

Supplementary Materials: Polymorphisms of *HLA-DM* on Treatment Response to Interferon/Ribavirin in Patients with Chronic Hepatitis C Virus Type 1 Infection

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Table S1. Primers and probes for TaqMan allelic discrimination.

Polymorphism		Sequence(5'-3')
rs23544	Primer	F: CCACTGTATTAGAGAGGACCTGGAA R: ACCACCCACTCCCAAGAAAAT
	Probe	FAM-AGATGGATTCCCC-MGB HEX-AGATGGGTTCCCC-MGB
rs3135029	Primer	F: TCGCTTGGGTGTTCTGTATAA R: CAGGGCCCCACGTGATCTG
	Probe	FAM-TAAGCTACAAATTCTGGCA-MGB HEX-ATAAGCTACAAATTCGGGCAA-MGB
rs1050391	Primer	F: AGGTCTTCTTCCAGGCAAGGA R: GAGCTATAGACAGGAAGTGCTGAA
	Probe	FAM-CTAGACGTAGAAGCAG-MGB HEX-AGCTAGACATAGAAGCAGA-MGB
rs1063478	Primer	F: CCACCCATGCTGACAGTGA R: AGTCCATCGACAGCTGAGACA
	Probe	FAM-ATCATTCCTCCCTGTG-MGB HEX-CATCATTCCTCCCTGT-MGB

Table S2. Association of SNPs in *HLA-DM* with EVR and cEVR.

Genotype	N-RVR <i>n</i> = 166	RVR <i>n</i> = 149	OR (95% CI)	<i>p</i> -Value	N-cEVR <i>n</i> = 98	cEVR <i>n</i> = 223	OR (95% CI)	<i>p</i> -Value
rs23544								
AA	73 (44.0)	61 (40.9)	1.00	-	43 (43.9)	92 (41.2)	1.00	-
AG	71 (42.8)	61 (40.9)	0.99 (0.59–1.67)	0.976	46 (46.9)	88 (39.5)	0.86 (0.49–1.48)	0.584
GG	22 (13.2)	27 (18.1)	1.30 (0.65–2.63)	0.455	9 (9.2)	43 (19.3)	2.11 (0.91–4.89)	0.081
Dominant			1.07 (0.66–1.73)	0.771			1.08 (0.65–1.79)	0.777
Recessive			1.31 (0.68–2.52)	0.420			2.27 (1.02–5.04)	0.044
Additive			1.11 (0.79–1.54)	0.544			1.25 (0.87–1.79)	0.221
rs3135029								
AA	116 (69.9)	96 (64.4)	1.00	-	69 (70.4)	145 (65.0)	1.00	-
AC	45 (27.1)	45 (30.2)	1.27 (0.74–2.18)	0.393	25 (25.5)	67 (30.0)	1.59 (0.89–2.87)	0.118
CC	5 (3.0)	8 (5.4)	1.83 (0.54–6.22)	0.328	4 (4.1)	11 (5.0)	1.45 (0.41–5.08)	0.566
Dominant			1.33 (0.79–2.23)	0.277			1.57 (0.90–2.75)	0.109
Recessive			1.72 (0.51–5.74)	0.379			1.26 (0.36–4.35)	0.713
Additive			1.30 (0.85–2.00)	0.224			1.41 (0.88–2.25)	0.147
rs1050391								
CC	116 (69.9)	97 (65.1)	1.00	-	68 (69.4)	148 (66.4)	1.00	-
CT	46 (27.7)	45 (30.2)	1.24 (0.72–2.14)	0.426	27 (27.5)	65 (29.1)	1.32 (0.74–2.34)	0.342
TT	4 (2.4)	7 (4.7)	1.73 (0.46–6.54)	0.416	3 (3.1)	10 (4.5)	1.53 (0.37–6.24)	0.553
Dominant			1.29 (0.77–2.17)	0.327			1.34 (0.78–2.33)	0.291
Recessive			1.63 (0.44–6.10)	0.463			1.42 (0.35–5.73)	0.092
Additive			1.27 (0.82–1.97)	0.282			1.29 (0.80–2.06)	0.053
rs1063478								
CC	70 (42.2)	65 (43.6)	1.00	-	52 (53.1)	88 (39.5)	1.00	-
CT	86 (51.8)	60 (40.3)	0.78 (0.47–1.29)	0.339	41 (41.8)	108 (48.4)	1.57 (0.93–2.64)	0.092
TT	10 (6.0)	24 (16.1)	2.31 (0.96–5.53)	0.059	5 (5.1)	27 (12.1)	2.85 (0.99–8.23)	0.053

Dominant	0.94 (0.58–1.52)	0.793	1.70 (1.02–2.82)	0.040
Recessive	2.65 (1.16–6.06)	0.021	2.25 (0.80–6.30)	0.122
Additive	1.19 (0.82–1.72)	0.357	1.63 (1.07–2.46)	0.021

Abbreviation: SNP, single nucleotide polymorphism; RVR, rapid virological response; N-RVR, non rapid virological response. OR, odds ratio; CI, confidence interval; EVR, early virological response; cEVR, complete early virological response; N-cEVR, non-complete early virological response; -, reference; Logistic regression analyses adjusted for age, gender, gamma-glutamyltranspeptidase, glucose, α -fetal protein, platelets, baseline RNA, T3, T4. Dominant model stands for (homozygous type + hybrid type) vs. wild type; recessive model stands for homozygous type vs. (hybrid type + wild type) and additive model stands for hybrid type vs. homozygous type vs. wild type.



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