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Contact networks of small mammals highlight potential transmission foci of Lassa mammarenavirus

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Introduction

Lassa fever, caused by *Mammarenavirus lassaense* (LASV), is an endemic zoonosis in several West African countries. Human infections primarily arise from rodent-to-human transmission, with *Mastomys natalensis*, a synanthropic species, serving as the principal reservoir. In Sierra Leone, small-mammal communities vary across land use gradients, potentially shaping LASV transmission risk in human populations. However, the extent to which anthropogenic environments facilitate small-mammal interactions conducive to viral transmission remains poorly understood.

Methods

We conducted small-mammal sampling over 43,266 trap nights, detecting 684 rodents and shrews in the LASV-endemic Eastern Province of Sierra Leone. To assess potential for within- and between-species transmission, we constructed space-sharing networks based on co-trapping within species-specific radii informed by home range estimates. These networks approximated shared space use rather than direct interaction, allowing comparison of potential encounter patterns across habitats.

Results

Small-mammal communities in agricultural settings had greater species richness and were more connected than those in villages and forests, although overall space-sharing rates did not differ substantially. Network topology varied by land use, with greater modularity in village networks. Notably, space sharing among *M. natalensis* individuals was more frequent in agricultural settings than in villages, suggesting that land use may modulate opportunities for intra-specific viral transmission. LASV seroprevalence across the small-mammal community was 5.7%,

with antibodies detected in nine species. We found no major differences in seroprevalence by land use or network complexity.

Conclusion

These findings underscore the importance of cross-habitat surveillance to understand host ecology and LASV transmission. Accounting for species-specific space use and habitat-dependent interaction structures is crucial for identifying key hosts and spillover settings.