	72.4	29	53.7	0.8731 [‡]	1.13	0.25 – 5.11	2.59	0.45 – 15.06
	b allele freq	0.448		0.352						
<i>TaqI</i>						0.5799 [†]				
	TT	10	34.5	25	46.3		1.0	Ref	1.0	Ref
	Tt	16	55.2	24	44.4		1.67	0.63 – 4.39	1.16	0.35 – 3.91
	tt	3	10.3	5	9.3		1.50	0.30 – 7.49	2.80	0.43 – 18.19
	Tt + tt	26	89.7	49	90.7	0.8731 [‡]	1.13	0.25 – 5.11	2.59	0.45 – 15.06
	t allele freq	0.414		0.324						

* Adjusted for other factors (skin, age, sun, tan) in a logistic model

[†] Distribution of 3 genotypes

[‡] Distribution of combined genotypes

eTable 4. Genotype Frequencies by Non-Melanoma Skin Cancer Type

		Basal Cell Carcinoma (n=40)		p-value*	Squamous Cell Carcinoma (n=33)		p-value*	Basal/Squamous Cell Carcinoma(n=25)		p-value*	p-value†	p-value‡
		N	(%)		N	(%)		N	(%)			
ApaI genotype	A	11	29.0	0.0952	3	9.7	0.0529	7	26.9	0.8825	0.2485	0.1286
	A	11	29.0		13	41.9		11	42.3			
	aa	16	42.1		15	48.4		8	30.8			
BsmI genotype	B	11	28.2	0.4630	9	28.1	0.5796	8	30.8	0.8319	0.9970	0.9915
	B	19	48.7		16	50.0		13	50.0			
	bb	9	23.1		7	21.9		5	19.2			
TaqI genotype	T	13	33.3	0.9945	11	34.4	0.6646	8	30.8	0.5489	0.9480	0.9784
	T	18	46.2		14	43.8		14	53.9			
	tt	8	20.5		7	21.9		4	15.4			

* Distribution of genotypes within each skin cancer type

† Distribution of genotypes among all skin cancer types

‡ Distribution of genotypes between individuals with basal cell carcinoma or squamous cell carcinoma, not both types