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were 100%, 100% and 98.6%. The five patients were relapsed. 80% of relapses were occcured on 12th weeek, 15.4% in 1b and 3% in 2a or 2c.

CONCLUSIONS: Most earlier studies have demonstrated, in Genotype 1b, the efficacy of eradication is poor than genotype non 1. But the virologic response is effective in any group of chronic hepatitis C infection by pegylated interferon and ribavirin combination therapy in our study. So, we think that more aggressive treatment is needed in any genotype of chronic hepatitis C and the standard regimen of pegylated interferon and ribavirin combination therapy can be effective in Korean chronic hepatitis C patients.

Table 1 Virologic responses according to genotype

Factor	Type 1b (n = 39)	Type 2a or 2c (n = 77)	p-value
Peg IFN α-2b/Peg IFN α-2a	5/34	14/63	0.461
EOT (%)	66.7	84.8	0.023
ETR (%)	96.2	100	0.624
EVR (%)	85.7	100	0.002
SVR (%)	85.2	98.6	0.005
Relapse (%)	15.4	3.0	0.029

Treatment Monitoring and Predictions of Therapeutic Response

P9

Distribution of genetic polymorphisms associated to hepatitis C virus (HCV) antiviral response in a multiethnic and admixed population

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Single-nucleotide polymorphisms (SNPs) near IL28B and ITPA genes have been described as predictors of response to antiviral treatment and ribavirin induced-hemolytic anemia in HCV patients, respectively. The prevalence of these polymorphisms differs among ethnic groups; however, there is a paucity of information about South American populations. Hence, the aim of this study was to determine the prevalence of these SNPs in the healthy population of different ethnic groups residing in Argentina.

DNA samples were obtained from 1287 unrelated anti-HCV [−] volunteers and grouped as follows: i) Argentines (n = 951) born in the Pampean region; and ii) immigrants (n = 336) from other Latin American countries (178 Bolivians; 88 Paraguayans and 70 Peruvians). SNPs rs1127354C>A (ITPA) and rs12979860C>T (IL28B) were PCR-amplified and characterized by nucleotide sequences. Ethnicity was assessed by analysis of Native American mitochondrial DNA and Y-SNPs (maternal and paternal haplogroups, respectively) using Real Time PCR followed by High Resolution Melting. Fisher's exact test was used for statistical analysis. A p value < 0.05 was considered as statistically significant. In regard to IL28B (rs12979860C>T) polymorphism, CC genotype -related to favorable treatment response- was observed in 51.9% of Argentines versus 35.9% of Bolivians ($p < 0.0001$), 37.1% of Peruvians ($p < 0.05$) and 39.8% of Paraguayans ($p < 0.05$). In regard to ITPA (rs1127354C>A) polymorphisms, CC genotype -related to higher risk of ribavirin induced-hemolytic anemia- was observed in 84.5% of Argentines versus 98.9% of Bolivians ($p < 0.0001$), 95.7% of Peruvians ($p < 0.01$) and 93.2% of Paraguayans ($p < 0.01$). As regards ancestry, 42.7% of Argentines, 94.6% of Bolivians, 94% of Peruvians and 98% of Paraguayans showed Native American maternal lineages ($p < 0.0001$); whereas, 1% of Argentines, 71% of Bolivians, 40% of Peruvians and 17.9% of Paraguayans showed Native American paternal haplogroups ($p < 0.002$).

This is the first systematic study of polymorphisms related to antiviral response in HCV infection and ethnicity characterization in the South American population. There is a significant bias in the distribution of predictive polymorphisms of response to HCV treatment according to the population ancestry. This study highlights the importance of the previous characterization of these variants to evaluate the risk-benefit of antiviral treatment according to the patient ancestry, particularly in a multiethnic and admixed population.

P10

Increasing uptake of hepatitis C treatment in England between 2002 and 2010

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BACKGROUND: The detection of anti-HCV antibodies is the primary diagnostic test for HCV in the UK. Evidence of anti-HCV positivity should be followed by testing for HCV-

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