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Resumo	The epidemiology of antimicrobial resistance (AMR) is complex, with multiple interfaces (human-animal-environment). In this context, One Health surveillance is essential for understanding the distribution of microorganisms and antimicrobial resistance genes (ARGs). This report describes a multicentric study undertaken to evaluate the bacterial communities and resistomes of food-producing animals (cattle, poultry, and swine) and healthy humans sampled simultaneously from five Brazilian regions. Metagenomic analysis showed that a total of 21,029 unique species were identified in 107 rectal swabs collected from distinct hosts, the highest numbers of which belonged to the domain *Bacteria*, mainly *Ruminiclostridium* spp. and *Bacteroides* spp., and the order *Enterobacterales*. We detected 405 ARGs for 12 distinct antimicrobial classes. Genes encoding antibiotic-modifying enzymes were the most frequent, followed by genes related to target alteration and efflux systems. Interestingly, carbapenemase-encoding genes such as $bla_{\text{AIM-1}}$, $bla_{\text{CAM-1}}$, $bla_{\text{GIM-2}}$, and $bla_{\text{HMB-1}}$ were identified in distinct hosts. Our results revealed that, in general, the

	bacterial communities from humans were present in isolated clusters, except for the Northeastern region, where an overlap of the bacterial species from humans and food-producing animals was observed. Additionally, a large resistome was observed among all analyzed hosts, with emphasis on the presence of carbapenemase-encoding genes not previously reported in Latin America.
Fomento	CAPES e CNPq