Institute, we found that the CHUGA-F75 strain was sensitive to gentamicin (MIC = 0.125 mg/L), doxycycline (MIC = 1 mg/L), and ciprofloxacin (MIC = 0.016 mg/L) and resistant to sulfamethoxazole/trimethoprim (MIC = 32 mg/L).

F. marina was described as responsible for systemic disease in fishes (*Lutjanus guttatus*, the cultured spotted rose snapper) in Central America, whereas 4 *F. salimarina* strains have been isolated from costal seawater in Guangdong Province, China, and 1 strain of *F. salina* has been grown from brackish seawater and seaweed off the coast of Galveston, Texas, USA (6–8). To our knowledge, these *Francisella* spp. were not responsible for human infection so far. This report, like previous descriptions of human infections caused by emergent *Francisella* spp., highlights that environmental or fishrelated *Francisella* spp. could be responsible for opportunistic human infections resembling tularemia.

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References

- Hennebique A, Boisset S, Maurin M. Tularemia as a waterborne disease: a review. Emerg Microbes Infect. 2019; 8:1027-42. https://doi.org/10.1080/22221751.2019.1638734
- Versage JL, Severin DDM, Chu MC, Petersen JM. Development of a multitarget real-time TaqMan PCR assay for enhanced detection of *Francisella tularensis* in complex specimens. J Clin Microbiol. 2003;41:5492–9. https://doi.org/ 10.1128/JCM.41.12.5492-5499.2003
- Kugeler KJ, Pappert R, Zhou Y, Petersen JM. Real-time PCR for *Francisella tularensis* types A and B. Emerg Infect Dis. 2006;12:1799–801. https://doi.org/10.3201/eid1211.060629
- Regoui S, Hennebique A, Girard T, Boisset S, Caspar Y, Maurin M. Optimized MALDI TOF mass spectrometry identification of *Francisella tularensis* subsp. *holarctica*. Microorganisms. 2020;8:E1143. https://doi.org/10.3390/ microorganisms8081143
- Meier-Kolthoff JP, Göker M. TYGS is an automated high-throughput platform for state-of-the-art genomebased taxonomy. Nat Commun. 2019;10:2182. https://doi.org/10.1038/s41467-019-10210-3
- Challacombe JF, Petersen JM, Gallegos-Graves LV, Hodge D, Pillai S, Kuske CR. Whole-genome relationships among *Francisella* bacteria of diverse origins define new species and provide specific regions for detection. Appl Environ Microbiol. 2017;83:e02589-16.

- Li L-H, Luo H-M, Feng J-H, Ming Y-Z, Zheng M-L, Deng G-Y, et al. *Francisella salimarina* sp. nov., isolated from coastal seawater. Int J Syst Evol Microbiol. 2020;70:3264–72. https://doi.org/10.1099/ijsem.0.004164
- Soto E, Griffin MJ, Morales JA, Calvo EB, de Alexandre Sebastião F, Porras AL, et al. *Francisella marina* sp. nov., etiologic agent of systemic disease in cultured Spotted Rose Snapper (Lutjanus guttatus) in Central America. Appl Environ Microbiol. 2018;84:e00144-18. https://doi. org/10.1128/AEM.00144-18

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Surveillance of Rodent Pests for SARS-CoV-2 and Other Coronaviruses, Hong Kong

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We report surveillance conducted in 217 pestiferous rodents in Hong Kong for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). We did not detect SARS-CoV-2 RNA but identified 1 seropositive rodent, suggesting exposure to a virus antigenically similar to SARS-CoV-2. Potential exposure of urban rodents to SARS-CoV-2 cannot be ruled out.

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was first identified in Wuhan, China, in late 2019 (1) and soon spread globally. Although its zoonotic origin remains unclear, animal species potentially susceptible to reverse-zoonotic transmission from humans have been identified (e.g., cats, dogs, minks, deer), some of which (e.g., mink) might maintain the virus and pose a risk of future spillback to humans (2,3). Domestic animals and urban wildlife are of particular concern (4) because of their potential exposure to viruses shed within urban environments. Analysis of the angiotensin-converting enzyme 2 (ACE2) receptor across diverse vertebrates suggests a potentially wide breadth of SARS-CoV-2–susceptible mammal host species (5).

The rapid transmission and adaptation of SARS-CoV-2 in humans has been characterized by the evolution of variants of concern (VOCs). Several VOCs, particularly the Alpha (B.1.1.7), Beta (B.1.351), and Gamma (P.1) variants, have convergently evolved an amino acid residue change in the receptor binding domain of the spike protein (N501Y) that was also observed following serial passage of SARS-CoV-2 in BALB/c mice (6). Recent in vitro and in vivo experiments have demonstrated that these VOCs are capable of infecting laboratory rats and mice (7; Montagutelli X et al., unpub. data, https://doi.org/10.1101/2021.03.18.436013). Such evolutionary processes indicate a possible risk for reverse-zoonotic transmission of VOCs into urban rodents.

We hypothesized that locations with positive

SARS-CoV-2 detection in sewage could also serve as key surveillance targets for potential exposure of pestiferous urban rodents to SARS-CoV-2 shed into the environment. We conducted sewage surveillance in Hong Kong to identify hidden infections and localized outbreaks of SARS-CoV-2 (*8*) during the fourth wave of COVID-19 in Hong Kong (Appendix, https://wwwnc.cdc.gov/EID/article/28/2/21-1586-App1.pdf).

During February 3–May 12, 2021, we sampled 217 rodents (*Rattus* spp.), 193 live-trapped rodents and 24 found dead near collection sites (Appendix Table 1). We collected 189 *R. norvegicus* and 28 *R. tan-ezumi* rats from 8 districts, the majority (n = 186) from Sham Shui Po, Yau Tsim Mong, and Kowloon City (Figure), where SARS-CoV-2 positive sewage has been reported.

We found samples from 1,702 swabs and tissues from 217 rats negative for SARS-CoV-2 by real-time quantitative PCR and 15 from 9 rats positive for murine alphacoronaviruses and betacoronaviruses using PCR and phylogenetic analysis (Appendix Table 2, Figure 1). Using ELISA, we identified 1 of 213 rodent serum samples from an R. norvegicus rat collected in Yau Ma Tei seropositive for SARS-CoV-2 (Table; Appendix Figure 2) and 11 samples inconclusive; only 1 of 2 replicates from 8 samples gave a positive absorbance result, and 1 or both replicates from 3 samples gave a borderline absorbance (Table; Appendix Figure 2). The unambiguously positive sample, from rat no. 213, was confirmed positive in surrogate virus neutralization testing (sVNT; 31.7% inhibition), but negative by plaque-reduction neutralization test (PRNT₄₀; <10 titers for 90% reduction). All 11 inconclusive samples were negative (<20% inhibition) by sVNT. As a pre-COVID-19 biological control to test for cross-sensitivity, 50 rodent serum samples collected in 2008 were examined by ELISA; none exhibited an unambiguously positive result.

Our rodent surveillance in Hong Kong revealed potential exposure to SARS-CoV-2, and although viral RNA was not detected, this could be a limitation of sample size if prevalence of active infection was low. One serum sample showed positive ELISA and sVNT results but negative PRNT₉₀ results. Previous research demonstrated that the sVNT used in our study has >98.8% specificity and sensitivity without cross-reaction to alphacoronaviruses and murine betacoronavirus (9). Some sVNT-positive COVID-19confirmed patients did not meet the threshold for positivity by PRNT₉₀ (9). This finding suggests that the seropositive result for SARS-CoV-2 or a closely related virus in the brown rat was unlikely to be attributable to past exposure to murine alphacoronaviruses or betacoronaviruses.

During our study period, SARS-CoV-2 infection was reported in several imported and local human cases in multiple locations and in multiple sewage results. Before December 2020, SARS-CoV-2 locally circulating in Hong Kong predominantly carried 501N with presumably lower rodent infectivity; however, during our study period, Hong Kong reported many imported cases of SARS-CoV-2 variants, including B.1.1.7 and B.1.351, carrying 501Y, which has been demonstrated in mouse experiments to be a critical genetic adaptation (6). These imported cases might disseminate virus into the environment near quarantine hotels, presenting an increased risk of spillover into urban rodent populations and requiring enhanced biosecurity to

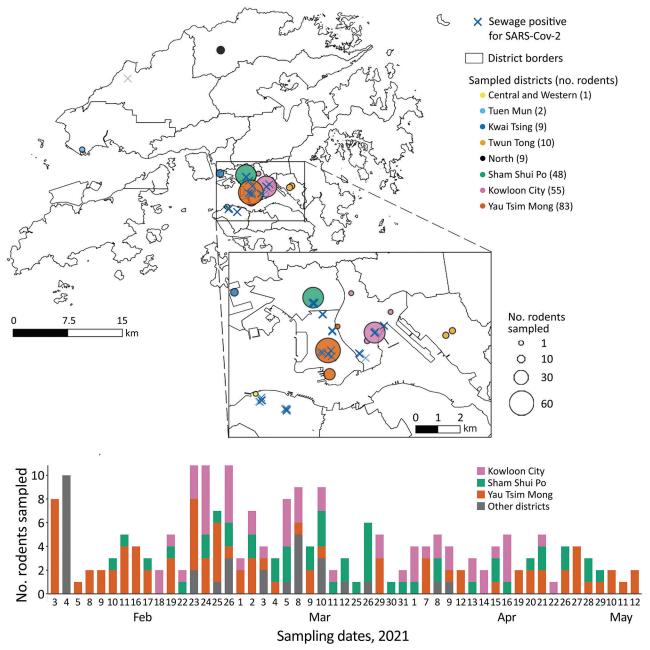


Figure. Surveillance of rodents for SARS-COV-2 conducted February–May 2021 in Hong Kong. A) Sampling sites, with number of rodents sampled and sewage testing positive for SARS-COV-2. Each circle represents a sampling location, color-coded by district and sized proportional to the number of captured rodents. Blue crosses represent locations where sewage was reported positive for SARS-COV-2during January 19–March 30, 2021. B) Number of sampled rodents, by collection dates and district. SARS-COV-2, severe acute respiratory syndrome coronavirus 2

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				ELISA A/CO		sVNT,
Animal code	Rattus species	Collection date	District	1st replicate	2nd replicate	inhibition, %
Rat-027	R. tanezumi	Feb 11	Sham Shui Po	0.019	0.855	1.281
Rat-069	R. norvegicus	Feb 24	Kowloon City	0.837	0.964	0.991
Rat-070	R. norvegicus	Feb 24	Kowloon City	1.199	0.472	-2.128
Rat-073	R. tanezumi	Feb 25	Yau Tsim Mong	1.445	0.033	2.224
Rat-076	R. norvegicus	Feb 25	Sham Shui Po	1.644	0.027	1.136
Rat-089	R. norvegicus	Mar 1	Yau Tsim Mong	1.324	-0.041	1.209
Rat-090	R. norvegicus	Mar 1	Yau Tsim Mong	1.636	-0.027	-0.532
Rat-096	R. norvegicus	Mar 2	Yau Tsim Mong	0.934	-0.007	3.748
Rat-097	R. norvegicus	Mar 2	Yau Tsim Mong	1.592	0.013	-4.666
Rat-098	R. tanezumi	Mar 2	Sham Shui Po	1.920	-0.724	-2.466
Rat-102	R. norvegicus	Mar 3	Kwai Tsing	0.992	-0.499	0.145
Rat-213†	R. norvegicus	May 10	Yau Tsim Mong	13.643	14.497	31.7

Table. Information on rodents with unambiguous (n = 1) or inconclusive (n = 11) positive serum samples in ELISA testing in study of surveillance of rodent pests for severe acute respiratory syndrome coronavirus 2 and other coronaviruses, Hong Kong^{*}

*A/CO was interpreted as negative if <0.9, borderline if 0.9–1.1, and seropositive if >1.1, according to manufacturer instructions. Serum was considered unambiguously positive if both replicates were seropositive. Positive cutoff for sVNT was 20% inhibition, as described elsewhere (9). A/CO, absorbance cutoff; sVNT, surrogate virus neutralization test.

†Positive in both ELISA and sVNT

limit potential exposure to urban rodents or other susceptible animals. Our finding of potential SARS-CoV-2 exposure in a pestiferous rat highlights the need for sustained monitoring of rodent populations to rapidly detect spillover events and subsequently put in place timely interventions (e.g., disinfestation using trapping and pesticide) to prevent potential establishment of new reservoirs.

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References

- Wu F, Zhao S, Yu B, Chen YM, Wang W, Song ZG, et al. A new coronavirus associated with human respiratory disease in China. [Correction in Nature. 2020;580:E7]. Nature. 2020;579:265–9. https://doi.org/10.1038/s41586-020-2008-3
- 2. Chandler JC, Bevins SN, Ellis JW, Linder TJ, Tell RM,

Jenkins-Moore M, et al. SARS-CoV-2 exposure in wild white-tailed deer (*Odocoileus virginianus*). Proc Natl Acad Sci U S A. 2021;118:e2114828118. https://doi.org/10.1073/ pnas.2114828118

- Oude Munnink BB, Sikkema RS, Nieuwenhuijse DF, Molenaar RJ, Munger E, Molenkamp R, et al. Transmission of SARS-CoV-2 on mink farms between humans and mink and back to humans. Science. 2021;371:172–7. https://doi.org/ 10.1126/science.abe5901
- Bosco-Lauth AM, Root JJ, Porter SM, Walker AE, Guilbert L, Hawvermale D, et al. Peridomestic mammal susceptibility to severe acute respiratory syndrome coronavirus 2 infection. Emerg Infect Dis. 2021;27:2073–80. https://doi.org/10.3201/ eid2708.210180
- Damas J, Hughes GM, Keough KC, Painter CA, Persky NS, Corbo M, et al. Broad host range of SARS-CoV-2 predicted by comparative and structural analysis of ACE2 in vertebrates. Proc Natl Acad Sci U S A. 2020;117:22311–22. https://doi.org/10.1073/pnas.2010146117
- Gu H, Chen Q, Yang G, He L, Fan H, Deng YQ, et al. Adaptation of SARS-CoV-2 in BALB/c mice for testing vaccine efficacy. Science. 2020;369:1603–7. https://doi.org/ 10.1126/science.abc4730
- Shuai H, Chan JF, Yuen TT, Yoon C, Hu JC, Wen L, et al. Emerging SARS-CoV-2 variants expand species tropism to murines. EBioMedicine. 2021;73:103643. https://doi.org/ 10.1016/j.ebiom.2021.103643
- Xu X, Zheng X, Li S, Lam NS, Wang Y, Chu DKW, et al. The first case study of wastewater-based epidemiology of COVID-19 in Hong Kong. Sci Total Environ. 2021;790:148000. https://doi.org/10.1016/j.scitotenv.2021.148000
- Perera RAPM, Ko R, Tsang OTY, Hui DSC, Kwan MYM, Brackman CJ, et al. Evaluation of a SARS-CoV-2 surrogate virus neutralization test for detection of antibody in human, canine, cat, and hamster sera. J Clin Microbiol. 2021;59:e02504–20. https://doi.org/10.1128/JCM.02504-20

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