

# Genomic dynamics and evolution of antibiotic resistance and bacterial virulence

Teresa Nogueira

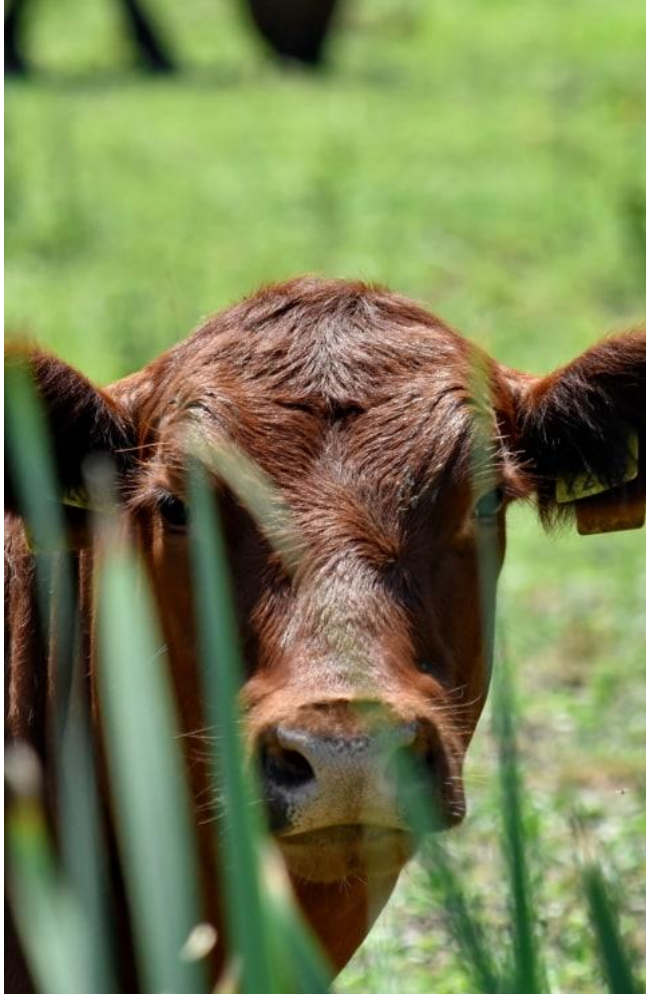


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Therapeutics

Prophylaxis



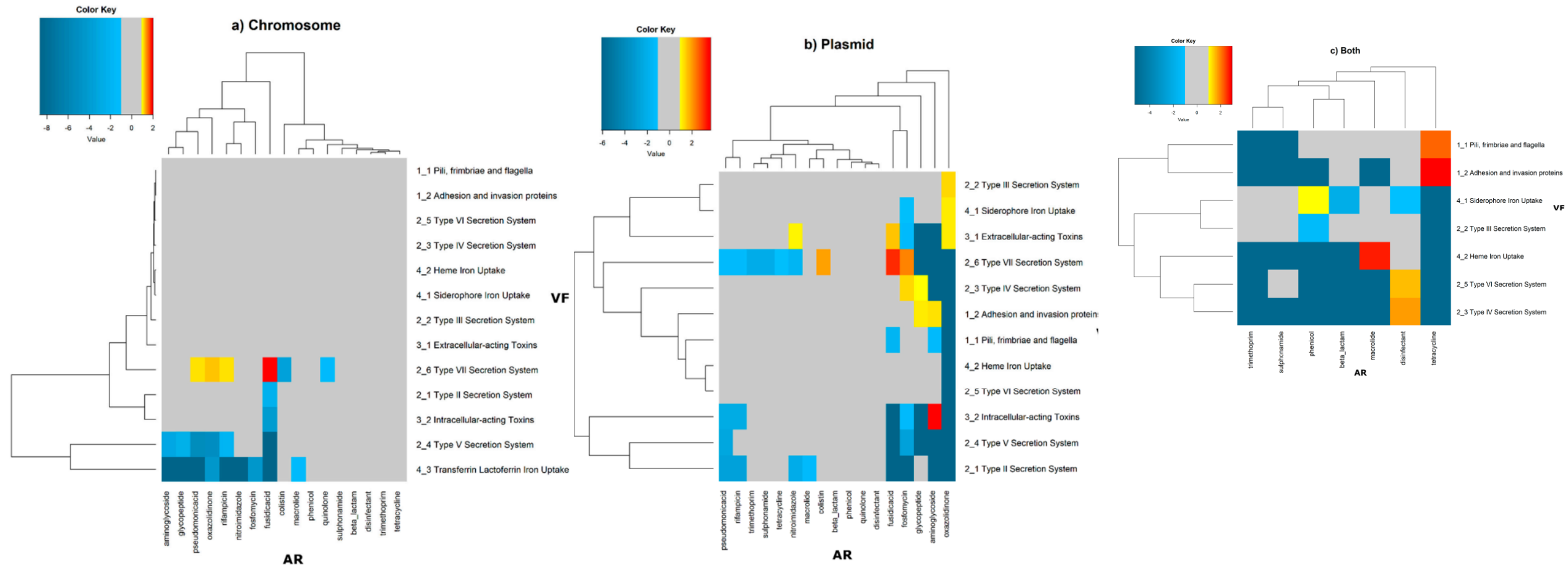
Environmental contamination



Agricultural use



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- We have also tested the hypothesis that there is a correlation between antibiotic resistance genes and virulence factor VF genes at the genomic level. We performed a comprehensive study of 16,632 reference bacterial genomes in which we identified and counted all orthologues of AR and VF genes in each of the locations: chromosomes, plasmids, or in both locations of the same genome. We found that, on a global scale, no correlation emerges. However, some categories of AR and VF genes co-occur preferentially, and in the mobilome, which supports the hypothesis that some bacterial pathogens are under selective pressure to be resistant to specific antibiotics, a fact that can jeopardize antimicrobial therapy for some human-threatening diseases.



# Take home messages

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- Since the connection between bacterial virulence and antibiotic resistance is so intricate, it requires multiple approaches.
- The diversity of antibiotic resistance genes and the virulence factors are correlated in the human gut and is influenced by antibiotic use.
- Our human network model predicts that antibiotic use and the spread of virulence and antibiotic resistance genes from one individual to another both contribute to the maintenance of the positive correlation between antibiotic resistance and virulence in microbiomes.
- Although there isn't conclusive proof that antibiotic resistance and virulence genes are related at the genome level, some patterns do appear at various genomic sites: plasmids or chromosomes



Instituto Nacional de  
Investigação Agrária e  
Veterinária, I.P.



Ciências  
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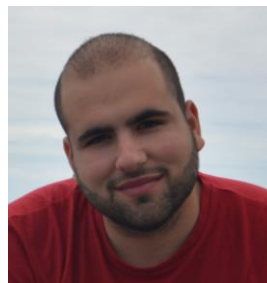
# Acknowledgments



Teresa Nogueira



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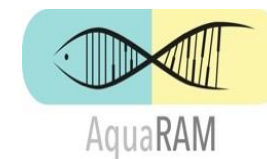
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