1   **Household secondary attack rates of SARS-CoV-2 by variant and vaccination status: an updated**

2   **systematic review and meta-analysis**

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17   Summary: Household secondary attack rates (SARs) were higher for Alpha and Delta variants than

18   previous estimates. SARs were higher to unvaccinated contacts than to partially or fully vaccinated

19   contacts and were higher from unvaccinated index cases than from fully vaccinated index cases.

1

20 **Abstract**

21 We previously reported a household secondary attack rate (SAR) for SARS-CoV-2 of 18.9% through

22 June 17, 2021. To examine how emerging variants and increased vaccination have affected transmission

23 rates, we searched PubMed from June 18, 2021, through January 7, 2022. Meta-analyses used generalized

24 linear mixed models to obtain SAR estimates and 95%CI, disaggregated by several covariates. SARs

25 were used to estimate vaccine effectiveness based on the transmission probability for susceptibility

26 ($VE_{S,p}$), infectiousness ($VE_{I,p}$), and total vaccine effectiveness ($VE_{T,p}$). Household SAR for 27 studies

27 with midpoints in 2021 was 35.8% (95%CI, 30.6%-41.3%), compared to 15.7% (95%CI, 13.3%-18.4%)

28 for 62 studies with midpoints through April 2020. Household SARs were 38.0% (95%CI, 36.0%-40.0%),

29 30.8% (95%CI, 23.5%-39.3%), and 22.5% (95%CI, 18.6%-26.8%) for Alpha, Delta, and Beta,

30 respectively. $VE_{I,p}$, $VE_{S,p}$, and $VE_{T,p}$ were 56.6% (95%CI, 28.7%-73.6%), 70.3% (95%CI, 59.3%-

31 78.4%), and 86.8% (95%CI, 76.7%-92.5%) for full vaccination, and 27.5% (95%CI, -6.4%-50.7%),

32 43.9% (95%CI, 21.8%-59.7%), and 59.9% (95%CI, 34.4%-75.5%) for partial vaccination, respectively.

33 Household contacts exposed to Alpha or Delta are at increased risk of infection compared to the original

34 wild-type strain. Vaccination reduced susceptibility to infection and transmission to others.

Introduction

A previous systematic review and meta-analysis of household transmission of SARS-CoV-2 published through June 17, 2021 reported an overall secondary attack rate (SAR) of 18.9% (95% CI, 16.2%-22.0%) [1]. Emerging variants of concern and increased vaccination have affected transmission rates. Delta (B.1.617.2) became the predominant variant in many parts of the world and Omicron (B.1.1.529) poses additional challenges given its high level of spike mutations and increased potential for transmissibility [2, 3]. Other variants of concern include Alpha (B.1.1.7), Beta (B.1.351), and Gamma (P.1).

Vaccine efficacies against symptomatic disease and death have been demonstrated in randomized controlled trials [4] and vaccine effectiveness has been corroborated in large observational studies in Denmark [5], Israel [6], and the United Kingdom [7]. Household studies can supplement efficacy trials to determine vaccine effectiveness. Vaccine studies based on secondary attack rates (SARs) can be used to estimate the protective effectiveness of a vaccine in vaccinated susceptible contacts compared to unvaccinated susceptible contacts who are exposed to an infected index case ($VE_{S,p}$) [8, 9]. Household studies also enable estimation of vaccine effectiveness in reducing infectiousness ($VE_{I,p}$) by comparing SARs from vaccinated and from unvaccinated index cases to household contacts, which was done for pertussis [10]. Total vaccine effectiveness ($VE_{T,p}$), or the combined effect of direct vaccine protection and indirect vaccine effectiveness, can also be estimated. It is unknown how effective the SARS-CoV-2 vaccines are in reducing susceptibility and infectiousness in the confines of the household where there is prolonged close contact between household members and index cases. Here, we aggregate evidence of household contact tracing studies to evaluate SARs for variants of concern and by index case or contact vaccination status.

Methods

59   This study followed the Preferred Reporting Items for Systematic Reviews and Meta-analyses

60   (PRISMA) reporting guideline using the same definitions and eligibility criteria as our original study [11].

61   Our last review identified studies published through June 17, 2018 [1]. Herein, we searched PubMed and

62   reference lists of eligible studies between June 18, 2021, and January 7, 2022, with no restrictions on

63   language, study design, or place of publication. Search terms were: "SARS-CoV-2", "COVID-19",

64   "severe acute respiratory syndrome", "SARS", "SARS-CoV", "coronavirus", "variant", "vaccination",

65   "immunization", "secondary attack rate", "secondary infection rate", "household", "family contacts",

66   "close contacts", "index case", "contact transmission", "contact attack rate", and "family transmission"

67   (S1 Table). Pre-prints were included. Citations were managed in EndNote 20 (Thomson Reuters, Toronto,

68   CA).

69   Articles with original data that reported at least 2 of the following factors were included: number

70   of infected household contacts, total number of household contacts, and household secondary attack rates.

71   Studies that reported infection prevalence, included populations that overlapped with another included

72   study, and tested contacts using antibody tests only or using antibody tests and another test but did not

73   disaggregate SARs by test were excluded. We first screened studies by titles and abstracts to identify

74   potential studies for inclusion. That reviewer then evaluated full-text articles and selected those that met

75   the inclusion criteria.

76   For this study, we extracted the following information: first author, location, index case

77   identification period, number of index cases, index case symptom status, household/family contact type,

78   test used to diagnose contacts, universal/symptomatic testing, number of tests per contact, and follow-up

79   duration. We also extracted the number of infected household contacts and total number of household

80   contacts and disaggregated by covariates including variant, index case vaccination status, household

81   contact vaccination status, and vaccine type.

82   To examine temporal patterns, we assessed household SARs by index case identification period

83   midpoint. We restricted this analysis to laboratory-confirmed infections and SARs from unvaccinated

84   index cases to unvaccinated household contacts to observe how transmission patterns changed

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85   independent of vaccination. Next, we evaluated household SARs by variants that were reported in ≥2

86   studies regardless of vaccination status and restricted to SARs from unvaccinated index cases to

87   unvaccinated contacts for comparison with SAR estimates from our original analyses of the

88   predominantly wild-type variant [1, 11].

89   Traditionally, vaccine efficacies for reducing susceptibility and infectiousness are estimated as

90    $VE_{S,p} = 1 - SAR_{01}/SAR_{00}$ and $VE_{I,p} = 1 - SAR_{10}/SAR_{00}$ respectively, where SAR_{ij} is the SAR

91   associated with vaccine status i (1=vaccinated, 0=unvaccinated) for the index case and j for the

92   household contact [8]. The total vaccine effectiveness is defined as $VE_{T,p} = 1 - (1 - VE_{S,p})(1 - VE_{I,p})$.

93   We examined SARs by index case vaccination status (unvaccinated, partially vaccinated, fully

94   vaccinated, all) and household contact vaccination status (unvaccinated, partially vaccinated, fully

95   vaccinated, all). The resultant SARs were used to estimate $VE_{S,p}$, $VE_{I,p}$, and $VE_{T,p}$. We created forest

96   plots of SARs by index case vaccination status to all household contacts regardless of vaccination status

97   and restricted to unvaccinated contacts only. We also created forest plots of SARs by contact vaccination

98   status from all index cases regardless of vaccination status and from unvaccinated index cases only.

99   Furthermore, we evaluated SARs by vaccine type and vaccination status for index cases and/or household

100   contacts if reported in ≥2 studies. Finally, we evaluated SARs by variant and vaccination status for index

101   cases and/or household contacts if reported in ≥2 studies.

102

103   *Evaluation of Study Quality and Risk of Bias*

104   To assess study quality and risk of bias, we used the same modified version of the Newcastle-

105   Ottawa quality assessment scale used by Fung *et al*. and in our first analysis [11, 12]. Studies received up

106   to 9 points based on participant selection (4 points), study comparability (1 point), and outcome of

107   interest (4 points). Studies were classified as having high (≤3 points), moderate (4-6 points), and low (≥7

108   points) risk of bias. When at least 10 studies were available, we also used funnel plots and Begg and

109   Mazumdar's rank correlation to evaluate publication bias with significance set at *P*<0.10 [13].

110

111   *Statistical Analysis*

112   We used generalized linear mixed-effects models to obtain SAR estimates and 95% CIs. For

113   comparisons across covariate subgroups (variant, index case vaccination status, household contact

114   vaccination status, vaccine type), study was treated as a random effect and the covariate as a fixed effect

115   moderator. For analyses of SARs by index case vaccination status and contact vaccination status,

116   comparisons between subgroups (e.g., fully vaccinated versus unvaccinated index cases) were restricted

117   to pairwise analyses (studies in which SARs were reported from both fully vaccinated and unvaccinated

118   index cases). For vaccine effectiveness measures, we also used generalized linear mixed models to obtain

119   the logit of the SAR and corresponding sampling variances, which were back-transformed to obtain VE

120   summary estimates and 95%CIs. Heterogeneity was measured using the I^2 statistic, with thresholds of

121   25%, 50%, and 75% indicating low, moderate, and high heterogeneity, respectively. All analyses were

122   performed using the metafor package in R software, version 4.1.2 (R Foundation for Statistical

123   Computing) [14, 15]. Statistical significance was set at a 2-tailed *P*-value≤0.05.

124

125   **Results**

126   We identified 1,291 records (1,281 from PubMed and 10 from reference lists of eligible articles)

127   published between June 18, 2021 and January 7, 2022 (S1 Figure). Forty-eight new studies [16-64] were

128   included in this review (S2 Table), 4 of which were preprints in our previous review that were

129   subsequently published [53-55, 64].

130   Forty-nine new studies[16-64] were combined with 77 studies from our previous review [1] for

131   our analysis of household SAR by study period (5 studies were excluded that did not include laboratory-

132   confirmed infections and 1 that included only asymptomatic index cases), resulting in 126 total studies

133   representing 1,437,696 contacts from 35 countries (see S3 Table for references). Figure 1 demonstrates

134   large heterogeneity in SAR over time but estimates with midpoints after July 2020 are generally higher

135   than the earliest estimates. The household SAR for 27 studies with midpoints in 2021 was 35.8% (95%CI,

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136   30.6%-41.3%), whereas the household SAR for 62 studies with midpoints through April 2020 was 15.7%

137   (95%CI, 13.3%-18.4%). Begg and Mazumdar's rank correlation was statistically significant for studies in

138   2021 (*P*=0.001), but not studies through April 2020 (S2 Figure). Excluding one study in 2021 [54] that

139   had a relatively low SAR improved the funnel plot symmetry and resulted in a SAR of 33.9% (95%CI,

140   29.4%-38.7%) for studies with midpoints in 2021. When restricting to unvaccinated contacts only, the

141   household SAR for studies with midpoints in 2021 was 35.4% (95%CI, 30.0%-41.2%).

142   Eight new studies [23, 28, 31, 39, 50, 52, 55, 56] were combined with 1 study [65] from our

143   previous review for our analysis of Alpha variant. Figure 2 summarizes results from these 9 studies as

144   well as 12 [23, 25, 29, 32, 41, 43, 48, 52, 56, 61-63] and 3 [20, 23, 56] new studies reporting household

145   SARs for Delta and Beta variants, respectively. Estimated mean household SAR for Alpha was 38.0%

146   (95%CI, 36.0%-40.0%), Delta was 30.8% (95%CI, 23.5%-39.3%), and Beta was 22.5% (95%CI, 18.6%-

147   26.8%) (Figure 2). SARs between Alpha/Delta and Delta/Beta were not significantly different, but Alpha

148   was significantly higher than Beta (*P*<0.001). High heterogeneity was found among studies for Delta

149   (98.0%), and low for Alpha (16.7%) and Beta (2.6%). Begg correlation was not significant for studies of

150   Delta (S3 Figure). SARs did not significantly change for Alpha (37.8%, 95%CI, 35.7%-39.9%) (5

151   studies) [23, 28, 31, 50, 55] or Delta (27.0%, 95%CI, 18.5%-37.4%) (7 studies) [23, 29, 32, 43, 48, 61,

152   62] when restricting to studies with low risk of bias (S4 Table). Restricting to unvaccinated contacts only,

153   mean estimated SAR for Delta was 34.9% (95%CI, 26.7%-44.1%) (S4 Figure).

154   Eight studies [24, 26, 34, 39, 43, 48, 54, 62] reported SARs by vaccination status of the index

155   case to all household contacts regardless of vaccination status, seven of which were at low risk of bias and

156   one was moderate (Figure 3). Overall estimated mean SAR was 26.6% (95%CI, 18.7%-36.4%) from

157   unvaccinated (8 studies) [24, 26, 34, 39, 43, 48, 54, 62], 16.2% (95%CI, 8.3%-29.4%) from partially

158   vaccinated (5 studies) [24, 43, 48, 54, 62], and 14.4% (95% CI: 10.5%-19.4%) from fully vaccinated (7

159   studies) [24, 26, 34, 39, 43, 48, 62] index cases to household contacts. For 7 paired studies [24, 26, 34, 39,

160   43, 48, 62], estimated mean SAR from unvaccinated index cases (29.9%; 95%CI, 23.0%-37.7%) was

161   significantly higher than from fully vaccinated index cases (*P*<0.001). For 5 paired studies [24, 43, 48,

7

162   54, 62], SARs were not significantly different from unvaccinated index cases (19.7%; 95%CI, 13.9%-

163   27.3%) than from partially vaccinated index cases. Three studies included only Delta infections [43, 48,

164   62]. Restricting to those 3 studies, we found no significant difference in SAR by index case vaccination

165   status to all contacts regardless of vaccination status. Excluding those 3 studies, the estimated mean SAR

166   was significantly higher from unvaccinated index cases (36.3%; 95%CI, 31.3%-41.6%) than from fully

167   vaccinated index cases (10.7%; 95%CI, 9.0%-12.8%) ($P<0.001$) (4 paired studies) [24, 26, 34, 39], but

168   not from partially vaccinated index cases (2 paired studies) [24, 54]. Restricting to unvaccinated

169   household contacts, SARs were also significantly higher from unvaccinated index cases (30.9%, 95%CI,

170   23.9%-38.8%) than from fully vaccinated index cases (12.0%, 95%CI, 10.0%-14.2%) ($P<0.001$) (4 paired

171   studies) [24, 26, 48, 62], but not from partially vaccinated index cases (3 paired studies) [24, 54, 62] (S5

172   Figure). SARs were generally lower from fully vaccinated index cases regardless of contact vaccination

173   status (S6 Figure). Direct comparison of these studies is compromised, however, because of differences

174   between studies in terms of vaccine types, definition of vaccination status (e.g., time elapsed since

175   vaccination or dosage) (S5 Table), vaccination coverage among contacts, characteristics of the study

176   population, duration of follow-up, diagnostic procedures and tools, location, magnitude of the pandemic,

177   and circulating variants.

178   Figure 4 summarizes 9 studies [24, 26, 34, 38, 43, 48, 56, 62, 63] reporting household SARs by

179   contact vaccination status regardless of index case vaccination status, eight of which were at low risk of

180   bias and two were moderate. Overall estimated mean SAR was 33.8% (95%CI, 28.0%-40.2%) to

181   unvaccinated contacts (9 studies) [24, 26, 34, 38, 43, 48, 56, 62, 63], 23.7% (95%CI, 19.1%-28.9%) to

182   partially vaccinated contacts (6 studies) [24, 38, 43, 48, 56, 63], and 14.1% (95%CI, 10.6%-18.6%) to

183   fully vaccinated contacts (9 studies) [24, 26, 34, 38, 43, 48, 56, 62, 63]. In the 9 paired studies, estimated

184   mean household SARs were significantly higher to unvaccinated contacts than to fully vaccinated

185   contacts ($P<0.001$). For 6 paired studies [24, 38, 43, 48, 56, 63], SARs were significantly higher to

186   unvaccinated contacts (33.1%, 95%CI, 27.8%-38.8%) than to partially vaccinated contacts ($P=0.020$), but

187   SARs were not significantly different to partially vaccinated contacts than to fully vaccinated contacts

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188   (16.6%, 95%CI, 11.9%-22.9%). SARs were consistent when restricting to only unvaccinated index cases

189   (4 studies [24, 26, 48, 62]) (S7 Figure). When restricting to 4 studies [43, 48, 62, 63] that targeted Delta,

190   SARs were also significantly higher to unvaccinated contacts (24.4%, 95%CI, 19.3%-30.4%) than to fully

191   vaccinated contacts (14.3%, 95%CI, 9.3%-21.3%) (*P*=0.027). We also estimated vaccine effectiveness

192   based on the SARs (Table 1).

193   Next, we examined SARs by vaccine type and index case vaccination status regardless of

194   vaccination status of household contacts. SARs were included in 2 studies [26, 39] for BNT162b2 and the

195   mean estimated SAR from fully vaccinated index cases was 8.3% (95%CI, 5.6%-12.1%) compared to

196   35.9% from unvaccinated index cases (95%CI, 34.1%-37.6%) (S8 Figure).

197   We also examined SARs by vaccine type and contact vaccination status regardless of index case

198   vaccination status (3 studies [24, 38, 56]). Mean estimated SAR to household contacts fully vaccinated

199   with Ad26.COV2.S (1 dose) (42.7%, 95% CI: 13.6%-77.9%) (*P*=0.005) or BNT162b2 (15.8%, 95%CI,

200   15.0%-16.7%) (*P*<0.001) was significantly higher than to contacts fully vaccinated with mRNA-1273 (2

201   doses) (6.2%, 95% CI: 2.8%-13.0%) (S9 Figure). Additionally, mean estimated SAR was higher to

202   contacts partially vaccinated with ChAdOx1-S (29.5%, 95% CI: 24.0%-35.7%) than contacts partially

203   vaccinated with mRNA-1273 (17.5%, 95%CI, 13.7%-22.3%) (*P*=0.008). There was no significant

204   difference in SAR to contacts fully vaccinated for ChAdOx1-S and BNT162b2, Ad26.COV2.S, or

205   mRNA-1273; or to contacts partially vaccinated for BNT162b2 and mRNA-1273or ChAdOx1-S.

206

207   **Discussion**

208   We aggregated household studies to examine how variants of concern and vaccination affected

209   household transmission rates of SARS-CoV-2. Household SARs from fully vaccinated index cases were

210   lower than from unvaccinated index cases. Fully and partially vaccinated household contacts were less

211   susceptible to SARS-CoV-2 infection than unvaccinated contacts. SARs for Delta and Alpha were

212   significantly higher than estimates for the original wild-type variant.

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213   Several individual studies included in this analysis reported that full vaccination of index cases

214   significantly reduced the risk of transmission to household contacts [24, 34]. Conversely, other studies

215   included in this analysis reported that vaccination status of the index case was not associated with

216   household contact infection [43, 48]. A meta-analysis allows us to aggregate all the evidence of index

217   case vaccination status from multiple studies and control for differences between the studies. We found

218   lower transmission to household contacts from fully vaccinated index cases than from unvaccinated index

219   cases, but not from partially vaccinated index cases. An observational cohort study from England which

220   included contacts outside the household also reported that two doses of BNT162b2 or ChAdOx1 reduced

221   onward transmission of Delta, but by less than Alpha, and the impact of vaccination against onward

222   transmission waned over time [66]. Our estimate for $VE_{I,p}$ of 56.6% was within the 41%-79% range

223   reported for VE_I from a modeling study that used household data from Israel before Delta became

224   widespread [67]. Potential mechanisms for reduced infectiousness following vaccination include

225   decreases in the respiratory tract viral load and severity of symptoms [68].

226   Fully vaccinated and partially vaccinated contacts had significantly lower SARs than

227   unvaccinated contacts. Other observational studies demonstrated reduced susceptibility to infection

228   among high risk or household contacts vaccinated with BNT162b2 or ChAdOx1 in Scotland [69],

229   BNT162b2 in Sweden [70], and BNT162b2 or mRNA-1273 in Belgium [71]. Studies have reported that

230   full vaccination with mRNA vaccines or ChAdOx1 effectively prevent infection against the original wild-

231   type, Alpha, and Beta variants, but are less protective against infection for Delta [72, 73]. Our estimates

232   of $VE_{S,p}$ (70.3%, 95%CI, 59.3%-78.4%) and $VE_{T,p}$ (86.8%, 95%CI, 76.7%-92.5%) were slightly lower

233   than the age-adjusted VE_S (80.5%, 95%CI, 78.9%-82.1%) and VE_T (88.5%, 95%CI, 82.3%-94.8%)

234   reported by *Prunas et al* [67]. Myriad factors preclude our ability to make direct comparisons of vaccine

235   effectiveness across studies including differences in the study population (e.g., age, comorbidities,

236   serostatus), viral characteristics, vaccine type, time period defining vaccination status, intensity of the

237   epidemic, community behavior, and use of nonpharmaceutical interventions (masks, social distancing)

238 [74]. For example, in this analysis *Singanayagam et al*. [48] included households of any size with

239 contacts ≥5 years, whereas *Gazit et al.* [26] restricted to households with only one contact other than the

240 index case. Moreover, *Ng et al.* in Singapore reported that all identified close contacts were placed under

241 a legally-binding quarantine for 14 days during which they were not allowed to leave their homes [43],

242 whereas contacts in other studies may have had a higher risk of infection outside the household.

243 With the addition of 49 studies since our last review [1], we observed higher SARs in 2021 than

244 earlier in the pandemic. This pattern may be attributed in part to the emergence of more contagious

245 variants. SAR estimates for Alpha (38.0%) and Delta (30.8%) variants were both higher than the overall

246 SAR previously reported (18.9%) for study periods earlier in the pandemic when the wild-type variant

247 was prevalent [1]. Public Health England (PHE), which tracks SARs for variants of concern and variants

248 of interest regardless of vaccination status for index cases and household contacts, found SARs similar for

249 Alpha (10.2%, 95%CI, 10.1%-10.3%) and Delta (10.4%, 95%CI, 10.4%-10.5%) variants [75]. They note,

250 however, that direct comparisons between variants are not valid as vaccination levels and social

251 restrictions in England have varied over this period. Similarly, SARs for Delta and Alpha were not

252 significantly different in this study even when restricting to unvaccinated contacts only, which may be

253 partially attributed to an increase in population immunity consequent to infection. A prospective cohort

254 study [22] and case-control study [76] in England demonstrated increased household transmission for

255 Delta compared to Alpha. Increased transmissibility may be attributed to higher viral loads, shorter

256 incubation periods, and mutations in the spike glycoprotein of the virus, which may confer immune

257 escape potential [77]. Delta infections produced more viral RNA copies per mL than Alpha infections

258 [78], its *in vitro* replication rate is higher than Alpha [79], and its spike protein binds more efficiently to

259 the host cell entry receptor ACE2 protein [80].

260 There was large heterogeneity in SARs over time which may be attributed to variations in study

261 methods, environmental factors, and contact patterns. Comparisons of SARs by vaccination status

262 between studies were also hindered by differences between studies and there were few studies

263 disaggregating SARs by both vaccination status of the index cases and contacts. The studies included in

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264   this review are from contact tracing investigations which are more likely to identify symptomatic index

265   cases than asymptomatic individuals, which could inflate the crude SAR. This may also underestimate the

266   reduction in transmission from vaccination for people infected with Delta [81]. Our analyses by vaccine

267   type and Beta variant were limited to three studies. There was insufficient data to determine vaccine

268   effectiveness for specific subgroups (e.g., by age group) and whether that varied by variant.

269   Household contacts exposed to Delta or Alpha variants are at increased risk of infection

270   compared to the original wild-type variant from Wuhan. Vaccination was demonstrated to reduce

271   susceptibility to infection and infectiousness. The household remains an important venue of transmission

272   for SARS-CoV-2. Other public health measures such as hygiene, increased testing, isolation, and

273   improved ventilation may help limit its spread. Preliminary analyses from PHE demonstrate increased

274   odds of household transmission from Omicron index cases than from Delta index cases, adjusting for

275   index case vaccination status and other factors [82]. A study from Denmark reported higher transmission

276   rates for Omicron than Delta for fully vaccinated individuals but not unvaccinated individuals [61]. The

277   transmissibility and virulence of Omicron is only now being elucidated and other variants are likely to

278   emerge.

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498

499   **Figure Legends**

500

501   **Figure 1. Household secondary attack rates over time (by study midpoint), 126 studies**

502   **(unvaccinated index cases, unvaccinated contacts).** Restricted to laboratory-confirmed results only.

503   The blue line is a loess smoothing line and bands are 95% confidence intervals. Bicolored points

504   represent studies with 2 predominant variants.

505   **Figure 2. Household secondary attack rates for Alpha (B.1.1.7), Delta (B.1.617.2), and Beta**

506   **(B.1.351) variants.**

507   **Figure 3. Household secondary attack rates by index case vaccination status.** All contacts are

508   included regardless of vaccination status. *For Harris *et al.*, most of the vaccinated index cases (93%) had

509   received only the first dose of vaccine and secondary attack rates were not disaggregated by dose.

510   **Figure 4. Household secondary attack rates by contact vaccination status.** All index cases are

511   included regardless of vaccination status.

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Table 1. Estimated vaccine effectiveness (95%CI) estimates from household secondary attack rates.		
Vaccine effectiveness	Full Vaccination	Partial Vaccination
$VE_{I,p}$	56.6% (28.7%-73.6%)	27.5% (-6.4%-50.7%)
$VE_{S,p}$	70.3% (59.3%-78.4%)	43.9% (21.8%-59.7%)
$VE_{T,p}$	86.8% (76.7%-92.5%)	59.9% (34.4%-75.5%)
$VE_{I,p}$: vaccine effectiveness for infectiousness based on the transmission probability p; $VE_{S,p}$: vaccine effectiveness for susceptibility; $VE_{T,p}$: total vaccine effectiveness		

Author, Location	Infected	Total	Estimates	SAR (95% CI)
Alpha (B.1.1.7)				
Julin et al., Oslo/Viken, Norway	13	21		0.62 [0.40, 0.82]
Cohen et al., South Africa	4	7		0.57 [0.19, 0.92]
Watanapokasin et al., Bangkok, Thailand	17	35		0.49 [0.32, 0.65]
Meyer et al., Germany	14	31		0.45 [0.28, 0.63]
Gorgels et al., Netherlands	99	249		0.40 [0.34, 0.46]
Tanaka et al., Osaka Prefecture, Japan	48	124		0.39 [0.30, 0.47]
Lyngse et al., Denmark	637	1719		0.37 [0.35, 0.39]
Loenenbach et al., Germany	34	92		0.37 [0.27, 0.47]
Sachdev et al., San Francisco, USA	2	8		0.25 [0.01, 0.62]
Subgroup Estimate	0.380 (0.360, 0.400)			
Delta (B.1.617.2)				
Hwang et al., Daejeon, South Korea	52	82		0.63 [0.53, 0.74]
Dougherty et al., Oklahoma, USA	42	80		0.52 [0.41, 0.63]
Ministry of Health NZ, New Zealand	902	1976		0.46 [0.43, 0.48]
Watanapokasin et al., Bangkok, Thailand	15	43		0.35 [0.21, 0.50]
Cohen et al., South Africa	115	359		0.32 [0.27, 0.37]
Sachdev et al., San Francisco, USA	5	16		0.31 [0.10, 0.56]
Singanayagam et al., UK	53	205		0.26 [0.20, 0.32]
Yi et al., Jeju, South Korea	11	46		0.24 [0.13, 0.37]
Ng et al., Singapore	169	753		0.22 [0.20, 0.25]
Kang et al., Guangdong, China	38	173		0.22 [0.16, 0.28]
Lyngse et al., Denmark	4923	23156		0.21 [0.21, 0.22]
De Gier et al., Netherlands	1063	7130		0.15 [0.14, 0.16]
Subgroup Estimate	0.308 (0.235, 0.393)			
Beta (B.1.351)				
Cheng et al., Hong Kong	7	25		0.28 [0.12, 0.47]
Cohen et al., South Africa	81	366		0.22 [0.18, 0.27]
Sachdev et al., San Francisco, USA	1	5		0.20 [0.00, 0.68]
Subgroup Estimate	0.225 (0.186, 0.268)			

Secondary Attack Rate

Author, Location	Infected	Total	Estimates	SAR (95% CI)
De Gier et al.1, Netherlands				
Unvaccinated	43069	139802		0.31 [0.31, 0.31]
Partially vaccinated	587	2032		0.29 [0.27, 0.31]
Fully vaccinated	79	706		0.11 [0.09, 0.14]
De Gier et al.2, Netherlands				
Unvaccinated	711	4022		0.18 [0.17, 0.19]
Partially vaccinated	58	735		0.08 [0.06, 0.10]
Fully vaccinated	294	2373		0.12 [0.11, 0.14]
Gazit et al., Israel				
Unvaccinated	1005	2814		0.36 [0.34, 0.37]
Fully vaccinated	21	269		0.08 [0.05, 0.11]
Harris et al., England, U.K.				
Unvaccinated	96898	960765		0.10 [0.10, 0.10]
Partially vaccinated*	567	9363		0.06 [0.06, 0.07]
Layan et al., Israel				
Unvaccinated	261	641		0.41 [0.37, 0.45]
Fully vaccinated	8	43		0.19 [0.08, 0.32]
Meyer et al., Germany				
Unvaccinated	12	22		0.55 [0.33, 0.75]
Fully vaccinated	2	9		0.22 [0.01, 0.56]
Ng et al., Singapore				
Unvaccinated	127	552		0.23 [0.20, 0.27]
Partially vaccinated	13	63		0.21 [0.11, 0.32]
Fully vaccinated	29	138		0.21 [0.15, 0.28]
Singanayagam et al., U.K.				
Unvaccinated	23	100		0.23 [0.15, 0.32]
Partially vaccinated	13	35		0.37 [0.22, 0.54]
Fully vaccinated	17	69		0.25 [0.15, 0.36]
Unvaccinated Estimate	0.266 (0.187, 0.364)			
Partially Vaccinated Estimate	0.162 (0.083, 0.294)			
Fully Vaccinated Estimate	0.144 (0.105, 0.194)			

Secondary Attack Rate

0   0.25   0.5   0.75   1

Author, Location	Infected	Total	Estimates	SAR (95% CI)
De Gier et al.1, Netherlands				
Unvaccinated	32086	91528		0.35 [0.35, 0.35]
Partially vaccinated	573	1917		0.30 [0.28, 0.32]
Fully vaccinated	280	2528		0.11 [0.10, 0.12]
De Gier et al.2, Netherlands				
Unvaccinated	606	2941		0.21 [0.19, 0.22]
Fully vaccinated	457	4189		0.11 [0.10, 0.12]
Gazit et al., Israel				
Unvaccinated	1060	2827		0.37 [0.36, 0.39]
Fully vaccinated	41	545		0.08 [0.05, 0.10]
Layan et al., Israel				
Unvaccinated	247	559		0.44 [0.40, 0.48]
Fully vaccinated	19	122		0.16 [0.10, 0.23]
Martínez–Baz et al., Navarre, Spain				
Unvaccinated	2869	6494		0.44 [0.43, 0.45]
Partially vaccinated	522	2319		0.23 [0.21, 0.24]
Fully vaccinated	1248	7492		0.17 [0.16, 0.18]
Ng et al., Singapore				
Unvaccinated	137	530		0.26 [0.22, 0.30]
Partially vaccinated	17	90		0.19 [0.11, 0.28]
Fully vaccinated	15	133		0.11 [0.06, 0.17]
Sachdev et al., San Francisco, USA				
Unvaccinated	6	18		0.33 [0.13, 0.57]
Partially vaccinated	2	15		0.13 [0.00, 0.36]
Fully vaccinated	12	38		0.32 [0.18, 0.47]
Singanayagam et al., U.K.				
Unvaccinated	15	40		0.37 [0.23, 0.53]
Partially vaccinated	7	39		0.18 [0.07, 0.32]
Fully vaccinated	31	125		0.25 [0.18, 0.33]
Yi et al., Jeju, South Korea				
Unvaccinated	5	18		0.28 [0.09, 0.51]
Partially vaccinated	5	20		0.25 [0.08, 0.47]
Fully vaccinated	1	8		0.12 [0.00, 0.46]
Unvaccinated Estimate	0.338 (0.280, 0.402)			
Partially Vaccinated Estimate	0.237 (0.191, 0.289)			
Fully Vaccinated Estimate	0.141 (0.106, 0.186)			

Secondary Attack Rate

0   0.25   0.5   0.75   1