


## Hepatitis C virus genotypes in Cordoba, Argentina. Unexpected high prevalence of genotype 2

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### RESUMEN

To determine hepatitis C virus (HCV) genotypes circulating in the central region of Argentina, 96 consecutive anti-HCV positive subjects were studied. The presence of HCV RNA was detected in 60 samples by RT-nested PCR of the 5' noncoding region (5' NCR). Genotyping was performed by restriction fragment length polymorphism analysis of 5' NCR region combined with PCR using type-specific primers of the core region. The groups of individuals in this study included hemophilia and hemodialysis patients, injecting drug users, screened blood donors, and patients with acute or chronic liver disease, all from Córdoba, Argentina. Overall, genotype 2 was the most prevalent (55.0%), followed by genotypes 1 (38.3%), and 3 (5.0%). Within genotype 1, subtype 1b was the most prevalent. An unexpected high prevalence of genotype 2 (61.9%) was found among patients with acute or chronic HCV infection (without known risk factors). These figures differ from other cohorts from East-Argentina where genotype 1 has been found as the most prevalent. This indicates that regional differences of genotype distribution might exist between Central and East Argentina.

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