Use of Zoo Mice in Study of Lymphocytic Choriomeningitis Mammarenavirus, Germany

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DOI: http://doi.org/10.3201/eid2912.230334

To the Editor: Mehl et al. (*1*) report high prevalence of lymphocytic choriomeningitis mammarenavirus (LCMV) in mice captured in a zoo in Germany; mice were screened after detection of LCMV in a golden lion tamarin. Similarly high LCMV prevalences have been detected in mouse breeding facilities (MBFs) (*2*). Mehl et al. suggested the zoo LCMV strains do not support the biogeographic hypothesis for LCMV distribution proposed by Fornůsková et al. (*3*). We feel obliged to point out that data collected from zoos cannot inform regarding biogeographic hypotheses, either way.

Fornůsková et al. (*3*) surveyed LCMV in natural (low-prevalence) house mouse populations. Their findings showed that an apparently random distribution of LCMV lineages in human infections, taken from public databases, is resolved by tracing viral origins not to diagnosing institutes, but instead through patient history. With origin tracing, most current data are consistent with the hypothesis that LCMV lineage I (sensu; *4*) originates in the range of *Mus musculus domesticus* mice, whereas LCMV lineage II originates in the range of *M. m. musculus* mice.

Regarding the infected lion tamarin (*1*), numerous LCMV infections have been reported in zoo primates (*5*); zoos in Europe exchange primates, including lion tamarins. Regarding the zoo-captured mice, zoos either maintain their own MBFs or receive live mice from external MBFs to feed reptiles, raptors, and other small carnivores. Presence of MBF mice in zoos breaks origin tracing of wild mouse pathogens because domesticated mice are crosses of 3 wild subspecies; origins of strains used to mass-produce animal food are unregulated. Mehl et al. (*1*) found multiple LCMV strains in a high-density host-pathogen transport hub. Whether such hubs might in the future lead to a breakdown in the current biogeographic pattern of LCMV lineages remains an open question.

The Czech Science Foundation supports the authors' work on house mouse viruses (grant no. 22-32394S).

References

1. Mehl C, Wylezich C, Geiger C, Schauerte N, Mätz-Rensing K, Nesseler A, et al. Reemergence of lymphocytic choriomeningitis mammarenavirus, Germany. Emerg Infect Dis. 2023;29:631–4. https://doi.org/10.3201/eid2903.221822
2. Knust B, Ströher U, Edison L, Albariño CG, Lovejoy J, Armeanu E, et al. Lymphocytic choriomeningitis virus in employees and mice at multipremises feeder-rodent operation, United States, 2012. Emerg Infect Dis. 2014;20:240–7. https://doi.org/10.3201/eid2002.130860
3. Fornůsková A, Hiadlovská Z, Macholán M, Piálek J, Goüy de Bellocq J. New perspective on the geographic distribution and evolution of lymphocytic choriomeningitis virus, Central Europe. Emerg Infect Dis. 2021;27:2638–47. https://doi.org/10.3201/eid2710.210224
4. Albariño CG, Palacios G, Khristova ML, Erickson BR, Carroll SA, Comer JA, et al. High diversity and ancient common ancestry of lymphocytic choriomeningitis virus. Emerg Infect Dis. 2010;16:1093–100. https://doi.org/10.3201/eid1607.091902
5. Childs JE, Klein SL, Glass GE. A case study of two rodent-borne viruses: not always the same old suspects. Front Ecol Evol. 2019;7:35. https://doi.org/10.3389/fevo.2019.00035

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DOI: http://doi.org/10.3201/eid3001.231521

In Response: Gouy de Bellocq et al. question in their letter whether data from zoos can be used to test a biogeographic hypothesis regarding lymphocytic choriomeningitis mammarenavirus (LCMV) (*1*). We agree that this should be done with caution because zoos may act as hubs for pathogen transfer through captive animal transfer and the use of feeder rodents. As we stated in our article (*2*), the occurrence of LCMV in house mice in western Germany was already described in the 1960s, although

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.

References

1. Goüy de Bellocq J, Baird SJE, Fornůsková A. Use of zoo mice in study of lymphocytic choriomeningitis mammarenavirus, Germany. Emerg Infect Dis. 2024;30:XXX. https://doi.org/10.3201/eid3001.230334
2. Mehl C, Wylezich C, Geiger C, Schauerte N, Mätz-Rensing K, Nesseler A, et al. Reemergence of lymphocytic choriomeningitis mammarenavirus, Germany. Emerg Infect Dis. 2023;29:631–4. https://doi.org/10.3201/eid2903.221822
3. Ackermann R, Bloedhorn H, Küpper B, Winkens I, Scheid W. Über die Verbreitung des Virus der lymphocytären Choriomeningitis unter den Mäusen in Westdeutschland. *Zentralblatt* für *Bakteriologie, Parasitenkunde.* I nfektionskrankheiten und Hygiene. 1964;194:407–30.
4. Asper M, Hofmann P, Osmann C, Funk J, Metzger C, Bruns M, et al. First outbreak of callitrichid hepatitis in Germany: genetic characterization of the causative lymphocytic choriomeningitis virus strains. Virology. 2001;284:203–13. https://doi.org/10.1006/viro.2001.0909
5. Fornůsková A, Hiadlovská Z, Macholán M, Piálek J, de Bellocq JG. New perspective on the geographic distribution and evolution of lymphocytic choriomeningitis virus, central Europe. Emerg Infect Dis. 2021;27:2638–47. https://doi.org/10.3201/eid2710.210224
6. Pankovics P, Nagy A, Nyul Z, Juhász A, Takáts K, Boros Á, et al. Human cases of lymphocytic choriomeningitis virus (LCMV) infections in Hungary. Arch Virol. 2023;168:275. https://doi.org/10.1007/s00705-023-05905-4

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

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DOI: https://doi.org/10.3201/eid3001.230208

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*).