

Secondary attack rate and superspreading events for SARS-CoV-2

A basic reproduction number, R_0 , of about 2 was estimated for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in Wuhan, China, early in the outbreak.^{1,2} However, this value only captures the average dynamics of transmission; a crucial question for control is whether specific situations and settings might be driving the outbreak. The secondary attack rate (SAR), defined as the probability that an infection occurs among susceptible people within a specific group (ie, household or close contacts), can provide an indication of how social interactions relate to transmission risk.

Increasingly, outbreak investigations are providing insights into the risk of transmission in different settings. Drawing on data from nine recent reports of secondary transmission associated with a specific event such as a meal or holiday visit (table), we estimated 48 secondary infections occurred among 137 attendees. Assuming that all these secondary infections were generated by a single

primary case, which is probable given the short-term nature of the exposure events, would imply a SAR among close contacts of 35% (95% CI 27–44).

If transmission is stratified by contacts within and outside of the household, the relationship between R_0 and household risk is: $R_0 = SAR_H N_H + SAR_C N_C$, where SAR_H and SAR_C are the secondary attack rates within household and wider community (ie, outside household), respectively, and N_H and N_C are the numbers of at-risk contacts made, respectively.³ An infection with a high household SAR but a modest R_0 would therefore suggest transmission is driven by a relatively small number of high-risk contacts. A large household SAR further suggests that between-household transmission risk is lower; otherwise the observed R_0 would be larger.

More data are needed to reliably estimate the true within-household and between-household transmission for SARS-CoV-2; recent reports might be biased towards larger transmission events. However, if it transpires that most at-risk contacts have a close relationship with cases, and superspreading events tend to occur at large gatherings of these close contacts,

measures to reduce infection risk during such gatherings and subsequent tracing of close contacts of cases might have a disproportionate effect on reducing overall transmission.

We declare no competing interests.

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	Date of exposure	Setting	Number at gathering (excluding primary case)	Subsequently infected
Harbin, Heilongjiang, China	Jan 24, 2020	Meal (home)	8	8
Shuangyashan, Heilongjiang, China	Jan 24, 2020	Meal (home)	13	4
Hangzhou, Zhejiang, China	Jan 17, 2020	Meal (unknown location)	1	1
Nanjing, Jiangsu, China	Jan 23, 2020	Meal (unknown location)	8	7
Nanjing, Jiangsu, China	Jan 24, 2020	Meal (restaurant)	14	3
Enshi, Hubei, China	Unknown	Meal (unknown location)	17	2
Enshi, Hubei, China	Unknown	Meal (unknown location)	47	10
Haute-Savoie, France	Jan 24–28, 2020	Chalet	11	5
Hong Kong	Unknown	Meal (home)	18	8

Full details are provided in the appendix.

Table: Summary of severe acute respiratory syndrome coronavirus 2 transmission events where the numbers of people exposed and subsequently infected were known, assuming a single primary case, by location

See Online for appendix
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