


Ratio between contagion probability and resistance genes loss rate is key for the emergence of a positive correlation between the diversity of virulence and antibiotic-resistance genes


Célia P. F. Domingues*¹, João S. Rebelo¹, Teresa Nogueira^{1,2}, Joël Pothier³, Francisca Monteiro¹, and Francisco Dionisio¹


¹ cE3c – Centre for Ecology, Evolution and Environmental Changes, Faculdade de Ciências, Universidade de Lisboa, 1749-016 Lisboa, Portugal
² INIAV, National Institute for Agrarian and Veterinary Research, 2780 -157 Oeiras, Portugal
³ Atelier de bioinformatique, ISYEB, UMR 7205 CNRS MNHN UPMC EPHE, Muséum National d’Histoire Naturelle, CP 50, 45 rue buffon F-75005 Paris, France

*email: celiapfd@hotmail.com


Ciências
research
day 2020

 A recent study found that human gut metagenomes with a higher diversity of resistance genes tend to have a higher diversity of virulence genes¹.

 We aim to understand the cause for this positive correlation through computational simulations.

 Since bacterial pathogens and resistance and virulence genes encoded by commensal bacteria circulate in the community, we simulated the contagion between people in a population organized in a social network.

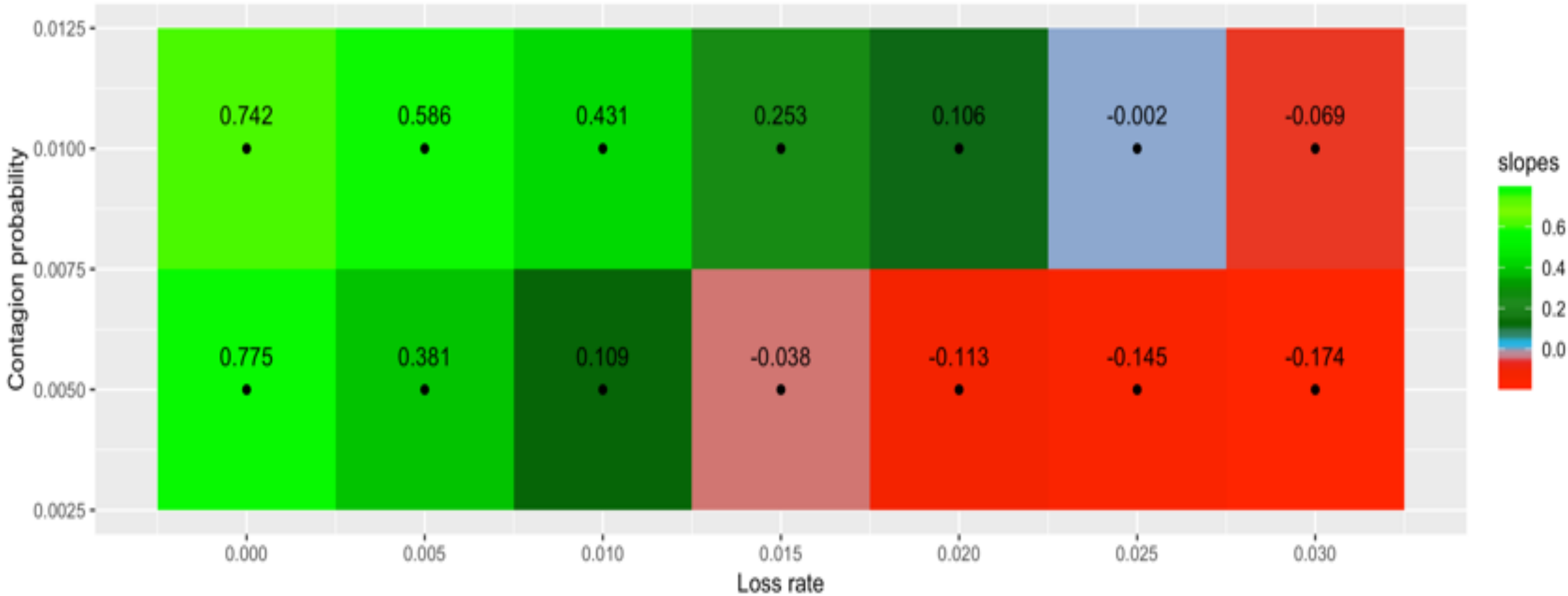
Health implications:

 The co-presence of a higher diversity of resistance and virulence genes may potentiate the emergence of virulent and multi-resistant bacteria in people’s metagenomes. These superbugs may then circulate in the community.

Reference:

(1) Escudeiro, P., Pothier, J., Dionisio, F., & Nogueira, T. (2019). Antibiotic resistance gene diversity and virulence gene diversity are correlated in human gut and environmental microbiomes. *Msphere*, 4(3).

Our simulations show that the critical factor for the emergence of the positive correlation is the ratio between the contagion probability between individuals and the loss rate of resistance genes.



Importantly, if the gene contagion probability is higher than the loss rate of resistance genes, the positive correlation emerges.

This finding maintains even when we change several simulations’ parameters, such as the total diversity of virulence genes and antibiotic resistance genes, the contagion probability between individuals, the loss rate of resistance genes, whether or not the population uses antibiotics, or the network type (regular, small-world, or random).