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Landscape fragmentation and rural land-use drive antimicrobial resistance gene diversity in a wild primate

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Antimicrobial resistance is a global health concern caused by the overuse of antimicrobials and environmental contamination. Wildlife exposed to disturbed environments can acquire resistant microorganisms, indicating environmental ARG (antimicrobial resistance genes) contamination and serving as ARG reservoirs. Here, we used a landscape-scale approach to test whether metrics of anthropogenic disturbance influence the abundance and diversity of ARG in brown howler monkeys (*Alouatta guariba*). We collected 377 fecal samples from 20 groups of howler monkeys. We extracted total DNA from pooled samples and performed shotgun metagenomic sequencing. We used the *SqueezeMeta* pipeline for metagenomic assembly and ARG identification based on the CARD database. We extracted landscape metrics representing habitat loss and fragmentation using ArcGIS. We applied generalized linear models to test the influence of landscape disturbance on ARG metrics. We identified 441 ARGs, mainly associated with aminoglycoside, carbapenem, and cephalosporin resistance. ARG richness increased with higher agricultural cover, habitat fragmentation, and water bodies in the landscape. ARG diversity and evenness were positively associated with pasture cover and water bodies. Landscapes with rural interfaces and higher fragmentation tend to increase the richness and diversity of ARGs in howler monkeys. Water bodies and pasture cover likely act as important environmental pathways for ARG dissemination.

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Professional Status of the Speaker

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Junior Scientist Status

Yes, I am a Junior Scientist.

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