

## Effect of atmospheric pollution on the taxonomic composition, diversity, and antibiotic resistance of the culturable bacterial community of the aerobiome in the Región Metropolitana of Chile.

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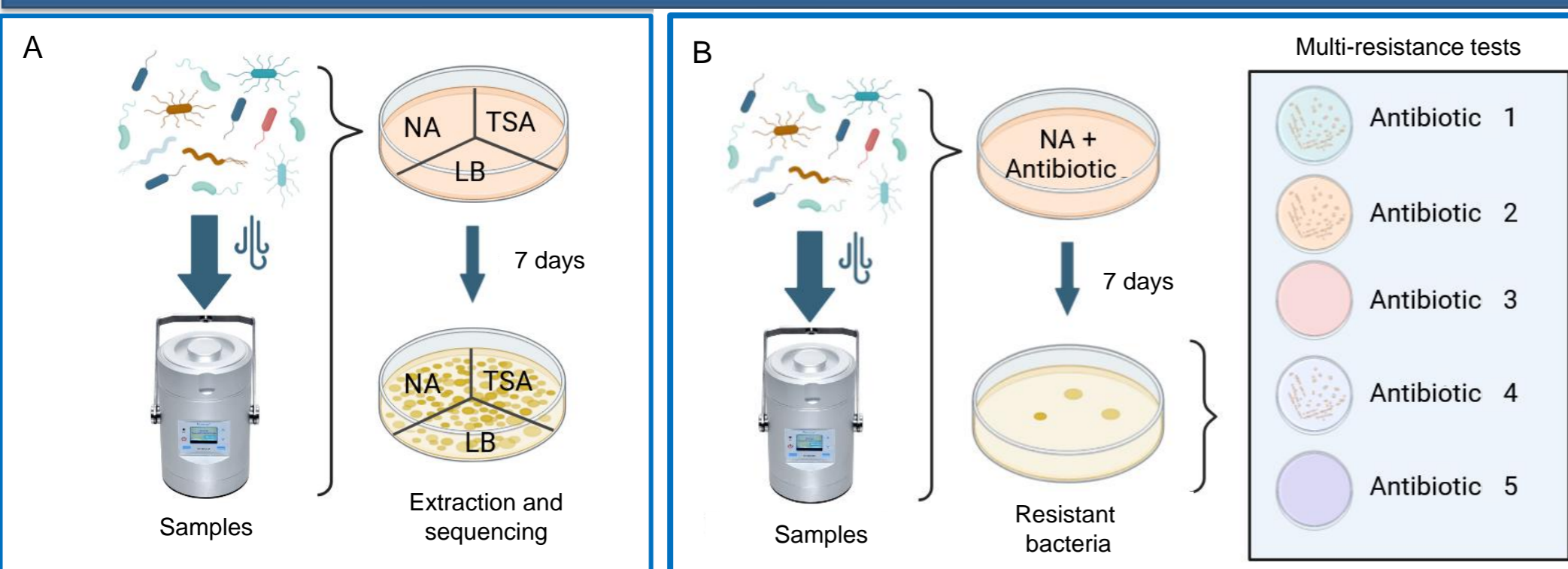
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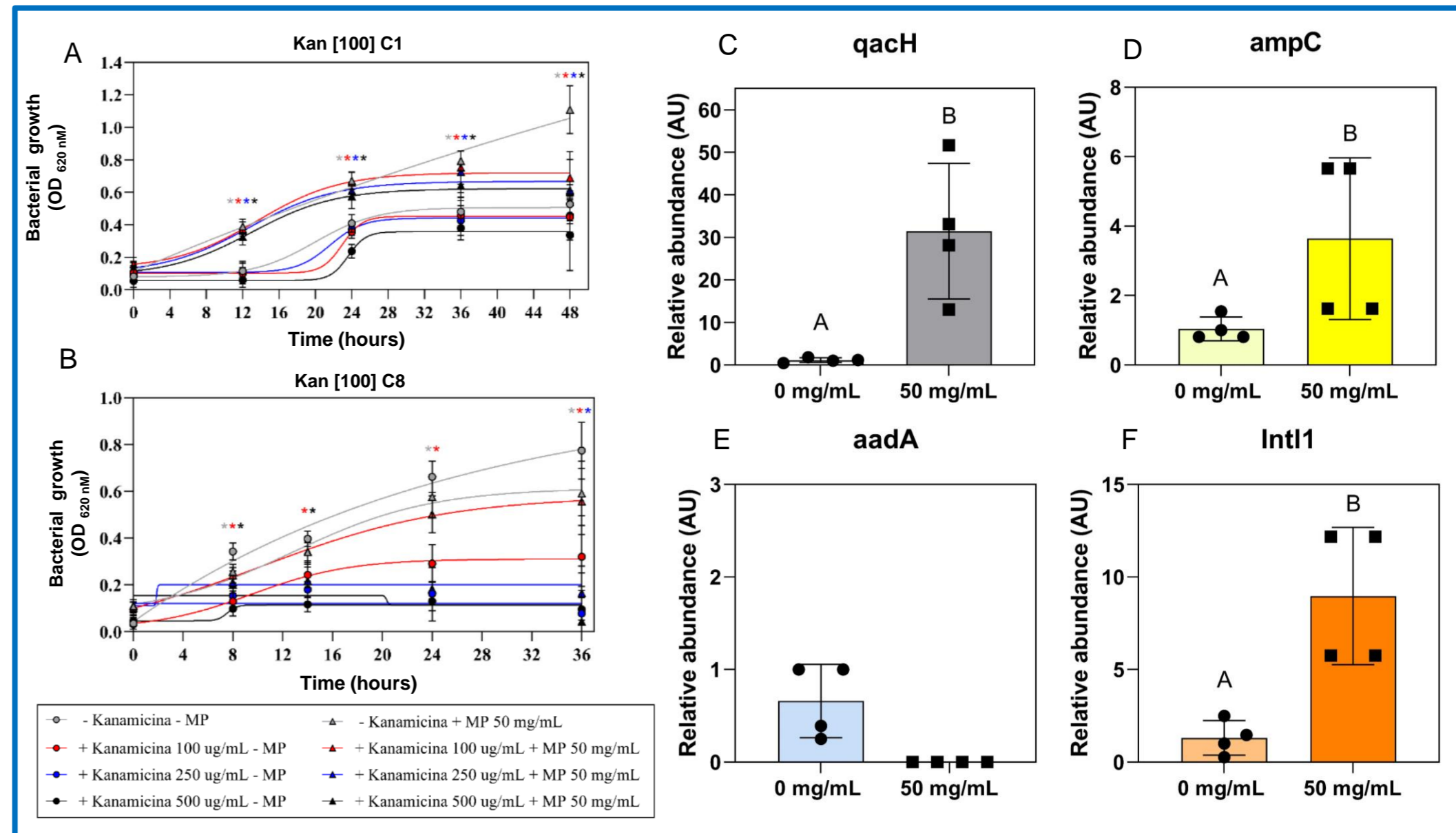
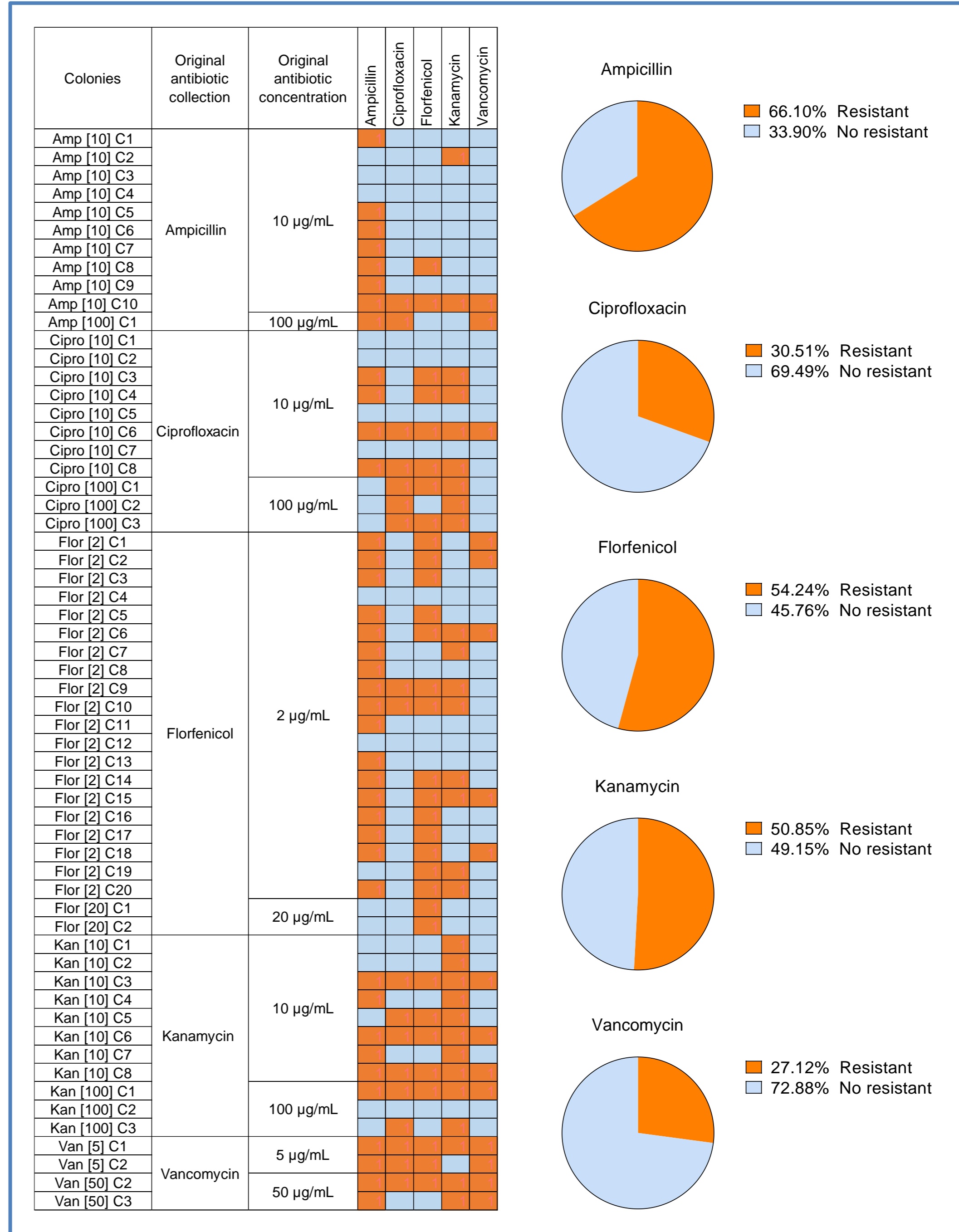
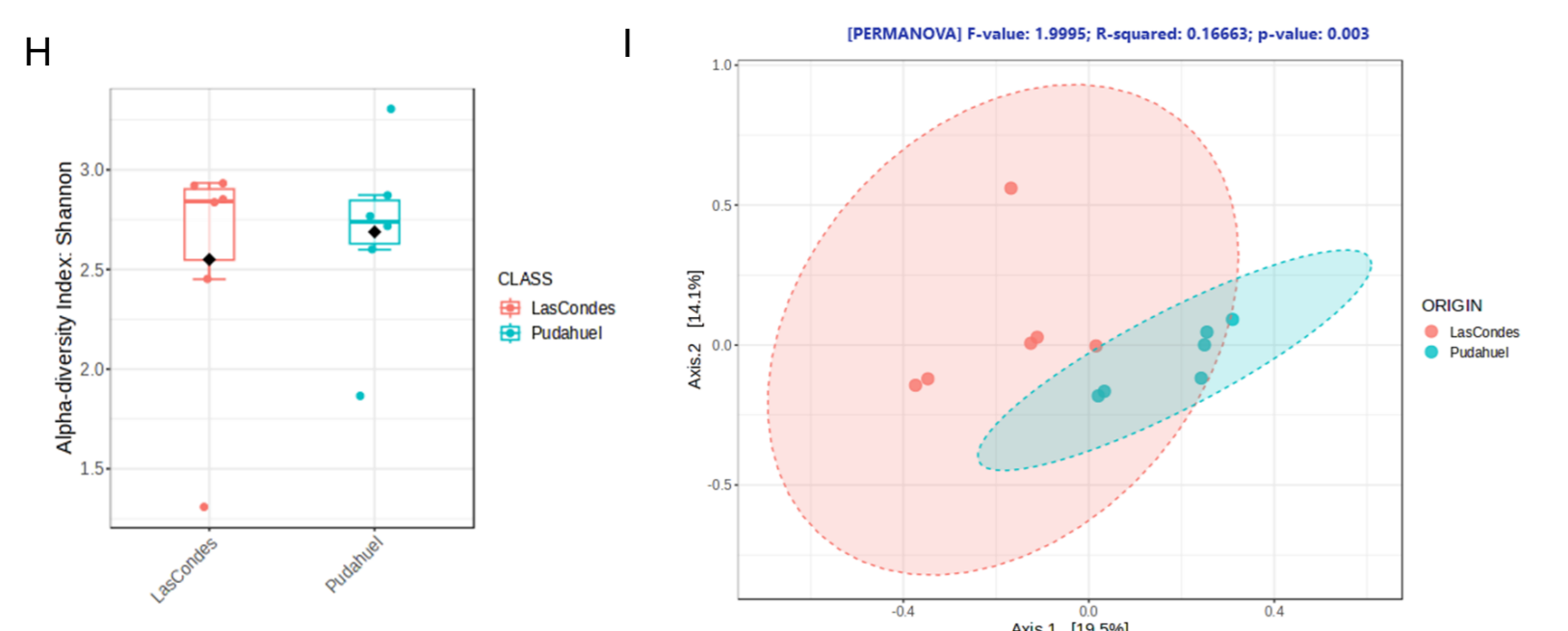
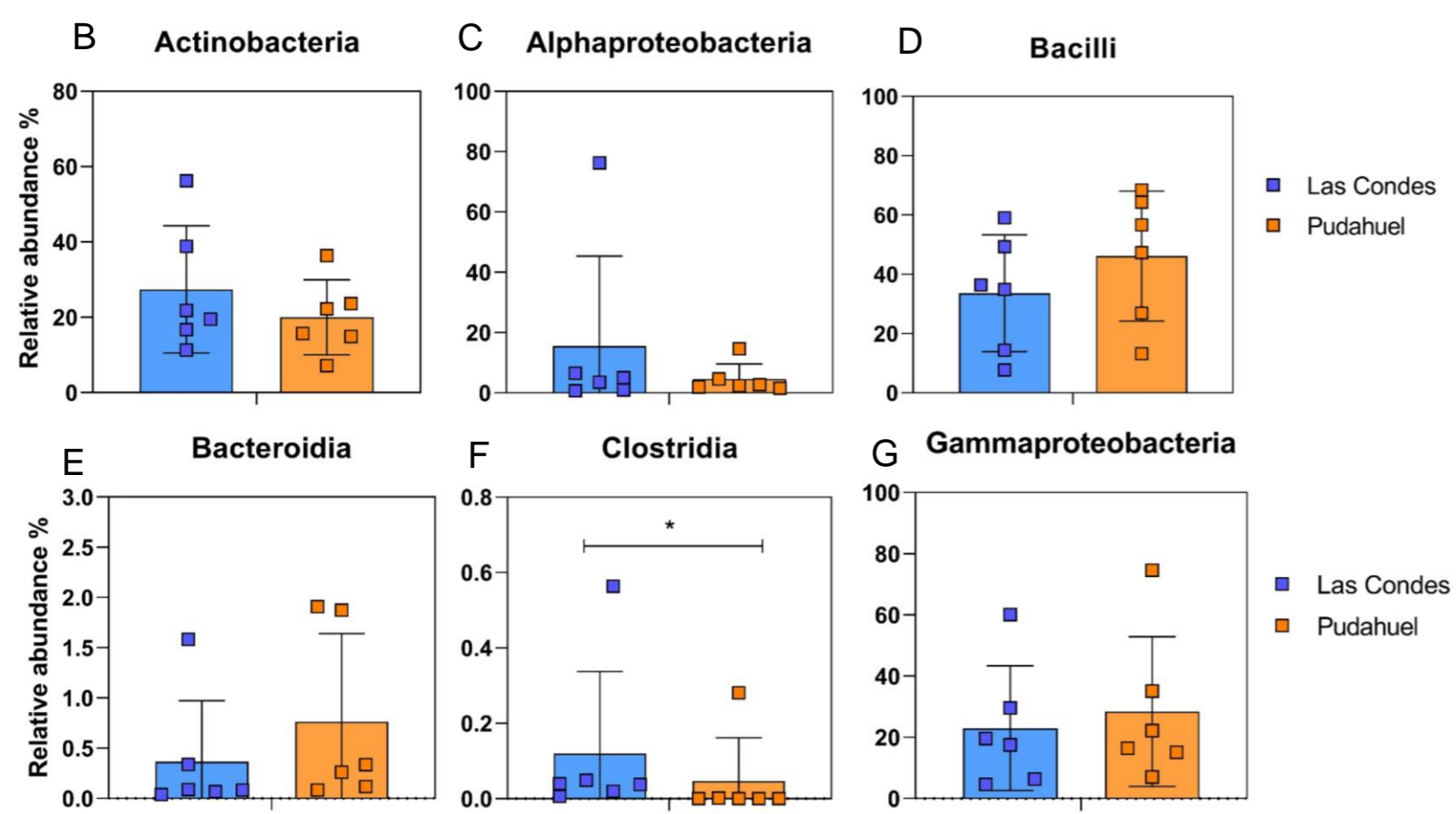
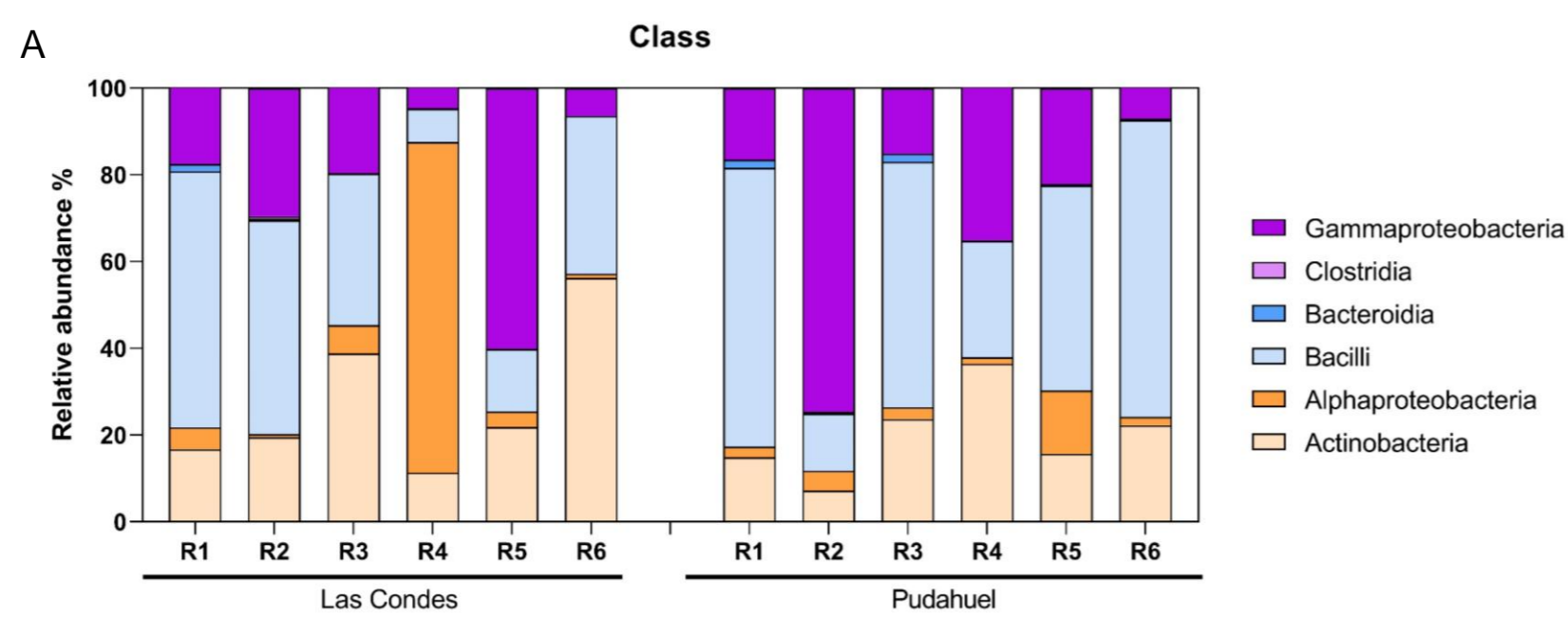
### INTRODUCTION & AIM

The bacteriome varies according to environmental conditions, such as pollution. These atmospheric variables also generate genetic and phenotypic changes in them, including antibiotic resistance. One way to study the bacteriome is using culturable communities, allowing the evaluation of changes in the community through controlled interventions. Our objective was to characterize and analyze the antibiotic resistance profile of the cultivable bacteriome of the Región Metropolitana. For this purpose, active air collections were obtained in Petri dishes with culture media from two areas of the Región Metropolitana that were differentially contaminated. After 7 days of growth, the composition and diversity were evaluated by high-throughput sequencing of the bacterial members. In addition, the resistant bacteriome was sampled in culture media supplemented with antibiotics at selective concentrations, and the multi-resistance quality of the isolates was evaluated. Finally, kanamycin-resistant isolates were selected and grown in a liquid medium supplemented with particulate matter, and their tolerance to antibiotics and the abundance of resistance gene transcripts were evaluated.

### METHOD



### RESULTS & DISCUSSION



### CONCLUSION

The sequencing of the bacterial community allowed us to detect 170 bacterial ASVs. The most abundant bacterial phyla in the samples were Proteobacteria and Firmicutes. Although there were no significant differences in the alpha diversity of the culturable bacteriome samples, there were significant differences in beta diversity. Also, we obtained 59 bacterial isolates resistant to antibiotics, of which more than 37% were multi-resistant. We detected resistance to aminoglycosides, beta-lactams, phenicols, glycopeptide antibiotics, and quinolones. Bacterial isolates subjected to particulate matter significantly increased their tolerance to kanamycin, which could be explained by an increase in the relative abundance of the antibiotic-resistance genes *qacH* and *ampC*. This study allowed us to determine the effects of pollution on the air bacterial community and antibiotic resistance, contributing to the generation of knowledge in the areas of microbial ecology and environmental sciences.

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