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Characterizing the burden of hepatitis C infection among entrants to Pennsylvania state prisons, 2004–2012

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Abstract

Although hepatitis C infection (HCV) is common among prisoners, relatively few undergo evaluation for treatment. This study reports the prevalence of chronic infection and the genotype distribution among an incarcerated population. HCV antibody testing was provided to adults entering Pennsylvania prisons; confirmatory and genotype testing were offered to those eligible for treatment. Antibody prevalence among 101,727 individuals was 18.1%. Among 7,633 individuals who underwent confirmatory testing, 69.3% had detectable RNA. Among 3,247 individuals who underwent genotype testing, genotype 1 was the most common (76.6%). The rate of chronic infection after HCV exposure is similar to that reported in the community, as is genotype distribution. Correctional facilities provide access to a population with a high disease burden, creating a public health opportunity for evaluation and treatment.

Keywords

correctional health; chronic hepatitis c infection; hepatitis c genotype distribution; prevalence

Hepatitis C virus (HCV) infection is highly prevalent among prisoners (Larney et al., 2013). Using data from 12 state prison systems, it was recently estimated that HCV antibody prevalence among US prisoners was 17.4% in 2006 (Varan, Mercer, Stein, & Spaulding, 2014). Few studies that have examined HCV prevalence among incarcerated populations have included women. Even fewer studies have investigated the prevalence of chronic

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infection or genotypic variability among persons with chronic infection, which is important for guiding treatment and predicting achievement of sustained virologic response (SVR). The development of new agents for the treatment of HCV makes this a particularly relevant time to further characterize the disease among incarcerated populations (Liang & Ghany, 2013).

Materials and Methods

The Pennsylvania Department of Corrections (DOC) is one of few state prison systems to implement universal screening of prisoners for HCV exposure. All incoming adults are screened on an opt-out basis for HCV antibodies by enzyme-linked immunosorbent assay (ELISA). Positive tests are confirmed by HCV RNA testing by polymerase chain reaction (PCR), which is offered to all inmates who are eligible for treatment. The main exclusion criterion for treatment eligibility is short sentence duration; less often, there are medical contraindications to treatment. Prisoners with confirmed infections are entered into a formal protocol for evaluation and treatment, including education and counseling about risk reduction. They are also offered immunization against hepatitis A and B when indicated. We previously reported the results of this HCV testing program (Larney et al., 2014). In this study, we retrospectively reviewed HCV RNA results and HCV genotype results from the available records. Records were de-identified; each prisoner was given a unique identifier to account for retesting on subsequent incarcerations.

There were 131,791 HCV antibody records for 101,727 individuals over nine years. 1,296 duplicate records were deleted, leaving 130,495 unique test results for 101,727 individuals. Viral load data included 24,275 records for 7,633 individuals. Participants were defined as HCV RNA detectable if they had at least one positive viral load result. We initially obtained 3,430 records from genotype testing; 183 duplicates were deleted, leaving 3,247 unique records.

HCV antibody prevalence was calculated with 95% binomial confidence intervals. RNA and genotype data were analyzed using frequency counts. Differences between men and women on these outcomes were assessed using the χ^2 test. The Brown University Research Protections Office deemed that this study did not require Institutional Review Board oversight. The study was approved by the Research Review Committee of the Pennsylvania DOC.

Results

A blood sample was provided for HCV antibody testing in an estimated 93% of prison receptions. Of 101,727 unique participants, 9.4% (n=9534) were women. The median age at first observed HCV antibody test was 32 years (min-max 17–95 years).

Overall HCV antibody prevalence from 2004–2012 was 18.1% (95% CI 17.9, 18.4). HCV antibody prevalence was significantly higher among women (31.3%; 95% CI: 30.4%, 32.3%) than men (16.8%; 95% CI: 16.5%, 17.0%) ($\chi^2=1230.4$, df=1, $p<.0001$).

Although women comprised 16.1% of HCV antibody positive individuals, only 6.8% of the 7633 individuals with PCR test results were women. Of all PCR tests, 69.3% (n=5288) had detectable HCV RNA. Men were significantly more likely than women to be chronically infected (69.7% vs 63.2%, $\chi^2=9.7$, $df=1$, $p=.002$).

Based on 3,247 genotype tests, the most common genotype was genotype 1 (76.6%), followed by genotype 3 (11.7%) and genotype 2 (9.3%) (Table 1). Women were more likely than men to be infected with genotypes 2 and 3 and less likely to be infected with genotype 1, although this result was not statistically significant.

Discussion

There have been few recent epidemiological analyses of HCV in US prisons to guide policy and clinical practice. As expected, in this sample of entrants to Pennsylvania state prisons between 2004 and 2012, HCV antibody seroprevalence is much higher than the estimated seroprevalence of 1.3% for the non-institutionalized American population (Ditah et al., 2013). An overall seroprevalence of 18.1% is lower than the summary global prevalence reported in a recent meta-analysis of HCV in prisons (Larney et al., 2013), and close to the recently reported national estimate of 17.4% in US state prisons (Varan et al., 2014). Consistent with international findings, the prevalence of HCV antibody positivity in this sample was almost twice as high among women as men (Larney et al., 2013).

According to a survey of non-institutionalized Americans, 67% of all HCV-exposed persons were chronically infected (Ditah et al., 2013), which is similar to our findings in an incarcerated population (69.3%). Our results should be viewed with caution, however, as substantial numbers of those who tested positive for HCV antibody did not complete HCV RNA testing. Although the treatment history of patients is unknown, the prevalence of prior treatment in this population is likely to be quite low. Other studies of chronic infection among prisoners have reported higher rates of detectable RNA (Meyer et al., 2007); the lower rate found among this sample should be the subject of further investigation. Women were underrepresented in PCR testing, most likely due to their shorter sentences. This finding highlights that shortened treatment courses will be particularly important for incarcerated women, who historically have shorter sentences (Mustard, 2001), and, therefore, are less likely to be eligible for treatment (Chew, Allen, Taylor, Rich, & Feller, 2009). Women in this sample were less likely to be chronically infected than men.

The same national survey reports that 68% of those chronically infected have genotype 1 (Ditah et al., 2013), compared with 77% of our study population. These patients will be highly treatable with new, more effective, interferon-free therapeutic agents, which are approaching 90% achievement of SVR in patients with HCV and genotype 1 (Kowdley et al., 2014). Studies of HCV treatment in prison using combination interferon and ribavirin demonstrated that rates of SVR achieved among patients in prisons are similar to those achieved in the community (Allen et al., 2003); we see no reason why this will not also be the case with interferon-free therapies.

There is great need for increased treatment of incarcerated patients with chronic HCV infection. A 2011 census reported the American correctional population to be 6,977,700; 1,504,150 persons were incarcerated in prisons (Glaze & Parks, 2011). If our results are applicable to other regions, nearly 200,000 persons in American prisons may be chronically infected with HCV, and many more will transition through jails, some with long enough stays to undergo at least initial testing. Since many Americans are unaware of their infections, diagnosis, even if treatment were unavailable, would be an opportunity for education, counseling, and vaccination.

One impediment toward wider availability of testing and treatment for HCV in prisons is the disproportionate burden of disease concentrated in correctional systems. Costs associated with treatment of chronic HCV among prisoners will be substantial; unfortunately, at present, there are insufficient data to generate a plausible estimate. A complete health economics analysis would necessarily account for more than the costs of evaluation, monitoring, and pharmaceuticals. Additional important considerations include the possible costs of disease progression that could be averted by treatment, including cirrhosis, hepatocellular carcinoma, and liver transplantation, as well as the potential for re-infection and forward transmission due to ongoing risk behaviors within prison and after release.

Modeling has shown that treatment of HCV, in addition to opiate substitution therapy, is crucial to reducing disease prevalence (Martin, Hickman, Hutchinson, Goldberg, & Vickerman, 2013). Constrained correctional resources will be hard-pressed to fund the upfront expenses of HCV treatment, no matter how cost-effective they would prove to be in the long run, and it is likely that prison systems will treat only those patients who need it most instead of all of those whom it could benefit.

Conclusions

The prevalence of HCV among inmates of Pennsylvania state prisons is much higher than that reported in the community, particularly among women. The rate of chronic infection after HCV exposure is similar to that reported in the general population, as is genotype distribution. The Pennsylvania DOC demonstrates that universal screening is feasible, and the high concentration of infection makes correctional settings high-yield venues for the expansion of HCV testing and treatment, especially among a population of patients who may have relatively increased access to healthcare while incarcerated and who may be at risk of ongoing transmission.

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Table 1

Distribution of genotypes among Pennsylvania state prisoners with chronic hepatitis C virus infection, 2004–2012 (n=3247)

	Total <i>n</i> (%)	Men <i>n</i> (%)	Women <i>n</i> (%)
Genotype			
1	2488 (76.6)	2302 (77.1)	186 (71.5)
2	302 (9.3)	273 (9.1)	29 (11.2)
3	380 (11.7)	340 (11.4)	40 (15.4)
4	45 (1.4)	42 (1.4)	3 (1.2)
Other	32 (1.0)	30 (1.0)	2 (0.8)