

Phylodynamics of HCV genotypes 3a and 1a in Pakistan

Aniqa Shahid^{1,2}, Francois Cholette^{3,4}, Don Kirkby², Christina Daniuk⁴, Laura H. Thompson⁵, John Ho⁴, James F. Blanchard⁵, Faran Emmanuel⁵, Tahira Reza⁶, Paul Sandstrom^{3,4}, Zabrina L. Brumme^{1,2}, **Jeffrey B. Joy**^{2,7,8}

¹Faculty of Health Sciences, Simon Fraser University, Burnaby, Canada; ²British Columbia Centre for Excellence in HIV/AIDS, Vancouver, Canada; ³Department of Medical Microbiology and Infectious Diseases, University of Manitoba, Winnipeg, Canada; ⁴National HIV and Retrovirology Laboratories, JC Wilt Infectious Diseases Research Centre, Public Health Agency of Canada, Winnipeg, Canada; ⁵Community Health Sciences, University of Manitoba, Winnipeg, Canada; ⁶National AIDS Control Program, Chak Shezhad, Islamabad, Pakistan; ⁷Department of Medicine, University of British Columbia, Vancouver, Canada; ⁸Bioinformatics Programme, University of British Columbia, Vancouver, Canada

Contact us at: ashahid@cfenet.ubc.ca, jjoy@cfenet.ubc.ca

Presenting author declaration: I HAVE NO CONFLICTS OF INTEREST TO DECLARE



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BACKGROUND

Characterizing the molecular dynamics of the HCV epidemic in Pakistan is crucial for optimizing public health interventions to control the rapidly growing HCV epidemic.

In this study, we analyze HCV sequences from PWID in Pakistan to:

- quantify the prevalence of mixed HCV genotype infections.
- characterize the extent of phylogenetic clustering.
- investigate whether HCV spread is temporally and geographically concordant with the HIV epidemic.

METHODS

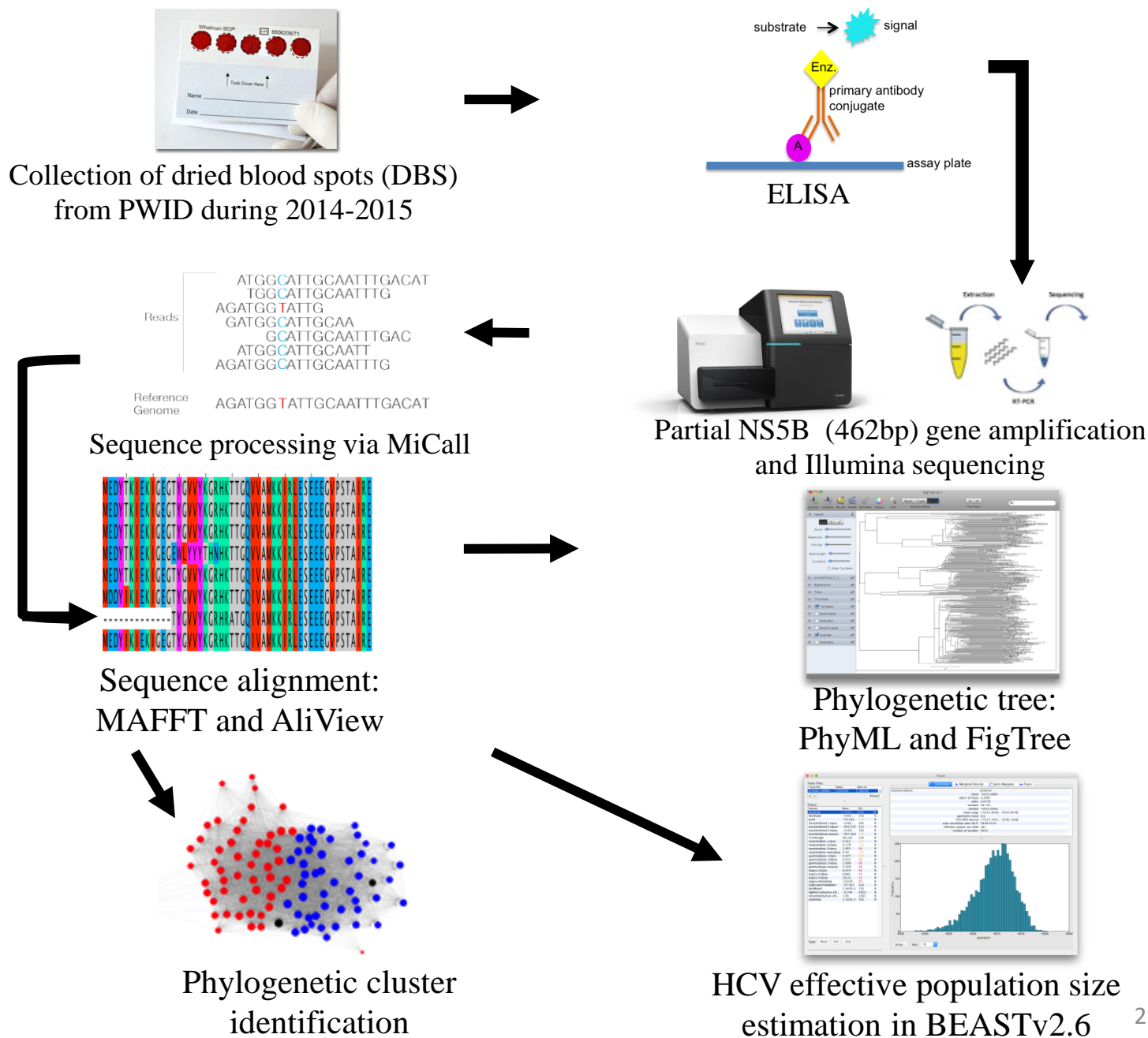


Table 1: Success rate of HCV NS5B amplification from DBS

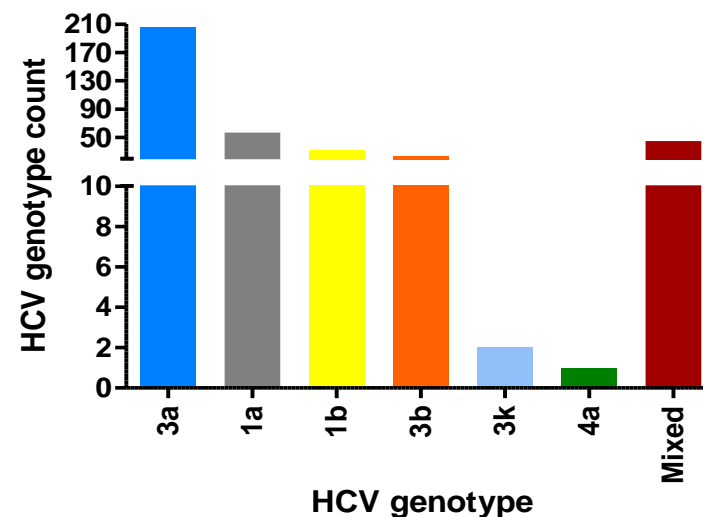
City	DBS collected	NS5B amplified
Karachi	300	181
Hyderabad	300	80
Larkana	300	55
Peshawar	253	43
Quetta	300	8
Total	1453	367 (25%)

Table 2: Characteristics of all male PWID with available sequences

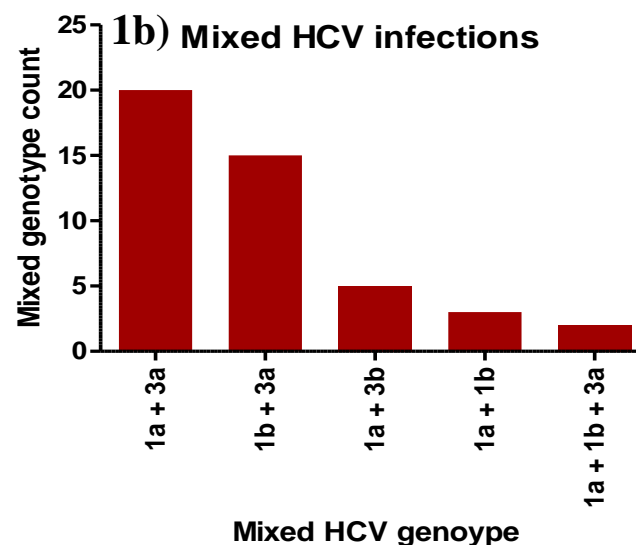
Category	Characteristics	Count
Age	Mean	29.8
	≤25	124
	>25	243
Help with injecting drugs	Took help	161
	Did not seek help	205
	Unknown	1
HIV co-infection	Yes	190
	No	177

Figure 1: HCV genotypes distribution

1a) Overall HCV infections



1b) Mixed HCV infections



1c) HCV genotype distribution in each city

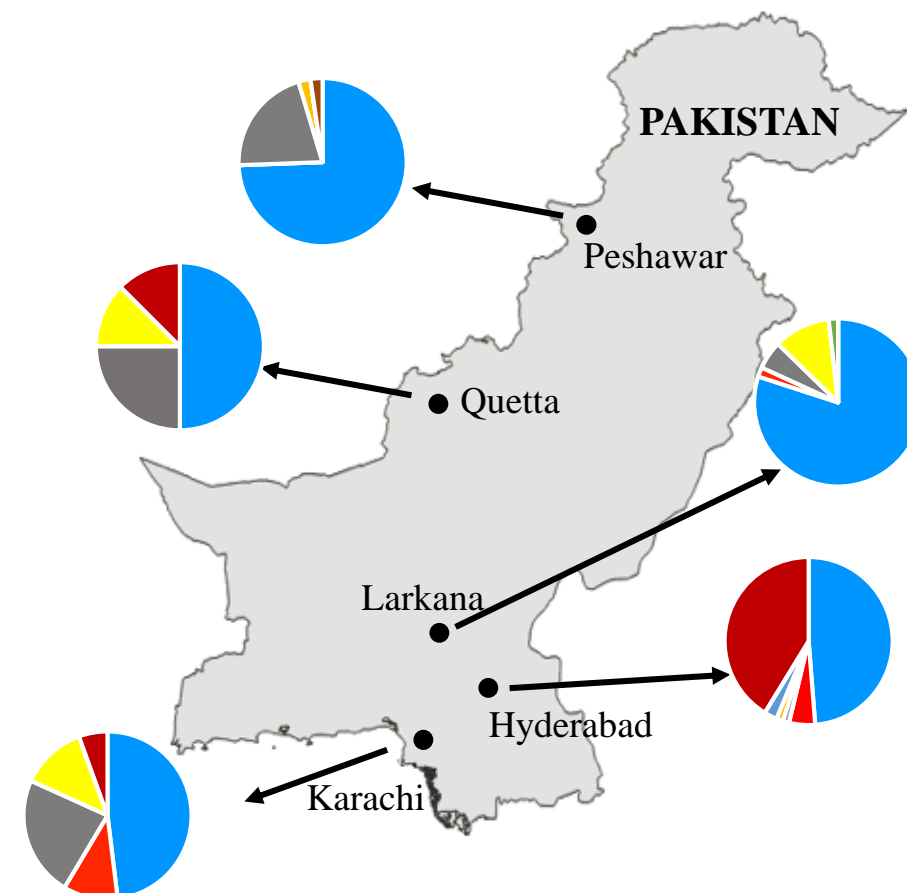


Figure 2: Maximum Likelihood Phylogenetic tree

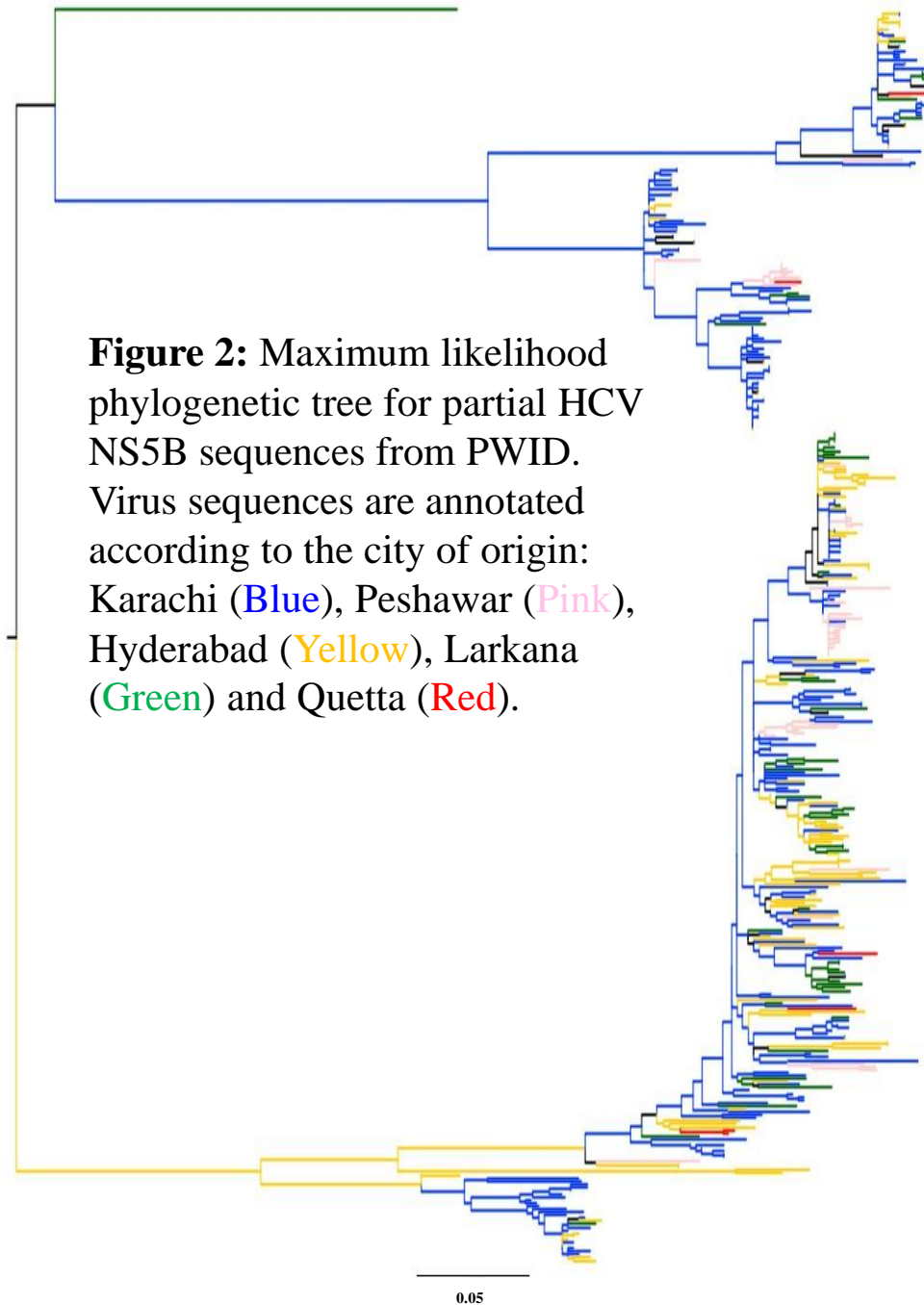


Figure 3: Phylogenetic cluster analysis

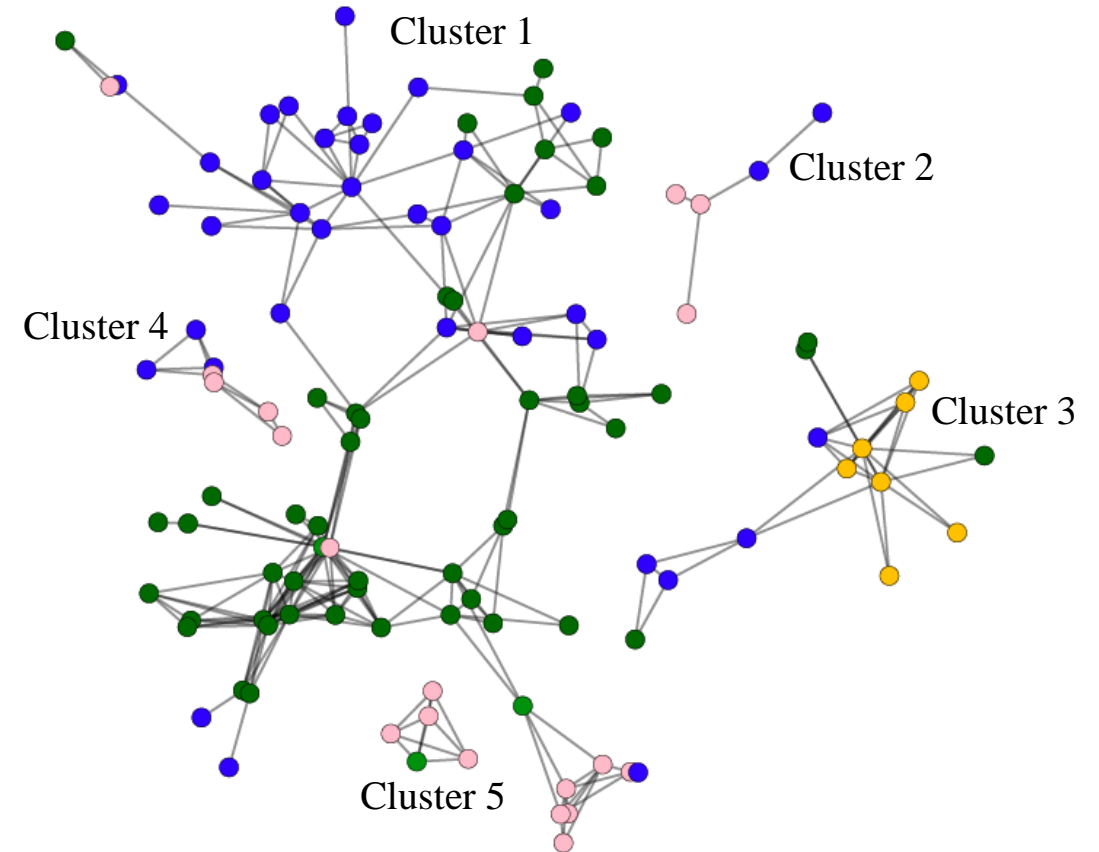


Figure 4: Coalescent analysis on most dominant HCV genotypes

Table 3. Additional Pakistani HCV NS5B sequences included

Genotype	Our dataset	GenBank	Total
3a	243	255	498
1a	87	21	108

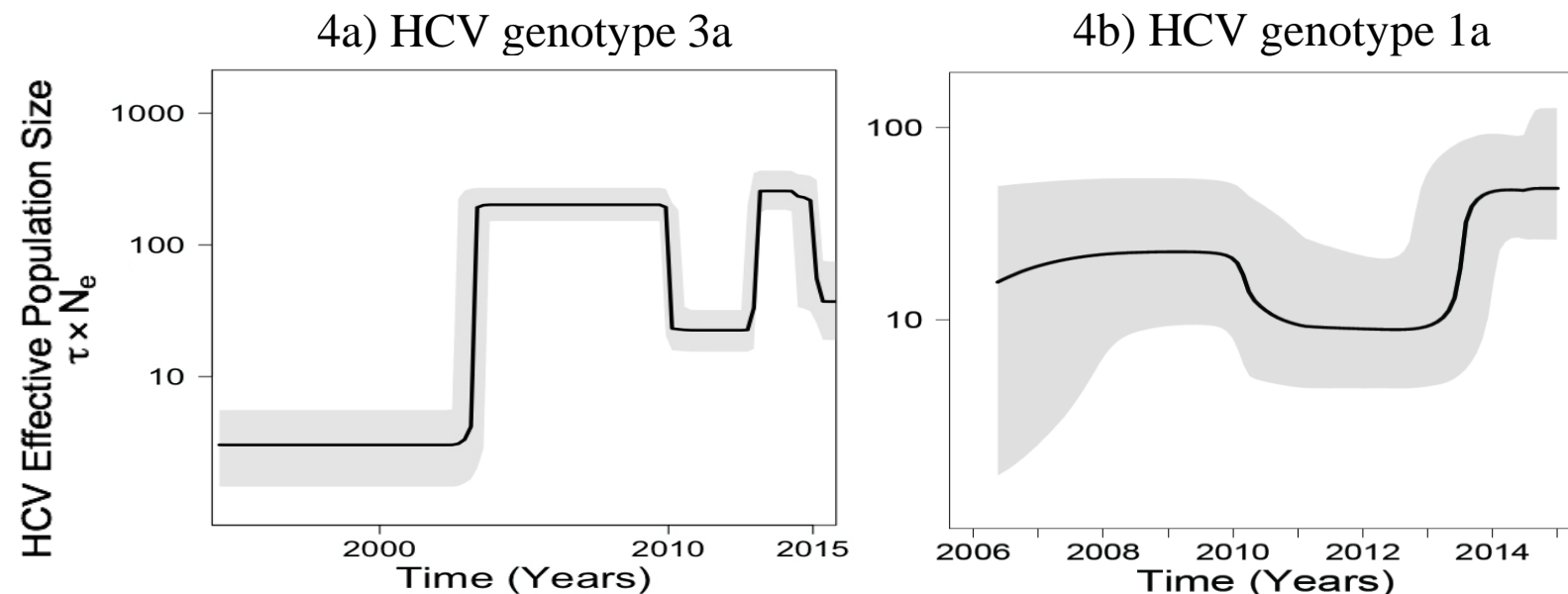


Figure 4: Bayesian skyline plots (BSP) showing the epidemic history of the most prevalent HCV genotypes in Pakistan: a) 3a and b) 1a, consisting of sequences from PWID defined in this study, and additional sequences downloaded from NCBI GenBank database (Table 3). The solid black line in both plots shows the median change in the effective population size (N_e) x generation time (τ) in a natural logarithmic scale on y-axis, versus time on the x-axis. The grey shaded areas correspond to the 95% highest posterior density (95% HPD) intervals. BSP of HCV genotypes 3a and 1a suggest periods of exponential growth from 2005 to 2010, followed by a decline & subsequent exponential growth during 2014-2015.

Burden of HCV in Pakistan is increasing

- The identification of transmission clusters, mixed infections, and recent exponential growth suggest rapid HCV spread; concordance with published HIV epidemic dynamics suggests common routes of infection by both HIV and HCV.
- Expansion of harm reduction strategies and treatment as prevention for PWID are urgently needed to reduce HCV-related incidence and mortality in Pakistan.