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Seroprevalence of SARS-CoV-2 in slums versus non-slums in Mumbai, India

Estimating seroprevalence is crucial for controlling the transmission of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). There are few published serosurveys in low-income and middle-income countries, which comprise over two-thirds of confirmed cases of COVID-19.[1] India has 6·1 million confirmed cases—a fifth of the worldwide total. Socioeconomic disparities and population density might drive disease dynamics in megacities that account for a large share of India's cases. To address these issues, we estimated prevalence in six slum and non-slum communities across three wards (one each from the three zones) of Mumbai, India.

This study was approved by the Indian Government and Institutional Review Boards at participating institutions (appendix p 1). On the basis of power calculations to estimate a 1·5 percentage-point difference in prevalence in a two-sided test with 95% CI in each study site, we aimed to test a total of 8870 individuals from both slum and non-slum communities across three wards: 2249 from Matunga, 1622 from Chembur West, and 576 from Dahisar (appendix p 11). We confined sampling between June 29 and July 19, 2020, to ensure that prevalence did not change substantially during the study. Individuals aged 12 years or older were eligible; those who did not consent or had contraindications to venipuncture were excluded.

Working in eight of the largest slums per ward, we divided each slum into areas covering roughly 400 homes. We sampled 100 homes per area, starting from the centroid of each area and selecting every fourth home. We divided the non-slum areas of each ward into cells of equal size so that sampling 100 persons per cell would meet our target sample size for that ward. Starting from a building at the centre of each cell, we obtained consent from resident associations to recruit one household per floor. We sampled adjacent buildings this way until the target was met or the study period ended.

Surveyors sought voluntary consent from one person per household, rotating through a list of eight demographic groups (female and male participants from four age strata) across households. Our final sample is a function of the population distribution across groups and consent rate per group.

We collected data on household demographics and 5 mL of blood from participants via venipuncture. Samples were tested for IgG antibodies to the nucleocapsid via chemiluminescence by use of Abbott Diagnostics Architect test (Abbott, IL, USA), for which sensitivity ranged from 90·0% (95% CI 74·4–96·5)[2] to 96·9% (89·5–99·5)[3] and specificity from 100·0% (95·4–100·0)[2] to 99·9%.[3]

We estimated the proportion of tests that were positive using Abbott's recommended cutoff (1·4) and score CIs. We used binomial regression of test results on indicators for age and sex to estimate demographic correlates of positive tests. By use of weights that matched the demographic distribution in samples and their respective sites, we calculated age-weighted and sex-weighted proportions. We used data from India's 2011 Census to aggregate adjusted proportions to the slum and non-slum level across wards. We derived adjusted seroprevalence from adjusted proportions using the Rogan–Gladen[4] correction for imperfect test accuracy, assuming low and high estimates of sensitivity and associated specificity. CIs for adjusted proportions are adjusted Wald intervals and those for seroprevalence are unadjusted Wald intervals; statistical comparisons employ Wald tests. We examined sensitivity to the cutoff recommended by Abbott by plotting the distribution of underlying IgG scores and estimated proportions under different cutoffs. We mapped the proportion of positive tests to location using latitude and longitude rounded to 4 significant digits. We analysed 4202 samples from slums and 2702 samples from non-slums (appendix pp 11–13).

Consent rates in slums were comparable with other studies.[1] For instance, in slums in Matunga, we recruited 45·6% of households visited. Based on field notes, over half of the households not sampled were due to homes being empty rather than non-consent. Recruitment fell short of sample-size targets in non-slum areas due to low consent rates. However, such rates cannot be quantified because we do not have information on the number of flats per building.

The proportions of positive tests by age and sex in different sites (appendix p 9) show markedly higher proportions in slums than in non-slums. Regression estimates (appendix p 14) suggest that unadjusted positive proportions were higher among women than among men (slums p<0·001; non-slums p<0·001). Intriguingly, although proportions of positive tests among individuals aged older than 60 years were lower in non-slums (*vs* age 12–24 years; p<0·0223), it was higher in slums (*vs* age 25–39 years; p<0·001).

Reweighting our sample to account for population demographics (appendix p 12) and population in each ward showed that 54·1% of samples in slums and 16·1% of those in non-slums tested positive (appendix p 8)—a significant difference (p<0·001). Our estimates of adjusted seroprevalence are higher in slums (means ranging from 55·1% to 61·4%) than in non-slums (mean ranging from 12·0% to 18·9%) across wards (appendix p 8). Underlying IgG scores are higher and the positive rate is more sensitive to the manufacturer's recommended cutoff in slums than in non-slums (appendix pp 16–17).

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See Online for appendix

Mapping our estimates to locations (appendix p 10) showed sharp differences over distances as little as 100 m. Our estimates of seroprevalence suggest a high reproductive rate of SARS-CoV-2 in slums. Combined with reported COVID-19 cases and numbers of death in sampled wards, our findings suggest a high asymptomatic spread of the infection and an infection fatality rate of 0·076% in slums and 0·263% in non-slums. The higher prevalence in slums could be driven by population density, lower adherence to distancing measures, and poorer hygiene. This stark variation in prevalence within wards also highlights the importance of geographic variation for epidemiological modelling[5] and policy discussions of herd immunity. Although moderate consent rates might bias our estimates of proportions of positive tests, the unadjusted age-weighted and sex-weighted proportions are not significantly different (appendix p 15).

JS reports to the Municipal Corporation of Greater Mumbai. All other authors declare no competing interests. The author list is provided in alphabetical order on first name basis.

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1 Hallal PC, Hartwig FP, Horta BL, et al. SARS-CoV-2 antibody prevalence in Brazil: results from two successive nationwide serological household surveys. *Lancet Glob Health* 2020; **8:** e1390–98.

2 US Food and Drug Administration. EUA authorized serology text performance. https://www.fda.gov/medical-devices/coronavirus-disease-2019-covid-19-emergency-use-authorizations-medical-devices/eua-authorized-serology-test-performance (accessed Oct 25, 2020).

3 Bryan A, Pepper G, Wener MH, et al. Performance characteristics of the Abbott Architect SARS-CoV-2 IgG assay and seroprevalence in Boise, Idaho. *J Clin Microbiol* 2020; **58:** e00941–20.

4 Rogan WJ, Gladen B. Estimating prevalence from the results of a screening test. *Am J Epidemiol* 1978; **107:** 71–76.

5 Britton T, Ball F, Trapman P. A mathematical model reveals the influence of population heterogeneity on herd immunity to SARS-CoV-2. *Science* 2020; **369:** 846–49.