genetic information is not available (*3*). The detection of LCMV lineage I in house mice from this zoo and the previous detection of a closely related strain in another zoo in this part of Germany (*4*) is in line with a biogeographic pattern.

We note that we made no claims toward the biogeography of LCMV lineages or of the wild house mice in the zoo. Rather, the study provided multiple evidence that did not support the subspecies host specificity because both LCMV lineages were found in the same population of wild *Mus musculus domesticus* mice in the zoo. The high similarity between LCMV genome sequences from a primate and a wild house mouse suggests a transmission link between captive and wild animals in the zoo. The primate was born in the zoo, and the zoo did not breed mice and has not fed mice to primates for decades; thus, the route through which LCMV might have entered the zoo remains unknown. More detailed analyses will be necessary to test the association of LCMV lineages with their reservoir hosts. The scarcity of LCMV detection in wild rodent populations and pet rodents (*5*) and the co-detection of both LCMV lineages (*2*,*6*) will continue to pose a challenge to biogeographic hypothesis testing.

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SARS-CoV-2 Incubation Period during Omicron BA.5–Dominant Period, Japan

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To the Editor: Ogata and Tanaka (*1*) estimated the mean incubation period was 2.9 (95% CI 2.6–3.2) days for SARS-CoV-2 strain Omicron BA.1 and 2.6 (95% CI 2.5–2.8) days for Omicron BA.5 during the Omicron-dominant period in Japan. Their earlier study reported a similar mean incubation period of 3.1 days for BA.1 (*2*). Their findings were derived from data collected through contact tracing efforts in Ibaraki Prefecture, Japan, which provided high accuracy in determining exposure time windows.

A potential concern is that their study only included cases that had a single exposure event and a 1-day exposure window. Although this concern was recognized by the authors as a study limitation, we emphasize that those criteria might bias results downward, especially when the disease is widespread. Persons that had longer incubation periods might have more opportunity for contacts or multiple exposure dates; thus, those with shorter incubation periods would be favored for inclusion. A more flexible case-selection approach might reduce bias, even though this approach would require methods to address uncertainty in actual infection timing.

In Taiwan, we collected data from the first 100 local symptomatic cases during the BA.1–dominant period (December 25, 2021–January 18, 2022), which were characterized by intensive case finding and contact tracing (A. Akhmetzhanov et al., unpub. data, https://doi.org/10.1101/2023.07.20.23292983. Among 69 cases with an identified exposure, only 4 had a 1-day exposure window. Using more comprehensive exposure windows, the estimated mean incubation period in Taiwan was 3.5 (95% CI 3.1–4.0) days, longer than Tanaka et al.'s estimates (*1*,*2*) but similar to estimates of 3.5 days from Italy (data collected during January 2022) (*3*) and South Korea (data collected during November–December 2021) (*4*) and estimates from a systematic review (3.6 days) (*5*). The estimates from Japan (*2*) appear to be the shortest periods reported across previously reviewed studies (*5*).

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In Response: We thank Dr. Cheng and colleagues (*1*) for their valuable comments regarding our study of incubation periods observed for the SARS-CoV-2 Omicron BA.5 subvariant in Japan (*2*). As we indicated in our study limitations paragraph, "patient pairs with long incubation periods might be censored during observational periods, and selection bias might result in underestimation" (*2*). We have several other comments to make regarding our study. First, our previous study during the increasing dominance of the Omicron BA.1 subvariant only included patients who had 1 exposure day; we reported incubation periods of 3.0 days for L452R mutation–negative patients and 3.3 days for unvaccinated patients (*3*), which was similar to 3.2 days reported in a study of patients with BA.1 infections who had multiple exposure days (*4*). Therefore, the effect of only including patients who had 1 exposure day should be further evaluated. Second, the incubation period for the BA.5 subvariant in our study was 3.0 days for patients with infectors who were ≤19 years of age and 2.1 days for patients with infectors who were ≥60 years of age (*2*). Because those data are considerably different, adjustment for demographic factors for both infectors and infectees might be necessary to compare incubation periods. Third, although including patients with multiple exposure days decreases selection bias, it might increase uncertainty regarding the actual time of infection (*5*). Therefore, comparing incubation periods in studies that use various methods and evaluating corresponding study limitations are useful for review and discussion.

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