polymerase chain reaction for detection and genotyping of hepatitis c virus in blood donors

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Summary and ConclusionsHCV is the major cause of posttransfusion hepatitis. Even with the most sensitive HCV ELISA there remains a gap of several weeks between infection and first appearance of antibody. Blood donors presenting at such a time will be ELISA negative and the blood processed for use. In countries with low HCV prevalence such transmissions will be rare but in high prevalence countries their frequency could be sufficient to justify a PCR approach (Vrielink et al., 1995).The aim of the present study were (i) to determine the seroprevalence of HCV among block' donors; (ii) to evaluate the need of PCR technique for the detection of HCV infection in blood banks by comparing its results by the results of ELISA technique; and (iii) to assess the distribution of HCV genotypes among blood donors.This work was carried out on 201 apparently healthy blood donors attended to blood bank of Benha University hospital. Their sera were examined for the presence of antibodies to hepatitis "C" (HCV) using second generation ELISA technique. The examination of their sera also included liver enzymes (ALT and AST) and screening for HBs Ag. Fifty HCV Ab positive sera and eleven of HCV Ab negative sera were tested for the presence of HCV RNA by (RT-PCR). HCV genotypes were determined for 20 HCV RNA positive sera. The presence of anti-HCV antibodies was found in 56 (27.86%) blood donors. 25 samples of 50 HCV Ab positive sera were found to contain HCV RNA. Qf 11 antibody-negative samples, 2 were positive for HCV-186-RNA. Genotyping analysis revealed the presence of genotype 4 in(95%) of cases. In one (5%) sample mixed genotypes la-4e was detected.This work concluded that:•High prevalence of circulating HCV RNA in the age group between 30and 39 years decreasing in older subjects probably due to higher mortality from chronic liver disease.•Schistosomiasis and dental manipulation could be a major risk factor for HCV infection in Egypt.•At the current time the majority of infected individuals are unaware of their infection.•HCV infection may persist for several years without biochemicalevidence of liver disease due to low empathic effect of the virus of healthy HCV carriers.•Significant proportion of symptom-free anti-HCV positive individualswith normal ALT values have both HCV antibodies and circulating HCV RNA.•Even with the high specificity of anti-HCV2. generation EL/SA, false positive result may be common specially among blood donors.•Possibility of an HCV infection could not be excluded by the lack ofdetectable specific antibodies, especially during the acute phase of infection.-187-71717"111117117IIRIL rirtirrr" "T " yr' r'•Detection of primary HCV by PCR might be the crucial marker for

establishing a diagnosis of primary HCV infection early in the course of the disease and in discriminating between past and active HCV infection in patients with persistent or fluctuating antibody patterns.•PCR can detect HCV infection in subjects with raised ALT that are missed by the best antibody-screening tests, thus -continued ALT testing in blood bank is recommended to complement routine anti HCV screening.•Genotyping of HCV by line probe assay (INNO-DPA) is a simple and reliable technique that can rapidly define the dominant circulating HCVgenotype.•HCVgentoype 4 is the most predominant genotypes in Egypt.•11CV genotyping might be complementary to routine HCV diagnosis. HCV types and subtypes may have important implications in studying the epidemiologic, routes of transmission, pathogenicity, clinical aspects, complications, and response of HCV to -interferon.Recommendation:•11CV RNA testing should be considered for both anti HCV positive andnegative blood donors in order to obtain correct information about the state of infectivity.•Until a safe and effective HCV vaccine is available for wide application,precaution for preventing parenteral spread are likely to be the only way of limiting transmission of HCV.-188-•Further studies on larger scales are highly recommended to study probable HCV heterogeneity particularly type - 4 diversity in Egypt, their implication in therapy, clinical course, autoimmunity, and immune response. This could be achieved by studying nucleotide sequences in the 5’ UTR, core region and other parts of the genome.•More cosmopolitian ELISAs containing antigens from all major gentoypes or at least targeted ELISAs contatining antigens relevant to the country where the blood is screened would be a significant step to ensure the maximum possible safety of transfused blood.-189-I I IllittiOMPOIHM91101111,01111111f !Mr 11 I rir111’11 111111111H1111I. ir 111,77. riv,.„ Tip