CEIP Sentinel

California Emerging
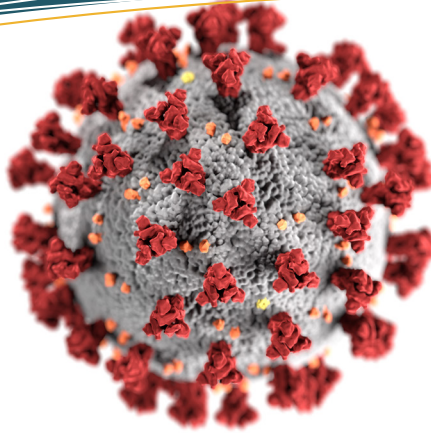Infections Program
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Tracking of SARS-CoV-2 Infections among Healthcare Personnel

The California Emerging Infections Program (CEIP) began interviewing healthcare personnel (HCP) with SARS-CoV-2 positive test results in April 2020. This project is ongoing. Cases were detected by screening cases reported to CalREDIE, the California Department of Public Health's electronic disease reporting and surveillance reporting system. The case definition includes having a positive SARS-CoV-2 test, residing in Alameda, Contra Costa, or San Francisco counties, and working in a healthcare facility or providing patient care. The latter portion of the case definition encompasses a wide array of healthcare personnel, including administration, environmental services, emergency responders, in-home healthcare providers, and dental professionals. The aims of the project are to determine the incidence of SARS-CoV-2 infection among HCP working in various types of healthcare settings and to describe characteristics of HCP exposed to or infected with SARS-CoV-2, including clinical activities and personal protective equipment (PPE) use.

As of September 13, 2021, 8,147 cases have been detected and CEIP staff have interviewed 1,673 HCP. The reasons for not interviewing cases included: not speaking English or Spanish (1%), phone disconnected/wrong number (2.8%), unable to reach after five attempts (24.4%), and being greater than 60 days after the test date (56.9%). The number of cases detected during the winter peak outpaced CEIP staffing levels for this project. For this reason we decided to stop contact or not begin contact of HCP if 60 days or more had elapsed from the test date.

Of the 1,673 case interviewed, 76.5% were female, 74.6% were symptomatic, and the median age was 39 years (min 18, max 79). The top five healthcare roles of interviewed HCP were, in descending order, home health caretakers, registered nurses, certified nursing assistants, administrative staff, and medical assistants. The top three facility types where interviewed HCP worked were, in descending order, acute care hospitals, nursing homes/skilled nursing facilities, and outpatient clinics.

The introduction of SARS-CoV-2 vaccines led to the addition of questions regarding vaccination to the questionnaire. The collection of these data will help evaluate post-introduction effectiveness of the vaccines in preventing severe disease among HCP with laboratory-confirmed symptomatic COVID-19. CEIP staff will continue to collect these data through the end of 2021, with a potential of continuing in 2022.

Contributed by Joelle Nadle, MPH, Health Program Manager

Photo Credit: CDC Public Health Image Library

Many questions about the safety and effectiveness of the SARS-CoV-2 vaccines have arisen after seeing the vaccines develop in less than one year, faster than any vaccine in United States history (Ball 2020). By the end of 2020, there were two vaccines, Pfizer-BioNTech and Moderna, ready for Phase 1 distribution among healthcare workers (CDC 2021). In December 2020, CEIP, in collaboration with Zuckerberg San Francisco General Hospital (ZSFG) and the Centers for Disease Control and Prevention (CDC), with 33 other sites nationwide, began evaluating the effectiveness of COVID-19 vaccines in preventing symptomatic cases of COVID-19 among healthcare personnel (HCP). HCP who have tested positive for COVID-19 are cases and compared with controls, those who have tested negative. Through comparison of vaccination status and other factors, cases and controls have been evaluated to determine the effectiveness of the COVID-19 vaccine.

We have interviewed 74 ZSFG HCP: 23 cases and 51 controls. Our data collection methods include interviewing healthcare workers, collecting vaccination records, and abstracting information from medical records. We are interviewing HCP to understand potential relationships between exposures in the community and workplace, underlying medical conditions, vaccination status, and demographic factors. Study staff have contacted medical providers and vaccine registries to verify underlying medical conditions and COVID-19 vaccination information.

The CDC has published a MMWR report with the interim analysis regarding the ongoing pandemic and expects to continue data collection until the data are able to inform meaningful analysis and results (Pilishvili 2021). As with SARS-CoV-2 itself, research to understand new variants and vaccine effectiveness continues to evolve and adapt.

[i.] Ball P. The lightning-fast quest for COVID vaccines - and what it means for other diseases [Internet]. Nature News. Nature Publishing Group; 2020 [cited 2021Apr9]. Available from: https://www.nature.com/articles/d41586-020-03626-1

[ii.] CDC's COVID-19 Vaccine Rollout Recommendations [Internet]. Centers for Disease Control and Prevention. Centers for Disease Control and Prevention; [cited 2021Apr9]. Available from: https://www.cdc.gov/coronavirus/2019-ncov/vaccines/recommendations.html

[iii.] Pilishvili T, Fleming-Dutra KE, Farrar JL, et al. Interim Estimates of Vaccine Effectiveness of Pfizer-BioNTech and Moderna COVID-19 Vaccines Among Health Care Personnel — 33 U.S. Sites, January–March 2021. MMWR Morb Mortal Wkly Rep 2021;70:753–758. DOI: http://dx.doi.org/10.15585/mmwr.mm7020e2external icon.

Contributed by Jane Lee, MPH

Disparities in Hospitalization Rates of Persons Infected with SARS-CoV-2 in Three San Francisco Bay Area Counties, March 1 through July 31, 2020

Background: Racial and ethnic disparities are occurring among cases of Coronavirus Disease 2019 (COVID-19) reported in California (CA). Using San Francisco Bay Area data collected for the CDC's 14-state COVID-19-Associated Hospitalization Surveillance Network (COVID-NET), we describe trends in disparities during the first five months of the pandemic.

Methods: The California Emerging Infections Program (CEIP) identified COVID-NET cases through active, population-based laboratory surveillance in Alameda, Contra Costa, and San Francisco counties. A case was defined as a resident of the catchment area with a laboratory-confirmed SARS-CoV-2 infection from March 1-July 31, 2020, who was hospitalized within 14 days of specimen collection. Cases were categorized by month of first positive SARS-CoV-2 test. Incidence rates and 95% confidence intervals (CIs) were calculated using population estimates from the CA Department of Finance. Rate ratios were calculated for each race/ethnicity and age group using non-Hispanic White as the reference group, then compared to the published all-site COVID-NET data.

Results: 3,062 patients met the case definition. The mean age was 56 years; 44.4% were Hispanic, followed by non-Hispanic White (15.7%), Asian/Pacific Islander (14.8%), African-American (12.2%), Unknown (11.7%), and Other (1.3%). Case rates for all age and race/ethnicity groups increased from March to July (Fig. 1). The rate ratio among Hispanics of all ages compared to non-Hispanic Whites increased from 2.4 (95% CI 1.8, 3.3) in March to 5.6 (95% CI 4.7, 6.8) in July (Fig. 2). The largest disparities were in those aged 30-49 years, with rates among Hispanics and African-Americans being 13.1 (95% CI 9.8, 17.5) and 5.9 (95% CI 4.1, 8.4) times that of non-Hispanic Whites, respectively (Table 1). Compared to all COVID-NET data, rate ratios for Hispanics compared to non-Hispanic Whites were higher in all age categories, with the largest difference among those 18-49 years (11.7 CEIP vs 9.1 all COVID-Net).

Conclusion: Disparities in COVID-19 hospitalizations are occurring and have increased among multiple racial/ethnic groups. Detailed data on potential exposures, such as household, occupational, and community sources will be useful in addressing disparities among COVID-19 hospitalizations.

Race/ Ethnicity	Asian/Pacific-Islander		African-American		Hispanic		Other		Non-Hispanic, White	
Age Group (years)	Rate	Rate Ratio*	Rate	Rate Ratio*	Rate	Rate Ratio*	Rate	Rate Ratio*	Rate	Rate Ratio*
0-17	0.6	0.6	5.9	6.8	11.3	12.9	1.9	2.2	0.9	1
18-29	13.3	1.3	36.9	3.7	92.1	9.3	6.3	0.6	10.0	1
30-49	**24.2**	**1.7**	**84.3**	**5.9**	**186.6**	**13.1**	**29.8**	**2.1**	**14.3**	1
50-64	67.6	1.7	121.5	3.1	292.0	7.5	91.5	2.4	39.0	1
65-79	86.3	1.3	236.2	3.6	369.5	5.6	93.0	1.4	66.5	1
80+	164.0	1.0	435.6	2.6	472.7	2.8	149.9	0.9	170.9	1
ALL AGES	41.9	1.2	100.2	3.0	158.1	4.7	27.0	0.8	34.0	1

*when compared to non-Hispanic White

Table 1. Cumulative Incidence Rates (cases per 100,000) and Rate Ratios* by Race/Ethnicity and Age Group from March 1 to July 31, 2020 in the San Francisco Bay Area
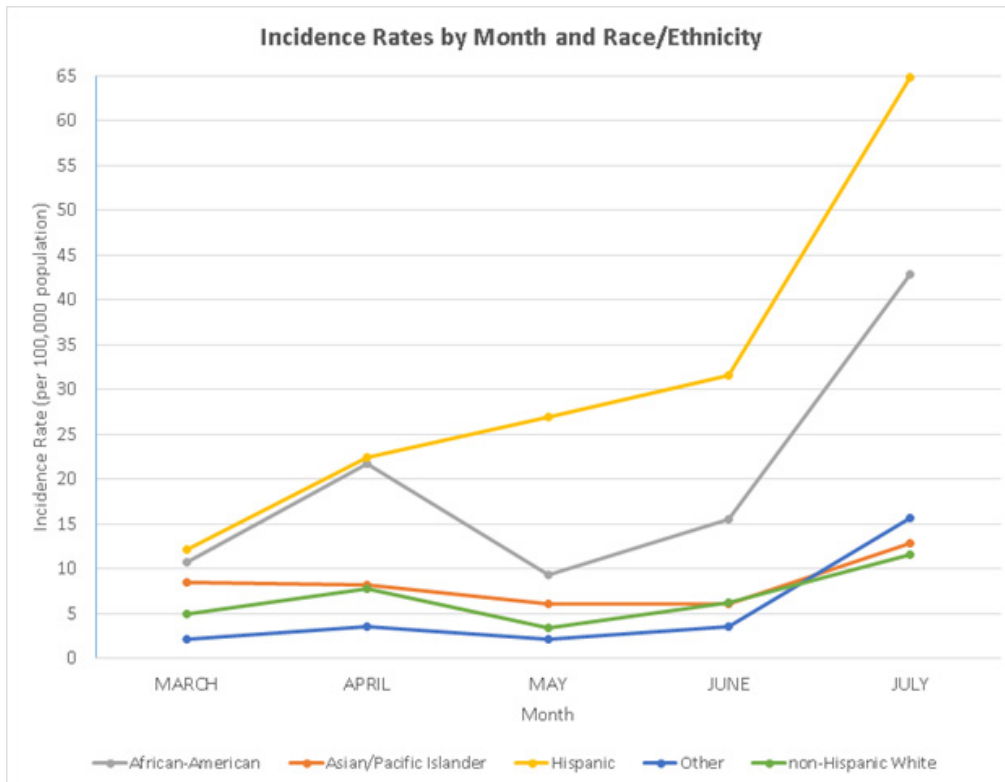
Figure 1. Monthly Incidence Rates of COVID-19-Associated Hospitalizations from March 1 to July 31, 2020 by Race/Ethnicity in the San Francisco Bay Area
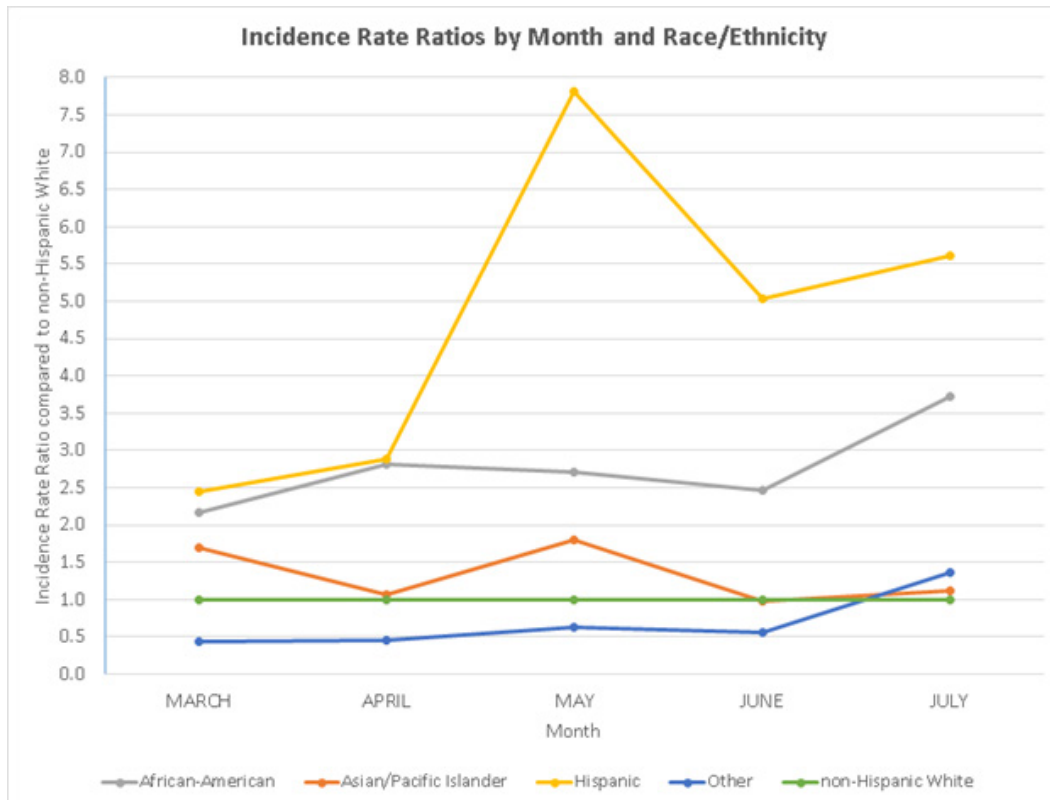

Figure 2. Incident Rate Ratios of COVID-19-Associated Hospitalizations by Race/Ethnicity from March 1 to July 31, 2020 in the San Francisco Bay Area

Contributed by Kareena Hundal, MPH

SARS-CoV-2 and CEIP's Effort in Tackling the Pandemic

The Coronaviridae family of viruses cause respiratory tract infections in humans that range from the mild common cold to severe diseases like SARS, MERS, and COVID-19. The disease spectrum tends to be different depending upon the type of animals these viruses infect and for humans, the health status of the individuals. The viruses can be classified in different ways based on their structure and function. They can be naked or enveloped. The viruses' genetic material can be DNA or RNA. Further classification of these viruses can be based on the number of strands of the genome (single-stranded or double-stranded), the genome's capability to make proteins (positive or negative) and the shape of the genome (linear or circular).

The novel coronavirus, SARS-CoV-2, is enveloped and has a positive single-stranded linear RNA genome. The genome behaves as a messenger RNA, that codes for its viral proteins and allows the viruses entering a host cell to utilize the host cell's machinery. To make more viral particles as the virus jumps through multiple hosts, it multiplies itself millions of times, which is the process known as replication. When errors occur in the genetic material synthesis during replication or changes occur in the genetic material for adaptation to the environment, the genetic material often changes in subsequent generations of viruses. These changes are called mutations. While mutations are changes in the genetic material, not all mutations lead to significant changes in the properties or structure of the viruses. The viruses with different genetic materials but similar properties are called variants. When mutations lead to significant changes in structure and properties of the viruses, such variants are called new strains. New strains can evade host defense mechanisms (natural or vaccine-induced) and can also infect new species and be more efficient in transmission among humans.

Similar to the flu virus, the SARS-CoV-2 virus that causes COVID-19 is constantly changing. Ongoing global characterization of SARS-CoV-2 viruses has shown that different variants have been identified in multiple countries. These variants are spreading globally. Of the variants identified, as of September 2021, the variants of particular concern are the ones that have been first identified in the following countries: B.1.1.7 (Alpha) in the United Kingdom, P.1 (Gama) in Brazil, B.1.351 (Beta) in South Africa, and B.1.617.2 (Delta) in India. Websites (links below) from CDC and CDPH have updated data about the variants of concern in the US and California.

https://www.cdc.gov/coronavirus/2019-ncov/transmission/variant-cases.html
https://www.cdph.ca.gov/Programs/CID/DCDC/Pages/COVID-19/COVID-Variants.aspx

The Delta variant (B1.617.2) has spread rapidly in the United States. In California, this variant accounts for over 97% of SARS-CoV-2 specimens undergoing genetic sequencing as of August 28, 2021. The Delta variant is twice as contagious compared to the earlier variants and can cause more severe illness, with increased likelihood of hospitalization, particularly in unvaccinated individuals. Although rare, fully vaccinated people who get infected (breakthrough infections) can still transmit the Delta variant to others but for a shorter period of time as compared to other variants and as compared to unvaccinated individuals. It is not yet clear whether fully vaccinated people with an asymptomatic Delta variant infection can still transmit the virus. Due to these unknown factors, masks must be worn in areas of high transmission by everyone who is able to do so, including vaccinated individuals.

https://www.cdc.gov/coronavirus/2019-ncov/variants/delta-variant.html

COVID-19 vaccines have been highly effective in preventing severe disease and death, even with the Delta variant. According to data released by CDC on September 10, 2021, the overall effectiveness of vaccination in preventing COVID-19-related hospitalization was 84 % among individuals admitted to the hospital before Delta variant.

https://www.cdc.gov/mmwr/volumes/70/wr/mm7037e3.htm

The California Emerging Infections Program (CEIP) is collaborating with the U.S. Centers for Disease Control and Prevention (CDC) and 13 other sites in the COVID-19-Associated Hospitalization Surveillance Network (COVID-NET). Population based surveillance for COVID-19 hospitalizations is being conducted in Alameda, Contra Costa, and San Francisco counties. The surveillance data are used to determine hospitalization rates, characteristics of cases, clinical characteristics, the severity of disease, and outcomes in people hospitalized with a laboratory-confirmed COVID-19 infection. As a part of COVID-NET activities, CEIP is initiating a pilot project that focuses on collecting and genetic sequencing of SARS-CoV-2 specimens from patients to identify variants of SARS-COV-2. The combination of epidemiologic surveillance data and variant identification will assist CDC in describing the epidemiology of SARS-CoV-2 variants among hospitalized patients. In addition, the information will be helpful in evaluating disease severity and outcomes among hospitalized patients with different variants of the virus in the vaccinated and the non-vaccinated hospitalized patients.

CEIP would not be able to conduct these much-needed public health activities without the dedication and perseverance of our excellent team, as well as the continued support from our local laboratory partners, hospital affiliates and local and state public health colleagues.

Contributed by Utsav Pokharel, MD

The California Emerging Infections Program (CEIP), a Program of Heluna Health, is a joint project of the California Department of Public Health, U.C. Berkeley School of Public Health, and Centers for Disease Control and Prevention, in collaboration with the Alameda County Health Care Services Agency, San Francisco Department of Public Health, Contra Costa County Health Services Department, and the City of Berkeley Health and Human Services Department.

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www.helunahealth.org

www.ceip.us

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