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Predicting environmental susceptibility to antimicrobial-resistant bacterial invasion using biodiversity and phylogenetic structure

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Antimicrobial resistance (AMR) can spread through freshwater systems when resistant bacteria enter river biofilms, yet predicting which communities resist such introductions remains difficult. Biotic resistance theory predicts lower invasion success in more diverse communities, but whether this applies to natural biofilms under change is unclear.

We collected epilithic biofilms from 30 river sites across seven European countries and transferred them into standardized flumes. A model antibiotic-resistant *E. coli* was introduced, and its persistence quantified over 14 days. Diversity was characterized at collection, after acclimation, and maturation.

Using leave-one-out cross-validated models, we tested whether resistance could be predicted from diversity, phylogenetic structure, and diversity change during ecosystem transfer. In established flume biofilms, resistance was best explained by Shannon diversity and mean phylogenetic distance to the invader, supporting niche saturation and phylogenetic limiting similarity. During river-to-flume transfer, resistance depended on initial diversity and proportional diversity loss, indicating that community stability shapes invasion outcomes.

These findings show that freshwater biofilm invasion is structured by measurable community properties. Biodiversity and phylogenetic structure may help identify systems vulnerable to resistant bacterial colonization, supporting One Health surveillance and environmental AMR risk assessment.

Keywords

Antimicrobial resistance; freshwater biofilms; microbial invasion; biodiversity; phylogenetic structure; biotic resistance; One Health; environmental surveillance

Registration ID

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Professional Status of the Speaker

Senior Scientist

Junior Scientist Status

No, I am not a Junior Scientist.

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