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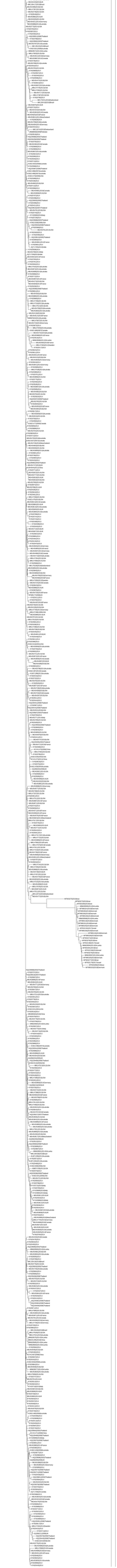
Phylogenetic Analysis of Spread of Hepatitis C Virus Identified during HIV Outbreak Investigation, Unnao, India

Appendix

Appendix Table. Characteristics of anti-HCV reactive and nonreactive persons identified during HIV outbreak investigation, Unnao, India, by HIV serostatus*

Characteristic	Anti-HCV reactive	Anti-HCV nonreactive	p-value
Total no. persons	98 (100)	60 (100)	
Mean age, y	41	38	0.289
Sex			
M	42 (42.86)	29 (48.33)	0.515
F	56 (57.14)	31 (51.67)	
Area of residence			
Chakmeerapur	44 (44.90)	26 (43.33)	0.419
Kirvidyapur	03 (3.06)	05 (8.33)	
Premganj	51 (52.04)	29 (48.33)	
Occupation			
Unemployed	46 (46.94)	19 (31.67)	0.157
Farmer	17 (17.35)	15 (25.00)	
Non-agricultural	35 (35.71)	26 (43.33)	
Ever had sex with female casual partner as reported by male participants†			
Yes	03 (7.50)	03 (10.71)	0.684
No	37 (92.50)	25 (89.29)	
Ever had sex with male casual partner as reported by female participants†			
Yes	01 (1.82)	0	1.000
No	54 (98.18)	31 (100)	
Condom use during last sex†			
Yes	14 (15.91)	13 (24.07)	0.273
No	74 (84.09)	41 (75.93)	
Intravenous injection in last 5 years			
Yes	74 (75.51)	37 (62.71)	0.104
No	24 (24.49)	22 (37.29)	
Intramuscular injection in last 5 years			
Yes	72 (73.47)	38 (63.33)	0.213
No	26 (26.53)	22 (36.67)	
Syringe and needle used while receiving intramuscular injection in last 5 years†			
Injected by used syringe and needle	12 (12.24)	02 (3.33)	0.046
Injected by new syringe and needle	73 (74.49)	54 (90.0)	
HIV infection			
Seropositive	28 (28.57)	05 (8.33)	0.002
Seronegative	70 (71.43)	55 (91.67)	

*Values are no. (%) except where indicated. HCV, hepatitis C virus.
†Because of nonresponse from some participants, numbers may not sum to total.



Appendix Figure 1. Phylogenetic tree of HCV global isolates derived using NS5B gene by maximum-likelihood method. Samples isolated from Unnao, India, sequenced in this study are shown in red for HIV/HCV co-infection cases and in blue for HCV monoinfection cases.

Appendix Figure 2. Phylogenetic tree of HCV global isolates derived using core gene by maximum-likelihood method. Samples isolated from Unnao, India, sequenced in this study are shown in red for HIV/HCV coinfection cases and in blue for HCV monoinfection cases.