Tulane researchers use AI to improve diagnosis of drug-resistant infections

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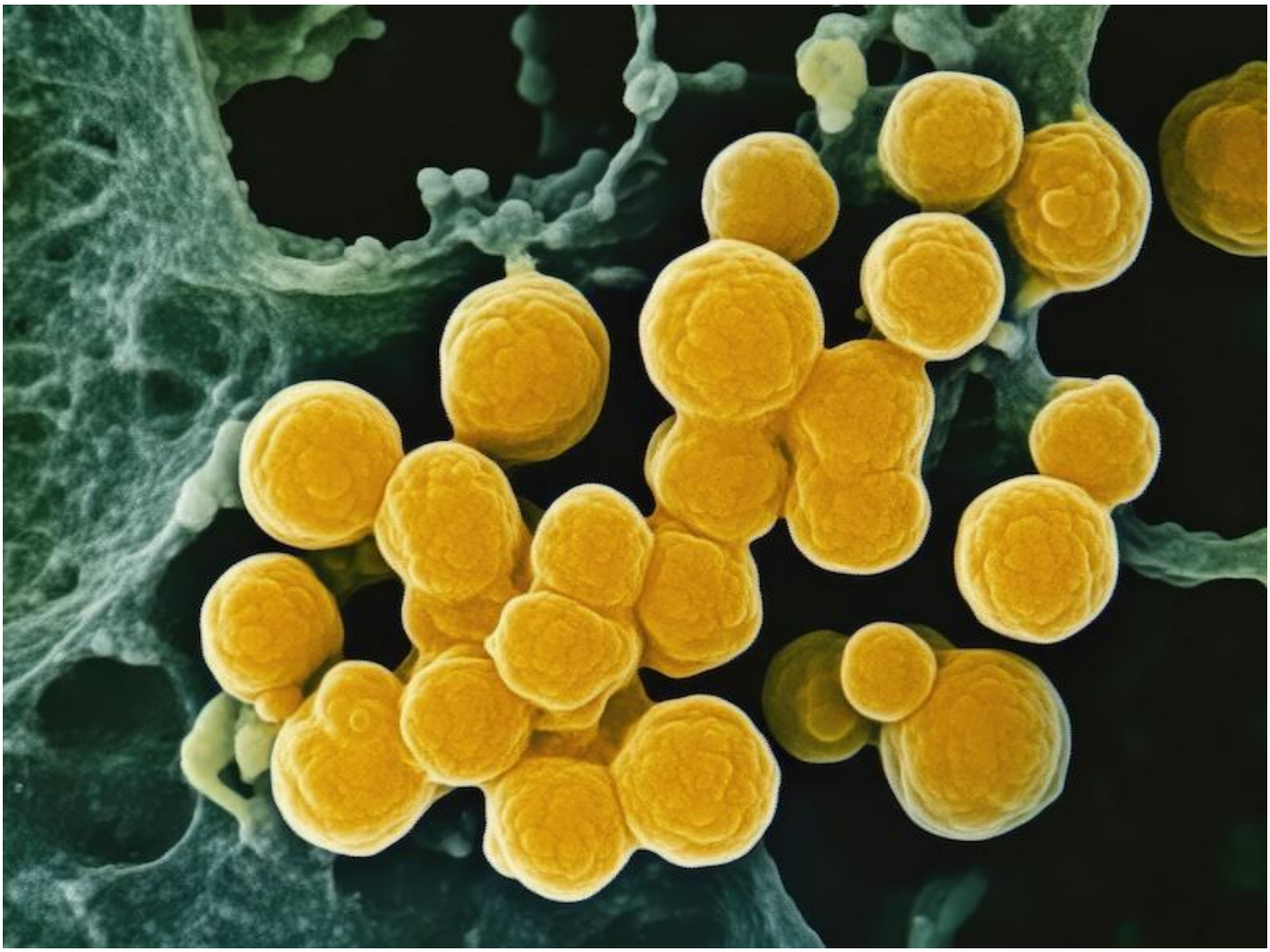

Tulane University scientists have developed a new artificial intelligence-based method to more accurately detect antibiotic resistance in deadly bacteria such as tuberculosis and staph (pictured above). The breakthrough could lead to faster and more effective treatments and help mitigate the rise of drug-resistant infections, a growing global health crisis. (Photo by Adobe Stock)

Drug-resistant infections — especially from deadly bacteria like tuberculosis and staph — are a growing global health crisis. These infections are harder to treat, often require more expensive or toxic medications and are responsible for longer hospital stays and higher mortality rates. In 2021 alone, 450,000 people developed multidrug-resistant tuberculosis, with treatment success rates dropping to just 57%, according to the World Health Organization.

Now, Tulane University scientists have developed a new artificial intelligence-based method that more accurately detects genetic markers of antibiotic resistance in *Mycobacterium tuberculosis* and *Staphylococcus aureus* — potentially leading to faster and more effective treatments.

A Tulane study, published in *Nature Communications*, introduces a new Group Association Model (GAM) that uses machine learning to identify genetic mutations tied to drug resistance. Unlike traditional tools, which can mistakenly link unrelated mutations to resistance, GAM doesn't rely on prior knowledge of resistance mechanisms, making it more flexible and able to find previously unknown genetic changes.

Current methods of detecting resistance used by organizations such as the WHO either take too long — like culture-based testing — or miss rare mutations, as with some DNA-based tests. Tulane's model addresses both problems by analyzing whole genome sequences and comparing groups of bacterial strains with different resistance patterns to find genetic changes that reliably indicate resistance to specific drugs.

"Think of it as using the bacteria's entire genetic fingerprint to uncover what makes it immune to certain antibiotics," said senior author Tony Hu, PhD, Weatherhead Presidential Chair in Biotechnology Innovation and director of the Tulane Center for Cellular & Molecular Diagnostics. "We're essentially teaching a computer to recognize resistance patterns without needing us to point them out first."

In the study, the researchers applied GAM to over 7,000 strains of *Mtb* and nearly 4,000 strains of *S. aureus*, identifying key mutations linked to resistance. They found

that GAM not only matched or exceeded the accuracy of the WHO's resistance database but also drastically reduced false positives, wrongly identified markers of resistance which can lead to inappropriate treatment.

"Current genetic tests might wrongly classify bacteria as resistant, affecting patient care," said lead author Julian Saliba, a graduate student in the Tulane University Center for Cellular and Molecular Diagnostics. "Our method provides a clearer picture of which mutations actually cause resistance, reducing misdiagnoses and unnecessary changes to treatment."

When combined with machine learning, the ability to predict resistance with limited or incomplete data improved. In validation studies using clinical samples from China, the machine-learning enhanced model outperformed WHO-based methods in predicting resistance to key front-line antibiotics.

This is significant because catching resistance early can help doctors tailor the right treatment regimen before the infection spreads or worsens.

The model's ability to detect resistance without needing expert-defined rules also means it could potentially be applied to other bacteria or even in agriculture, where antibiotic resistance is also a concern in crops.

"It's vital that we stay ahead of ever-evolving drug-resistant infections," Saliba said. "This tool can help us do that."

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