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Epidemiological changes in Hepatitis C virus infection in Europe

The epidemiological parameters of hepatitis C virus infection in Europe have changed during the past 15 years. The risk of transfusion-associated hepatitis C has decreased with blood safety, but strong evidence supports that HCV is still spreading throughout Europe. This review summarizes recently published data on the epidemiology of HCV infection in Europe focusing on the factors currently shaping the epidemic.

The epidemic of hepatitis C virus (HCV) infection in Europe is continuously evolving and epidemiological parameters such as prevalence (number of infected persons), incidence (number of new infections), disease transmission patterns and genotype distribution, have changed substantially during the last 15 years, together with genotype distribution (HCV has been classified into 6 genotypes (1-6) and subtypes 1a,1b, etc.).

HCV prevalence in blood donors and/or general population is shown in Figure 1, and genotype distribution in Figure 2. Prevalence is not homogenously distributed between countries and even between regions, and goes from 0,1-1% in Northern Europe to 2,5-3% in Southern countries with 0,2-1,2% in Center Europe and 0,9-5% in Est countries.

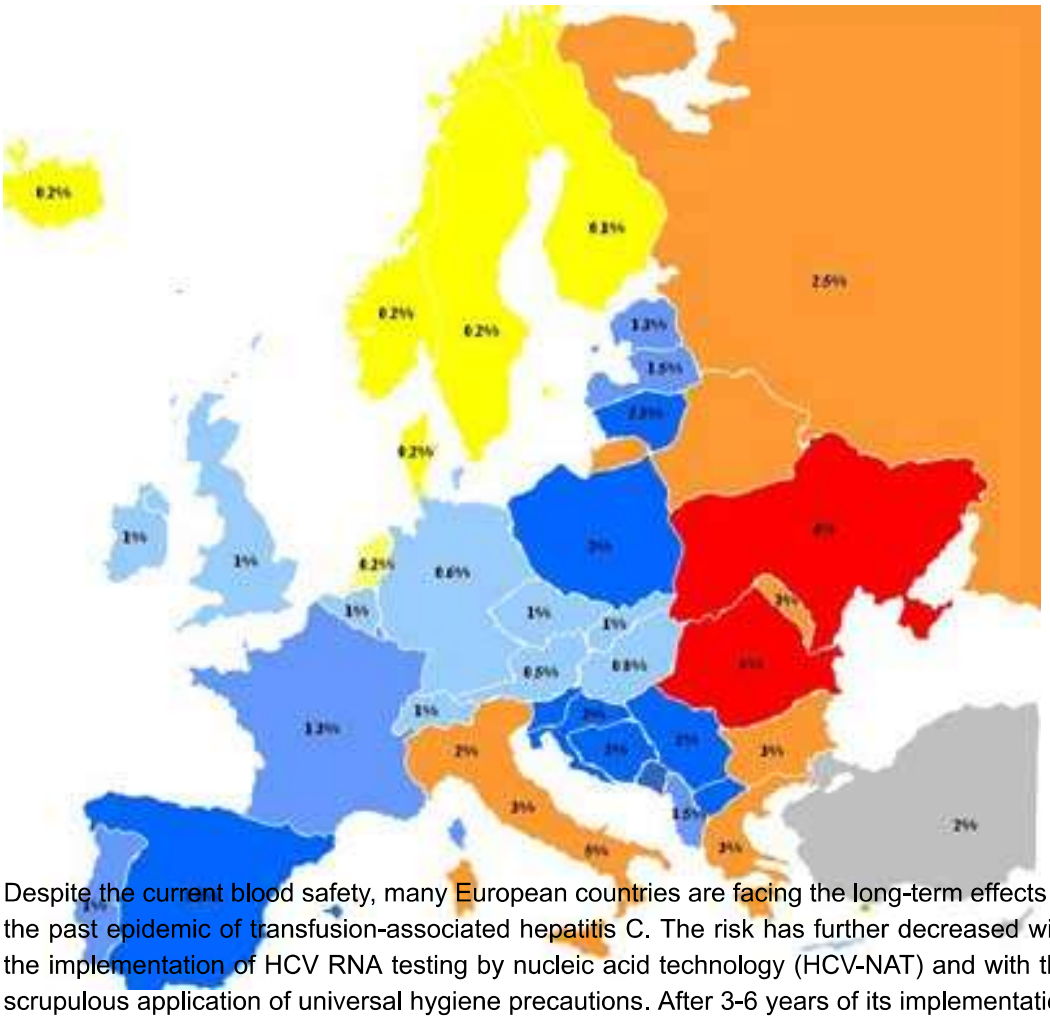

Figura 1 *HCV prevalence in Europe*

Despite the current blood safety, many European countries are facing the long-term effects of the past epidemic of transfusion-associated hepatitis C. The risk has further decreased with the implementation of HCV RNA testing by nucleic acid technology (HCV-NAT) and with the scrupulous application of universal hygiene precautions. After 3-6 years of its implementation risk estimates range between 0.1 and 2.33 per million donations. With the current blood transfusion safety, and the availability of recombinant clotting factors, newly diagnosed haemophilia and thalassemia patients are no longer at risk for HCV infection. Similarly, blood safety along with the use of erythropoietin (EPO) and improvement in infection control practices have greatly decreased HCV infection among haemodialysis patients. Blood safety has also paved the way to intravenous drug use (IDU) to become the main risk factor for HCV transmission and has switched the HCV genotype distribution (among patients younger than 50) (from 1b and 2 to 1a, 3a and 4d). Molecular epidemiological studies have revealed that HCV exchange between European IDU patients has occurred on a large scale and following a epidemic profile (large number of isolates with short genetic distances). Multiple genotype infection of a single patient after repetitive IDU has been proposed as the cause of recombinant HCV virus (1b/2k) appearance that may alter detection and/or antiviral response. Strong evidence supports that HCV is still spreading among European general population.

Other cases and outbreaks of HCV transmission have been associated with several medical procedures when standard precautions are not strictly followed, especially with the use of contaminated multi-dose vials, invasive surgical interventions, or tests that involve parenteral treatment.

The incidence of HCV associated with immigration varies among countries, with a significant impact in North European countries that have the lowest prevalence and depending on the origin of immigrants. Immigration may have not changed HCV prevalence in South European

countries with higher prevalence. In any case, immigration has increased the diversification of genotype distribution.

Hence, prevalence data from studies conducted a decade ago may not be useful to estimate the current and future burden of HCV infection and additional epidemiological studies should be conducted, and new preventive strategies implemented to control the silent epidemic. This review summarizes recently published data on the epidemiology of HCV infection in Europe focusing on the factors currently shaping the epidemic.

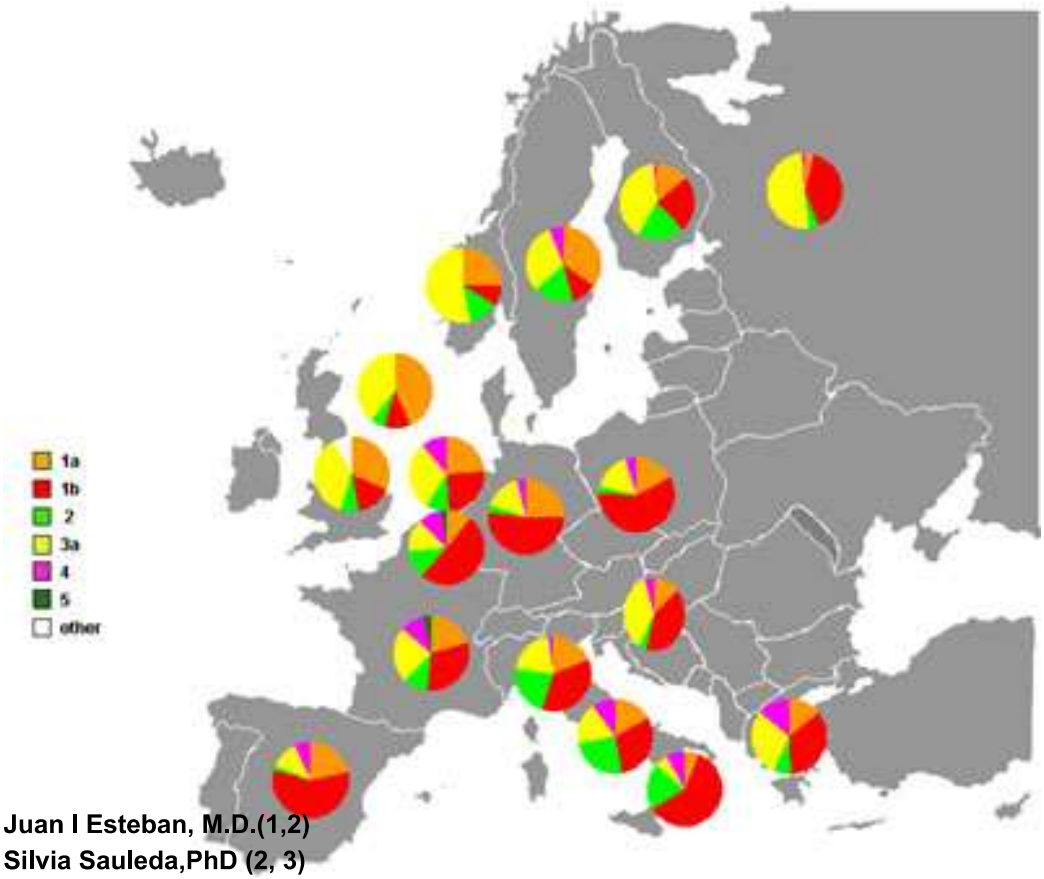

Figura 2. HCV genotype distribution.

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