IL28B SINGLE NUCLEOTIDE POLYMORPHISMS GENOTYPE INDEPENDENT PREDICTOR OF SUSTAINED VIRAL RESPONSE IN HEMODIALYSIS PATIENTS WITH CHRONIC HEPATITIS C

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OBJECTIVES

The host and viral factors have important role in achieving sustained viral response (SVR) in treated patients with chronic hepatitis C virus (HCV) infection.

The genome wide analysis studies performed in different geographic locales identified that single nucleotide polymorphisms (SNPs) near IL28B gene were associated with treatment response in patients with chronic HCV infection.

The aim of the study was to determine the predictors of SVR in hemodialysis patients with chronic hepatitis C treated with pegylated interferon alpha-2a (PEG IFN α-2a).

METHODS

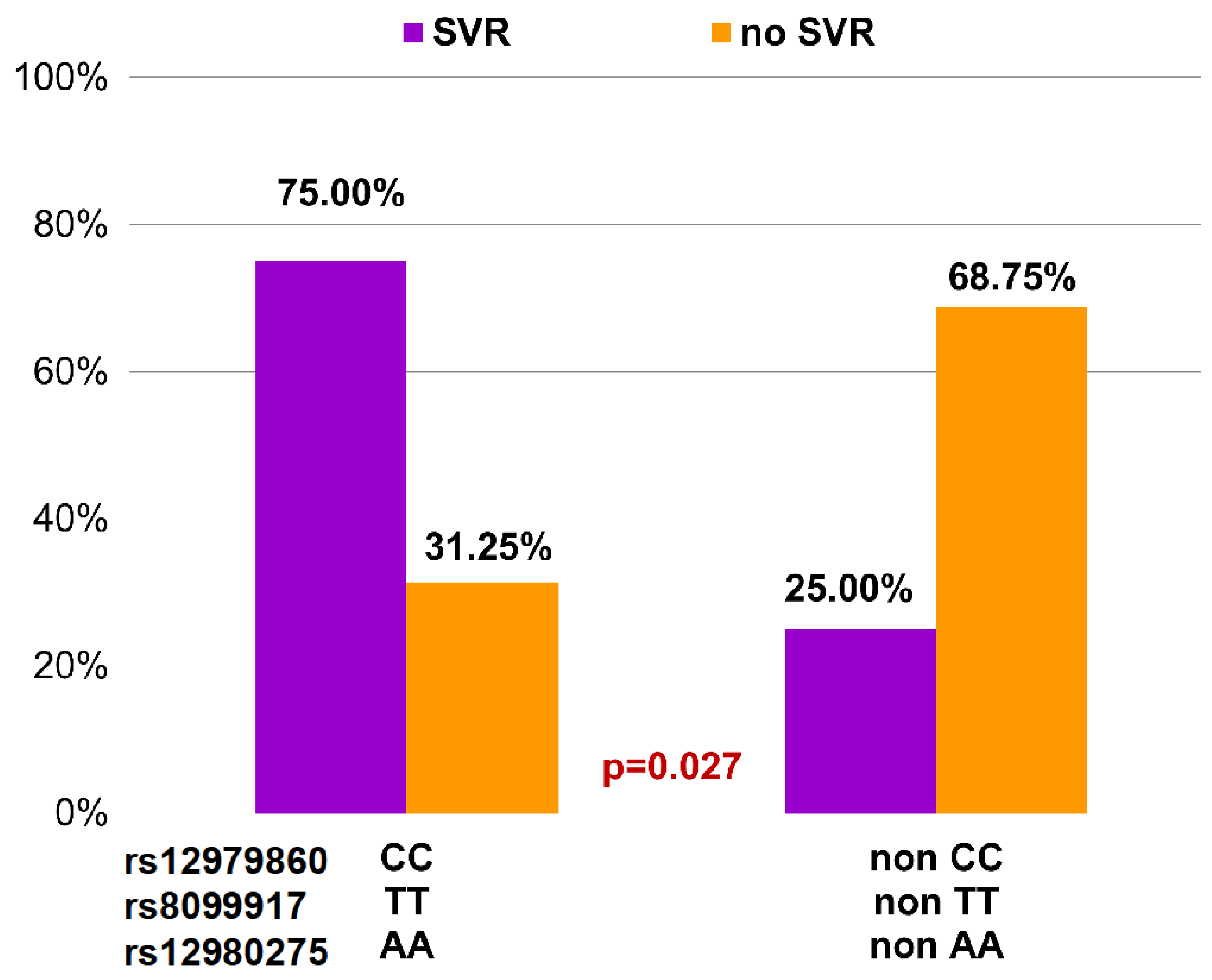
- Twenty eight hemodialysis (HD) patients with chronic HCV infection were treated with 135 μg of pegylated interferon alfa-2a
- Twenty six patients infected with HCV genotype 1 & 4 were treated for 48 weeks, and two patients with HCV genotype 2 were treated for 24 weeks
- Sustained viral response (SVR) is defined as an absence of detectable HCV RNA in the serum examined by an assay with a sensitivity of at least 50 IU/mL, 6 months after completion of the antiviral treatment
- Gender, age, renal disease, HBV co-infection, HCV genotype, early viral response, end treatment viral response, and single nucleotide polymorphisms (SNPs) near IL28B gene were evaluated as possible predictors of the SVR in treated HD patients with chronic HCV infection.
- The IL28B SNPs (rs12979860, rs8099917, rs12980275) were determined using SNP Genotyping Assays.
- Univariate logistic regression was used to identify the association between the different variables and SVR. The independent predictors of the SVR were determined with the multiple logistic regression analysis.

RESULTS

Table 1 Demographic, clinical, viral and treatment response features of the treated patients

	No	
HD patients	**28**	
Gender	No	%
male	25	89.3
female	3	10.7
Age	X	SD
	47.21	11.1
Renal disease	No	%
Glomerylopathy	14	50.0
Nephroarteriosclerosis	3	10.7
APKD	4	14.3
Tubulo interstitial nephritis	3	10.7
Unknown	4	14.3

HBV co-infection	No	%
	2	7.1
HCV genotype	No	%
G1	24	85.7
G2	2	7.1
G4	2	7.1
Treatment response	No	%
Early viral response	21	75.0
End treatment viral response	20	71.4
SVR	12	42.8



Graph 1 Association of SVR with IL28B SNPs genotype in HD patients

Table 2 Predictors associated with the SVR identified by univariate logistic regression

Predictor	*OR*	*95% CI (OR)*	*p*
Early viral response	1.77	1.21 – 2.59	0.006
End treatment viral response	1.82	1.28 – 2.59	0.002
IL28B SNPs genotype	1.53	1.08 – 2.16	0.021

Table 3 Predictor associated with the SVR identified by multiple logistic regression

Predictor	*OR*	*95% CI (OR)*	*p*
IL28B SNPs genotype	1.43	1.06 – 1.92	0.046

CONCLUSIONS

- The independent predictor of SVR in the treated hemodialysis patients was IL28B SNPs genotype
- The single nucleotide polymorphisms near IL28B gene are useful for prediction of the response to treatment with pegylated interferon alpha-2a in hemodialysis patients with chronic hepatitis C.

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