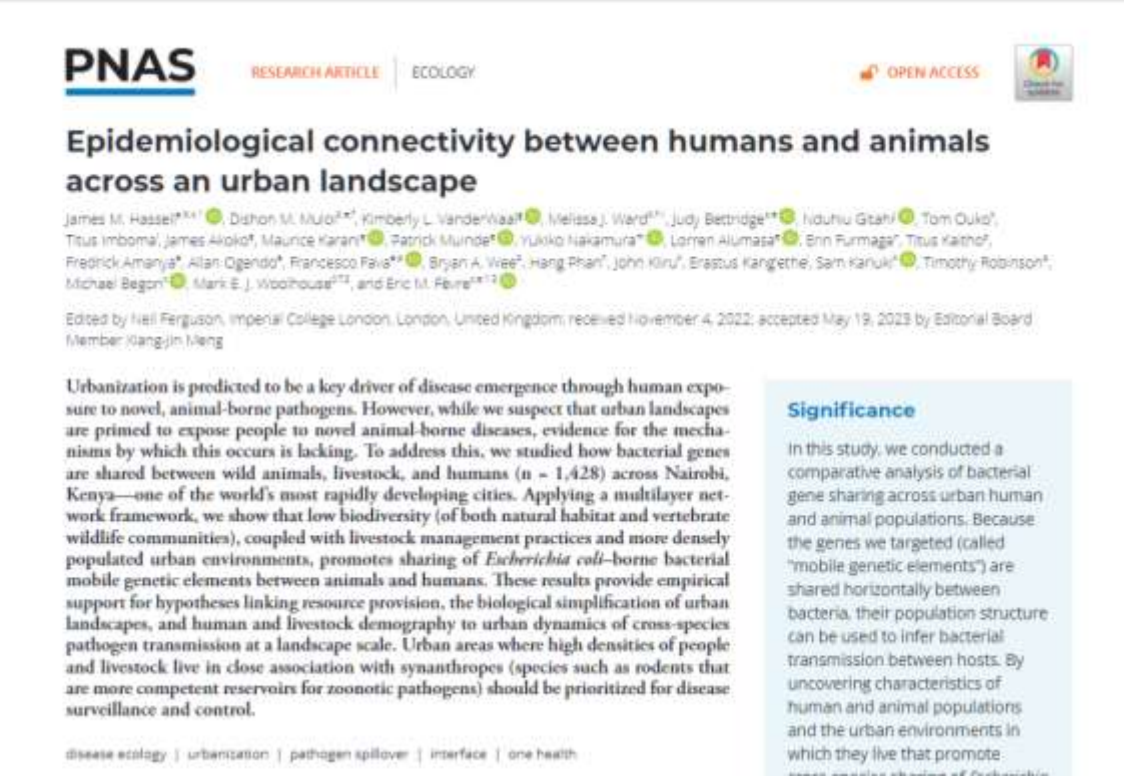

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Epidemiological connectivity between humans and animals across an urban landscape

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Urbanization is predicted to be a key driver of disease emergence through human exposure to novel, animal-borne pathogens. However, while we suspect that urban landscapes are primed to expose people to novel animal-borne diseases, evidence for the mechanisms by which this occurs is lacking. To address this, we studied how bacterial genes are shared between wild animals, livestock, and humans ($n = 1,428$) across Nairobi, Kenya—one of the world's most rapidly developing cities. Applying a multilayer network framework, we show that low biodiversity (of both natural habitat and vertebrate wildlife communities), coupled with livestock management practices and more densely populated urban environments, promotes sharing of *Escherichia coli*–borne bacterial mobile genetic elements between animals and humans. These results provide empirical support for hypotheses linking resource provision, the biological simplification of urban landscapes, and human and livestock demography to urban dynamics of cross-species pathogen transmission at a landscape scale. Urban areas where high densities of people and livestock live in close association with synanthropes (species such as rodents that are more competent reservoirs for zoonotic pathogens) should be prioritized for disease surveillance and control.

disease ecology | urbanization | pathogen spillover | interface | one health

Significance

In this study, we conducted a comparative analysis of bacterial gene sharing across urban human and animal populations. Because the genes we targeted (called "mobile genetic elements") are shared horizontally between bacteria, their population structure can be used to infer bacterial transmission between hosts. By uncovering characteristics of human and animal populations and the urban environments in which they live that promote