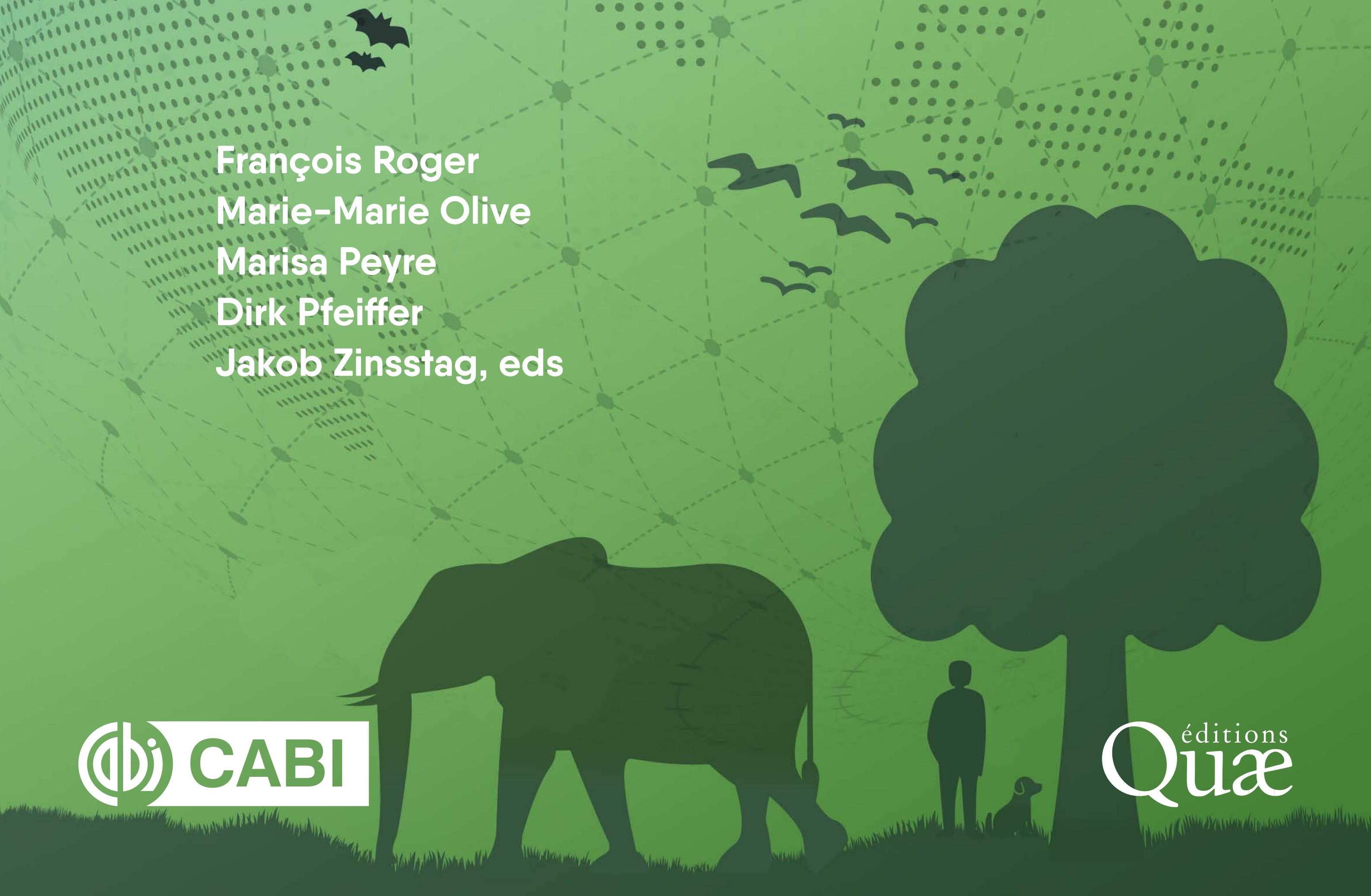
ONE HEALTH ATLAS

François Roger
Marie-Marie Olive
Marisa Peyre
Dirk Pfeiffer
Jakob Zinsstag, eds



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One Health and the spread of antibiotic resistance

Adrien Rieux, Noellie Gay,
Éric Cardinale, Étienne Loire

Escherichia coli that produces extended-spectrum β-lactamase (ESBL-Ec) is a pathogen that poses a threat to healthcare and is a crucial marker for epidemiological surveillance of antimicrobial resistance (AMR). While the epidemiology and transmission of ESBL-Ec has been widely investigated in animals, humans and the environment, global studies performed on several of these reservoirs simultaneously are rare, particularly in low- and middle-income countries in which the threat of AMR is of major concern.

To assess the risk of resistance genes being transmitted between bacteria from different sources, we collected 1,454 bacterial isolates from various human and animal hosts (humans, pigs, chicken, ducks, cattle, etc.) and the environment (drinking and irrigation water) in rural Madagascar. The isolates underwent whole genome sequencing and were analysed using cutting-edge phylogenomic methods to characterize population genetic structure and infer presumed transmission events.

ESBL-Ec were detected in almost 40% of the samples taken (Figure 1), regardless of the source. By sequencing and analysing the core genomes of 510 strains, we reconstructed their phylogenetic relationships, identified the genes that confer AMR, and estimated transmission events. Our results revealed a prominent level of bacterial genetic diversity within a limited geographical zone, including new, previously unknown groups of ESBL-Ec. The most unexpected finding, in clear contrast with previous observations made in Global North countries (in this case, England), was the ease with which bacterial and resistance genes seemed to circulate between different hosts and source compartments. Transmission events were so frequent that our reconstructed phylogeny showed a total lack of association between genomic diversity and compartment structure (Figure 2).

This study, one of the first performed on such a large scale in a country in the Global South, illustrates the need for an integrated approach encompassing human, animal and environmental health to combat a phenomenon as complex as AMR. In-depth knowledge of the various mechanisms that lead to the emergence and dissemination of AMR on a global level, in both the Global South and Global North, is vital for building appropriate, effective surveillance and control strategies.

References

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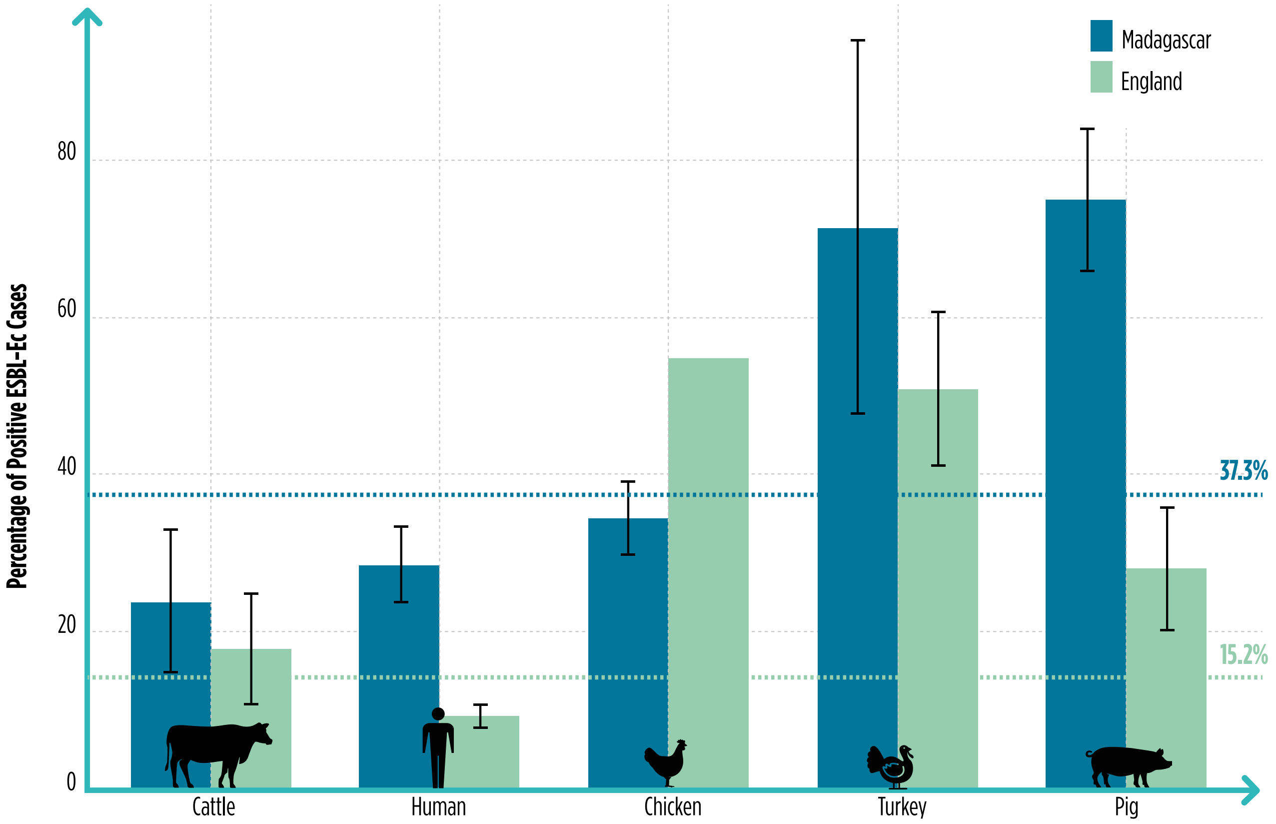

Figure 1. Significant differences were observed in humans, chickens and pigs (no significant difference in cattle or turkeys) may be due to variations in healthcare, veterinary and agricultural practices, antibiotic usage, or environmental factors between Madagascar and England. New epidemiological studies should be conducted to confirm or refute these hypotheses about the different ESBL-Ec profiles between Madagascar and England.

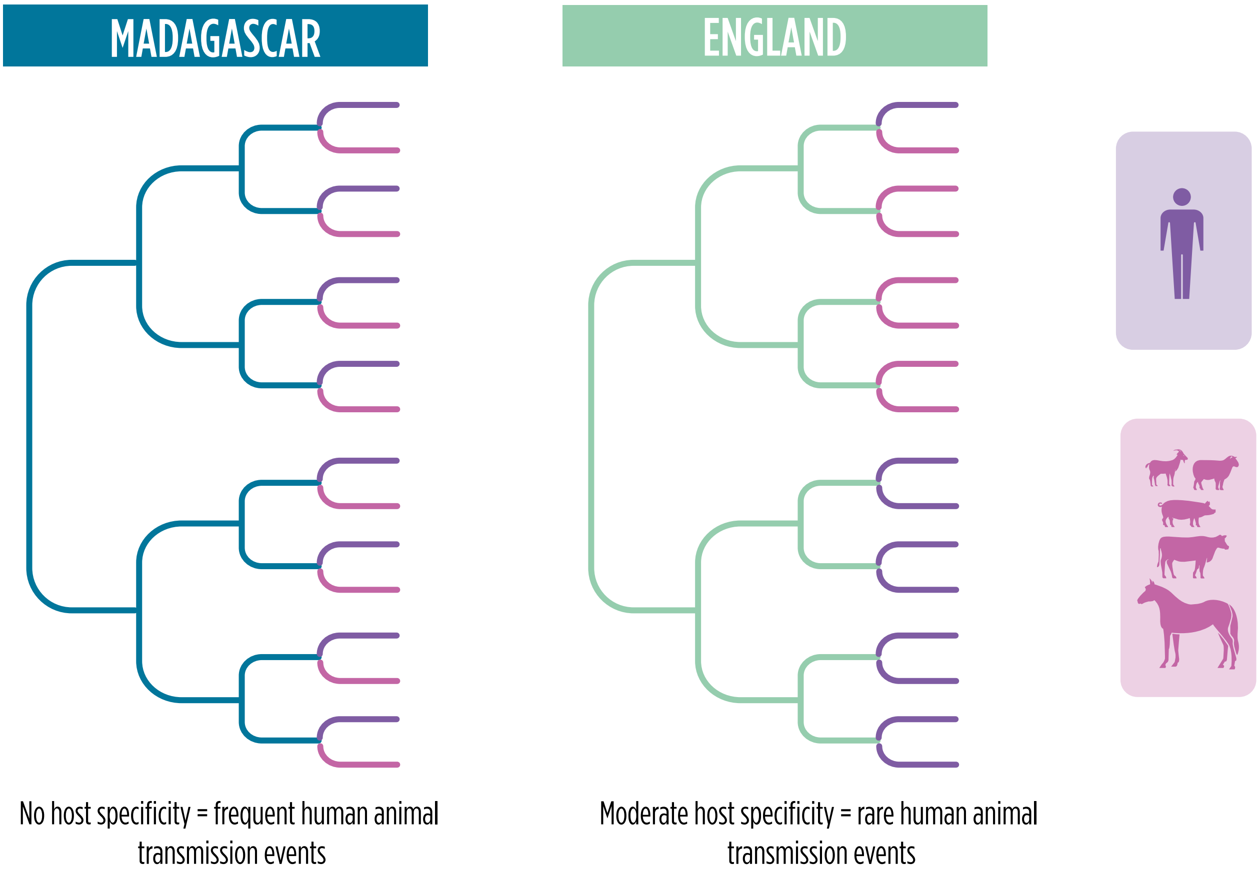

Figure 2. Schematization of global phylogeny obtained from ESBL-Ec strains sampled in Madagascar (left panel) and England (right panel). Hosts are indicated in violet (humans) and pink (animals).