[6]*Infectious Diseases Unit, University Hospital of Valme, Sevilla, Spain*
[7]*Infectious Diseases Unit, University Hospital of Puerto Real, Cádiz, Spain*
[8]*Infectious Diseases, University Hospital Reina Sofía, Murcia, Spain*
[9]*Infectious Diseases Unit, University Hospital Donostia, San Sebastian, Spain*
[10]*Infectious Disease Unit, University Hospital Santa Lucía, Cartagena, Murcia, Spain*
[11]*Infectious Diseases Unit, University Hospital Reina Sofía, Córdoba, Spain*
[12]*Hepatology Unit, Hospital Carlos Haya, Málaga, Spain*
[13]*Center for Global Health and Tropical Medicine, Microbiology Unit, Institute of Hygiene and Tropical Medicine, University Nova Lisbon, Lisbon, Portugal*
*Corresponding authors. Address: KU Leuven, Department of Microbiology, Immunology and Transplantation, Rega Institute for Medical Research, Leuven, Belgium. LC: Tel.: +32 16 32 11 76 or BV: +32 16 37 44 00.
E-mail addresses: bram.vrancken@kuleuven.be (B. Vrancken) lize.cuypers@kuleuven.be (L. Cuypers)

[#] These first authors contributed equally to this article.

Reply to: "Cross-country migration linked to people who inject drugs challenges the long-term impact of national HCV elimination programmes"

To the Editor:
We appreciate the interest and comments by Vrancken *et al.* They had previously found that the most prevalent HCV genotype in Spain, genotype 1a, was linked to transmission networks outside the country.[1] Specifically, the origin of those strains could be traced to a number of European countries, including France, Germany and Italy among others.[1] In their letter, Vrancken *et al.* expand their data to HCV genotype 3a, most frequently found among people who inject drugs (PWID) in Spain. This is very relevant information. In our paper, we showed that PWID with and without opiate agonist therapy can achieve high sustained virological response rates with direct-acting antiviral combinations. However, the overall efficacy of direct-acting antivirals in active drug users is lower, mainly due to losses to follow-up. Efforts to reduce their risk of abandoning follow-up are needed to reach HCV elimination targets in Spain. Another potential threat for the elimination efforts in Spain is stressed by Vrancken *et al.* An increasing number of HCV genotype 1a[1] and 3a infections are being introduced to Spain from the rest of Europe, essentially through drug use networks. Thus, HCV elimination plans should be developed with a broader perspective than the national level. Otherwise, successful reductions in the burden of HCV infection in Spain could be counteracted by waves of imported infections.

Conflict of interest
Please refer to the accompanying ICMJE disclosure forms for further details.

Supplementary data
Supplementary data to this article can be found online at https://doi.org/10.1016/j.jhep.2019.09.002.

References
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Juan Macías
Infectious Diseases and Microbiology Unit, Hospital Universitario de Valme, Seville, Spain
E-mail address: jmacias@cica.es

Assessment of liver phenotype in adults with severe alpha-1 antitrypsin deficiency (Pi*ZZ genotype)

To the Editor:
We would like to congratulate Clark *et al.* for their pioneering work characterizing histological liver injury in patients with the classic severe alpha-1 antitrypsin (AAT) deficiency (genotype Pi*ZZ).[1] The Pi*ZZ genotype is seen in 1:3,000 Caucasians and the associated liver disease is greatly understudied despite the fact that it is more frequent than several well-established liver disorders such as autoimmune hepatitis or primary sclerosing cholangitis.[2,3] While Clark *et al.* greatly enhanced our understanding of the clinical, biochemical and histological liver phenotype of these individuals, we would like to further discuss the following topics: (i) a high occurrence of liver steatosis in