Heterogeneity

There was considerable differences between the study populations, locations, design. It is also likely that the people were infected by several variants of the SARS-CoV-2 virus as the pandemic went on. We see these differences reflected in the strong evidence for statistical heterogeneity of the results. In a post-hoc investigation of heterogentiety, we

METHODS

We conducted post-hoc investigations of heterogeneity to assess how bias and sample size might affect the estimates. We performed six sensitivity analyses in which we included only (1) studies at low risk of selection bias (i.e., the sample was representative of the target population and the non-respondents did not differ from respondents); (2) studies at low risk of information bias (i.e., the symptoms were thoroughly assessed and recorded frequently and/or systematically); (3) studies at low risk of misclassification bias (i.e., the follow up was at least 14 days after exposure and 7 days after testing or until a negative PCR test); (4) studies at low risk of attrition bias (i.e., all participants were followed up for symptom status and included); (5) studies at low risk of bias in every domain (i.e., selection, information, misclassification, and attrition bias); and (6) studies with a sample size of at least 10. We also performed meta-regressions on sample size and individual study precision.

RESULTS

The sensitivity analyses are summarised in table X. The prediction intervals for all estimates were large and there was strong evidence of heterogeneity in all analyses (I2 ≥ 84%). The pooled estimate for the contact and outbreak investigations remained similar (between 0.16 and 0.25) in all scenarios. In analyses 4 (studies at low risk of information bias) and 7 (studies at low risk of bias in every domain), the pooled estimate for the screening studies was much lower than in the main results.

Notes on subgroup analyses

Selection bias

Potential reasons for heterogeneity

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| Population | We include studies from many different populations. While in some studies the target population was the general population of a country or region, many studies included specific subpopulations such as travellers, pregnant women, hospitalised patients, healthcare workers, nursing home residents, nursing home staff, and employees at a workplace. The people in these groups differ systematically from each other in terms of age, income, and health status. Therefore there could be systematic differences in how they are exposed to the SARS-CoV-2 virus, their physical reaction to the virus, and how they report symptoms. |
| Variants | The SARS-CoV-2 virus has many genetic variants and mutations. Some mutations could affect the likelihood of developing symptoms. The studies included have information on several different variants therefore we may not be comparing the same virus. |
| Locations | The studies come from several different countries and regions. There could be cultural differences in how people report symptoms in different places. |
| Reporting | We have extracted data on how symptoms were assessed, recorded, and how long follow-up was. However, this information may not be reliable. In some cases, it was not clear if symptoms were assessed systematically even if a long list was provided in the paper. |
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