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# Adherence to Public Health Measures Mitigates the Risk of COVID-19 Infection in Older Adults: A Community-Based Study

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## Abstract

**Objective:** To assess the prevalence and characteristics of coronavirus disease 2019 (COVID-19) cases during the reopening period in older adults, given that little is known about the prevalence of COVID-19 after the stay-at-home order was lifted in the United States, nor the actual effects of adherence to recommended public health measures (RPHM) on the risk of COVID-19.

**Patients and Methods:** This was a cross-sectional study nested in a parent prospective cohort study, which followed a population-based sample of 2325 adults 50 years and older residing in southeast Minnesota to assess the incidence of viral infections. Participants were instructed to self-collect both nasal and oropharyngeal swabs, which were tested by reverse transcription polymerase chain reaction–based severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) assay between May 8, 2020, and June, 30, 2020. We assessed the prevalence of COVID-19 cases and characteristics of study subjects.

**Results:** A total of 1505 eligible subjects participated in the study whose mean age was 68 years, with 885 (59%) women, 32 (2%) racial/ethnic minorities, and 906 (60%) with high-risk conditions for influenza. The prevalence of other Coronaviridae (human coronavirus [HCoV]-229E, HCoV-NL63, and HCoV-OC43) during the 2019 to 2020 flu season was 109 (7%), and *none* tested positive for SARS-CoV-2. *Almost all participants* reported adhering to the RPHM (1,488 [99%] for social distancing, 1,438 [96%] for wearing mask in a public space, 1,476 [98%] for hand hygiene, and 1,441 [96%] for staying home mostly). Eighty-six percent of participants resided in a single-family home.

**Conclusion:** We did not identify SARS-COV-2 infection in our study cohort. The combination of participants' behavior in following the RPHM and their living environment may considerably mitigate the risk of COVID-19.

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**O**n March 6, 2020, the United States declared a national emergency for coronavirus disease 2019 (COVID-19) with individual states issuing stay-at-home orders soon thereafter. Two community-based population surveillance studies in Europe reported the prevalence of COVID-19 (1% in a random sample of 2283 residents in Iceland [April 1-4]<sup>1</sup> and 1.2% in 2343 residents of Vo in Italy [February 23-March 8]<sup>2</sup>).

The nationwide issuance of the stay-at-home order significantly reduced the burden and transmission of COVID-19. For example, the orders were associated with a 30% to 49% reduction of cases and a 60% reduction of COVID-19–related deaths during the first 3 weeks of issuance of the orders,<sup>3</sup> and this is true for the state of Minnesota.<sup>4</sup> As the states lifted the stay-at-home orders, resurgence of COVID-19 was observed at a national level.<sup>5</sup> In the state of

Minnesota, the stay-at-home order was enforced from March 27, 2020, through May 18, 2020.

To date, no community-based population surveillance studies have assessed the prevalence of COVID-19 after the stay-at-home orders were lifted in a well-defined population in a mixed rural-urban setting of the United States. In addition, few studies assessed the influence of adherence to the recommended public health measures and social determinants of health (SDH) as factors characterizing COVID-19 cases and healthy individuals in the community. For example, a meta-analysis, which compiled 44 studies for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), severe acute respiratory syndrome—associated coronavirus, or Middle East respiratory syndrome coronavirus primarily in health care settings, reported that adhering to the recommended public health measures including physical distancing, masks, and eye protection reduced the risk of transmission of COVID-19, SARS, or Middle East respiratory syndrome.<sup>6</sup> However, none of these studies assessed such effects in the community. Also, although environmental conditions and SDH have been reported to be one of the major risk factors for the transmission of COVID-19 in the community,<sup>7-11</sup> little is known about the role of SDH in the risk of COVID-19 transmission in the community.

Therefore, we assessed the prevalence of COVID-19 cases and characteristics of study subjects in a community-based sample of adults 50 years and older residing in southeast Minnesota (SEMN) via community-based population surveillance during a period when restrictions for the stay-at-home order were being lifted.

## PATIENTS AND METHODS

The ongoing parent study assessing a viral infection was designed to follow adults 50 years and older residing in SEMN between October 2019 and April 2021. According to US census data in 2010, the age, sex, and ethnic characteristics of Olmsted County residents (89% of the study subjects) were

similar to those of the state of Minnesota and the Upper Midwest<sup>12</sup> except for a large proportion of residents working in the health care industry. We enrolled patients paneled in the primary care practice of Mayo Clinic's campus in Rochester, Minnesota. For this study, we identified all individuals who resided in SEMN (largely from 4 counties including Olmsted, Dodge, Wabasha, and Goodhue) on April 1, 2019, by using electronic health records.

The first COVID-19 case in Olmsted County was reported on March 11, 2020. As of July 1, 2020 (at the end of our present study between May 8, 2020, and June 30, 2020), the total number of COVID-19 cases were 37,210 in the state of Minnesota, 1076 in Olmsted (a population of 158,293), 83 in Dodge (a population of 20,934), 31 in Wabasha (a population of 21,627), and 127 in Goodhue (a population of 46,340) counties. The virus circulation remained relatively constant over the study period in the counties. The study was approved by the Mayo Clinic Institutional Review Board.

The study was designed as a cross-sectional study nested in a parent prospective cohort study, which enrolled a population-based sample of adults 50 years and older residing in SEMN and represents a stratified random sample by age, sex, race/ethnicity, and socioeconomic status (SES). Inclusion/exclusion criteria for the parent study can be found in the [Supplemental Material](#) (available online at <http://www.mayoclinicproceedings.org>). Subjects who agreed to participate in the present study were screened for COVID-19 symptoms and then were instructed to self-collect swabs (regardless of COVID-19 symptoms) of both the anterior nares and oropharynx (throat) using packaged testing kits distributed to consented participants between May 8, 2020, and June 30, 2020. Specimens were returned to the performing laboratory by a prearranged courier service within 24 hours for testing for SARS-CoV-2 by reverse transcription polymerase chain reaction (PCR). The study aims were to assess the prevalence and characteristics of COVID-19 cases on the basis of symptom

status via a questionnaire survey completed by the participants at the time of swab collection. The institutional process for handling positive cases of COVID-19 was to be activated for positive results.

#### **Assessment of Exposure to and Symptoms of COVID-19 by a Survey at the Time of Testing**

We established detailed exposure and symptom screening algorithms on the basis of the institutionally recommended guidelines derived from the Centers for Disease Control and Prevention (see [Supplemental Material](#) for details).

#### **Instructions for Self-collecting Swabs of Anterior Nares and Oropharynx**

We developed instructions and workflow for self-collecting swabs of anterior nares and oropharynx (see [Supplemental Material](#) for details) as reported by others.<sup>13-16</sup> The concordance rates for positive PCR test results for both influenza and respiratory syncytial virus between swabs performed by research staff and self-swabs were 99% (95% CI, 94% to 100%) in our parent study (N=98).

#### **Severe Acute Respiratory Syndrome Coronavirus 2 Testing**

Testing for SARS-CoV-2 was performed according to manufacturer's instructions for the real-time reverse transcription PCR-based cobas SARS-CoV-2 assay (Roche Molecular Systems, Inc.) that has received emergency use authorization from the US Food and Drug Administration. This assay detects the SARS-CoV-2 *ORF1ab* and *E* gene sequences, and test results were reported as target detected, target not detected, presumptive positive (when only the *E* gene sequence was detected), or inconclusive (when PCR inhibition was present).

#### **Other Pertinent Variables**

We also collected both nasal and oropharyngeal swabs in the same fashion as described above during the flu season (from November 1, 2019, through April 30, 2020) when our parent study cohort developed acute

respiratory illnesses (see [Supplemental Material](#) for details of non-SARS-CoV-2 virology, sociodemographic, and clinical data for the parent study).

#### **Data Analyses**

We collated descriptive statistics summarizing characteristics of study subjects. Among those participating in this study, the proportion (prevalence) of subjects with confirmed COVID-19 by PCR and their characteristics were also evaluated.

## **RESULTS**

### **Characteristics of Study Subjects**

Characteristics of study subjects are summarized in [Table 1](#). Of the 2325 adults who participated in the parent study, 1508 participated in this present study and 3 subjects were excluded as 2 subjects did not have reverse transcription PCR results for SARS-CoV-2 and 1 subject had missing survey data. There were no marked differences in demographic and clinical characteristics between those who participated and those who did not (data not shown). The mean age of subjects was 68±9.6 years, and women were represented by 59%. Although minority subjects (32 [2%]) were underrepresented in our study, 313 (21%) were rural residents, 566 (43%) were those with less than 4-year college education, 536 (38%) were those with SES below the median of our study population, 514 (35%) were current or former smokers, and 906 (60%) were those who had high-risk comorbidities for influenza (also for COVID-19).

### **Exposure to SARS-CoV-2 in Study Subjects**

Characteristics of exposure to SARS-CoV-2 cases at the time of testing for SARS-CoV-2 are summarized in [Table 2](#). Only 28 (2%) study subjects reported being exposed to laboratory-confirmed COVID-19 cases at the time of testing, and most exposures were outside the household (27 [96%]). One hundred sixty subjects (11%) reported to have at least 1 clinical symptom at the time of testing. One hundred thirty nine participants (9%) were health care workers and

**TABLE 1. Sociodemographic and Clinical Characteristics of Study Participants (N=1505)<sup>a,b</sup>**

Characteristic	Value
COVID-19 positive by RT-PCR	0 (0)
Age at the time of testing (y)	68 ± 9.6
Sex	
Female	885 (58.8)
Male	620 (41.2)
Race/ethnicity	
American Indian/Alaskan Native	4 (0.3)
Asian	11 (0.7)
Black	6 (0.4)
Hispanic or Latino	11 (0.7)
Non-Hispanic white	1457 (96.8)
Unknown	16 (1.1)
Rurality	
Living in rural area	312 (20.7)
Living in urban area	1193 (79.2)
Socioeconomic status (HOUSES index in quartile)	
1 (lowest)	174 (12.3)
2	362 (25.5)
3	402 (28.3)
4 (highest)	482 (33.9)
Missing	85 (5.6)
Education level	
High school or less	139 (10.6)
Some college	427 (32.4)
Four year college graduate	406 (30.8)
Graduate or professional school	345 (26.2)
Missing	188 (12.5)
Smoking status	
Never	951 (64.9)
Former	477 (32.6)
Current	37 (2.5)
Missing	40 (2.7)
Chronic illness <sup>c</sup>	
Any conditions	908 (60.3)
Hypertension	576 (38.3)
Coronary heart disease	23 (1.5)
Obesity (BMI ≥ 30 kg/m <sup>2</sup> ) 72 (4.8)	
Chronic kidney diseases	119 (7.9)
Chronic liver diseases	32 (2.1)
Immune suppressive conditions	70 (4.7)
Malignant tumor	212 (14.1)
Congestive heart failure	44 (2.9)
Asthma	118 (7.8)
Chronic obstructive pulmonary disease	70 (4.7)

*Continued on next column*

**TABLE 1. Continued**

Characteristic	Value
Obesity (BMI ≥ 30 kg/m <sup>2</sup> ) 72 (4.8), continued	
Any other heart or lung disease	304 (20.2)
Diabetes mellitus	164 (10.9)

<sup>a</sup>BMI, body mass index; COVID-19, coronavirus disease; HOUSES, Housing-based Socioeconomic Index; RT-PCR, reverse transcription polymerase chain reaction.

<sup>b</sup>Data are presented as mean ± SD or as No. (percentage).

<sup>c</sup>Chronic illnesses were defined using electronic health records within 1 y of enrollment in the parent study.

12% had traveled outside Minnesota. Most study subjects (86%)(1,282 [86%]) resided in a single family home, whereas only 216 participants (14%) resided in multiunit dwellings, mobile home communities, or other group quarters.

**Prevalence of COVID-19 and Characteristics Mitigating the Risk of Transmitting COVID-19**

Of the 1505 subjects tested for COVID-19, *none* came back positive during the study period (May through June 2020). For this unexpected study result, given the multiple individual risk factors (eg, prevalent comorbidities and older age) for COVID-19 in our study subjects, we focused our analyses on identifying factors potentially mitigating the risk of transmitting COVID-19, which may have led to a significant reduction in the burden of COVID-19 cases in our study subjects and community. The results are summarized in [Tables 3 and 4](#).

As shown in [Table 3](#), on the basis of self-reported public health measures for COVID-19, *almost all study subjects* followed the recommended public health measures (1,488 [99%] for social distancing, 1,438 [96%] for wearing mask in a public space, 1,476 [98%] for hand hygiene, and 1,441 [96%] for staying home as much as they can).

[Table 4](#) summarizes virology data on the basis of specimens collected during the past flu season (October 2019 through April

**TABLE 2. COVID-19–Related Exposures at the Time of Testing for COVID-19 in Study Participants<sup>a,b</sup>**

COVID-19–related exposure	Variable
Close contact (ever) <sup>c</sup> with laboratory-confirmed COVID-19 cases	
No	1344 (89.4)
Yes	28 (1.9)
Unknown	132 (8.8)
Missing	1 (0.1)
Relationship with COVID-19 cases among those who had contact with COVID-19 cases	
Patient in health care setting	8 (28.6)
Household	1 (3.6)
Coworker	5 (17.9)
Other	14 (50.0)
Self-reported any symptoms within 14 d at the time of screening	
No	1297 (89.0)
Yes	160 (11.0)
Missing	48 (3.2)
Health care provider (eg, physicians, nurses)	
No	1361 (90.7)
Yes	139 (9.3)
Missing	5 (0.3)
Been outside Minnesota in the past 14 d	
No	1312 (87.6)
Yes	185 (12.4)
Missing	8 (0.5)
Been outside the United States in the past 14 d	
No	1504 (100)
Yes	0 (0)
Missing	1 (0.1)
Primary residence	
Single family home	1282 (85.6)
Multiunit dwelling	199 (13.3)
Nursing home	4 (0.3)
Room in home (others home)	0 (0)
Other community dwelling	13 (0.9)
Missing	7 (0.5)

<sup>a</sup>COVID-19, coronavirus disease 2019.<sup>b</sup>Data are presented as No. (percentage).<sup>c</sup>Close contact was defined as being within ~6 ft (2 m) of another person for a prolonged period of time, which could occur while caring for or living with someone else, visiting, socializing, working, or sharing a health care waiting area.

2020) when they had upper or lower respiratory symptoms. One hundred nine (7%) had infections by 1 or more seasonal coronaviruses—HCoV-NL63, HCoV-229E, and HCoV-OC43—during the flu season (October through April), and 7% had influenza A or B. Influenza vaccination within 1 year before enrollment in the parent study and

pneumococcal vaccination ever before enrollment in the parent study were 452 (30%) and 803 (53%), respectively.

## DISCUSSION

To our knowledge, this is the first community-based population surveillance study in a well-defined population after the stay-at-home order was lifted, which comprehensively characterized the study population using clinical, virological, and behavioral data in the United States. Our results indicated that although the prevalence of non-SARS-CoV-2 infections (HCoV-NL63, HCoV-229E, and HCoV-OC43) in our study cohort (7%) was higher than the national average (4%) during the flu season, there were *no* COVID-19 cases among the 1505 study participants during the study period (between May 8, 2020, and June 30, 2020). Despite the large proportion of study subjects affected by risk factors for COVID-19 (eg, high-risk comorbidities for influenza and older age), *almost all* subjects followed the recommended public health measures and 86% of participants resided in a single family housing units instead of high-density housing units (eg, apartments). Although our study results were unexpected and did not have a comparative reference group, they nonetheless provide an important insight into the characteristics of a population protected from COVID-19, where such protection is potentially rooted in adherence to public health recommendations and thus would support the current public health recommendations to be more fully implemented at the community, state, and national levels.

Our study results are unexpected given the reported prevalence of asymptomatic COVID-19 cases in various study settings including the community. For example, 2 community-based population surveillance studies, which are similar to our study, reported the prevalence of COVID-19 (13 [0.6%] in a random sample of 2283 residents in Iceland [April 1-4]<sup>1</sup> and 1.2% in a sample of 2343 residents of Vo (out of 3275) in Italy [February 23-March 8]<sup>2</sup>) and asymptomatic COVID-19 (7 of 13 [54%] in the Iceland



study and 30 of 73 [41%] in the Italian study at the time of testing). As our study results were based on self-swab at home, one might be concerned about systematic performance biases (from subject’s specimen collection) leading to potential false negativity. However, during our study, the concordance rates for both respiratory syncytial virus and influenza between self-swab and swab by research staff were 99%. In addition, although it is not part of the present report, our ongoing work assessing the prevalence of COVID-19 during the flu season using the same processes and methods as the present study indeed found a positive case, suggesting that our study findings are unlikely to be due to performance biases or errors leading to false negativity.

Although our study participants overrepresented the White race as a protective factor for COVID-19 raising a selection bias, it is unlikely to account for our study finding. For example, the prevalence of non-SARS-CoV-2 infections in our study cohort (7%; see Table 4) was higher than the national average (4%) during the flu season.<sup>17</sup> The National Respiratory and Enteric Virus Surveillance System by US laboratories (117 laboratories reported 854,575 HCoV tests) from July 2014 through June 2017 (ie, pre-COVID-19 pandemic) reported that 2.2% were positive for HCoV-OC43, 1.0% for HCoV-NL63, 0.8% for HCoV-229E, and 0.6% for HCoV-HKU1.<sup>17</sup> Also, the prevalence of influenza in our study participants during the COVID-19 pandemic was 7% whereas that of an older cohort during the pre-COVID-19 pandemic was 7%.<sup>18</sup> Our study subjects exhibited a high health care worker rate (9%), which may mean a potentially higher chance of contacting people including patients as essential workers, but also they might have had better personal protective equipment, of which the net effects are unknown but presumably higher for COVID-19.

Our study results provide guidance to communities in terms of how to minimize the spread of COVID-19.

First, as shown in Table 1, our study cohort encompasses population features

**TABLE 3. Proportions of Study Participants Who Followed the Recommended Public Health Measures for COVID-19<sup>a,b</sup>**

Variable	Value (%)
Social distancing by maintaining 6 ft from others when in a public space	
No	11 (0.7)
Yes	1488 (99.3)
Missing	6 (0.4)
Wearing a face covering or mask when in a public space	
No	65 (4.3)
Yes	1438 (95.7)
Missing	2 (0.1)
Practicing hand hygiene	
No	24 (1.6)
Yes	1476 (98.4)
Missing	5 (0.3)
Staying home as much as you can	
No	62 (4.1)
Yes	1441 (95.9)
Missing	2 (0.1)
Self-quarantine if necessary	
No	1247 (84.0)
Yes	237 (16.0)
Missing	21 (1.4)
Wearing gloves if necessary	
No	1185 (78.8)
Yes	318 (21.2)
Missing	2 (0.1)

<sup>a</sup>COVID-19, coronavirus disease 2019.

<sup>b</sup>Data are presented as No. (percentage).

representing both reported protective (eg, predominant White race and higher proportion of women) and risk (eg, high frequency of high-risk comorbidities and older age) factors for COVID-19. Apart from these non-modifiable risk and protective factors, our study results indicated that *almost all study subjects* followed the recommended public health measures for COVID-19, as shown in Table 3. The literature suggested that only about 70% to 90% of people followed social distancing policy, depending on age.<sup>19-21</sup> Given the reported evidence for preventing transmission of SARS-CoV-2,<sup>4,11,22,23</sup> this behavioral feature is likely to be a *key mitigating factor* protecting our study subjects from acquiring COVID-19, even though they were a high-risk population as reflected in influenza vaccination rate (lower than the national average, 60% for those older than 65 years),<sup>24</sup> a history

**TABLE 4. Exposures to Other Viral Infections Between the Past Flu Season (October Through April) and Vaccinations in Study Participants<sup>a,b</sup>**

Variable	Value
Previous vaccination	
Influenza vaccination (past year <sup>c</sup> )	452 (30.0)
Pneumococcal vaccination (ever <sup>d</sup> )	803 (53.4)
Viral infections during the flu season	
Any seasonal coronavirus (HCoV-NL63, HCoV-229E, and/or HCoV-OC43)	109 (7.2)
Seasonal coronavirus HCoV-NL63	24 (1.6)
Seasonal coronavirus HCoV-229E	7 (0.5)
Seasonal coronavirus HCoV-OC43	85 (5.6)
Any influenza	105 (7.0)
Influenza A	91 (6.0)
Influenza B	14 (0.9)

<sup>a</sup>COVID-19, coronavirus disease 2019; HCoV, human coronavirus.

<sup>b</sup>Data are presented as No. (percentage).

<sup>c</sup>Influenza vaccination was defined using electronic health records within 1 y before enrollment in the parent study.

<sup>d</sup>Pneumococcal vaccination was defined using electronic health records before enrollment in the parent study.

of smoking (national average of former smoking in adults, 21% in 2018),<sup>25</sup> socioeconomic background (~40% of subjects were below the median of the Housing-based Socioeconomic Index of the community population measuring SES), and rural residence (similar to the national average, 19.3%).<sup>26</sup> Although the prevalence of exposure to laboratory-confirmed COVID-19 in the general population is not known, in our study only 2% were exposed to laboratory-confirmed cases, presumably because of almost all subjects following the recommendation of avoiding high-risk settings for exposures. Given the current unnecessary skepticism and controversies over current public health recommendations to preventing transmissibility of COVID-19, our study findings based on subjects who were protected from COVID-19 should provide guidance and reinforcement for following the recommended simple public health measures at the community, state, and national levels, as found in recent reports.<sup>6,27</sup>

Second, as shown in Table 2, 86% of our study subjects resided in single family housing units, which is higher than the national average single family homeownership rate (68% in 2020)<sup>28</sup> and could be another important factor mitigating the risk of COVID-19 as one of the important risk

factors for COVID-19 is crowded residential units.<sup>29</sup> This finding highlights the importance of at least 1 social determinant of health, such as housing or even arranging a temporary place for isolation or quarantine of the affected family members for those living in crowded residential units (eg, apartments) beyond testing and tracing to mitigate the risk of COVID-19 transmissibility in the community.<sup>8-10</sup>

Third, as shown in Table 4, among our study subjects, 8% had seasonal coronavirus infections (HCoV-229E, HCoV-NL63, and HCoV-OC43) during the past flu season (October 2019 through April 2020). Recent studies reported lymphocytes from 20% to 50% of unexposed individuals display significant reactivity to SARS-CoV-2 antigen peptide pools,<sup>30-33</sup> and it is hypothesized, but not yet proven, that this might be due to immunity from cross-reactivity to other coronaviruses and have implications for COVID-19 severity, herd immunity, and vaccine development.<sup>34,35</sup> The role of non-SARS-CoV-2 Coronaviridae-associated preexisting immune reactivity in the risk of COVID-19 needs to be determined in future studies.<sup>17</sup>

The main limitations of our study include no inclusion of a concurrent control or reference group and collection of specimens for SARS-CoV-2 testing by self-swab



instead of collection by research staff (ie, possibility of false negativity for our study results). However, we believe that the present single group analysis still provides a valuable insight into the epidemiology of COVID-19 without including an arbitrary reference group. The community prevalence of COVID-19 in this setting is relatively low compared with the national level (68 per 1,000,000 vs 847 per 1,000,000 as of July 1, 2020), so the results may not be generalizable to other study settings. Desirability bias through phone interview might have played a role in the high percentage of adhering to public health measures, although it is unlikely.

## CONCLUSION

Although the prevalence of non-SARS-CoV-2 infections in our study cohort (7%) was higher than the national average (4%) during the flu season, we did not observe subjects in this cohort testing positive for COVID-19. The combination of participants' behavior in following the recommended public health measures and a social determinant of health, such as access to a single family housing, may significantly mitigate the risk of COVID-19. The biological effect of the preceding infections with non-SARS-CoV-2 Coronaviridae and its associated preexisting immune reactivity on the risk of COVID-19 remains to be determined.

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## SUPPLEMENTAL ONLINE MATERIAL

Supplemental material can be found online at: <http://www.mayoclinicproceedings.org>.

Supplemental material attached to journal articles has not been edited, and the authors take responsibility for the accuracy of all data.

**Abbreviations and Acronyms:** COVID-19 = coronavirus disease 2019; HCoV = human coronavirus; PCR = polymerase chain reaction; RPHM = recommended public health measures; SARS-CoV-2 = severe acute respiratory syndrome coronavirus 2; SDH = social determinants of health; SEMN = southeast Minnesota; SES = socioeconomic status

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