

ASSOCIATION BETWEEN VITAMIN D RECEPTOR Taq I (rs731236) GENE POLYMORPHISM AND DENTAL CARIES SUSCEPTIBILITY IN EGYPTIAN CHILDREN

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ABSTRACT

Objective: Dental caries is a complex infectious illness resulting from the interaction of several genetic and environmental variables. The purpose of this work is to evaluate the association among the genetic polymorphism TaqI (rs731236) in vitamin D receptor (VDR) with susceptibility to dental caries and/or severity in Egyptian children. **Subject and Methods:** A total of 300 children (144 males, 156 females) aged between 6 and 12 years were included in the study. The subjects were divided into 3 groups as high caries group (DMFT/dmft >4; n=100), moderate caries group (DMFT/dmft =1-4; n=100), and caries free group (n=100). From each individual, the genomic DNA was extracted from buccal swabs, and the VDR TaqI (rs731236) gene polymorphism was determined by qRT-PCR. **Results:** The genotypic distribution and allelic frequency of both A and G alleles were evaluated in controls and dental caries subjects under different genetic models. A substantial association among the G allele of the VDR gene (rs731236) and dental caries susceptibility and/or severity were found compared to controls (p= 0.01). Moreover, a significant association with dental caries severity risk was observed under one of the co-dominant models used (GG versus AA, p= 0.01), dominant model (p= 0.02) and recessive model (p= 0.045). There was no significant association between the other co-dominant model utilized in this study (AG versus AA, p= 0.08) and the over-dominant model (p= 0.36) contrasted to the controls. **Conclusion:** VDR-Taq I gene polymorphism might be correlated with dental caries susceptibility and/or severity in Egyptian children with raised risk of dental caries.

KEYWORDS: Dental caries, Single Nucleotide Polymorphism, Vitamin D Receptor

INTRODUCTION

Dental caries is a significant public health concern and is the most prevalent chronic disorder. The dental caries prevalence in young children is affected by disparities in socio-demographic circumstances, limited oral health knowledge, and obstacles to accessing preventive and dental care

services ⁽¹⁾. In the 2015 Global Burden of Disease Study, deciduous tooth decay was identified as the 12th most widespread disorder, impacting 560 million children ⁽²⁾. Dental caries is a complex illness that may impact individuals of all ages due to several factors. The condition is closely associated with and impacted by the patient's habits of eating,

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consumption of sugar, amount of saliva produced, level of fluoride in saliva, and preventative actions⁽³⁾.

Despite the high frequency of dental caries in Egypt, there is a scarcity of published epidemiological studies on the topic⁽⁴⁾. The World Health Organization (WHO) conducted the most widely-published epidemiological research on Egypt's oral health condition in 2014 in partnership with the Egyptian Ministry of Health^(4,5).

One of the greatest epidemiological indices in dentistry that represents oral and dental health in the community is the Decay-Missing-Filled Teeth (DMFT) index. Another name for it is the caries index⁽⁶⁾. To assess the frequency of coronal caries, Klein et al. suggested an index of decaying, filled, and missing permanent teeth⁽⁷⁾. Buccal swabbing is now a commonly used non-invasive method for collecting DNA samples from numerous species⁽⁸⁾.

Vitamin D (Vit D), a group of lipophilic steroids, helps in calcium and phosphate absorption in the intestinal tract, so supporting the ideal structure, functioning, and preservation of bones⁽⁹⁾. Vit D has been shown to be correlated to caries and plays a major role in the mineralization of enamel⁽¹⁰⁾. The action of vitamin D-related bio mineralization is believed to be facilitated by the vitamin D receptor (VDR). In the process of developing mineralized tissues including bone and tooth enamel, VDR is implicated in bio mineralization. Genetic mutations in the VDR gene may have significant impacts on gene being activated, affecting the metabolism of calcium, cell growth, immunological responses, and chronic pain syndromes⁽¹¹⁾.

A polymorphism is a mutation in a gene that occurs at a frequency of no less than 1% in a population⁽¹²⁾. There are several polymorphs present in the human VDR gene⁽¹³⁾. Multiple investigations have shown a correlation between caries and single-nucleotide polymorphisms (SNPs) in the VDR gene. One of the main SNPs in VDR gene is TaqI rs731236 A>G SNP⁽¹³⁻¹⁵⁾. As far as we know, just

two investigations have evaluated the genotype and allele prevalence of the VDR TaqI polymorphism in Chinese and Turkish populations with caries of the teeth^(15,16). However, no study has been conducted on Egyptian populations.

Therefore, the primary purpose of this study was to determine the genotype distributions and allelic frequency of Vitamin D receptor Taq I SNP (rs731236) between dental caries and control group. Secondly is to assess the correlation between the VDR Taq I SNP (rs731236) and the dental caries risk/severity in Egyptian children.

SUBJECTS AND METHODS

A total of 300 children, aged 6-12 years, consisting of 144 boys and 156 girls, were chosen from the first of January 2022 to the end of August 2023 and categorized into three groups: severe dental caries, moderate dental caries and dental free caries groups. This classification was determined by their Decayed, Missing, and Filled Teeth (DMFT)/dmft index scores expressed in Figure (1). Children were selected from the Pedodontics Outpatients Clinic, Faculty of Dental Medicine, Boys, Al-Azhar University, Cairo, Egypt.

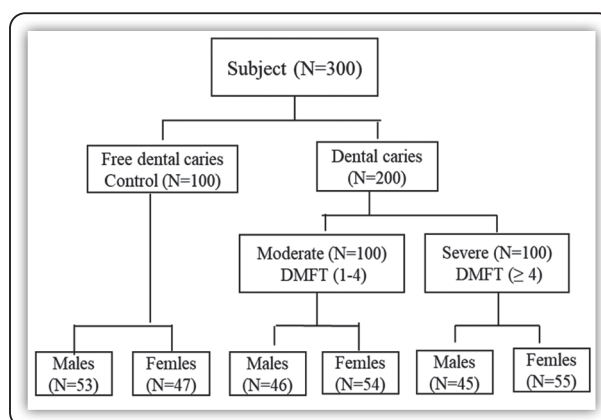


FIG (1) Flowchart Diagram

Written informed consent was obtained from each parent, and ethical approval was obtained by the Institutional Review Board and Ethical

Committee of the Faculty of Dental Medicine, Boys, Al-Azhar University, Cairo, Egypt (EC Ref NO. 640/3631). Children with any kind of systemic illness and inadequately completed questionnaires were excluded from the research. A structured questionnaire was used to record the following: the frequency of tooth brushing (less than once, once, twice), the dietary habits that were consumed each day (0–2 times, >2 times).

Assessment and categorization of patients

Dental examinations of the children were conducted by a pediatric dentist under natural light with the aid of a dental mirror and explorer. Dental plaque scores were recorded according to Silness & Loe index⁽¹⁸⁾. The mesial, distal, lingual and buccal surfaces of all erupted teeth were scored by one observer on a scale of 0–3. The mean surface score per tooth was determined by dividing the total score of all surfaces by four.

The caries diagnosis criteria adhered to the guidelines set out by the WHO⁽¹⁹⁾. The DMFT (D: decayed, M: missing, F: filled, T: tooth for permanent teeth) and dmft (d: decayed, m: missing, f: filled, t: tooth for deciduous teeth) indices were recorded and all children were classified according to the DMFT scores; High caries group (dmft/DMFT >4, n=100), moderate caries group (dmft/DMFT=1–4, n=100) and caries-free group (dmft/DMFT=0, n=100).

DNA extraction

The extraction and purification of Genomic DNA had been gathered from the buccal swabs of participants with a DNA extraction kit (GeneJET™ buccal swab genomic DNA purification mini kit, Thermo Scientific, Wilmington, Delaware, USA). The concentration of DNA was assessed by utilizing a NanoDrop 2000 Spectrophotometer (Thermo Scientific, Wilmington, Delaware, USA) at wavelength 260 nm. Then DNA aliquots were stored at -80 °C in until required.

SNP Genotyping TaqMan® Assay

The VDR TaqI SNPrs731236 [A/G] was assessed utilizing a TaqMan® allelic discrimination test with quantitative real time-polymerase chain reaction (qRT-PCR) following the guidance provided by the manufacturer. The TaqI rs731236 TaqMan® probes had been pre-designed by Applied Biosystems (ID: rs731236, C_2404008_10; **Cat. No. 4351379**; Applied Biosystems, California, USA). Genetic investigations were carried out at the Department of Biochemistry and Molecular Biology, Faculty of Pharmacy, Al-Azhar University, Cairo, Egypt.

Statistical Analysis

Graph pad prism 9.0 (GraphPad software 2018, San Diego, CA, USA) was used for analysis. The difference among the studied groups for quantitative variables will be evaluated either by one-way analysis of variance (ANOVA) test after by post hoc Tukey's multiple comparisons test for parametric parameters or by Kruskal-Wallis test, then by post hoc Dunn's multiple comparisons test for nonparametric variables. The Hardy-Weinberg equilibrium was evaluated utilizing Chi square test (χ^2). The variations in allele and genotype frequencies among the studied groups had been analyzed by utilizing Fisher's exact. A P-value <0.05 was deemed statistically significant.

RESULTS

The demographic data and oral health practices, dietary habits intake, and plaque index in relation to dental caries among study groups are expressed in Table (1). No statistically substantial variation was existed in term of age, and sex distribution between the studied groups. Regarding the environmental factors, 108 children (36%) underwent teeth brushing a minimum of once daily, and 49 children (16%) underwent teeth brushing twice daily. The other children (47.6%) underwent teeth brushing sporadically or never (P>0.001, Table 1). The prevalence of dental caries was substantially greater in children

who consumed carbohydrates and dairy products (milk) daily ($P < 0.001$). Additionally, it was substantially greater in children who consume soft drinks regularly on a daily basis ($P < 0.001$, Table 1).

A significant gender differences was observed ($p < 0.05$) for dmft/DMFT caries indices between males and females. When analyzing the severity of tooth decay in relation to age and gender, majority of

the factors showed statistically substantial variations ($p < 0.05$) (Figure 2). Children under the age of 7 had substantially lower average dmft scores contrasted with children aged 10-12 (2.5 ± 1.14 vs. 3.6 ± 1.3 , $P = 0.001$, correspondingly, Figure 2A). In contrast, the older age group had a substantially greater average DMFT score (3.4 ± 1.15) contrasted to the younger group (2.3 ± 1.11 , $P = 0.001$; Figure 2B).

TABLE (1) Sociodemographic data and oral health practices, dietary habit intake, and plaque index in relation to dental caries among study groups

Variables	Children caries free (n=100)	Children with caries (n=200)	X ²	P value	OR (CI 95%)
Age years (M±SD)	7.21 ± 1.1	9.89 ± 2.3	8.92	0.52	0.41 (0.23-0.68)
Gender					
Males	53 (53%)	91 (45.5%)	0.51	0.47	0.85 (0.77-1.77)
Females	47 (47%)	109 (54.5)	0.48	0.48	1.16 (0.76-1.77)
Tooth Brushing					
- Once a day	56 (56%)	52 (26%)	11.5	0.007	0.46 (0.3-0.7)
- Twice a day	27 (27%)	22 (11%)	8.6	0.003	0.4 (0.22-0.76)
- No brushing	5 (5%)	114 (57%)	38.5	< 0.001	11.4 (4.7-26.6)
Dietary Habits					
Carbohydrates	12 (12%)	82 (41%)	14.9	0.0001	3.41 (1.78-6.59)
Fruits/Vegetables	37 (37%)	32 (16%)	9.89	0.001	0.43 (0.25-0.72)
Milk product	69 (69%)	28 (14%)	42.8	< 0.001	0.20 (0.12-0.33)
Soft drinks	18 (18%)	68 (34%)	4.84	0.027	1.88 (1.06-3.39)
Plaque Index					
Low	55 (55%)	26 (13%)	31.68	< 0.001	0.23 (0.14-0.39)
Moderate	30 (30%)	48 (24%)	0.72	0.39	0.80 (0.48-1.32)
High	15 (15%)	126 (63%)	25.6	< 0.001	4.20 (2.35-7.57)

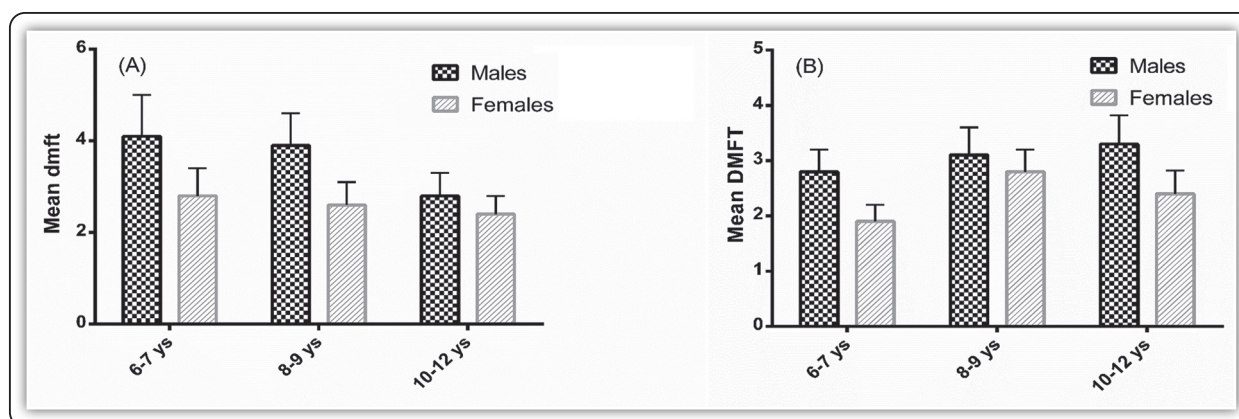


FIG (2) Mean dmft for primary teeth (A) and DMFT for permanent teeth (B) scores, according to age and gender

The genotypic distribution and allelic frequency of both A and G alleles for VDR Taq I (rs731236) gene were calculated in both control and dental caries groups under different genetic models (co-dominant, dominant, recessive, over dominant and allele) as shown in Table (2). In the present study, the genotype distribution and allele frequency for VDR Taq I A<G SNP (rs731236) were revealed no deviation from Hardy–Weinberg equilibrium (HWE).

The statistical analysis of our findings revealed that the prevalence of the (A) allele was substantially greater between the control group (n, %) (141, 70.5%) than in dental caries group (235, 58.75%). In addition, the (G) allele was more predominant in dental caries group (165, 41.25 %) than in control

group (59, 29.5%) as shown in Figure (3). Thus, indicates a significant association was observed among the (G) allele of VDR Taq I (rs731236) gene and the risk of dental caries (OR= 1.68, 95% CI= 1.16 – 2.40 and P=0.005) as illustrated in Table (2).

Furthermore, a significant association with dental caries susceptibility was revealed under one of the two co-dominant models utilized (GG versus AA, OR = 2.66, 95% CI = 1.22 – 5.59, p = 0.01), dominant model (OR = 1.8, 95% CI = 1.11 – 2.98, p = 0.02) and recessive model (OR = 2.1, 95% CI = 1 – 4.3, p = 0.047). While no substantial correlation was existed under the other co-dominant model utilized in this study (AG versus AA, p = 0.09) and over-dominant model (p = 0.39) as shown in Table (2).

TABLE (2) Genotype distribution and allele frequencies of VDR gene rs731236 for dental caries groups versus control group

Models	Genotype and allele distribution n (%)			ORs	95% CI	P-value
	Genotype allele	Dental caries groups (n = 200)	Control group (n = 100)			
Codominant	AA	73 (36.5%)	51 (51%)	1.00 (ref.)		
	AG	89 (44.5%)	39 (39%)	1.6	0.95 – 2.63	0.09
	GG	38 (19.0%)	10 (10%)	2.66	1.22 – 5.59	0.01*
Dominant	AA	73 (36.5%)	51 (51%)	1.00 (ref.)		
	AG + GG	127 (63.5%)	49 (49%)	1.8	1.11 – 2.98	0.02*
Recessive	AA + AG	162 (81%)	90 (90%)	1.00 (ref.)		
	GG	38 (19%)	10 (10%)	2.1	1 – 4.3	0.047*
Over dominant	AA + GG	111 (55.5%)	61 (61%)	1.00 (ref.)		
	AG	89 (44.5%)	39 (39%)	1.25	0.77 – 2.03	0.39
Allele	A	235 (58.75%)	141 (70.5%)	1.00 (ref.)		
	G	165 (41.25%)	59 (29.5%)	1.68	1.16 – 2.4	0.005*
HWE		P = 0.25	P = 0.53			

HWE: Hardy-Weinberg equilibrium; X2: Chi square; *Statistically significant different at $p < 0.05$ using Fisher's exact test. ref.: reference.

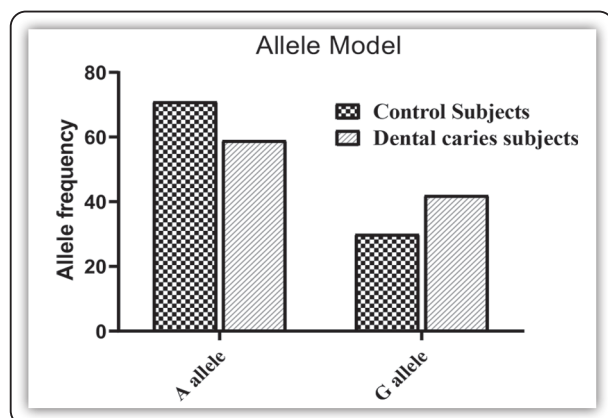


FIG (3) The allelic frequency of VDR A/G single nucleotide polymorphism in the studied groups (Allele Model)

The genotypes percentage and allelic frequencies of both A and G alleles were calculated in both moderate and severe dental caries groups under all genetic models as illustrated in Table (3). A statistical analysis of our findings showed that the prevalence of the (G) allele was substantially greater in

the severe dental caries group (n, %) (95, 47.5%) when compared to moderate dental caries group (70, 35%). Moreover, the (A) allele was more predominant in moderate dental caries group (130, 65%) than in severe dental caries group (105, 52.5%). Thus, indicates a significant association was found between the G allele of VDR Taq I (rs731236) gene and dental caries susceptibility and/or severity (OR = 1.68, 95% CI = 1.13 – 2.5, $p = 0.01$).

Besides, a significant correlation between VDR Taq I SNP (rs731236) and dental caries severity risk was observed under one of the two co-dominant models used (GG versus AA, OR = 2.6, 95% CI = 1.15 – 5.59, $p = 0.03$), dominant model (OR = 1.8, 95% CI = 1.11 – 2.98, $p = 0.02$) and recessive model (OR = 2.04, 95% CI = 0.98 – 4.23, $p = 0.045$). While, there was no significant association between the other co-dominant model utilized in this study (AG versus AA, $p = 0.1$) and the over-dominant model ($p = 0.57$) as shown in Table (3).

TABLE (3) Genotype distribution and allele frequencies of VDR gene rs731236 variant for Moderate dental caries group versus severe dental caries group.

Models	Genotype and allele distribution n (%)			ORs	95% CI	P-value
	Genotype allele	Moderate Dental Caries (n = 100)	Severe Dental Caries (n = 100)			
Codominant	AA	44 (44%)	29 (29%)	1.00 (ref.)		
	AG	42 (42%)	47 (47%)	1.7	0.93 – 3.2	0.1
	GG	14 (14%)	24 (24%)	2.6	1.15 – 5.9	0.03*
Dominant	AA	44 (44%)	29 (29%)	1.00 (ref.)		
	AG + GG	56 (56%)	71 (71%)	1.8	1.11 – 2.9	0.02*
Recessive	AA + AG	86 (86%)	76 (76%)	1.00 (ref.)		
	GG	14 (14%)	24 (24%)	2.0	0.98 – 4.2	0.4*
Over dominant	AA + GG	58 (58%)	53 (53%)	1.00 (ref.)		
	AG	42 (42%)	47 (47%)	1.2	0.69 – 2.2	0.57
Allele	A	130 (65%)	105 (52.5%)	1.00 (ref.)		
	G	70 (35%)	95 (47.5%)	1.68	1.13 – 2.5	0.01*
HWE		$P = 0.25$	$P = 0.53$			

HWE: Hardy-Weinberg equilibrium; χ^2 : Chi square; *Statistically significant different at $p < 0.05$ using Fisher's exact test. ref.: reference.

DISCUSSION

The occurrence of dental caries is the result of an intricate interplay between hereditary factors and the surrounding environment⁽²⁰⁾. Studies involving families and genomes have shown that over 40% of the risk for tooth decay may be attributable to hereditary factors⁽¹²⁾. Regarding the general characteristics of these study participants, our findings revealed no statistically substantial variation in the demographic data including participants' number, age, and sex distribution in all the studied groups which were in agreement with Abbass et al.⁽²¹⁾.

The current study reported that the dental caries incidence in youngsters in Egypt was greater in their primary teeth (dmft) contrasted to their permanent teeth (DMFT). The results of our study align with the findings previously published in India⁽²²⁾. Deciduous teeth are more prone to dental caries because they contain lower levels of calcium and structural variations⁽²³⁾. The present investigation found a substantial and favorable association between dmft and age, consistent with prior research done in Brazil and Colombia with children aged 3 to 5 years⁽²⁴⁾.

This work was aiming to assess the correlation among the *TaqI* SNP (rs731236) of VDR gene and dental caries in caries-active (moderate-severe) and caries-free Egyptian children. Results of the present study have been investigated by performing association under several genetic models (co-dominant, dominant, recessive, and allele) to avoid potential biases.

The current study has revealed that the rs731236 variant of the VDR gene is substantially associated with dental caries risk in Egyptian children under all genetic models. These findings were in agreement with the previous studies of SNPs in the VDR gene that was correlated with dental caries^(15,16). In case-control research done by Hu et al. in China, it was shown that persons from northwestern China

who had the VDR *TaqI* genotype have a greater sensitivity to caries⁽¹⁵⁾. Furthermore, this aligns with the research done by Cogulu et al. in Turkey, which indicated that the genotype in VDR *TaqI* may potentially elevate the chance of developing caries⁽¹⁶⁾. However, research done by Holla et al. in Czech Republic found that genetic variants in the VDR *TaqI* gene can't serve as a reliable indicator for detecting the risk of dental caries⁽²⁵⁾.

The current study showed that the co-dominant model for *TaqI* rs731236 variant genotype, (AA, AG, and GG) genotypes frequencies across the healthy children's individuals are 51 %, 39 %, and 10 %, while the frequencies among dental caries children are 36.5%, 44.5%, and 19 % respectively. Instead, across Indian people the frequencies of *TaqI* variants had been 49%, 43%, and 8%⁽²⁶⁾ while a Japanese work revealed 77%, 22%, and 1%⁽²⁷⁾, and a Turkish, the work revealed the frequency of 40.8%, 47.9% and 11.2% respectively⁽²⁸⁾. This contradiction was explained by differences in the sample size of studied populations, geographical regions, race, age, and gender of subjects⁽²⁹⁾.

Moreover, the analysis of allelic frequencies demonstrated that the prevalence of the mutant (A) allele was notably greater in control subjects compared to dental caries subjects, while the wild (G) allele was more prevalent in dental caries subjects than in control subjects. This indicates a substantial correlation among the wild allele and elevated risk of dental caries development in Egyptian children.

These findings had been in agreement with that noticed by Bahareh et al., in the Iranian population⁽³⁰⁾. Moreover, our result was in agreement with those noticed by Hu et al.⁽¹⁵⁾, who indicated that the VDR *TaqI* genotype could potentially raise the likelihood of developing dental caries in persons living in the northwest region of China. Likewise, Cogulu et al.⁽¹⁶⁾, reported that the *TaqI* VDR genotype increases the risk of dental caries incidence in Turkish children.

Conversely, the work done by Li et al. found no correlation among the VDR -1056 T/C gene polymorphism and serious periodontitis in the Chinese population⁽³¹⁾. Furthermore, research performed by Chantarangsu et al. found no correlation among the VDR gene polymorphism and persistent periodontitis in the Thai people⁽³²⁾. Ho et al. performed a work on the VDR -1056 T/C gene polymorphism and found no association between this genetic variation and serious periodontitis in the Taiwanese population⁽³³⁾.

The limitation of this study was that we only focused on TaqI SNP (rs731236) of VDR gene in dental caries disease, and the sample size was small.

CONCLUSION

Dental caries is a major public health issue affecting more than 500 million children globally⁽²⁾. Dental caries is caused by a complex interaction between genetics and the environment⁽³⁴⁾. One of the genes that have a role in enamel formation is the VDR gene⁽³⁵⁾. The TaqI G > A (rs731236) SNP of the VDR gene has been evaluated in the existing study. Our findings reported that the wild (G) allele was more predominant in children with dental caries than in controls suggesting a considerable association between the G allele and risk of dental caries incidence. Thus, the TaqI (rs731236) SNP of VDR gene may be correlated to dental caries severity and risk in Egyptian children.

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