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Association of *TaqI* VDR Polymorphism with the Response to Directly Acting Antiviral Treatment in Hepatitis C Patients

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NHHA: Designed the study, collected the data, did genetic analysis, performed statistical analysis, and wrote the manuscript. Soumble Z: Supervised and reviewed the genetic analysis work. MFH: Participated in data collection. ARS: Supervised the research and reviewed the study and the manuscript. Sibgha Z and MI: Supervised the research and reviewed the manuscript.

Key words
Hepatitis C, Vitamin D receptor polymorphism, *TaqI* VDR polymorphism, Response to treatment

ABSTRACT

The objective of this study was to determine the association between *TaqI* Vitamin D receptor (VDR) polymorphism and the response to directly acting antiviral treatment in hepatitis C patients. This case control study included 132 participants, out of which 66 were chronic hepatitis C (CHC) genotype 3 patients who received directly acting antiviral treatment, responded to the treatment, and achieved sustained virologic response (SVR) i.e. negative HCV-RNA three months after completion of the treatment (responders), and 66 were CHC genotype 3 patients who received the same treatment and did not achieve SVR (non-responders). After taking informed consent from each participant, demographic data was collected. Under aseptic conditions, 5 mL of blood was drawn for DNA extraction, polymerase chain reaction (PCR), restriction fragment length polymorphism analysis (RFLP), and gel electrophoresis. Data was analysed using SPSS 24. *TaqI* genotypes distribution was found to be 31 (47%), 26 (39.4%), and 9 (13.6%) for the genotypes TT, Tt, and tt in responders and 33 (50%), 26 (39.4%), and 7 (10.6%) in non-responders, respectively. For the T and t alleles, the distribution was 88 (66.7%) and 44 (33.3%) in responders and 92 (69.7%) and 40 (30.3%) in non-responders, respectively. No significant association was found between *TaqI* VDR polymorphism and the response to directly acting antiviral treatment nor between *TaqI* VDR polymorphism and cirrhosis in CHC patients (p-values > 0.05). In conclusion, *TaqI* VDR polymorphism has no association with the response to directly acting antiviral treatment in CHC genotype 3 patients.

INTRODUCTION

Hepatitis C is a global health problem with about 50 million people world-wide infected with chronic hepatitis C (CHC) virus. One million new cases in 2022 were reported by WHO. The largest burden of hepatitis C infections is found in Pakistan, India, China, the United States of America, Indonesia, and Russia (WHO, 2024). Hepatitis C is still one of the major health concerns (Manikat *et al*., 2024) and is one of the most common causes of chronic liver disease and cirrhosis (Moon *et al*., 2020). Hepatitis C is a risk factor for hepatocellular carcinoma. Globally, cirrhosis and hepatocellular carcinoma are the 11th and 16th causes of death respectively, accounting for 3.5% of the worldwide deaths (Asrani *et al*., 2019).

Directly acting antiviral drugs have revolutionized the treatment of CHC infection and have led to viral eradication in majority of the patients. However, some patients remain as difficult to treat (Manns and Maasoumy, 2022). The high cost of directly acting antiviral drugs and the high incidence of hepatitis C infection constitute an economic burden which makes it important to have adequate cure rates. Therefore, it is crucial to address the factors that might have led to failing DAA treatment (Schwander *et al*., 2022; Abdelaziz *et al*., 2024). Multiple factors can affect the course of the HCV infection including host as well as viral factors. It is suggested that host genetics may

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play an important role in affecting the clinical course of the disease (Nahon and Cobat, 2020).

Among the host genetic factors, vitamin D receptor (VDR) gene variations were reported to modulate the progression of the disease (Malicki *et al*., 2025). VDR polymorphisms may affect inflammation, response to treatment, and progress of fibrosis (Al-Aqmer *et al*., 2022; Lima *et al*., 2025). One of these VDR gene variations is *TaqI* VDR polymorphism. Beka *et al*. (2022) reported *TaqI* VDR genotype to be associated with the degree of liver fibrosis and Neamatallah *et al*. (2022) found more frequency of *TaqI* VDR polymorphism in patients with CHC as compared to those who had spontaneous virus clearance. Moreover, Abdelsalam *et al*. (2016) reported that *TaqI* VDR polymorphism was associated with successful treatment and was a predicting factor for the response to pegylated interferon and ribavirin therapy. In another study, *TaqI* VDR polymorphism was not found to be associated with cirrhosis, however, it was found to be associated with low VDR levels in CD14+ cells in hepatitis C patients. It was also found to affect the expression of the genes that regulate oxidative stress, proliferation and differentiation of cells, and intracellular signalling (Tourkochristou *et al*., 2023).

On the other hand, some studies found no association between *TaqI* VDR polymorphism and the response to treatment. Thanapirom *et al*. (2019) reported no relationship of *TaqI* VDR polymorphism with the response to pegylated interferon therapy nor with advanced liver disease in CHC patients. Similarly, Arai *et al*. (2015) reported no association between *TaqI* VDR genotypes and the response to pegylated interferon and ribavirin with Telaprevir in CHC patients.

Whether *TaqI* VDR polymorphism relates to the response to the treatment in HCV patients remains unclear. Moreover, there is no data on the association of *TaqI* VDR genotypes with the response to directly acting antiviral treatment in CHC genotype 3 patients. Our study aimed at finding out the association between *TaqI* VDR polymorphism and the response to the directly acting antiviral treatment in HCV genotype 3 patients.

MATERIALS AND METHODS

This case-control study included 132 participants, in which 66 CHC genotype 3 patients, males and females, aged ≥ 18 years, who received directly acting antiviral treatment, daclatasvir and sofosbuvir (with ribavirin in cirrhotic patients), and responded to the treatment by achieving a sustained virologic response (SVR) i.e. were HCV-RNA negative three months after the treatment was completed (Responders), and 66 CHC genotype 3 patients who received the same treatment and did not achieve a sustained virologic response (SVR) i.e. were HCV-RNA positive three months after the treatment was completed (Non-responders). Both the groups were matched in age, gender, and cirrhosis status. The study excluded CHC patients with hepatitis B, HIV, advanced liver disease, or renal disease. Informed written consent was taken from the participants and their demographic data was recorded. Test reports of platelet count, prothrombin time, INR, liver function tests, and haemoglobin were recorded. Under aseptic conditions, 5 mL blood was drawn from each participant for DNA extraction, polymerase chain reaction (PCR) of the sequence containing the *TaqI* restriction site (rs731236), restriction fragment length polymorphism (RFLP) analysis, gel electrophoresis, and visualization under UV light.

DNA extraction was done using ThermoScientific #K0781 and was followed by PCR. The primers used were:

F 5'CAGAGCATGGACAGGGAGCAA3'

R 5'GCAACTCCTCATGGCTGAGGTCTC3'.

The PCR reaction mixture of 20 µL contained 5 µL DNA, 3 µL 25 mM $MgCl_2$, 3 µL 2.5 mM dNTPs, 2 µL 10X $(NH_4)_2SO_4$ buffer, 0.5 µL 5U/µL Taq polymerase, 1.5 µL 10 µM forward primer, 1.5 µL 10 µM reverse primer, and 3.5 µL water. PCR reaction mixture underwent initial denaturation for 5 min at 95°C, 35 cycles each comprising of denaturation for 30 sec at 95°C, annealing for 45 sec at 65°C, extension for 45 sec at 72°C, and final extension for 10 min at 72°C. The PCR product containing *TaqI* VDR polymorphism (rs731236) was of 744 base pairs.

For *TaqI* VDR genotyping, restriction fragment length polymorphism (RFLP) analysis was done using Thermo Scientific *TaqI* (#ER0671). The mixture comprised of 10 µL PCR product (0.1-0.5 µg DNA), 2 µL *TaqI* enzyme, 2 µL 10X buffer *TaqI*, and 16 µL nuclease free water making up a total volume of 30 µL. The mixture tube was sealed with paraffin film and incubated at 65°C in water bath for 8-16 h. The samples were run on 2% agarose gel and visualized under UV light.

Statistical analysis

Data was entered and analysed using SPSS 24. T-test (for normally distributed data) and Mann-Whitney test (for not-normally distributed data) were used to compare age and BMI between responders and non-responders. Frequencies of *TaqI* polymorphisms were studied in accord with the Hardy-Weinberg equilibrium. The association of *TaqI* VDR polymorphism with the response to treatment, cirrhosis, and gender was studied using Chi Square test and Exact Fisher's test accordingly. ANOVA (for normally distributed data) and Kruskal Wallis test (for not-normally distributed data) were used to compare platelets count, prothrombin time, INR, liver function tests and haemoglobin among the TT, tt, and Tt genotypes. A

p-value < 0.05 was considered significant.

RESULTS

There were 132 participants with 66 in the responders group and 66 in the non-responders group. No significant differences were found in age and BMI between the two groups (p-values > 0.05) (Table I). The restriction of the PCR product (744 base pairs) containing *TaqI* VDR polymorphism (rs731236) yielded two bands for the wild homozygous TT genotype (TT) of 494 and 250 base pairs, three bands for the mutant homozygous tt genotype (CC) of 293, 250, and 201 base pairs, and four bands for the heterozygous Tt genotype (CT) of 494, 293, 250, and 201 base pairs (Fig. 1).

The frequencies of the *TaqI* VDR genotypes were 48.5%, 39.4%, and 12.1% for the TT, Tt, and tt genotypes respectively with 68.2% frequency for the T alleles and 31.8% for the t alleles (Table II). In the responders and non-responders groups, the distribution of *TaqI* VDR genotypes was 47% and 50% for the wild homozygous *TaqI* genotype (TT), 39.4% for the heterozygous *TaqI* genotype (Tt) in both the groups, and 13.6% and 10.6% for the homozygous mutant *TaqI* genotype (tt), respectively. The distribution of the T and t alleles was 88 (66.7%) and 44 (33.3%) in responders and 92 (69.7%) and 40 (30.3%) in non-responders, respectively. There was no significant association between *TaqI* VDR genotypes and the response to treatment (p-value = 0.855) (Table III). There was no significant association between *TaqI* VDR polymorphism and cirrhosis nor between *TaqI* VDR polymorphism and gender (Table IV).

No significant differences were found in platelets count, prothrombin time, INR, total bilirubin, direct bilirubin, aspartate transaminase (AST), alanine transaminase (ALT), alkaline phosphatase (ALP), albumin, and haemoglobin levels among the TT, tt, and Tt genotypes (p-values > 0.05) (Table V).

Table I. Age (yrs) and BMI (kg/m^2) in responders and non-responders.

Variables	Responders [a] (n=66)	Non-responders [b] (n=66)	p-value
Age Median (IQR) [c]	53.5 (44-55)	51.0 (43-55)	0.360
BMI Mean±SD [d]	26.97±6.81	28.01±6.46	0.369

* p-value < .05 is considered significant. [a] Responders are HCV patients who achieved sustained virologic response (SVR) three months after completing the treatment; [b] Non-Responders are HCV patients who did not achieve sustained virologic response (SVR) three months after completing the treatment; [c] Mann-Whitney test was used; [d] T-test was used. IQR, Interquartile range; BMI, Body mass index.

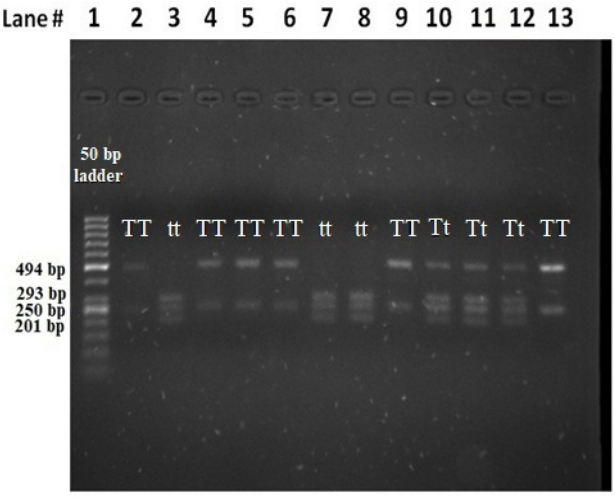

Fig. 1. RFLP analysis of *TaqI* VDR polymorphism (rs731236) in 2% agarose gel showing the bands 494 and 250 bp in the TT genotype (Lanes# 2, 4, 5, 6, 9, and 13), the bands 494, 293, 250, and 201 bp in the Tt genotype (Lanes# 10, 11, and 12), and the bands 293, 250, and 201 bp in the tt genotype (Lanes# 3, 7, and 8).

Table II. Frequencies of *TaqI* VDR genotypes and alleles (n=132).

Genotypes/Alleles	Count (%)
Genotypes	
TT	64 (48.5 %)
Tt	52 (39.4 %)
tt	16 (12.1 %)
Total	132 (100 %)
Alleles	
T	180 (68.2 %)
t	84 (31.8 %)
Total	264 (100 %)

Table III. Association between *TaqI* VDR polymorphism and the response to directly acting antiviral treatment.

Genotypes	Responders[a] (n=66)	Non-responders [b] (n=66)	Chi-Square test	p value
TT	31	33	0.313	0.855
Tt	26	26		
tt	9	7		

* p-value < .05 is considered significant. Responders and non-responders are explained in Table I.

Table IV. Association of *TaqI* VDR polymorphism with cirrhosis and gender in responders and non-responders.

TaqI VDR genotypes	Responders [a] (n=66)		Non-responders [b] (n=66)	
	With cirrhosis (n=33)	Without cirrhosis (n=33)	With cirrhosis (n=33)	Without cirrhosis (n=33)
Association with cirrhosis				
TT	16	15	19	14
tt	5	4	2	5
Tt	12	14	12	14
p-value	0.891		0.356	
	Males (n=40)	**Females (n=26)**	**Males (n=40)**	**Females (n=26)**
Association with gender				
TT	17	14	21	12
tt	7	2	4	3
Tt	16	10	15	11
p-value	0.460		0.936	

* p-value < .05 is considered significant. Responders and non-responders are explained in Table I.

DISCUSSION

Our study found no significant association between *TaqI* VDR polymorphism and the response to directly acting antiviral treatment in chronic hepatitis C genotype 3 patients indicating no role of *TaqI* VDR polymorphism in affecting the response to therapy. Similar to our results, Arai *et al*. (2015) found no association between *TaqI* VDR polymorphism and the response to Telaprevir and pegylated interferon with ribavirin in CHC patients in Japan. Also, Wang *et al*. (2016) and Hung *et al*. (2016) reported the same in their studies conducted in China and Thailand with Taiwan, respectively on CHC patients who received pegylated interferon plus ribavirin therapy therapy.

On the contrary, Baur *et al*. (2012) found TT genotype to be a predictive marker for the treatment failure in CHC patients genotypes 1, 2, and 3 in Switzerland and Abdelsalam *et al*. (2016) reported t allele to be protective and associated with success of treatment.

The different reported results could be due to the differences in the hepatitis C virus genotypes and ethnicities as both factors may affect the response to treatment (Navaneethan *et al*., 2009; Ansaldi *et al*., 2014). Moreover, the above mentioned studies were on patients who received interferon and ribavirin whereas our study was on patients who received directly acting antiviral HCV treatment and pharmacogenetics might affect the results.

We found no association between *TaqI* polymorphism and cirrhosis, and no significant differences in platelets count, PT, INR, liver function tests, and haemoglobin among *TaqI* genotype groups. Our results aligned with the results of Tsounis *et al*. (2022) who also reported no association between *TaqI* polymorphism and cirrhosis. They also found no significant differences in platelets count, alanine transaminase (ALT), aspartate transaminase (AST), alkaline phosphatase (ALP), and albumin levels amongst the three *TaqI* genotype groups. On the contrary, Triantos *et al*. (2018) found that the *TaqI* VDR genotype TT was associated with advanced Child-Pugh stage and with the severity of liver cirrhosis. This could not be assessed in our study as advanced liver disease patients were excluded.

Table V. Platelets count, PT, INR, liver functions tests, and haemoglobin among the TT, tt, and Tt genotype groups.

Variables (Median (IQR)[a]/ Mean±SD[b])	*TaqI* VDR genotypes			p-value
	TT	tt	Tt	
Platelets count (×1000/µL)	260 (152-291) [a]	252 (178-268) [a]	260 (164.5-292) [a]	.887
PT (sec)	14.8 (14.2-15.9) [a]	14.3 (14.0-14.8) [a]	14.5 (14-15.5) [a]	.141
INR	1.1 (1.1-1.2) [a]	1.1 (1.0-1.2) [a]	1.1 (1-1.2) [a]	.406
Total bilirubin (mg/dL)	1 (0.5-1.6) [a]	0.7 (0.5-1.4) [a]	0.8 (0.5-1.3) [a]	.585
Direct bilirubin (mg/dL)	0.3 (0.2-0.9) [a]	0.2 (0.1-0.7) [a]	0.2 (0.1-0.7) [a]	.280
AST (U/L)	67.5 (52.0-80.8) [a]	61.5 (50.5-81.8) [a]	61.0 (47.0-80.0) [a]	.671
ALT (U/L)	71.0±21.6[b]	70.4±25.3[b]	69.2±22.0[b]	.910
ALP (IU/L)	110.1±22.0[b]	109.9±22.7[b]	107.4±19.4[b]	.779
Serum albumin (g/dL)	3.5 (3.0-4.2) [a]	3.6 (2.9-4.0) [a]	3.2 (3.0-3.9) [a]	.380
Haemoglobin (gm/dL)	13.2 (12.0-14.1) [a]	12.9 (11.9-14.3) [a]	13.1 (11.7-14.1) [a]	.840

* p-value < .05 is considered significant. [a] Kruskal-Wallis test was used; [b] ANOVA test was used. PT, prothrombin time; INR, international normalized ratio; AST, aspartate transaminase; ALT, alanine transaminase; ALP, alkaline phosphatase.

CONCLUSION

We concluded that there is no significant association between *TaqI* VDR polymorphism and the response to daclatasvir and sofosbuvir (with ribavirin for cirrhotic patients) in chronic hepatitis C genotype 3 patients. This finding suggests that *TaqI* VDR polymorphism may not play a major role in influencing the response to treatment within the studied population. While this contrasts with the results of some of the previous studies, it highlights that the relationship between *TaqI* VDR polymorphism and the response to therapy in CHC patients may be influenced by other factors.

DECLARATIONS

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Ethical statement and IRB approval

This study was conducted after approval from the Ethical Review Board of Pakistan Kidney and Liver Institute, Lahore.

Generative AI and AI assisted technology statement

The authors declare that no generative AI and AI assisted technology was used in the creation of this manuscript.

Statement of conflict of interest

The authors have declared no conflict of interest.

REFERENCES

Abdelaziz, A.I., Abdelsameea, E., Abdel-Samiee, M., Ghanem, S.E., Wahdan, S.A., Elsherbiny, D.A., Zakaria, Z. and Azab, S.S., 2024. Effect of immunogenetics polymorphism and expression on direct-acting antiviral drug response in chronic hepatitis C. *Clin. Exp. Med.*, **24**: 184. https://doi.org/10.1007/s10238-024-01432-x

Abdelsalam, A., Rashed, L., Salman, T., Hammad, L. and Sabry, D., 2016. Molecular assessment of vitamin D receptor polymorphism as a valid predictor to the response of interferon/ribavirin-based therapy in Egyptian patients with chronic hepatitis C. *J. Dig. Dis.*, **17**: 547-553. https://doi.org/10.1111/1751-2980.12353

Al-Aqmer, N.H.H., Aamir, Z., Hanif, M.F., Zulfiqar, S., Zulfiqar, S., Izhar, M. and Shakoori, A.R., 2022. *ApaI* VDR polymorphism as a risk factor of treatment failure in chronic hepatitis C patients. *Pakistan J. Zool.*, **54**: 2055-2060. https://doi.org/10.17582/journal.pjz/20210909030800

Ansaldi, F., Orsi, A., Sticchi, L., Bruzzone, B. and Icardi, G., 2014. Hepatitis C virus in the new era: Perspectives in epidemiology, prevention, diagnostics and predictors of response to therapy. *World J. Gastroenterol.*, **20**: 9633–9652. https://doi.org/10.3748/wjg.v20.i29.9633

Arai, T., Atsukawa, M., Tsubota, A., Kondo, C., Shimada, N., Abe, H., Itokawa, N., Nakagawa, A., Okubo, T., Aizawa, Y. and Iwakiri, K., 2015. Vitamin D-related gene polymorphisms do not influence the outcome and serum vitamin D level in pegylated interferon/ribavirin therapy combined with protease inhibitor for patients with genotype 1b chronic hepatitis C. *J. med. Virol.*, **87**: 1904–1912. https://doi.org/10.1002/jmv.24244

Asrani, S.K., Devarbhavi, H., Eaton, J. and Kamath, P.S., 2019. Burden of liver diseases in the world. *J. Hepatol.,* **70**: 151-171. https://doi.org/10.1016/j.jhep.2018.09.014

Baur, K., Mertens, J.C., Schmitt, J., Iwata, R., Stieger, B., Frei, P., Seifert, B., Ferrari, H.A.B., von Eckardstein, A., Müllhaupt, B., Geier, A. and Swiss Hepatitis C Cohort Study Group, 2012. The vitamin D receptor gene *bAt* (CCA) haplotype impairs the response to pegylated-interferon/ribavirin-based therapy in chronic hepatitis C patients. *Antivir. Ther.*, **17**: 541–547. https://doi.org/10.3851/IMP2018

Beka, A.A., Papadopoulos, V., Mylopoulou, T., Panopoulou, M., Karakasiliotis, I., Mavromara, P., Mimidis, K. and Veletza, S., 2022. Association between vitamin D receptor gene polymorphisms and fibrosis susceptibility in Greek patients with HCV infection. *Germs*, **12**: 384–393. https://doi.org/10.18683/germs.2022.1342

Hung, C.H., Hu, T.H., Lu, S.N., Chen, C.H., Wang, J.H. and Lee, C.M., 2016. Association of vitamin D receptor gene polymorphisms with response to peginterferon plus ribavirin in Asian patients with chronic hepatitis C. *J. Formos. Med. Assoc.,* **115**: 278–283. https://doi.org/10.1016/j.jfma.2015.11.008

Lima, S.P.S., Fernandes-Ferreira, R., Brait, B.J., Aguiar,

F.L., Pinhel, M.A.S., Abreu, A.D.S., Silva, R.F., Silva, R.C.M.A. and Souza, D.R.S., 2025. Influence of genetic variants of the vitamin D receptor on clinical profile in cirrhosis and hepatocellular carcinoma. *E-cancer*, **19**: 1990. https://doi.org/10.3332/ecancer.2025.1990

Malicki, D., Bisaga, W., Sternak, A., Wrześniewska, N., Nowak, A., Jabłońska, A., Stępień, W. and Janczura, J., 2025. The role of vitamin D3 deficiency in hepatitis C treatment: A systematic review. *Rev. Méd. Hosp. Gen. México*. https://doi.org/10.24875/HGMX.25000033

Manikat, R., Ahmed, A. and Kim, D., 2024. Current epidemiology of chronic liver disease. *Gastroenterol. Rep.*, **12**: goae069. https://doi.org/10.1093/gastro/goae069

Manns, M.P. and Maasoumy, B., 2022. Breakthroughs in hepatitis C research: from discovery to cure. *Nat. Rev. Gastroenterol. Hepatol.*, **19**: 533–550. https://doi.org/10.1038/s41575-022-00608-8

Moon, A.M., Singal, A.G. and Tapper, E.B., 2020. Contemporary epidemiology of chronic liver disease and cirrhosis. *Clin. Gastroenterol. Hepatol*, **18**: 2650–2666. https://doi.org/10.1016/j.cgh.2019.07.060

Nahon, P. and Cobat, A., 2020. Human genetics of HCV infection phenotypes in the era of direct-acting antivirals. *Hum. Genet.*, **139**: 855-863. https://doi.org/10.1007/s00439-020-02136-4

Navaneethan, U., Kemmer, N. and Neff, G.W., 2009. Predicting the probable outcome of treatment in HCV patients. *Therap. Adv. Gastroenterol.*, **2**: 287–302. https://doi.org/10.1177/1756283X09339079

Neamatallah, M., Serria, M.S., El-Bendary, M., El-Gilany, A.H., Alhawarey, A., Abed, S., Setate, Y.A. and Ammar, O.A., 2022. Association of vitamin D gene polymorphisms with HCV infection outcome. *Br. J. biomed. Sci.*, **79**: 10237. https://doi.org/10.3389/bjbs.2021.10237

Schwander, B., Feldstein, J., Sulo, S., Gonzalez, L., ElShishiney, G. and Hassany, M., 2022. Pursuing elimination of hepatitis C in Egypt: Cost-effectiveness and economic evaluation of a country-wide program. *Infect. Dis. Ther.*, **11**: 1193–1203. https://doi.org/10.1007/s40121-022-00631-x

Thanapirom, K., Suksawatamnuay, S., Sukeepaisarnjaroen, W., Tangkijvanich, P., Thaimai, P., Wasitthankasem, R., Poovorawan, Y. and Komolmit, P., 2019. Genetic associations of vitamin D receptor polymorphisms with advanced liver fibrosis and response to pegylated interferon-based therapy in chronic hepatitis C. *PeerJ*, **7**: e7666. https://doi.org/10.7717/peerj.7666

Tourkochristou, E., Tsounis, E.P., Tzoupis, H., Aggeletopoulou, I., Tsintoni, A., Lourida, T., Diamantopoulou, G., Zisimopoulos, K., Kafentzi, T., de Lastic, A.L., Rodi, M., Tselios, T., Thomopoulos, K., Mouzaki, A. and Triantos, C., 2023. The influence of single nucleotide polymorphisms on vitamin D receptor protein levels and function in chronic liver disease. *Int. J. mol. Sci.*, **24**: 11404. https://doi.org/10.3390/ijms241411404

Triantos, C., Aggeletopoulou, I., Kalafateli, M., Spantidea, P.I., Vourli, G., Diamantopoulou, G., Tapratzi, D., Michalaki, M., Manolakopoulos, S., Gogos, C., Kyriazopoulou, V., Mouzaki, A. and Thomopoulos, K., 2018. Prognostic significance of vitamin D receptor (VDR) gene polymorphisms in liver cirrhosis. *Sci. Rep.*, **8**: 14065. https://doi.org/10.1038/s41598-018-32482-3

Tsounis, E.P., Tourkochristou, E., Sapsani, A., Aggeletopoulou, I., Lourida, T., Zisimopoulos, K., Tzikopoulos, T., Diamantopoulou, G., Tsintoni, A., Thomopoulos, K., Mouzaki, A. and Triantos, C., 2022. The role of vitamin D receptor polymorphisms in the course of chronic hepatitis C infection. *Annls. Gastroenterol.*, **35**: 203–212.

Wang, C., Wu, Q., Wei, X.T., Li, Z.Z. and Lei, X.Z., 2016. Association of vitamin D receptor polymorphisms with response to antiviral therapy in patients with chronic hepatitis C. *J. Sichuan Univ. (Med. Sci.)*, **47**: 227–231.

World Health Organization, 2024. *Global hepatitis report 2024: action for access in low- and middle-income countries.* Available at: https://www.who.int/publications/i/item/9789240091672 (accessed 3 Jan 2026).