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Zoe Schneider _____ March 5th, 2021 _____

[Student's name typed] Date

Approval Sheet

An Analysis of Risk Factors for Household Spread of COVID-19 in a Hispanic Population Associated with Meat Packing Plants

By

Zoe Schneider
MPH

Department of Epidemiology

_____

Jodie L. Guest, PhD, MPH
Committee Chair

Abstract Cover Page

An Analysis of Risk Factors for Household Spread of COVID-19 in a Hispanic Population Associated with Meat Packing Plants

By

Zoe Schneider

BA Genetics, AB Cognitive Science
University of Georgia
2018

Faculty Thesis Advisor: Jodie L. Guest, PhD, MPH

An abstract of
A thesis submitted to the Faculty of the
Rollins School of Public Health of Emory University
in partial fulfillment of the requirements for the degree of
Master of Public Health in the Department of Epidemiology
2021

Abstract

An Analysis of Risk Factors for Household Spread of COVID-19 in a Hispanic Population Associated with Meat Packing Plants

By Zoe Schneider

Introduction: The COVID-19 pandemic has disproportionately affected racial and ethnic minorities in the United States. This analysis aims to further examine the household-level risk factors in Hispanic people in Georgia who are connected with the meat processing industry and compare them to risk factors in the general population.

Methods: Hispanic employees at a poultry plant who tested positive for COVID-19 and their families received follow-up PCR and antibody tests 1 month after their first positive test. Odds ratios were calculated for current and/or prior infection and all individual level risk factors collected. Multiple linear regression was used to determine household risk factors predicting the percent of individuals in a household with a positive PCR or antibody test result.

Results: 49 out of 194 (25%) employees at a meat processing plant tested positive for COVID-19 in May 2020. The odds of working in a meat processing plant among individuals who tested positive was 4 times the odds among those who tested negative (OR= 4.10, 95% CI 1.62 - 10.93). No other variables were significantly associated with infection at the individual level. Household spread from an incident case was more common for those with higher household density (ß = 0.43, p-value = 0.003) and fewer children under 18 in the household (ß = -0.59, p-value = 0.02).

Discussion: Identification and consideration of population-specific risk factors is essential when responding to the COVID-19 pandemic and making appropriate recommendations. The risk factors for this population are similar to risk factors identified in previous studies, but higher average household density and working in a meat processing plant contributed to a higher risk of household and individual spread of COVID-19 from an incident case in this population in comparison with the general population.

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Table of Contents

Introduction:

The first case of COVID-19 was reported in the state of Georgia on March 2nd, 2020. Despite the lack of availability of COVID-19 tests, reported cases continued to rise through March and early April, and an MMWR published in May highlighted the increased risk of COVID-19 among workers in meat processing facilities (1).

As the outbreak progressed, it became increasingly apparent that COVID-19 disproportionately effects racial and ethnic minorities in the United States. This observation has been attributed to a variety of factors, including a correlation to living in urban areas, poorer baseline health, and higher proportions of essential workers in these groups (2). In Hall County, Hispanic workers at poultry plants at the intersection of these risk factors have been hit particularly hard, with testing events finding 14-30% of workers positive for COVID-19 (unpublished Emory Outbreak Response Team data).

The household contacts of these workers are also at high risk of contracting COVID-19. Understanding the unique risk factors in this situation may help keep these families safer from COVID-19. Early studies conducted in China (3,4) found an increased risk of household transmission to contacts who are over 60 years of age and when the index case was unable to quarantine. More recently, a study of household infections in Tennessee and Wisconsin found higher rates of secondary infections within households in Hispanic members and female index patients, although the differences were not statistically significant (5).

However, these data may not be directly applicable to the Hispanic population in Georgia because of differences in the prevalence of risk factors and the accessibility of testing or public health messaging. In a study COVID-19 infections in a similar

population of with high levels of occupation in meat packing factories, basic summary statistics of cases showed higher percentages of infections in children under 18 years in comparison to White, Non-Hispanic individuals in the same area (6).

This analysis aims to further examine the household-level risk factors in Hispanic people in Georgia in order to evaluate potential prevention strategies.

Methods:

Recruitment: Data for this analysis was collected from two COVID-19 testing events for employees of Vital Foods and their families, coordinated by the Emory Outbreak Response team. At the initial event, held May 22 through May 24, 2020, all Vital Foods employees were given the opportunity to receive a free COVID-19 test during their paid work hours. All employees who tested positive were given paid sick leave for their 14-day quarantine period in order to minimize personal risk to the employee for choosing to get tested. All employees who tested positive and members of their household were invited to a follow-up testing event one month later, on June 20 and 21, 2020.

Data collection: Trained teams consisting of one translator and one healthcare professional administered PCR nasal tests and serum antibody tests. Basic demographic information was also collected, including race, ethnicity, sex, age, number of people in the household, and employment with a meat packing plant.

Laboratory Testing: Real-Time PCR assays for SARS-CoV-2 from anterior nares swabs were performed by Molecular Testing Labs (MTL) for the qualitative detection of SARS-CoV-2 N protein, S protein and ORF1ab. This is an FDA EUA diagnostic test and MTL is a CLIA approved lab. Anterior nares swab specimens underwent nucleic acid extraction using the Thermo Kingfisher platform (ThermoFisher Scientific, Waltham, MA). Extracts were tested for human RNase P by reverse transcriptase RT-PCR with Thermo SARS CoV-2 testing kit v1. SARS-CoV-2 serological tests were performed to identifying antibodies (e.g., IgG, IgM) to SARS-CoV-2 from clinical specimens using lateral flow SARS-CoV-2 serological tests from MTL.

Statistical analysis: All data cleaning and analysis was performed with R Studio version 1.4.1103. Demographics were summarized for all participants at the June testing events and for the limited sample of qualified households, where at least 2 members received a PCR test and at least one member of the household was identified as a positive case at a previous testing event. Odds ratios were calculated for all participants using a positive PCR and/or antibody test as the outcome and the demographic variables collected as the exposure.

Final multiple linear regression analysis was limited to the data set of qualified households. All available variables were initially included in the model, and backwards elimination was performed until only significantly associated variables remained.

Results:

Of the 194 initial participants on May 22-24 who worked at a meat packing factory, 49 (25%) tested positive. All of these individuals as well as 14 individuals who tested positive at an earlier event at the meat packing factory were contacted and invited to return with members of their household for additional testing. Through this recruitment as well as word-of-mouth advertising, a total of 95 individuals participated in the second testing event.

Demographic trends are similar for the full dataset of participants and the individuals in the household analysis (Table 1). The primary difference is a lower antibody positivity among those in the household analysis.

In all participants for the second testing event (not factoring in household correlations between participants) the odds of working in a meat packing plant among those who had a positive PCR or antibody test was 4.1 times the odds of working in a meat packing plant among those who did not have a positive test (Table 2). Other variables considered were not significantly associated with COVID-19 infections at the individual level.

Data was then limited to households where at least one member received a positive PCR test at a previous testing event and at least two household members returned for follow-up testing. This resulted in a final sample size of 22 households consisting of 62 individuals (Figure 1). Using multiple linear regression to model the percent of a household with a positive antibody and/or PCR test, there was a significant correlation with household density, percent of children in the household, and number of people in the household who work in meat processing plants (Table 3). Increased

household density was associated with a higher percent of household infections (ß = 0.43), while an increased number of children and number of members working in a meat processing plant was associated with a decreased percent of household infections (ß = -0.59 and -0.21, respectively).

Discussion:

Although previous household analyses have been done, this is the first one to focus on the population of Hispanic workers at Hall county meat processing plants and their families. These results were in agreement with previous studies that found the risk of COVID-19 household transmission was increased among individuals who identified as Hispanic (5) and decreased for children (7). In this analysis, working in a meat-processing plant was identified as a factor that increased the risk of an individual testing positive for COVID-19, but decreased the percent of COVID-19 positive individuals in a household. This discrepancy is likely because all households analyzed in this study contained at least one family member who worked at the meat processing plant. Therefore, this parameter only represents the effect for each additional member of the household, which is a less meaningful question. In similar populations, 38% of household clusters have been attributed to an initial case in a meat packing plant worker (6), although it is unclear if this percentage is higher than expected given the number of people in the population working in meat packing factories.

This analysis confirmed a higher risk of transmission in high density households that was seen in previous studies (8). Quarantine of infected family members is a commonly recommended strategy for preventing household transmission, and these data suggest that this may be more difficult to do in higher density households and thus the risk is increased for all members of the household when one person tests positive.

Beyond the analysis, the testing events discussed provided an opportunity to intervene in the transmission chain and communicate information about COVID-19 prevention to families at high risk of infection. As discussed above, the data collected

confirms that previously observed population trends in COVID-19 household transmission risk hold true for this population in Hall County. This is important because most previous studies have been conducted with individuals who were recruited due to a positive test at a traditional testing site. Due to language barriers, lack of access, and anxiety about the safety of attending public testing sites, it is likely that Hispanic people are under-represented in these studies that recruit positive cases from general testing events.

Ultimately, the data used in this analysis were collected with the primary purposes of confirming the validity of a new antibody test and providing a high-risk population with the opportunity to be tested. Because of these priorities, there were several major limitations of the data. First, the true number of cases in the population were underestimated in multiple ways. Of the 49 incident cases who tested positive on May 20, 2020 and received a follow-up antibody test June 20 or 21, 22 (45%) had a negative antibody and PCR test on follow-up. As antibodies may take 1-3 weeks after infection to develop (9), other household members who were infected around this time period may have cleared an infection but not have developed antibodies yet. Three households (13.6%) also had at least one family member with a positive PCR test. If the information provided at the testing event was not sufficient to prevent transmission, it is possible that additional members of these families became infected or were already exposed at the testing event.

Selection bias was also present. All positive cases from the first testing event were contacted for the second event, and one of the more common reasons for refusal was not being able to travel to the event because they or a family member was sick.

Therefore, several households or individuals with active and symptomatic presumptive infections were not included in this analysis.

Finally, the definition of a household for this study was somewhat unclear. While the calculation of household density asked participants how many people slept in their house the previous night, two households had more individuals tested than the number of people they reported sleeping in their home. While an easy number to collect, number of people sleeping in the house may not fully reflect the reality of an individual's contacts in the house.

For future messaging and COVID-prevention strategies, it is important to consider the factors identified in this analysis. As discussed above, isolating the index case in their own bedroom and bathroom is not always an option. The median number of individuals per bedroom in this population was 1.5, which is higher than previous studies that had a median of 1 individual per bedroom (5). Providing more options for isolation or discussing these difficulties and stressing the importance of separation with high density households may help reduce transmission.

Some of the discrepancies in risk factors found in this analysis highlight the importance of focusing on societal factors that contribute to higher risk profiles of Hispanic populations, such as geography, pre-existing conditions, and county-level English fluency rates (10) that exist regardless of occupational status and overlap with the observed risk factors.

Through the COVID-19 pandemic and future infectious disease emergences, rapid detection and intervention of outbreaks in vulnerable populations is essential. As of February of 2021, 569 outbreaks at meat packing factories have directly resulted in

54,000 cases and 270 deaths from COVID-19 (11), and the total burden of cases associated with these meat packing plants has been estimated as high as 310,000 cases and 5,200 excess deaths (12). A variety of societal and individual level factors contribute to the increased risk to these workers and their communities, and consideration of these factors must be integrated into response efforts.

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Tables

Table 1: Demographics of all participants collected and the subset of participants who qualified for the household analysis

	All participants (n= 95)	Analyzed households (n= 62)
Age, Mean (SD)	35.2 (15.9)	34.8 (17.0)
Gender, N Female (Percent)	49 (51.6%)	29 (46.8%)
Hispanic, N (Percent)	88 (92.6%)	62 (100%)
Work at Meat Packing Plant, N (Percent)	37 (38.9%)	22 (35.5%)
PCR Positivity, N (Percent)	13 (13.8%)	7 (11.2%)
Antibody Positivity, N (Percent)	25 (29.8%)	9 (14.5%)

Table 2: Odds ratios for individual level risk factors

Characteristic	Odds Ratio (95% Confidence Interval)
Age (Under / Over 18)	0.64 (0.15, 2.27)
Sex (Female/male)	0.84 (0.35, 2.03)
Ethnicity (Hispanic/ Non-Hispanic)	3.63 (0.53, 99.4)
Occupation (meat plant / other)	4.10 (1.62, 10.93)
Density (1+ / <1 person per bedroom)	2.44 (0.65, 12.34)

Table 3: Results of multiple linear regression to model the percent of positive cases (PCR or antibody) within a household

	ß Estimate	95% CI	P-value
Household Density	0.43	0.16, 0.70	0.003
Percent Under 18	-0.59	-1.08, -0.1	0.02
Number working in meat processing	-0.21	-0.39, -0.03	0.03