Allele and Genotype Frequency of IL28B (rs12979860) in South Iranian population

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Hepatitis C virus (HCV) has chronically infected million peoples worldwide. Spontaneous viral clearance occurs in 25% of affected patients. The standard regimen to treat HCV infection is the combination of pegylated interferon and ribavirin.[1] The most important indicator of successful treatment is sustained virologic response (SVR), which is defined as undetectable HCV RNA 24 weeks after treatment. The HCV-1 genotype is the most prevalent and the least responsive genotype. In addition to the viral genotype, some racial groups spontaneously recover more from infection. Caucasians were more likely to respond to treatment and recover from acute HCV infection than African Americans population.[1] Interleukin (IL) 28B (rs12979860) is the best known polymorphism to predict the treatment response. The CC genotype (wild type) is associated with greater interferon (IFN) induction after IFN treatment with more spontaneous viral clearance.[2] The allelic frequency of rs12979860 IL28B in one hundred healthy unrelated individuals, from Shiraz, southern Iran was determined by PCR-RFLP method. The primer sequence was F-5′-CCCAGCAGGCGCCTCTCCTA-3′;R-5′-CCCAGCAGGCGCCTCTCCTA-3′ and the PCR product was digested using Hpy166II (Biolab, New England). Alleles and genotype frequencies were determined and compared with reported frequencies from other populations (tables 1, 2). The most common genotype in our population was CT (46%) followed by CC (45%) and TT (9%), and the most prevalent allele was C (68%). The frequency of CC, CT, and TT genotypes and C, T allele had been reported as 40.4%, 47.1%, 12.5% and 63.9%, 36.1% respectively from north of Iran.[3] The favorable C allele frequency is higher in south of Iran.[3] The previous studies from Caucasians in Eu¬rope, United State, and Australia revealed that the most common genotype was CT and then CC and TT.[4] Thomas and colleagues reported the allelic frequency of rs12979860 in different ethnicities.[4] The C allele is the most common allele worldwide. They found that the protective allele C was highly prevalent in East Asian individuals (90-100%), intermediate frequency in European/Caucasian populations (50-85%), and presented at low frequency in African people (38-54%).[4] The C allelic frequency is 68% in our population, which is near Caucasians (50-85%), much higher than Africans (38-54%),

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Table 1: Genotype and allele frequency of IL28B (rs12979860) in South Iranian population.

Genotype	CC	45 (45%)
	CT	46(46%)
	TT	9 (9%)
Allele	C	136(68%)
	T	64(32%)

Table 2: The IL28B rs12979860 C allele frequency in different populations

Region	Number	C allele frequency (%)
Africa (Ethiopian Jews)	21	54.8
Africa (Sandawe)	37	44.6
Africa (Ibo)	47	38.3
Europe (Hungarians)	142	65.1
Europe(Irish)	113	73.9
Europe (Russians)	32	64.1
Europe (Danish)	51	76.5
Europe(Khanty)	49	85.7
Europe(Adygei)	53	52.8
European American	92	67.4
Southwest Asia (Kuwaitis)	16	75.0
Southwest Asia (Druze)	96	77.6
Southwest Asia (Yemenite Jews)	41	69.5
South Asia (Indians)	29	65.5
South Asia (Kachari)	17	94.1
East Asia (Chinese, Taiwan)	47	93.6
East Asia (Japanese)	50	91.0
East Asia (Koreans)	54	93.5
East Asia(Atayal)	40	100.0
Oceania (Micronesians)	36	98.6
North America (Mexico)	99	55.5
South America (Karitiana)	54	82.4
North of Iran (Tehran)	104	63.9
South of Iran (Shiraz) (current study)	100	68.0

and lower than East Asian populations (more than 90%). Any population has a relatively unique pattern of genes polymorphism, which has significant role in disease susceptibility, immunogenetics and pharmacogenetics. As the C allele is the favorable allele for predicting SVR in patients with HCV, its application is important in personalized treatment plan to maximize the drug response and minimize the toxicity.

CONFLICT OF INTEREST

The authors declares no conflict of interest related to this work.

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