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Heterogeneity in Hepatitis B Virus (HBV) Seroprevalence Estimates from U.S. Adult Incarcerated Populations

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Hepatitis; Incarceration; Prison; Prisoners; Meta-Analysis

INTRODUCTION

Despite substantial declines over the past two decades in U.S. incidence rates for hepatitis B virus (HBV) infection, chronic HBV infection and its sequelae—chronic liver disease/cirrhosis and primary liver cancer—remain significant public health problems (1–7). These conditions may have a particularly strong impact on correctional health-care systems in the United States, as studies suggest that the prevalence of current or past HBV infection in incarcerated populations may be four to five times greater than that in the U.S. general population (6,8–30). However, HBV seroprevalence estimates from U.S. incarcerated populations appear to vary widely across studies, with prevalence estimates for HBV surface antigen (HBsAg) (current infection) ranging from 0.9% to 11.4% (12,28) and HBV core antibody (anti-HBc) (past or current infection) estimates ranging from 6.5% to 42.6% (12,19). Variation in HBV seroprevalence estimates across incarcerated populations has received limited attention in the literature (12–14), and several authors have suggested that HBV seroprevalence estimates reported in their studies were consistent with previous estimates (15,17,19,21,27–29). We conducted a systematic review of studies reporting HBV seroprevalence estimates from U.S. adult incarcerated populations to describe variation in these estimates across studies.

METHODS

Data Sources and Search

Medline via Ovid, Web of Science-Science Citation Index and Social Sciences Citation Index, National Criminal Justice Reference Service Abstracts Database, and UMI Proquest Digital Dissertations were searched using the keywords “hepatitis” and “prison*” for reports of HBV seroprevalence estimates in incarcerated adults that were indexed from January 1,

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1975 through August 31, 2005. Bibliographies of review articles and initially eligible studies were also searched.

Study Selection

The following eligibility criteria were pre-specified and applied in the order mentioned: (1) indexed in the time period noted above; (2) conducted in the United States; (3) primary study; (4) reporting prevalence estimates of HBV infection; (5) study population sampled from prisons, jails, or other correctional facilities; (6) measurement of one or more standard serologic markers for HBV (HBsAg, total anti-HBc, IgM anti-HBc, anti-HBs); (7) HBV seroprevalence estimates based on screening a defined population (i.e., not mathematical models (31) or surveys of medical directors (32–34)); (8) sample drawn exclusively from a prison, or correctional system, or facility housing primarily adults; (9) sample not drawn from a facility housing primarily non-U.S. residents; and (10) sample not restricted to those with another illness (e.g., HIV-positive prisoners). When unique citations reflected duplicate reports of the same data, HBV seroprevalence estimates and sample characteristics were drawn from the more complete report.

Data Extraction

HBV seroprevalence estimates and study characteristics considered potential sources of variation (35–37) were extracted independently by two authors (correlation coefficient, r = 94.4; percentage agreement [95% confidence interval (CI)] = 89.4% [87.5%–91.1%]). Discrepancies were resolved by A.J.H. and K.J.G.

Statistical Analysis

Data were analyzed using Stata 8.2 (38). Outcomes of interest were prevalence estimates for the most commonly reported seromarkers: HBsAg, total anti-HBc, and any positive HBV marker (i.e., one or more seromarkers positive when more than one seromarker was tested). Wilson 95% CIs (39) were calculated to display prevalence estimates using a common metric for precision.

The Q-statistic was used to test for heterogeneity in prevalence estimates overall and by study level strata for each seromarker. Prevalence estimates and corresponding standard errors were transformed into logits and weighted using the inverse variance method to calculate a Q-statistic [$Q=\Sigma w_i(L - \bar{L})^2$] (*meta* command) (40–44), for which a small p value indicates heterogeneity beyond what would be expected from random variation (i.e., the smaller the p value the greater, the departure from homogeneity) (40–44). Logit transformation of proportions has been recommended for meta-analysis because logits afford the advantages of a normal distribution and stable variance analysis (40,43). Statistical outliers among weighted logit prevalence estimates were identified using the method proposed by Hamilton (2003) (*iqr* command) (45). Analyses were repeated excluding outliers to examine their influence on Q-statistics.

RESULTS

Search and Study Selection

Of 579 unique citations screened, 23 eligible studies were initially identified. Two of these studies estimated HBV seroprevalence for two distinct populations, so these were treated as separate estimates (28,30). Thus, our systematic review included reported HBV seroprevalence estimates from 25 distinct U.S. incarcerated populations, with 15 estimates of HBsAg prevalence, 11 of anti-HBc prevalence, and 13 of any positive HBV marker prevalence.

Heterogeneity in HBV Seroprevalence Estimates

Q-statistics indicated heterogeneity of estimates for each of the 3 outcomes (Fig. 1). Outlier analysis indicated one mild outlier for HBsAg prevalence (Solomon et al., 2004, detainees) (28). After exclusion of the outlier, the *p* value for the heterogeneity test for HBsAg prevalence estimates remained extremely small ($p = 0.000$), indicating that substantial heterogeneity persisted. Q-statistics also indicated heterogeneity of seroprevalence estimates for all definable within-study subgroups (e.g., all males, all females, all injection drug users) and for nearly all study-level strata (e.g., all studies with mean age ≥31 years). Prevalence estimates of any positive marker for studies with 30% or less injection drug users appeared to be homogeneous ($p = 0.656$).

DISCUSSION

Results of this study confirmed that adult incarcerated populations in the United States are heterogeneous with respect to prevalence of 3 commonly reported HBV seromarker outcomes; that is, the dispersion of HBV seroprevalence estimates around their mean was far greater than would be expected from within-study sampling error alone. This heterogeneity and its potential sources should be considered in the future when interpreting study-specific HBV seroprevalence estimates from U.S. adult incarcerated populations, when comparing these estimates across studies, and when assessing studies that rely upon these estimates, such as cost-effectiveness analyses of HBV-related preventive and therapeutic strategies in correctional settings. Potential sources of heterogeneity may include across-study differences in sample demographic characteristics and behavioral risk factors, background disease prevalence, and methodologic factors (35–37). Because of the small number of HBV seroprevalence estimates and differences in reporting across studies, application of meta-regression techniques to HBV seroprevalence estimates from U.S. incarcerated populations provides only limited insight into the sources of heterogeneity across studies (37). A national, population-based study may be required to explore fully the factors affecting HBV seroprevalence estimates from U.S. incarcerated populations.

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Selected Abbreviations and Acronyms

HBV	hepatitis B virus
HBsAg	HBV surface antigen
anti-HBc	HBV core antibody

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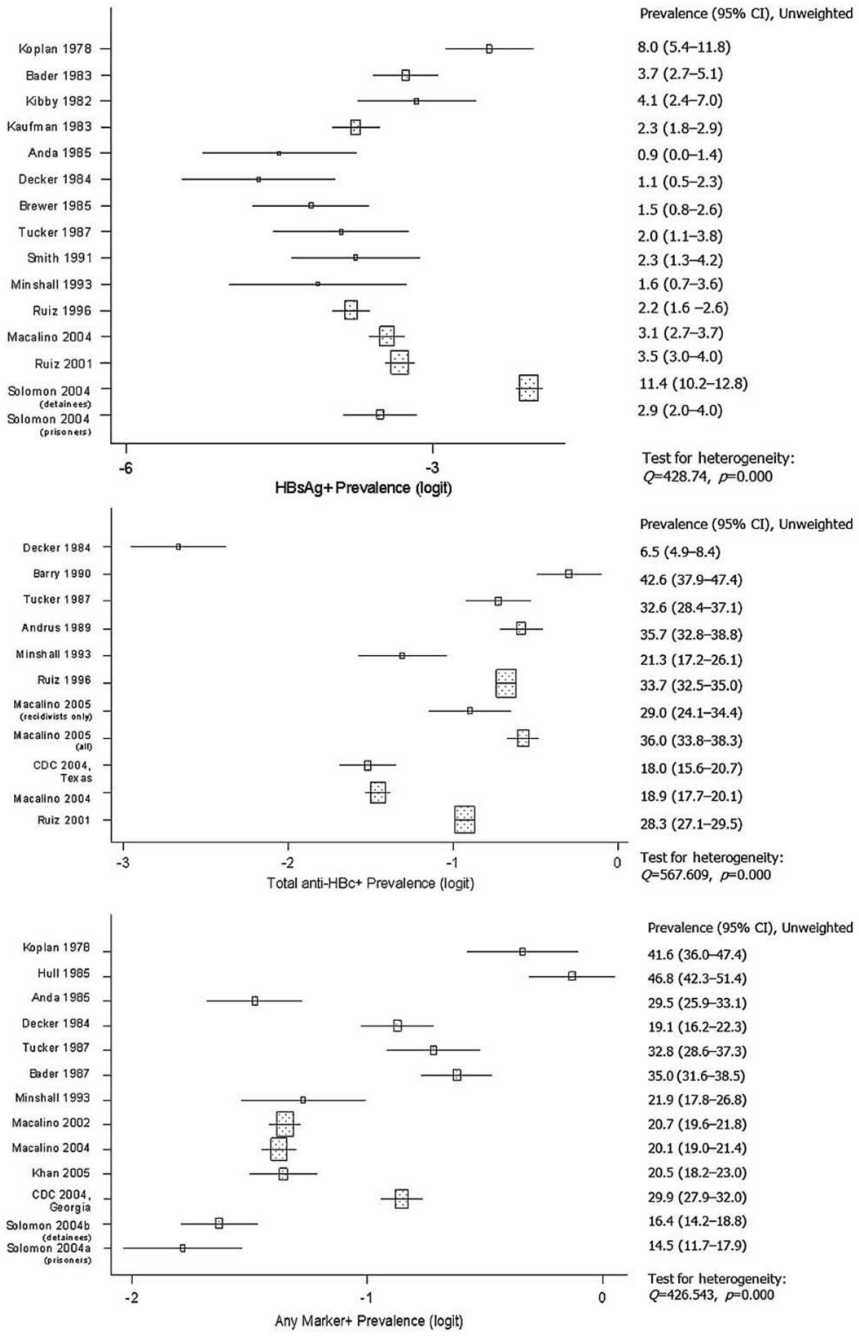

FIGURE 1.
HBV seromarker prevalence estimates with 95% confidence intervals and heterogeneity statistics.