

1 Title:

2 Closed environments facilitate secondary transmission of coronavirus disease 2019

3 (COVID-19)

4

5 Authors:

6 Hiroshi Nishiura, M.D., Ph.D.<sup>1,2</sup>

7 Hitoshi Oshitani, M.D., Ph.D.<sup>1,3</sup>

8 Tetsuro Kobayashi, M.D.<sup>1,2</sup>

9 Tomoya Saito, M.D., M.P.H., Ph.D.<sup>1,4</sup>

10 Tomimasa Sunagawa, M.D., Ph.D.<sup>1,5</sup>

11 Tamano Matsui, M.D., Ph.D.<sup>1,5</sup>

12 Takaji Wakita, M.D., Ph.D.<sup>1,5</sup>

13 MHLW COVID-19 Response Team<sup>1</sup>

14 Motoi Suzuki, M.D., Ph.D.<sup>1,5</sup>

15 1. Cluster Intervention Group, Ministry of Health, Labour and Welfare, 2. Graduate

16 School of Medicine, Hokkaido University, 3. Tohoku University Graduate School of

17 Medicine, 4. National Institute of Public Health, 5. National Institute of Infectious

18 Diseases

19 (Correspondence to Hiroshi Nishiura at: Address: Kita 15 Jo Nishi 7 Chome, Kita-ku,

20 Sapporo-shi, Hokkaido 060-8638, Japan, Tel: +81-11-706-5066; Fax: +81-11-706-7819;

21 Email: [nishiurah@med.hokudai.ac.jp](mailto:nishiurah@med.hokudai.ac.jp))

22

23

24

25 Main text:

26 Although the incidence of coronavirus disease 2019 (COVID-19) in China began to  
27 decrease in February 2020,<sup>1</sup> many countries are struggling with containment of the  
28 disease. To effectively reduce the spread of COVID-19, it is vital to identify common  
29 features of cases so as to better understand what factors promote superspreading events,<sup>2</sup>  
30 wherein an extraordinarily large number of secondary transmissions are produced by a  
31 single primary case. Commissioned by the Minister of the Ministry of Health, Labour,  
32 and Welfare of Japan (see Supplementary text), we collected secondary transmission data  
33 with the aim of identifying high risk transmission settings.

34 As of 26 February 2020,<sup>3</sup> we examined a total of 110 cases among eleven  
35 clusters and investigated who acquired infection from whom. The clusters included four  
36 in Tokyo and one each in Aichi, Fukuoka, Hokkaido, Ishikawa, Kanagawa and  
37 Wakayama prefectures. All clusters were associated with close contact in indoor  
38 environments, including fitness gyms, a restaurant boat on a river, hospitals, and a snow  
39 festival where there were eating spaces in tents with minimal ventilation rate.

40 The number of secondary cases generated by each primary case was calculated  
41 using contact tracing data. Of the 110 cases examined, 27 (24.6%) were primary cases  
42 who generated secondary cases. Figure 1 shows the distribution of these transmissions,  
43 of which the mean and variance were 0.6 cases and 2.5 cases<sup>2</sup>, respectively. The odds  
44 that a primary case transmitted COVID-19 in a closed environment was 18.7 times  
45 greater compared to an open-air environment (95% confidence interval [CI]: 6.0, 57.9).

46 If superspreading events are defined as events where the number of secondary  
47 cases generated by a single primary case is greater than the 95th percentile of the

48 distribution (i.e. transmission to three or more persons), then eleven of the 110 cases  
49 (10.0%) were involved in such events. Nine of these events (81.8%) took place in  
50 closed environments, and the odds ratio (OR) of superspreading events in closed  
51 environments was as high as 29.8 (95% CI: 5.8, 153.4).

52         It is plausible that closed environments contribute to secondary transmission of  
53 COVID-19 and promote superspreading events. Closed environments are consistent with  
54 large-scale COVID-19 transmission events such as that of the ski chalet-associated  
55 cluster in France and the church- and hospital-associated clusters in South Korea<sup>4</sup>. Our  
56 findings are also consistent with the declining incidence of COVID-19 cases in China, as  
57 gathering in closed environments was prohibited in the wake of the rapid spread of the  
58 disease.

59         Reduction of unnecessary close contact in closed environments may help  
60 prevent large case clusters and superspreading events. We hope that with such a  
61 reduction in contact the reproduction number of COVID-19 in Japan will be maintained  
62 below 1 and contact tracing will be sufficient to contain disease spread.<sup>5</sup> As the  
63 possibility of confounders and interactions was not assessed in this study, additional  
64 studies must be conducted to verify the importance of closed environments as  
65 facilitators for transmission of COVID-19.

66

67 **Conflict of interest:**

68 We declare that we have no conflict of interest.

69 **Acknowledgement:**

70 We sincerely thank staff of local governments, including health centers and prefectural  
71 institutes of public health, healthcare facilities, and associated companies and

72 organizations for cooperating us to collect and investigate secondary transmission data.

73

74 **References:**

75 1. The Novel Coronavirus Pneumonia Emergency Response Epidemiology Team. Vital

76 Surveillances: The Epidemiological Characteristics of an Outbreak of 2019 Novel

77 Coronavirus Diseases (COVID-19) — China, 2020. China CDC Weekly

78 2020;2(8):113-122.

79 2. Lloyd-Smith JO, Schreiber SJ, Kopp PE, Getz WM. Superspreading and the effect of

80 individual variation on disease emergence. Nature 2005;438:355-359.

81 3. Ministry of Health, Labour and Welfare, Japan. On the novel coronavirus infection.

82 Tokyo: Ministry of Health, Labour and Welfare, 2020. Available online from:

83 [https://www.mhlw.go.jp/stf/seisakunitsuite/bunya/0000164708\\_00001.html](https://www.mhlw.go.jp/stf/seisakunitsuite/bunya/0000164708_00001.html) (accessed

84 on 26 February 2020).

85 4. Promed mail. Subject: PRO/AH/EDR> COVID-19 update (19): China, global, Italy

86 & Iran. imported cases, WHO. Archive Number: 20200226.7029842

87 5. Grantz K, Metcalf JE, Lessler J. Dispersion vs. control. 2020. Available online from:

88 <https://hopkinsidd.github.io/nCoV-Sandbox/DispersionExploration.html> (accessed on

89 26 February 2020).

90

91 **Figure legend**

92 Figure 1. The distribution of the number of secondary cases generated by a single

93 primary case with novel coronavirus (COVID-19). The mean and variance were 0.6

94 cases and 2.5 cases<sup>2</sup>, respectively.

