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Surrey University leads research against anti-biotic resistance

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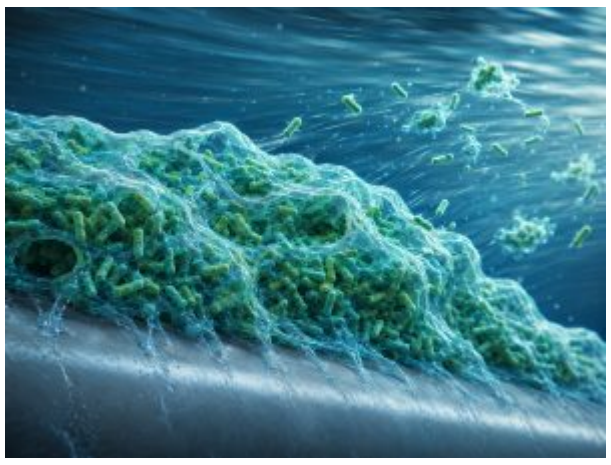

Faster and more effective ways to treat *pseudomonas aeruginosa*, a bacterium identified by the World Health Organization (WHO) as one of the most life-threatening pathogens, could be on the cards thanks to a first-of-its-kind 3D computer model developed by the University of Surrey.

The model has shown how *pseudomonas aeruginosa* grows and reshapes its protective layer and spreads to new surfaces. The WHO estimates that bacterial antimicrobial resistance – where antibiotics are no longer effective – was directly responsible for 1.27 million deaths worldwide in 2019 alone.

In a study published in npj Biofilms and Microbiomes, researchers used BioDynaMo, an open-source simulation platform developed as part of an international collaboration involving the University of Surrey and partners worldwide, to create a three-dimensional agent-based model (ABM) that recreates how *pseudomonas aeruginosa* forms biofilms.

Biofilms are communities of bacteria encased in a protective sticky layer made up of sugars, proteins and DNA that allows them to cling to surfaces and resist antibiotics. For Pseudomonas aeruginosa, these biofilms commonly form in flowing environments such as catheters and plumbing systems.

Unlike previous computer models, the Surrey-developed ABM captures how biofilms grow under constant fluid flow – similar to real-world conditions – and how the bacteria naturally break away from them to spread and colonise new surfaces. The team validated the simulation against laboratory experiments, demonstrating that it accurately reproduces the growth, structure and detachment patterns seen in real bacterial biofilms.

Ryan Bournes, postgraduate researcher at the University of Surrey and lead author of the study, said:

“Biofilms are incredibly difficult to study because many of the important interactions happen at a microscopic level. Our model allows us to simulate these processes in a virtual environment, making it much easier to test new ideas and understand how these bacteria spread without solely relying on costly and time-consuming laboratory experiments.”

As well as helping scientists study *pseudomonas aeruginosa*, the modelling framework could be adapted to investigate other biofilm-forming bacteria and predict how factors such as fluid flow, surface design and bacterial behaviour influence the spread of infection.

Dr Roman Bauer, Senior Lecturer at the University of Surrey’s Computer Science Research Centre and BioDynaMo spokesperson, said:

“Antimicrobial resistance is steadily rising due to the overuse and misuse of antibiotics, so finding faster and smarter ways to understand the behaviour of pathogens is essential.

“Using BioDynaMo, we’ve been able to recreate for the first time how Pseudomonas aeruginosa biofilms grow, change shape and spread under flowing conditions – biological processes that would be extremely difficult, expensive or even impossible to observe directly. This gives researchers a powerful new tool for virtual testing before moving into the laboratory.”

The research could help researchers optimise experiments, reduce laboratory costs and support the development of safer medical devices, hospital plumbing systems and other environments where harmful biofilms can form.

Surrey University

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Image: Artist’s impression of Pseudomonas aeruginosa bacteria encased within a protective biofilm under flowing conditions.

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