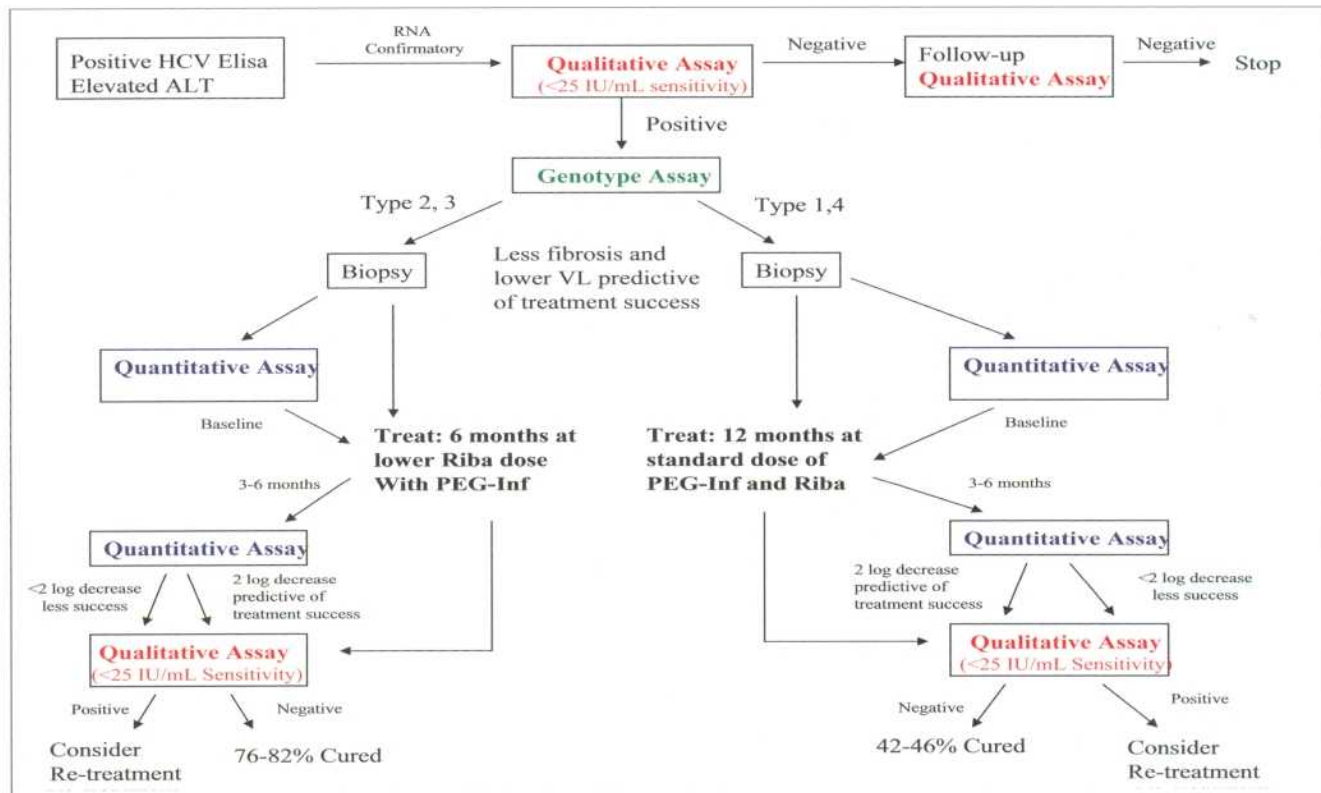


HCV FLOWCHART



Hepatitis C Viral RNA, LiPA

Purposes: Predict likelihood of therapeutic response; and determine the duration of treatment.

Hepatitis C virus (HCV), one of 6 hepatitis viruses (A-E and G), is a major cause of liver disease and the leading reason for liver transplantation in the United States. Although acute infection is usually asymptomatic, most patients (75%-85%) develop chronic infection; about 60% to 70% of chronically infected individuals develop active liver disease, which can progress to cirrhosis or hepatocellular cancer.

Favorable predictors of therapeutic response include low pretreatment HCV RNA levels (<2 million HCV RNA copies/

mL or <1.0 million IU/mL) and HCV genotypes 2 and 3. There are at least 6 major HCV types and more than 50 subtypes (eg, 1a). Type 1 accounts for about 70% of chronic HCV infections in the United States and is less responsive to current therapy. Patients with type 2 or 3 infection given combination therapy have maximum therapeutic response rates about twice those of patients with type 1 infection (eg, 73% vs. 30% and 69% vs. 28%⁹). Individuals with type 2 or 3 infection achieve a maximum response rate at 24 weeks of combination therapy, whereas those with genotype 1 infection may benefit by extending therapy

to 48 weeks. Several methods are available for genotyping HCV. The line probe assay (LiPA) is based on variations in the 5' untranslated region (UTR) of the HCV genome. Since it is quick and reproducible and correlates well with other methods, it is useful for predicting the likelihood of therapeutic response and determining optimal treatment duration. Unlike sequencing-based assays, LiPA does not detect novel sequence variations or provide sequence information from the coding region. However, it can provide a reportable genotype in samples with viral loads as low as 1,000 HCV RNA copies/mL.

References:

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