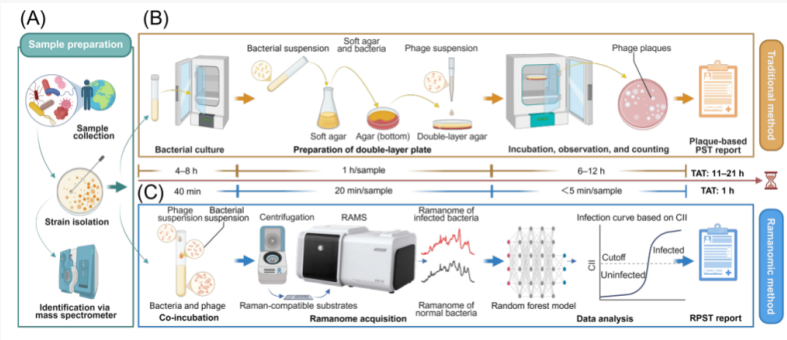
Rapid and quantitative phage susceptibility test by ramanome

GA, UNITED STATES, June 4, 2026 /EINPresswire.com/ -- As antibiotic resistance threatens to outpace available treatments, bacteriophage therapy has re-emerged as a precision alternative, but finding the right phage fast remains a critical bottleneck. Scientists have now developed a ramanome-based phage susceptibility test (RPST) that uses Raman spectroscopy to detect infection-induced changes in bacteria, delivering results in approximately 1 h with 96% agreement with gold-standard plaque assays. Central to RPST is a Composite Infection Index (CII), computed from four conserved Raman biomarkers that capture phage-induced remodeling of nucleic acids, proteins, and lipids. As a continuous, population-level score, CII enables not just susceptibility calls but quantitative ranking of phage potency and determination of the minimum effective dose, offering a rapid and quantitative framework for precision phage therapy.



Overview of ramanome□based phage susceptibility test (RPST)

This study(doi: https://doi.org/10.1002/mlf2.70089) was led by Prof. Jian Xu (Qingdao Institute of Bioenergy and Bioprocess Technology, Chinese Academy of Sciences) in collaboration with Prof. Hongzhou Lu (Shenzhen Third People's Hospital) and Prof. Jiadong Huang (University of Jinan). To address the lack of rapid and quantitative phage susceptibility test (PST) methods for precision phage therapy, scientists developed a ramanome-based PST (RPST), which uses label-free Raman spectroscopy to capture the biochemical remodeling that bacteria undergo during phage infection. Because these molecular-level changes occur within minutes—well before bacterial lysis becomes visible—RPST can classify infection outcomes within approximately 1 h, compared with the 11–21 h required by conventional plaque assays (Fig. 1).

To identify conserved ramanome biomarkers that distinguish infected from uninfected bacterial populations, scientists analyzed ramanomes from multiple representative phage-host systems, including T1- and T4-infected Escherichia coli strains, across multiple time points and MOI conditions. Four spectral regions capturing changes in nucleic acids, proteins, and lipids were identified as conserved biomarkers of phage infection across all systems tested (Fig. 2). These

biomarkers showed sustained, progressive shifts in phage-susceptible bacteria, while resistant strains showed only transient responses that quickly returned to baseline—enabling clear discrimination between susceptible and resistant populations.

To achieve robust and generalizable infection classification, the four biomarkers were integrated into a Composite Infection Index (CII) using a random forest model. Cross-validation demonstrated excellent performance, with an average AUC of 0.995 and a mean accuracy of 0.965 (Fig. 3). RPST successfully distinguished susceptible and resistant bacterial populations and achieved 96.0% concordance with conventional plaque assays across 25 phage-host systems spanning four clinically relevant bacterial species.

Beyond binary susceptibility testing, RPST enabled quantitative ranking of phage potency. Because the CII accurately reflected the fraction of infected cells in a population, it directly captures how effectively different phages infect the same host—information that plaque assays alone cannot resolve (Fig. 4). Critically, by tracking CII over time at different phage-to-bacterium ratios, RPST also determined the minimum phage dose at which infection can sustain and propagate through a bacterial population, a key parameter for predicting whether a phage will work under realistic clinical conditions (Fig. 5). Together, these findings establish RPST as a rapid, quantitative, and dynamic phenotypic framework for phage susceptibility test and precision phage therapy.

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