

CROI 2018 PRESS CONFERENCE ABSTRACTS: Wednesday, March 7, 2018
Abstracts # 135, 137, 141, 142LB, 128, 129, 130 embargoed until Wednesday,
March 7, 2018 at 12:00 pm ET
Abstract #81LB embargoed until Tuesday, March 6, 2018 at 12:00 pm ET
Abstract #166 embargoed until Wednesday, March 7, 2018, 1:15 pm ET

Abstract Number 130 - (Oral)

INTERNATIONAL VERSUS DOMESTIC HCV TRANSMISSION IN MSM: A PERSPECTIVE FOR THE DAA ERA

Clinical: (K) Hepatitis Viruses and Liver Complications

Authors: Luisa Salazar-Vizcaya¹, Roger Kouyos², Karin Metzner², Kamila Caraballo³, Cyril Shah², Jürg Böni², Manuel Battegay⁴, Enos Bernasconi⁵, Alexandra Calmy⁶, Matthias Cavassini⁷, Herbert A. Mbunkah², Olivia Keiser⁸, Andri Rauch¹ **Institutions:** ¹University Hospital of Bern, Bern, Switzerland, ²University Hospital Zurich, Zurich, Switzerland, ³Medical University of Warsaw, Warsaw, Poland, ⁴University Hospital Basel, Basel, Switzerland, ⁵Servizio di Malattie Infettive, Lugano, Switzerland, ⁶University Hospitals of Geneva, Geneva, Switzerland, ⁷Lausanne University Hospital, Lausanne, Switzerland, ⁸University of Geneva, Geneva, Switzerland

Presenting Author: *Luisa Salazar-Vizcaya, PhD*

Background: Rapid scale-up of early direct-acting antiviral (DAA) therapy for hepatitis C virus (HCV) in HIV-positive men who have sex with men (MSM) is ongoing in many European countries. It is expected to abate the high incidence of HCV associated with sexual practices. But isolated public health strategies in neighbouring countries might boost or hinder each other if international transmission is frequent. Switzerland is ideally placed to study international transmission due to its small population size and its high connectivity to international transmission networks. We used molecular epidemiology for estimating the contribution to the Swiss epidemic of HCV-infections acquired by contact with MSM from abroad, as a measure of potential vulnerability to foreign public health strategies.

Methods: HCV subtype 1a genomes from 29 HIV-positive MSM with incident HCV infections were sequenced using Illumina technology (study sequences). Subtype 1a accounts for 62% of replicating infections in this population. Sampling dates ranged between 1999 and 2013. We used RAxML to infer maximum-likelihood phylogenetic trees containing a 436-base-pairs fragment of the NB5B region of the study sequences and other circulating strains (including 84 from other HIV+ people in Switzerland and 220 from across Europe). We established the likely geographic origin of infection (Swiss-to-Swiss versus imported transmissions) by inferring transmission clusters and locating the study sequences in such clusters. Sufficient degree of certainty was defined as a bootstrap value above 70%.

Results: Ninety-seven percent of study sequences (28/29) were located in MSM clusters. Of those, ninety-six percent (27/28) were found amongst five transmission clusters within Europe (including Switzerland; Figure-A). Swiss-to-Swiss transmission was estimated to range between 38% and 76%. German-Swiss transmission was estimated to range between 7% and 41%. Transmissions linked to other European regions ranged between 0% and 28% (Figure-B).

Conclusion: Swiss-domestic transmission of HCV subtype 1a is ongoing and therefore national treatment scale-up is expected to reduce HCV-incidence. But at least a quarter of sequenced infections were likely acquired by contacts with MSM from other European countries, in particular the neighboring country Germany. Our findings suggest the need for joint European scale-up schemes. Time-updated phylogenies are valuable for assessing the impact of national DAA scale-up programs.