

New mathematical model challenges aggressive antibiotic treatments

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Facing the threat of a post-antibiotic era, a careful and more sustainable use of antibiotics is urgently needed. Credit: Photo via Flickr

Antibiotic resistance is one of the most challenging problems in modern medicine. A new study by Erida Gjini and Patricia H. Brito from the

Instituto Gulbenkian de Ciência (IGC; Portugal), provides a new mathematical model to evaluate the best treatment protocol to clear an infection, by taking into account the role of the host immune system. This new conceptual framework, published in the latest edition of the scientific journal *PLoS Computational Biology*, may be used in the future for personalised treatments.

Antibiotics are required to treat severe bacterial infections, but their misuse or overuse has contributed to a rise in bacterial resistance. In the presence of resistance, standard treatments are less effective or don't work at all. Because the discovery of new antibiotics does not always follow the rate at which new resistances develop, it is important to promote a more rational use of the available medicines. Erida Gjini, principal investigator at the IGC, and Patrícia H. Brito, researcher at the IGC and Faculdade de Ciências Médicas da Universidade Nova de Lisboa, addressed this issue by developing a mathematical framework to compare different treatment therapies. These included [aggressive treatments](#), with a highest possible dose of antibiotics, and moderate therapies that combine appropriate timing, reduced drug dosage, and short treatment durations. Based on mathematical analysis and computer simulations, the researchers compare treatments with a fixed drug dose and duration, and treatments where dose and duration closely follow patient symptoms, to understand how the drug-resistance problem can be minimized without compromising patient health.

"The host immunity is an important, but often overlooked factor in the process of infection clearance. A strong immune response can substantially reduce the need for aggressive treatments, we just have to find out how ", says Erida Gjini. Therefore, in addition to key parameters such as pathogen growth rate and antibiotics dosage, the interdisciplinary IGC team also considered information about the host's immune system, and integrated it in this model.

Patrícia H. Brito explains that with this model "we can quantify how the strength of the immune response, together with the appropriate timing, drug dosage and duration of therapy, determine the success or failure of antibiotic treatments. By using simulations we could also predict that some relapses may be caused by sensitive bacteria that could be treated with the same antibiotic, and not by resistant bacteria as it is usually assumed."

About the importance of this study, Erida adds: "Treatment optimization in the era of personalized medicine will increasingly require quantifiable indicators of the host [immune response](#), pathology, and recovery processes during infection. Mathematical and computational approaches, like the one adopted in this study, will be key to integrate such important information with clinical practice."

More information: Gjini, E., Brito, P. H. (2016); Integrating Antimicrobial Therapy with Host Immunity to Fight Drug-Resistant Infections: Classical vs. Adaptive Treatment; *PLoS Computational Biology*; [DOI: 10.1371/journal.pcbi.1004857.t001](https://doi.org/10.1371/journal.pcbi.1004857.t001)

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