Using Geographic Information Systems and Spatial Analyses to Depict Reported Hepatitis C Cases in Massachusetts, 2002-2013

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BACKGROUND

Deemed the most common chronic bloodborne infection in America today, the hepatitis C virus (HCV), infects between 3.4 and 4.9 million individuals in the United States.[1] In Massachusetts alone, it is estimated that 65,000 individuals are currently living with the virus; however, this approximation is likely under estimated.[2] Of these infected individuals, up to 85% will develop chronic HCV infection along with possible cirrhosis, liver cancer, liver failure, and/or death.[1,3] To help curb this common bloodborne infection, understanding the spatial distribution of the virus remains critical in providing care and treatment for the virus; however, few studies have investigated this spatial component, especially in the state of Massachusetts.[4] To help fill this gap in knowledge, the number of reported HCV cases, between the years 2002-2013 in Massachusetts, will be thematically mapped on the census tract level; focus will be given on rates per 1,000 individuals, along with spatial density analyses to understand the virus' spatial distribution.

METHODS

HCV surveillance data, between the years 2002-2013, was obtained from the Massachusetts Department of Public Health (MDPH) (n=99,787). Using data collected from the U.S. Census Bureau's American Fact Finder, HCV cases with a census tract (n=63,292) were aggregated at the year 2000 census boundary (n=1,361). Dot density and choropleth maps were generated, with choropleth maps detailing infection rates per 1,000 individuals by quintiles. Further, kernel density estimates were calculated for HCV rates per 1,000 individuals per square mile. On all maps, census tracts with a case number ≤4 were suppressed in accordance with MDPH's infectious disease data suppression guidelines.[5] Data management and aggregation took place in SAS, version 9.3 (SAS Institute Inc., Cary, NC); maps were created in ArcGIS, version 10.2.2 (Esri, Redlands, CA).

RESULTS

Reviewing Figure 1, larger clusters of reported HCV cases surround cites with higher populations, these include: Boston, Lowell, Worcester, and Springfield. Smaller clusters of the virus are seen in Brockton, Fall River, New Bedford, Lemoinster/Fitchburg, and Pittsfield areas. When adjusted for population (i.e., calculating infections per 1,000 individuals), Figure 2 indicates that higher rates of HCV cases (>17 to ≤317 per 1,000 individuals) are found in: Boston, Lowell, Worcester, Springfield, Pittsfield, Orange/Athol, and Provincetown areas. Similar results were also seen in the kernel density estimates, Figure 4, where larger HCV density per 1,000 individuals per square mile exists in: Boston, Lowell/Haverhill, Worcester, Springfield, Pittsfield, Brockton, Fall River, and New Bedford areas. Moving forward, it would be of interest to determine if these areas of high HCV clustering are statistically significant HCV clusters using hot spot cluster analyses.
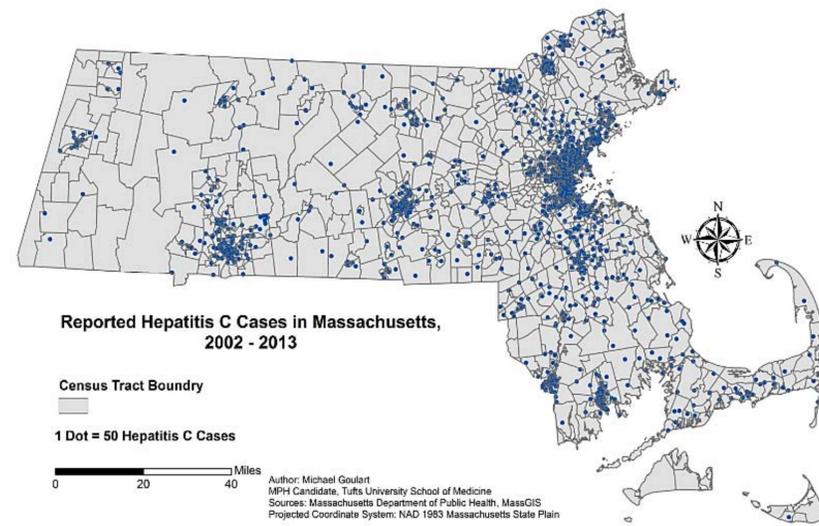

Figure 1: Reported Hepatitis C (HCV) Cases in Massachusetts at the Census Tract level, 2002-2013. One Dot = 50 HCV Cases.
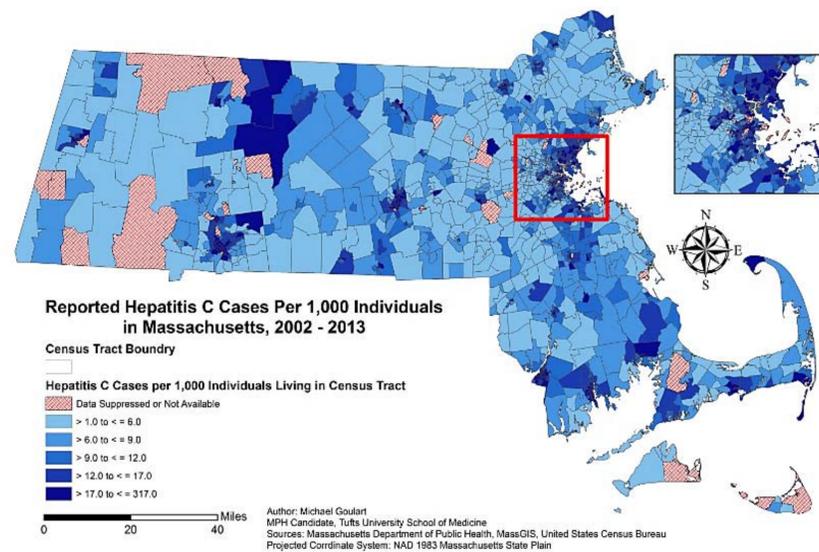

Figure 2: Reported Hepatitis C (HCV) Cases in Massachusetts at the Census Tract Level per 1,000 Individuals, 2002-2013.

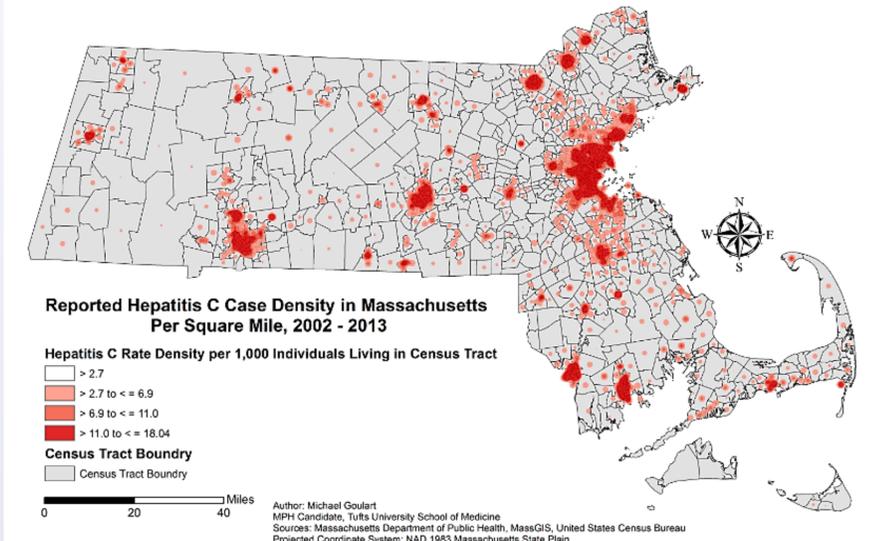Figure 3: Map of the United States; Massachusetts Shown in Red

Figure 4: Reported Hepatitis C (HCV) Case Density per Square Mile in Massachusetts at the Census Tract Level, 2002-2013.

DISCUSSION

Understanding the spatial distribution of HCV across Massachusetts, allows for improvements to made in hepatitis C prevention, treatment, and care. The findings outlined here can play a critical role in determining where HCV-care services and harm reduction programs can be targeted. These services have remained vital in not only curbing HCV morbidity and mortality, but also decreasing incident infections.[6] Strengths of these maps and spatial analyses come from the hypotheses that they can generate; however, interpretations should be done with caution. The surveillance data represents reported HCV cases through the years 2002-2013 only. Maps do not represent all HCV cases in Massachusetts, nor do they represent cases not reported to MDPH. Further, not all HCV cases reported to MDPH from 2002-2013 are represented; during data aggregation, reported cases that did not have an associated census tract (n=36,495), where excluded. Despite the limitations noted, policymakers and public health officials should utilize these analyses to determine locations where HCV prevention, treatment, and care would be best focused across the Commonwealth. Future research should determine if the clusters identified here are statistically significant through the use of hot spot cluster analyses.

REFERENCES

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