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Original article

Utilizing student-led contact tracing initiative to alleviate COVID-19 disease burden in central Pennsylvania

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Purpose: Contact tracing elicits probable contacts from COVID-19 cases. Our student-led contact tracing initiative promoted isolation of both confirmed and probable cases and quarantine of contacts to reduce disease in Central Pennsylvania.

Methods: Close contacts of COVID-19 cases were contacted by tracers, advised to quarantine, and monitored for 14 days for symptoms. Symptomatic contacts were classified as probable cases and advised to isolate. Data was collected from March 24, 2020 to May 26, 2020. Poisson regression and linear regression were utilized to examine the relationships between case and number of contacts and proportion of symptomatic contacts.

Results: Study sample comprised of 346 confirmed and 157 probable cases. Our results indicate a significant difference in percent of household contacts who became symptomatic between confirmed and probable cases (22% vs. 3%; adjusted P < .01). Similarly, probable cases had significantly fewer non-household contacts compared to confirmed cases (0.87 vs. 0.55; adjusted P < .01).

Conclusions: Timely notification of exposure to a COVID-19 positive individual by student contact tracers allowed for probable cases to quarantine early in the disease process. Our data suggests that early quarantine and/or isolation may have directly contributed to probable cases having fewer non-household contacts and a smaller proportion of symptomatic household-contacts compared to confirmed cases.

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Introduction

As infection rates of coronavirus disease 2019 (COVID-19) continue to increase globally, the impact of identification and isolation of confirmed cases of COVID-19 as well those who have been exposed to the disease, has become an important area of further study. COVID-19 is caused by Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) and has been shown to spread via aerosols, secretions, fomite droplets, and contact transmission [1]. Currently, the total COVID-19 infections in the United States have exceeded 32.3 million, and it has resulted in over 575,481 deaths [2]. Per the U.S. Centers for Disease Control (CDC), overall cumulative hospitalization rates since March 2020 associated with COVID-19 were 178.2 per 100,000 people, with the highest rate of hospitalization among people older than 65 years of age (at 481.5 hospitalizations per 100,000 people) [3]. Pennsylvania currently has a rate of 9176 coronavirus cases per 100,000 people [2]. Notably, a large-scale cohort study that examined the impact of COVID-19 intensive care unit (ICU) strain on COVID-19 mortality found significant association between strain on critical care capacity and increased ICU COVID-19 mortality [4]. As a result, further outbreaks may have devastating consequences on hospital systems and create major scarcities in healthcare resources [4,5].

A recent epidemiological modeling study examined the impact of mitigation (focused on slowing, not stopping spread) compared to suppression (focused on reducing the number of new cases by reducing reproduction number—R—below 1) [6]. Mitigation involves utilizing non-pharmacological interventions to slow the spread of a disease to prevent the healthcare system from being overwhelmed; it does not aim to stop the spread of disease.
For example, this strategy was undertaken during the 2009 swine flu pandemic caused by the H1N1 influenza virus when vaccines were initially provided to those with pre-existing medical conditions and thereby at higher risk of severe illness [6]. This allowed the at-risk population to be protected while herd immunity developed in the remaining population. Strategies focused on suppression aimed to reduce R_0 below 1, thereby reducing case numbers to lower levels or eliminating human-to-human contact (as in the case of SARS) [6]. Common suppression strategies include social distancing, closure of high transmission venues, and robust testing and tracing programs. Results from this model suggested that social distancing policies, when combined with other interventions such as closure of schools/universities and isolation of COVID-19 cases, could suppress transmission of the disease and also reduce the number of new cases [6]. Suppression was deemed more feasible based on this model, though the measures used to achieve suppression would need to evolve over time [6]. Contact tracing is a suppression strategy that can be employed to control transmission rate and limit the spread of disease by allowing for identification, patient education, and isolation of confirmed and probable cases of COVID-19 and quarantine of their close contacts. Suppression strategies could thereby allow for adequate time to develop mitigation techniques for the COVID-19 pandemic, such as vaccines.

Contact tracing involves the identification of individuals with disease (cases) and advising them of isolation protocols, communicating with them (case investigation) to determine close contacts, and ultimately notifying contacts of possible exposure to allow them to quarantine and prevent further spread of disease. Although contact tracing has been shown to be less effective in diseases in which infectiousness precedes the onset of symptoms (such as in SARS), it has also been shown to be beneficial in diseases where infectiousness and onset of symptoms overlap (such as in Ebola virus disease) [7–9]. Thus, the major epidemiologic variables that determine the effectiveness of contact tracing include the rate of transmission before symptom-onset as well as the number of new cases generated from every new infection [7,10]. A mathematical model sought to assess the value of contact tracing and subsequent isolation of COVID-19 cases in controlling COVID-19 outbreaks.

The study found that only high levels of contact tracing can help mitigate new outbreaks of COVID-19, specifically noting that around 80% of symptomatic contacts must be traced and isolated to contain around 80% of outbreaks in this model [10]. Additional model-based estimates also note that to control further spread of the disease, approximately 70% of contacts would need to be successfully traced [11]. Furthermore, a recent retrospective cohort study examined disease transmission and factors influencing transmission by comparing cases identified through symptomatic surveillance and contact tracing; the study included 391 cases and 1286 of their close contacts [12]. This study noted that cases began isolation 4.6 days after developing symptoms, and that contact tracing reduced this delay by 1.9 days [12]. The retrospective study also noted that household contacts and individuals travelling with confirmed COVID-19 cases were at an increased risk for infection [12].

Successful contact tracing can therefore help reduce the delay between symptom onset and isolation to prevent further spread of the disease. A major limitation in tracing processes is that prevention of disease spread from asymptomatic but infectious individuals requires tracing of cases who tested positive; many cases do not ultimately seek care (hence, are not being tested) due to being asymptomatic. A solution to this involves identification of probable cases, which may be colloquially referred to as “possible” or “presumed” cases; these are individuals who have been documented as being in contact with confirmed positive COVID-19 cases who report symptoms but have not yet been tested [13]. Ideally, contact tracing should help reduce the basic reproductive number for the disease (R_0, or number of new infections caused by an individual) to less than 1; tracing that can help cases isolate and identify/notify their contacts to quarantine will thereby lead to a more successful program [14].

In this report, we sought to examine contact tracing data and various key performance indicators (KPIs) of a successful contact tracing program to explore the role of a student-led contact tracing initiative in promoting isolation of infected and quarantine of exposed individuals and thereby reducing disease burden in the Central Pennsylvania community. We evaluate this here through the comparison of confirmed and probable cases and an examination of both their number of contacts and percentage of their contacts who became symptomatic.

Methods

Contact tracing program overview

To assist the community of Central Pennsylvania, health professional students at the Penn State College of Medicine (PSCOM) worked alongside health system leadership and faculty to design multiple health systems-aligned projects. Among these, the contact tracing taskforce was created to slow the spread of infection and transmission of COVID-19 in Central Pennsylvania. Building upon a student-run foundation, the contact tracing taskforce sought to ensure that confirmed and probable cases were notified of their disease status and ultimately followed isolation and/or quarantine measures. Detailed discussion regarding PSCOM’s contact tracing workflow, organization/team structure, as well as further follow-up and onboarding information have been recently published [15,16]. The general overview of PSCOM’s contact tracing workflow included identification of a COVID-19 positive patient and addition of this patient to our HIPAA compliant Research Electronic Data Capture (REDCap); a trained health professions student contact tracer from the case team then contacted the patient and conducted a case investigation, utilizing a pre-designed script with specific questions to identify any exposures and potential contacts. Another team in the contact tracing program would then add the contacts into REDCap (with unique identification numbers) and distribute them for further follow-up by student tracers. Contacts were followed for 14 days via daily phone calls and monitored for symptoms development. If contacts were noted to be symptomatic, they were classified as presumed cases, which triggered a case investigation, isolation, and referral to testing when available.

Data collection

Data, which was collected via phone calls with cases and contacts, were stored in HIPAA-compliant Research Electronic Data Capture (REDCap) [17]. The time period for this study was from the initiative’s start on March 24, 2020 to May 26, 2020. During this time, contacts who became symptomatic were offered access to a COVID-19 test. After May 26, all contacts regardless of symptoms, were offered a COVID-19 test.

A confirmed case was defined as an individual who tested positive for COVID-19 at Penn State College of Medicine. A probable case was defined as anyone who had a known exposure to a COVID-19-positive individual and who had symptoms consistent with COVID-19 [13]. A symptomatic contact who subsequently tested positive for COVID-19 remained designated as a probable case. Due to the scarcity of testing available at the time of data collection [18–21], theprobable cases were treated like confirmed cases, such that they were advised to isolate and interviewed for contacts. We collected basic demographic data from all cases.
We interviewed each case about contacts that they may have interacted with in the 48 hours preceding their COVID-19 test or the 48 hours prior to symptom onset (if symptoms began before testing if no testing was not available), as per guidance from the Centers for Disease Control and Prevention [22]. A contact was defined as anyone who was within 6 feet of the case for total of 15 minutes or more during the infectious period [22]. Mask wearing was not considered as part of contact identification [22]. Each contact was classified as a household (shares home with case) or non-household (does not share home with case) contact. Tracers attempted to call contacts a minimum of 4 times to inform them of their exposure and advise them to quarantine until 14-days after their exposure date. Contacts were called daily or sent a daily email during their quarantine period to assess for symptoms [15]. If contacts became symptomatic during their 14-day quarantine period, they were identified as probable cases.

Statistical analyses

Statistical analyses were performed using SAS 9.4 (SAS Institute, Cary, NC, USA).

We calculated frequencies of demographics for confirmed and probable cases. We calculated the mean number of total contacts, household contacts, and non-household contact for confirmed and probable cases. Among those with household contacts, we calculated the proportion of household contacts who became symptomatic. Among those with non-household contacts, we calculated the proportion of non-household contacts who became symptomatic.

We used Poisson regression to estimate the association between case type (confirmed vs. probable) and number of contacts. We did this separately for total contacts, household contacts, and non-household contacts. We estimated the unadjusted associations and associations adjusted for age (continuous) and case sex (male, female). Using the adjusted model, we estimated the predicted number of household and non-household contacts by case type.

We used linear regression to estimate the association between case type (confirmed vs. probable) and proportion of contacts who developed symptoms. We did this separately for household and non-household contacts. We first estimated the unadjusted associations and then estimated the associations adjusted for the age and sex of the case. Using the adjusted model, we estimated the predicted proportion of symptomatic household and non-household contacts by case type.

Results

The contact tracing program communicated via phone with 461 confirmed cases and 259 probable cases during the period of study. Among those, 115 confirmed cases and 102 probable cases reported zero contacts. Those individuals were excluded from this analysis. In total, our final sample consisted of 346 confirmed cases and 157 probable cases (N = 503).

Characteristics of confirmed and probable cases

Among the confirmed cases, 58% (n = 199) were female and the median age was 40 years. The probable cases were also 58% female, but the median age was 33 years (Table 1).

Confirmed and probable cases both reported an average of 3.5 total contacts per case.

The average number of household contacts reported by each probable case (2.9) was slightly higher than the average reported by each confirmed case (2.6). Both confirmed cases and probable cases reported, on average, less than 1 non-household contact per case, with confirmed cases reporting an average of 0.9 and probable cases reporting 0.6. Among those cases who reported any household contacts, a higher percentage of household contacts of confirmed cases reported symptoms (22%) compared to the household contacts of probable cases (3%). Among those cases who reported any non-household contacts, a higher proportion of non-household contacts of confirmed cases reported symptoms (17%) compared to non-household contacts of probable cases (10%). (Table 1).

Total contacts

Unadjusted Poisson regression evaluating the relationship of case status and number of total contacts per case revealed a non-significant relationship (P = .90), which remained unchanged after adjustment for age and sex of case (P = .25).

Household contacts

Unadjusted and adjusted (for age and sex) Poisson regression revealed no significant relationship between case status and number of household contacts (unadjusted P-value=.14; adjusted P-value=.53). Using the adjusted model, the predicted number of household contacts among probable cases is 3.65 (95% confidence interval [CI]: 3.16, 4.21) contacts and among confirmed cases is 3.51 (95% CI: 3.06, 4.03) contacts (Fig. 1).

Results from unadjusted linear regression indicated a significant relationship between case status and proportion of household contacts that reported symptoms (P<.01), which remained even after adjustment for age and sex (P<.01). The multivariable model predicted that, on average, the proportion of symptomatic household contacts among confirmed cases is 17% (95% CI: 9%, 24%) and the proportion among probable cases is 0% (95% CI: 0%, 7%). (Fig. 2).

Non-Household contacts

Poisson regression results indicated that case status was a significant predictor of non-household contact count (P<.05), even after adjustment for age and sex (P<.05). After adjustment for age and sex, confirmed cases have 57% more non-household contacts compared to probable cases. Using the adjusted model, the predicted number of non-household contacts is 0.87 (95% CI: 0.67, 1.13) among confirmed cases and 0.55 (95% CI: 0.41, 0.74) among probable cases (Fig. 1).

The relationship between case status and proportion of non-household contacts who reported symptoms, was not significant in unadjusted linear regression model (P = .17), nor after adjustment for age and sex (P = .20). The multivariable model predicted that, on average, after adjustment for age and sex of the case, the proportion of symptomatic non-household contacts among confirmed cases is 30% (95% CI: 17%, 43%) whereas the proportion among probable cases is 23% (95% CI: 8%, 37%). (Fig. 2).

Discussion

Contact tracing can bridge the gap between possible exposure to disease or onset of symptoms and isolation. Effective tracing of infected individuals and cases with potential exposure can help identify a majority of secondary infections [11,23,24]. Thereby, intensive contact tracing and subsequent isolation is critical in slowing the spread of COVID-19 given that a significant proportion of those infected are contagious/infectious before they are symptomatic [14,25,26].

In this report, we present the results of a student-led contact tracing initiative in Central Pennsylvania that suggest contact tracing can reduce spread of COVID-19 in this community. Our results indicate that despite the lack of significance when comparing total contacts and household contacts between confirmed and
Table 1
Characteristics of confirmed and probable cases of COVID-19 (N = 503)

|                          | Confirmed cases (n = 346) | Probable cases (n = 157) |
|--------------------------|---------------------------|--------------------------|
|                          | n (%)                     | n (%)                    |
| Sex                      |                           |                          |
| Male                     | 147 (42%)                 | 65 (41%)                 |
| Female                   | 199 (58%)                 | 91 (58%)                 |
| Missing                  | 0 (0%)                    | 1 (<1%)                  |
| Age (years)              | Median (IQR)              | Median (IQR)             |
|                          | 40 (26–55)                | 33 (21–46)               |
| Mean number of all contacts per case | 3.5 (1–21)               | 3.5 (1–13)               |
| Mean number of household contacts per case | 2.6 (0–8)                | 2.9 (0–9)                |
| Mean number of non-household contacts per case | 0.9 (0–19)               | 0.6 (0–10)               |
| Mean proportion of household contacts who became symptomatic (n = 472) | 22% (0%–100%)            | 3% (0%–100%)             |
| Mean proportion of non-household contacts who became symptomatic (n = 164) | 17% (0%–100%)            | 10% (0%–100%)            |

Fig. 1. Predicted number of contacts with 95% confident intervals, adjusted for age and sex of case.

probable cases, there was a statistically significant difference in the proportion of household contacts who became symptomatic between confirmed cases and probable cases. Similarly, a statistically significant difference was noted when comparing total non-household contacts among confirmed cases and probable cases. Thereby, probable cases in our contact tracing system had fewer symptomatic household contacts and fewer total non-household contacts than the confirmed cases. While the difference was not statistically significant, probable cases did also have a smaller proportion of symptomatic non-household contacts compared to confirmed cases.

In this contact tracing program, probable cases were directly contacted about a potential exposure to an individual with documented COVID-19 by our tracers. The probable cases were then provided with referral for testing, guidance for isolation, as well as resources for food/amenities. Prompt notification of exposure to a COVID-19 positive individual allowed these probable cases to quarantine early in the disease process. The data supports that this may have reduced their total number of non-household contacts and reduced the proportion of their household who became symptomatic.

The number of household contacts was similar between confirmed and probable cases. This highlights the difficulty in reduction and prevention of exposure within households without alternative housing options (hotels, motels, etc.). In general, the number of individuals living in a house is fixed and cannot be modified without significant external support. However, the significantly lower number of non-household contacts and symptomatic household contacts of probable cases likely indicates a change in behavior brought about by the contact tracing process. Ultimately, the contact tracing program played a substantial role in identifying probable cases early and advising them to isolate early, such that infection transmission was minimized.

As noted above, the number of symptomatic household contacts differed significantly between confirmed and presumptive cases. We believe this reflects that early action on presumptive cases re-
duced transmission to household members. However, it is possible that this finding reflects that presumptive cases were not infected with COVID-19 and, thus, were at no risk for transmitting to others.

A limitation of this analysis, attributable to the scarcity of COVID-19 testing available at the time of this study, is the inability to definitively confirm that all probable cases were correctly classified as incidents of COVID-19 infection. It is possible that the reduced number of symptomatic contacts of probable cases is a result of some of these probable cases being incorrectly classified and, therefore, not being infectious. This analysis is further limited by the very few contacts that were reported by both confirmed and probable cases. It is possible that this reflects the time period in which this data was collected. Individuals may have had very few contacts due to the state and local policies limiting abilities to travel, frequent businesses, and socialize [27,28]. Alternatively, another plausible explanation is that reported contacts were artificially low due to individuals being hesitant to disclose contacts because they knew that the expectation at the time was to minimize contact with others, an example of desirability bias.

Overall, results from this analysis highlight the value of our student-run contact tracing initiative in reducing number of contacts per case and, by extension, the spread of COVID-19 in the Central Pennsylvania community. The significant trend reflecting probable cases having fewer total non-household contacts and a lower percentage of their household contacts becoming symptomatic highlights the benefits of patients being followed by tracers. Our analysis also included demographic information of our cases, including age and sex, to control for possible sources of bias: i.e. older individuals may have been more likely to remain home during the peak of the COVID-19 pandemic due to concern for infection or possibly to care for their family. Interestingly, the analyses showed a stronger association upon controlling and adjusting for age and sex. With this report, we demonstrate the benefits of effective contact tracing and student-run initiatives in roles of alleviating disease burden in local communities.

**Ethics statement**

This project was reviewed by the Penn State College of Medicine Subjects Protection Office and determined to be consistent with quality improvement and not research.

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**Fig. 2.** Predicted proportion of contacts who became symptomatic with 95% confidence intervals, adjusting for age and sex of case.
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