Introduction and Objectives: Patients diagnosed with viral hepatitis often fail to follow up, a problem exacerbated by the pandemic. The "relink" strategy aims to reconnect these patients to ensure they receive the necessary follow-up and treatment.

The objective of our work was to generate a PANRELINK program based on the analysis of blood samples tested for HBsAg and anti-HCV antibodies from the reference laboratory database at Hospital El Cruce and to implement a relink strategy for patients with positive results.

Patients / Materials and Methods: We analyzed the results of blood samples tested for HBsAg and HCV antibodies by chemiluminescence, conducted at the reference laboratory from 2012 to 2022. Samples were stratified by origin (primary care centers [CAP] vs. medium and high complexity hospitals [MHC]). Statistical analyses chi-squared and t-tests.

Results and Discussion: A total of 108,261 blood samples were tested for HBsAg, with a test positivity rate (TPR) of 0.28% (306/108,261). For HCV, 106,917 samples were tested, with a TPR of 1.09% (1,162/106,917). When stratified by sample origin, TPR for HBsAg was 0.11% (101/86,609) in CAP and 0.96% (205/21,652) in MHC ($p<0.001$). For HCV, TPR was 0.43% (384/88,625) in CAP and 4.34% (778/17,130) in MHC ($p<0.001$). Among HBsAg-positive patients, 11% (34/306) were already in treatment at the time of relink, 16% (49/306) had died, 11% (33/306) were acute cases, and 52% (163/306) were potential candidates for relink. Among HCV-positive patients, 21% (242/1,162) had been treated, 25% (289/1,162) had died, 6% (67/1,162) were in treatment at the time of relink, 2% (26/1,162) were false positives, and 46% (538/1,162) were potential candidates for relink. In HCV-positive patients, a relink program was implemented. The phone contact rate with patients for reconnection was 16% (86/538) on the first call. The low contact rate was due to phone number changes. The attendance rate was 70% (60/86).

Conclusions: The study reveals that a significant proportion of patients with viral hepatitis do not receive adequate follow-up, highlighting the need for effective reconnection strategies. The PANRELINK strategy was effective in identifying patients from laboratory records. This PANRELINK modality can serve as a replicable high-volume model in other health contexts, improving long-term health outcomes and reducing the disease burden. Addressing communication barriers, such as phone number changes, is crucial to improve contact and attendance rates in future reconnection initiatives.

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O-12 DECIPHERING WILSON'S DISEASE IN COSTA RICA: AN INNOVATIVE GENETIC APPROACH

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Conflict of interest: No

Introduction and Objectives: In a recent article from the American Journal of Human Genetics, the genetic behavior of variants associated with Wilson's Disease (WD) is analyzed, alongside the worldwide discovery of the responsible gene. The variant c.3809A>G (p.Asn1270Ser) is highlighted, with a prevalence of 61% in Costa Rica, differing from that observed in Europe and the United States, and originally described in Sicily. The Genetics Center of the National Children's Hospital has been instrumental in identifying a specific genetic pattern among Costa Ricans with WD. Additionally, a novel worldwide variant in heterozygosity has been discovered in Nicaraguan patients, solidifying Costa Rica as a country with a high incidence of WD and significant contributions to the genetic study of the disease, which has documented over 1161 pathogenic variants. Objective: To analyze and describe the genetic spectrum of these variants in Costa Rica over the past two years, aiming to establish a comprehensive genetic map in a population with a high incidence of WD.

Patients / Materials and Methods: Molecular Sequencing (Sanger NGS) for molecular confirmation, as well as MLPA techniques and Copy Number Variations (CNVs) analysis.

Results and Discussion: During the period (2022-2023), 86 patients with WD variants were identified, including 19 homozygotes, 11 compound heterozygotes, and 56 carriers. There was a significant gender distribution, with a female predominance among homozygotes (58%) and male predominance among compound heterozygotes (64%). The ages of the patients varied widely, with an average age of 20 years for homozygotes and 21 years for compound heterozygotes. Multiple genetic variants were identified in genes such as ATP7B, including p.N1270S and others.

Conclusions: The importance of genetic research in understanding complex hereditary diseases like WD is underscored. The high prevalence of the c.3809A>G variant in Costa Rica highlights regional genetic diversity and the need to adapt diagnostic and treatment strategies to the specific genetic characteristics of each population.

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OP-13 CHOLANGIOCARCINOMA IN LATIN AMERICA: A MULTICENTER OBSERVATIONAL STUDY ALERTS ON ETHNICAL DISPARITIES IN TUMOR PRESENTATION AND OUTCOME

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Conflict of interest: No

Introduction and Objectives: Cholangiocarcinoma (CCA) represents a global health challenge, with rising incidence and mortality