GENETIC VARIABILITY OF HEPATITIS C VIRUSES STRAINS

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ABSTRACT

Hepatitis C virus (HCV) has high genomic variability and, since its discovery, at least six different types and an increasing number of sub-types have been reported. There is not knowledge about the degree of genetic variation among HCV strains circulating in the Andean region of South America. In order to study the degree of genetic variability of strains isolated at the HNERM, in this preliminary study it was obtained the sequences from the 5' non coding region (5' NCR) belonging to 12 patients and were reported to the GenBank obtaining the accession identifications.

Serum samples were obtained from 12 patients with chronic hepatic disease being assisted at the Gastroenterology Department of Hospital Nacional Edgardo Rebagliati Martins, (Lima, Peru). Patients were in each case evaluated through the biochemical levels of ALT, the enzyme immunoassay-Third generation from Innogenetics and the supplementary LIA test (also from Innogenetics). Viral loads were measured in each case using Amplicor HCV-Mv.2.0 from Roche. Patients under treatment with interferon plus ribavirin, as well as untreated patients were included in these studies. Once the immunological tests were performed and the viral loads obtained, the 5' non-coding region (5' NCR) of the samples that were reactive were amplified by PCR, as previously described [1]. Sequences were obtained using the automatic sequencer ABI PRISM model 377, v.3.0; or by the Sanger method with the use of Amershan reagents. The evaluated patients had a distribution by sex of 67% masculine and 33% femenine, with an age average of 47.63 for men and 50 years for women. The results of these studies are shown in Table 1. All patients had levels of ALT >100 UI/ml and were anti-HCV positives. The samples were positives for HCV PCR. The 5' NCR PCR showed a band of 250 bp in all cases.

Table 1. Evaluation of the HNERM patients.

Patient	Age[a]	Sex[b]	Viral Load[c]	Treatment[d]
PER40	46	M	217,880	YES
PER82	41	M	363,119	YES
PER16	42	M	365,119	YES
PER18	56	M	>850,000	YES
PER61	47	M	262,299	YES
PER96	40	F	821,291	YES
PER152	61	M	35,601	YES
PER108	39	F	701,273	NO
PER62	62	F	186,889	NO
PER99	46	M	453,158	NO
PER118	42	M	>850,000	NO
PER153	58	F	>850,000	NO

(a) In years.
(b) M means male, F means female.
(c) In International Units IU/ml.

The accession numbers for each sequence of strains reported in this work are AJ438626; AJ438623; AJ438624; AJ438625; AJ438627; AJ438622; AJ438619; AJ438618; AJ438628; AJ438621; AJ438617; AJ438620.

The study contributed to the diagnosis, follow up of patients and molecular epidemiology of HCV in peruvian cases.
Molecular nucleotidic study of hepatitis C RNA- 5' NCR was also compared with results found in Brazil [2], Argentina [3], Venezuela [4] and Perú [5].

These preliminary results were presented during the ICGEB – OPS – RELAB Workshop "Molecular Biology of Viruses" at the Universidade Federal do Rio de Janeiro – Brasil, may 6-7, 2004.

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