

**Surface enhanced Raman spectroscopy (SERS) of bacterial
metabolites for bacterial growth monitoring and diagnosis
of viral infection**

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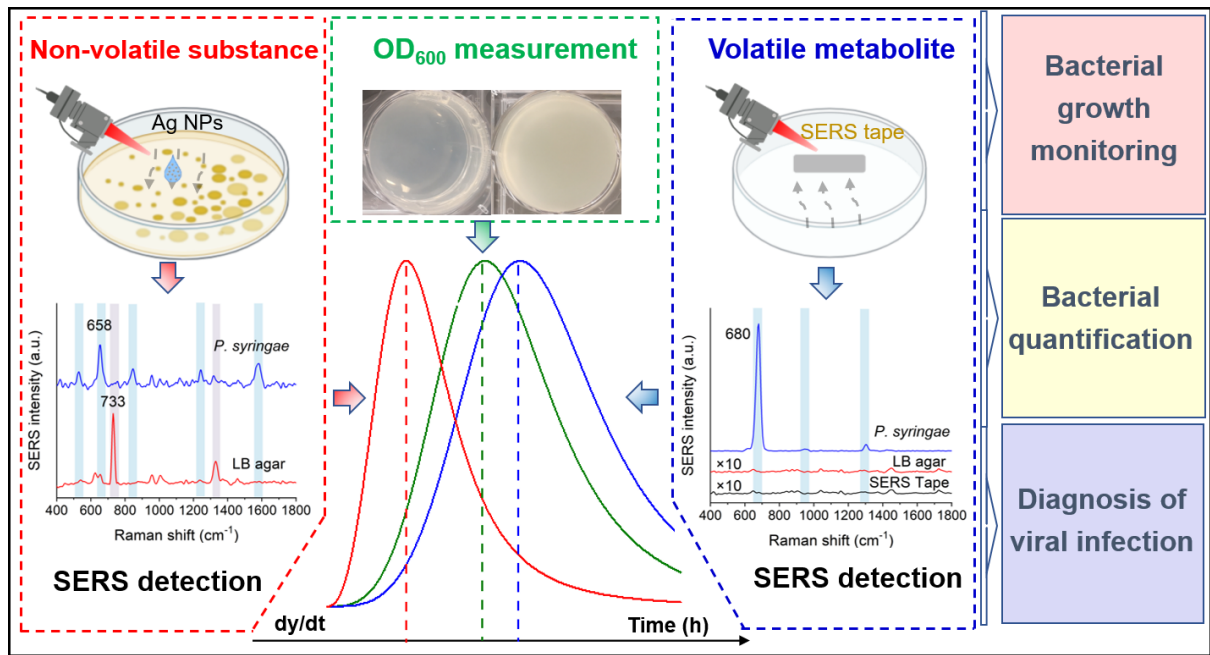
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ABSTRACT: Bacterial metabolites are intermediate products of bacterial metabolism and their production reflects metabolic activity. Herein, we report the use of surface enhanced Raman spectroscopy (SERS) for detection of both volatile and non-volatile metabolites and the application of this approach for bacterial growth quantification and diagnosis of viral infection. The time dependent SERS signal of the volatile metabolite dimethyl disulfide (DMDS) in the headspace above bacteria growing on an agar plate was detected and quantified. In addition, SERS signals arising from the plate reflected nutrient consumption and production of non-volatile metabolites. The measurement of metabolite accumulation can be used for bacterial quantification. In the presence of bacteriophage virus, bacterial metabolism is suppressed, and the relative decrease in SERS intensity reflects the initial virus concentration. Using multivariate analysis, we detect viral infection with a prediction accuracy of 93%. Our SERS based approach for metabolite production monitoring provides new insight towards viral infection diagnosis.

KEYWORDS: Surface enhanced Raman spectroscopy, detection, metabolite, bacteria, virus

SYNOPSIS: Surface enhanced Raman spectroscopy enables monitoring of volatile and non-volatile bacterial metabolites, the quantification of bacterial growth, and diagnosis of viral infection.

Graphical abstract:



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INTRODUCTION

Bacterial metabolites, the intermediate products of bacterial metabolism, reflect the growth, development, and interactions of bacteria with their environment.¹⁻³ Bacterial metabolites include both soluble and volatile compounds and some of them are highly specific to a given bacterial species.⁴ The types and concentrations of metabolites produced are often affected by the environment surrounding a bacterial cell.^{5,6} For example, quorum sensing bacteria produce and release autoinducer signaling molecules that regulate gene expression in response to population density fluctuations;⁷ and many bacteria produce bacteriocins (e.g., colicin⁸) to control competing species densities when hunting for nutrients or space.⁴ Metabolite sensing is considered an important requirement for controlling microbial growth and improving disease diagnosis.^{9,10}

Many bacterial metabolites are low molecular weight compounds and accordingly gas chromatography-mass spectrometry (GC-MS), liquid chromatography-MS (LC-MS) and their derivatives are often used for metabolite detection.¹¹⁻¹⁴ However, despite their accurate and robust utility, these conventional methods are complex, time-consuming, and expensive and are inappropriate for rapid point of care or real time measurements. Recently, colorimetric and electrochemical methods have been developed to enable precise *in-situ* metabolite detection.¹⁵⁻¹⁹ These newer detection methods are often designed for targeted sensing that may hinder their capacity to detect unknown chemical species within complex metabolite mixtures. Accordingly, new strategies for the detection of bacterial metabolites are attracting significant attention.

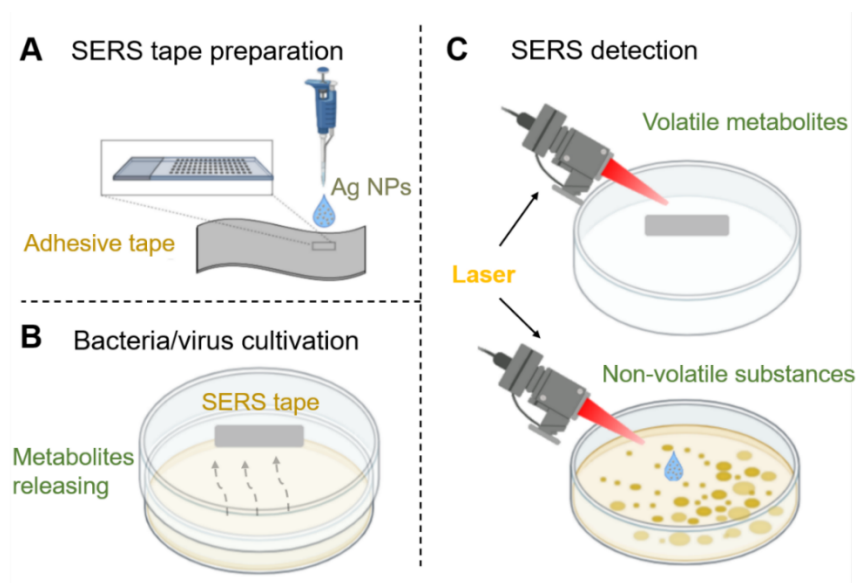
Surface-enhanced Raman spectroscopy (SERS) is an ideal approach for biological sensing due to its high sensitivity, real time response, and capacity for molecular fingerprinting.^{20,21} The Raman scattering of an analyte can be significantly enhanced when it is located within the strong electromagnetic field generated by the localized surface plasmon resonance (LSPR) of plasmonic nanoparticles.²² SERS can be used to capture spectral fingerprints of biomolecules

without the use of labels and can achieve ultrahigh sensitivity.²³ Recently, a number of researchers have used SERS for bacterial metabolite detection.²⁴⁻²⁷ SERS substrates can either be placed near bacteria to evaluate intracellular or local extracellular metabolites²⁷ or can be placed in the headspace to detect gaseous metabolites.²⁸⁻³⁰ *In-situ* SERS of signaling metabolites has been obtained using purposely designed substrates to understand both intraspecies communication^{27,31} as well as interspecies interactions within complex microbial communities.^{32,33} Besides end-point detection, time dependent SERS signals can provide real time information about metabolite production, which can then be used to define metabolic activity.^{30,34} These studies have collectively shown that SERS is a promising means for metabolite sensing. However, up until now, research has focused more on metabolite detection and only a few papers monitoring of bacterial growth or metabolite quantification.²⁷

Since metabolic activities can be affected by environmental conditions, SERS metabolite signals can be used to examine the effects of external stimuli such as antibiotic treatment.^{35,36} Bacteriophage viruses are well-recognized elements to bacterial mortality.³⁷ Following bacteriophage infection, the host bacterial metabolism is altered in favor of viral replication and in the case of lytic viruses may ultimately result in bacterial cell rupture. For this reason, bacteriophages have been suggested as an alternative means of bacterial inactivation in lieu of antibiotics.^{38,39}

In the present study, we report that bacterial metabolite SERS signals can be used for bacterial growth monitoring and the diagnosis of viral infection. Instead of focusing on one or two representative metabolites as done previously, we simultaneously detected both volatile and non-volatile metabolites. To do so, we prepared a low-cost plasmonic substrate that could be inverted inside the cover of a Petri dish to passively capture volatile metabolites formed during bacterial cultivation (**Scheme 1**). To detect non-volatile substances, colloidal nanoparticles were directly pipetted onto the culture plate. The collected SERS signals of the

metabolites were used to monitor bacterial growth and for bacterial quantification. To diagnose viral infection, variable virus titers were added to the bacterial culture, the resulting SERS signals were recorded, and multivariate analysis was used for classification. The lytic bacteriophage Phi6, a surrogate for enveloped viruses, such as SARS-CoV-2 and influenza virus,⁴⁰⁻⁴² and its host bacteria *Pseudomonas syringae* (*P. syringae*) were used in these proof-of-concept studies. The approach described in this work, based on SERS monitoring of bacterial host metabolites, provides new insight into viral infection diagnosis.



Scheme 1. Schematic illustration of (A) SERS substrate preparation; (B) bacterial cultivation with/without virus; (C) SERS detection for both volatile and non-volatile metabolites.

EXPERIMENTAL SECTION

Materials. Silver nitrate (AgNO_3 , 99%), hydroxylamine hydrochloride ($\text{NH}_2\text{OH}\cdot\text{HCl}$, 99%), sodium hydroxide (NaOH , $\geq 98.0\%$), dimethyl disulfide (DMDS , $\geq 99\%$), and 4-mercaptobenzoic acid (4-MBA, 99%) were purchased from Millipore Sigma. Luria-Bertani (LB) broth (Miller, powder) and agar (Difco, granulated) were obtained from Fisher Scientific. The adhesive tape (Scotch double sided adhesive tape) was purchased from the local market. Bacterial strains *Pseudomonas syringae* pv phaseolicola (*P. syringae*), *Escherichia coli* K 12 (*E. coli*), and bacteriophages Phi6, MS2 were obtained from Dr. Linsey Marr's group.^{40,43}

Deionized water from a Milli-Q-plus system was used throughout this work.

Synthesis of colloidal silver nanoparticles (AgNPs) and SERS substrate. The colloidal suspension of AgNPs was synthesized via a facile and fast preparation method at room temperature.⁴⁴ Briefly, 9 mL of 2 mmol/L freshly prepared $\text{NH}_2\text{OH}\cdot\text{HCl}$ solution (containing 3 mmol NaOH) was mixed with 1 mL of 10 mmol/L AgNO_3 in a centrifuge tube. The mixture was then vortexed for 1 min to achieve complete mixing. During the process, the solution was turned to yellow/greenish. The prepared colloidal AgNPs were stored in the dark at 4 °C for future use.

The low-cost SERS tape substrate was fabricated by depositing AgNPs on adhesive tape as reported in the literature.⁴⁵ Generally, 50 μL of the as-prepared AgNPs were uniformly pipetted on the surface of the adhesive tape. After being dried naturally at room temperature, AgNPs were readily immobilized on the tape without other modifications and the aggregation of the nanoparticles generated abundant SERS hot spots, where the highest SERS enhancement occurs.⁴⁶

Bacterial cultivation and viral propagation. Before cultivation, LB medium was prepared by dissolving LB broth (containing 10 g of tryptone, 5 g of yeast extract, and 10 g of NaCl) in 1 L water. LB agar plates were made by adding 1.5% agar to the prepared LB medium, autoclaved, and then poured into glass Petri dishes before cooling down. Bacterial strain *P. syringae* was streaked onto the LB agar plates and incubated at 25 °C for 48 h. A single colony was transferred to 15 mL of autoclaved LB medium and incubated at 25 °C with agitation (200 rpm) for 24 h. The obtained *P. syringae* suspensions were diluted in series and inoculated into LB agar plates and the concentration was obtained by counting colony forming units (CFU) after cultivating for another 48 h.

To propagate Phi6, LB soft agar (LB medium with 0.75% agar) was prepared and autoclaved. An aliquot of 4 mL of LB soft agar was pipetted to each culture tube and kept in a

130 50 °C water bath. Then, 200 µL of the *P. syringae* suspensions and 50 µL of Phi6 stock were
131 added to the culture tubes. The mixture was poured on top of a LB agar plate and cultured at
132 25 °C for 24 h. Phi6 was harvested by scraping soft agar from the plate into a 50 mL centrifuge
133 tube with 5 mL of LB medium. The tube was vortexed and centrifuged for 10 min at 1753×g.
134 Bacterial cells and debris were removed from the Phi6 suspension by filtering through a 0.22
135 µm cellulose acetate membrane. Plaque forming units (PFU) were counted by repeating the
136 abovementioned procedure with different Phi6 dilutions. *E. coli* and MS2 were cultured with
137 the same procedures but at 37 °C.

138 **SERS monitoring of bacterial metabolites.** The SERS tape was inversely attached inside the
139 cover of a *P. syringae* containing glass Petri dish. The plate was sealed by parafilm and the
140 released volatile metabolites were captured by the substrate. After 24 h incubation, the SERS
141 signals were recorded. The SERS signals of non-volatile substances were obtained by directly
142 pipetting 5 µL of prepared AgNPs onto the culture plate. To evaluate metabolite release and
143 cell growth, the bacterial optical density (OD₆₀₀) was measured at 10 min intervals and the
144 SERS signals were recorded at 3 h intervals over a 24 h period. To diagnose viral infection, 50
145 µL of Phi6 (10⁷ PFU/mL or diluted) was pre-added to 200 µL of 10⁹ CFU/mL *P. syringae*
146 suspension. SERS data were then collected after 24 h incubation. All the other procedures were
147 as stated previously.

148 **Instrumentation.** A field-emission Quanta 600 FEG environmental scanning electron
149 microscope (SEM) was used to observe the morphologies of AgNPs and SERS Tape.
150 Ultraviolet-visible (UV-Vis) spectrophotometer (Cary 5000, Agilent) and dynamic light
151 scattering instruments (DLS, Zetasizer Nano ZS) were used to obtain the UV-Vis spectrum and
152 hydrodynamic diameter of AgNPs, respectively. A microplate reader (Multi-mode, Synergy™
153 HTX) was adapted to measure OD₆₀₀. WITec alpha500R Raman spectrometer (WITec GmbH,
154 Ulm, Germany, spectral resolution = ~3.5 cm⁻¹) with a 785 nm laser and a 10× confocal

microscope objective was used to obtain the SERS spectra of all the samples. The silicon peak at 520 cm^{-1} was used for instrumental calibration before measurement. The signal was collected using a Peltier cooled charge coupled device (CCD) with 300 Groves per mm grating set. For each sample, 400 spectra (20×20 ; $X\times Y$) were acquired across a $100\times 100\text{ }\mu\text{m}^2$ area with an integration time of 0.1 s for each point.

SERS data analysis. The instrument embedded software (Project Five) was used for spectral cosmic ray removal, Savitzky-Golay smoothing, baseline subtraction, and peak identification. Subsequently, the SERS data was analyzed using MATLAB® 2019b (The MathWorks, USA) to calculate the absolute intensities of the peak of interests and the ratio of different peaks. Multivariate data analysis was also performed in MATLAB. Principal component analysis (PCA) was employed to identify the spectral features within 400 to 1800 cm^{-1} during bacterial growth. To diagnose viral infection, 18 spectral features were selected by the software from a total of 3600 spectra (2000 spectra for infected *P. syringae* and 1600 spectra for normal *P. syringae*). Support vector machine (SVM) classification with quadratic kernel function was performed to help differentiate multivariate SERS data.

RESULTS AND DISCUSSION

Characterization of AgNPs and SERS tape. AgNPs were synthesized by room temperature hydroxylamine hydrochloride reduction.^{44,47} As prepared, spherical AgNPs exhibited high uniformity and a TEM determined average size of $44.8 \pm 8.6\text{ nm}$ (**Figure S1**). When dispensed in water, the AgNPs exhibited the expected LSPR band at $\approx 410\text{ nm}$ ⁴⁷ and a DLS determined average hydrodynamic diameter (Z_{ave}) of $79.6 \pm 22.8\text{ nm}$. The SERS tape substrate was fabricated by uniformly depositing AgNP suspension ($\approx 2\times 10^9\text{ NPs/mL}$) on the sticky layer of commercially available double-sided adhesive tape. Once dried, the AgNPs aggregated and became embedded on the tape surface due to the swelling and deswelling action of the

adhesive.⁴⁵ After decoration, the morphology of the tape surface changed from smooth and flat to rough (**Figure S2**).

In proof-of-concept experiments, the SERS performance of both the AgNPs and the SERS tape was evaluated. The responsive, pH sensitive SERS molecule 4-MBA was chosen to verify our methods. AgNPs were mixed with 4-MBA and placed on the surface of aluminum foil as droplets, while the SERS tape dried naturally after 4-MBA solution was added. As shown in **Figure 1**, both AgNPs and SERS tape showed high SERS performance towards 4-MBA with SERS enhancement factors of 5×10^7 and 3×10^7 , respectively. The SERS results exhibited large spatial variations due to the heterogeneous distribution of hot spots, especially for SERS tape (coefficient of variation (CV) = 46.0%, **Figure 1E**). The AgNPs self-aggregated on the tape and the aggregation process was uncontrolled, thus resulting in the random spatial distribution of SERS hot spots. We have recently reported on the use of surface enhanced elastic scattering as a localized intrinsic internal standard to address hot spot variability and improve SERS reproducibility.⁴⁸⁻⁵⁰ Succinctly, a pseudo peak at $\sim 77 \text{ cm}^{-1}$ (I_{77}), which is the surface enhanced elastic scattering signal, is enhanced within the hot spots. Accordingly, I_{77} can be used as an internal standard for hot spot normalization. Following hot spot normalization, the CV of SERS tape declined to 14.1% (**Figure 1F**), a value comparable to many substrates.^{45,51,52} Similarly, the CV of AgNPs alone decreased from 15.2 to 5.9% (**Figures 1B and 1C**). High SERS enhancement, reproducibility, and deployability suggest the promise of SERS tape.

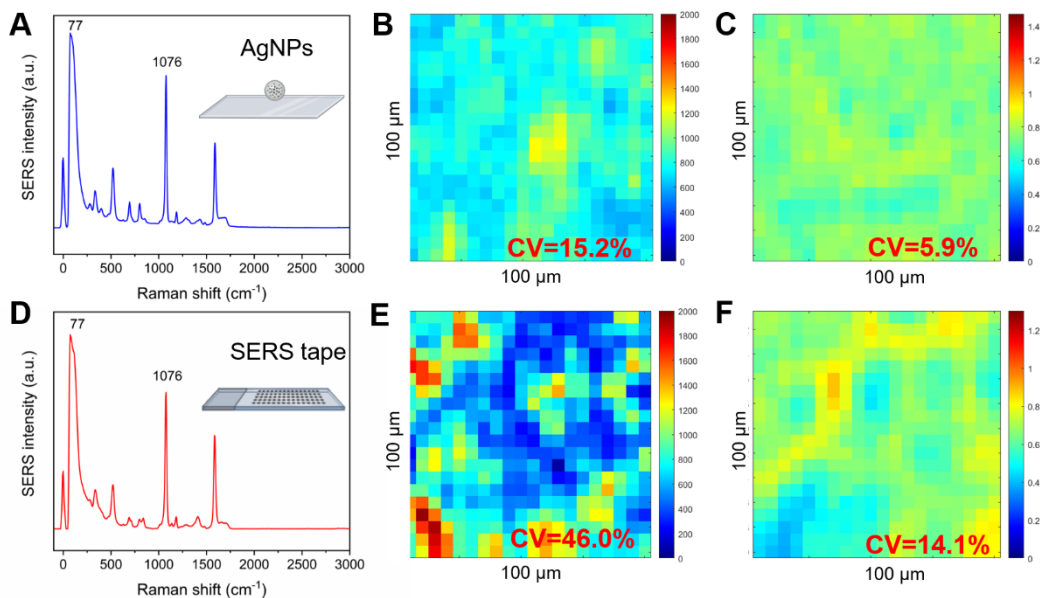


Figure 1. SERS spectra and maps of 4-MBA on AgNPs (A-C) and SERS tape (D-F). (A) and (D) average spectra of 4-MBA; (B) and (E) maps of peak intensity of 1076 cm^{-1} (I_{1076} , CCD cts); (C) and (F) maps of hot spot normalized peak intensity (I_{1076}/I_{77}). 400 spectra (20×20 , $X \times Y$) were acquired across a $100 \times 100 \mu\text{m}^2$ area.

SERS spectra of bacterial metabolites. We detected both volatile and non-volatile metabolites. To do so, SERS tape was inversely attached inside the cover of a Petri dish used for *P. syringae* cultivation. Volatile metabolites that partitioned to the headspace of the Petri dish interacted with the SERS tape during *P. syringae* growth. After a 24 h exposure period, the spectra of the SERS tape were recorded. In parallel, AgNPs were directly dropped onto the culture plate and the signals produced by non-volatile substances were detected. As shown in **Figure 2A**, compared to the fresh SERS tape and SERS tape in the control sample (LB agar plate without bacteria), a very strong peak appeared at $\sim 680 \text{ cm}^{-1}$ in the headspace above *P. syringae*. This peak reflects the $\nu(\text{C-S})$ vibration of methyl sulfide.²⁹ Previous studies have shown that many bacteria fermentatively produce volatile sulfide compounds, such as dimethyl disulfide (DMDS).^{53,54} Methyl sulfide is the expected dissociation product of DMDS on Ag and Au surfaces.³⁰ Less intense peaks at 950, 1305, and 2917 cm^{-1} reflect the $\nu_s(\text{CH}_3)$ vibration, CH_3/CH_2 twist, and $\nu(\text{CH})_{\text{syn}}$ vibration, respectively.^{30,55} These peaks have been reported

previously for volatile bacterial metabolites and reflect alkene, alcohol, ketone, or aromatic compounds in the metabolite mixture (**Table S1**).^{28-30,56}

The SERS signals of the non-volatile substances detected within the LB agar plates are complex due to their biological origin within bacterial cells that precludes simple identification.²⁰ In addition, there are several components (protein hydrolysates and nucleobase containing substances) in LB culture medium that contribute to the SERS spectra.^{57,58} As shown in **Figure 2B**, LB medium exhibits peaks at 626 cm⁻¹ (C-C twisting mode in phenylalanine), 733 cm⁻¹ (adenine or phosphatidylserine), 957 cm⁻¹ (phosphate or C=C deformation), 1006 cm⁻¹ (phenylalanine), 1328 cm⁻¹ (CH₂/CH₃ wagging mode present in collagen or purine bases) and 1450 cm⁻¹ (CH₂/CH₃ deformation of proteins and lipids).^{55,58} Following 24 h cultivation of *P. syringae* the majority of the original LB peaks disappeared, while other peaks appeared or increased in intensity (e.g., 658 cm⁻¹ (guanine), 842 cm⁻¹ (polysaccharides), and 1582 cm⁻¹ (phenylalanine, hydroxyproline, tyrosine, etc.)).^{55,59} These new peaks reflect production of metabolites or changes within the bacteria themselves. To explore the origin of these peaks, we selected an area in a LB agar plate where only a fraction of the selected scan area contained bacterial colonies (**Figure S3A**). The SERS signals across the full scan area did not significantly differ (**Figure S3B**), thus suggesting that the peaks did not arise from the bacterial cells. Previous Raman/SERS studies have shown that metabolite signals often dwarf those of bacterial cells.⁵⁸ We also cultivated *P. syringae* in LB broth for 24 h, centrifuged the sample to collect the supernatant, and resuspended the *P. syringae* pellet in PBS (**Figure S3C**). After resuspension in PBS there were no obvious peaks in the spectrum (**Figure S3D**). Instead, the SERS spectrum of the supernatant had very similar peaks to the original sample. This evidence collectively suggests that the new SERS peaks measured within the plate result from extracellular metabolites (**Table S1**) that are produced by bacteria and then diffuse within the agar.

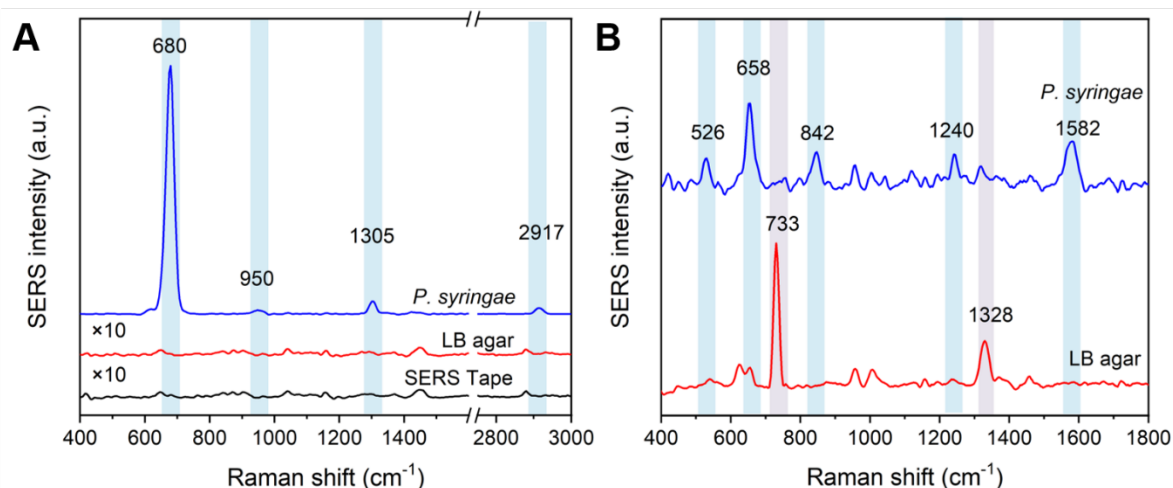


Figure 2. SERS spectra of (A) volatile metabolites in the headspace of *P. syringae* containing culture plate and control plate after 24 h cultivation, and (B) non-volatile substances in LB agar plate before and after 24 h cultivation of *P. syringae*. The light blue bars indicate the characteristic peaks of bacterial metabolites and the light red bars refer to the peaks of LB medium that disappear following cultivation.

Bacterial growth monitoring. To explore the kinetics of metabolite production, SERS spectra were recorded at 3 h intervals and the hot spot normalized peak intensity ($I_{\text{peak of interest}}/I_{77}$) was used for metabolite quantification. For DMDS, as shown in **Figure 3A**, I_{680}/I_{77} increased with time, due to its accumulation in the headspace. After 24 h, the I_{680}/I_{77} ratio was 0.133, corresponding to a headspace concentration of $\approx 43 \mu\text{M}$ DMDS (**Figure S4**). For the non-volatile substances, we utilized PCA to identify the peak features that contributed to the greatest differences in the spectra that arise due to bacterial growth (**Figure 3B**). The loading plot of the first principal component (PC1) indicates that spectral features arising from the LB medium (733, 1328, 1006 and 626 cm⁻¹) negatively contributed to the loadings (**Figure S5**) and that the normalized intensities of these peaks gradually decreased with time (**Figure S6**) – thus indicating consumption. Relative to the phenylalanine peaks (i.e., 1006 and 626 cm⁻¹), the peaks associated with purines (i.e., 733 and 1328 cm⁻¹) declined considerably within 9 h. The results are consistent with bacterial utilization of exogenous purines as a carbon or nitrogen source.^{60,61} Meanwhile, during bacterial growth, the peak initially at $\sim 733 \text{ cm}^{-1}$, which

primarily reflects adenine, gradually shifted to $\sim 725\text{ cm}^{-1}$ before it ultimately disappeared. The peak at 725 cm^{-1} reflects hypoxanthine,⁶² a typical metabolic intermediate in the formation of nucleic acids, or adenine containing substances⁵⁹, such as flavin adenine dinucleotide (FAD) and nicotinamide adenine dinucleotide (NAD). We also examined the normalized intensities of the four peaks that most positively contributed to the PC1 loadings. These peaks reflect production of nucleic acids (658 cm^{-1}), carbohydrates (842 cm^{-1}), and proteins ($526, 1582\text{ cm}^{-1}$). The most dramatic increase in the four peaks happened between 6-18 h (**Figure S6**), demonstrating production and accumulation of such substances during exponential growth (**Figure 3C**).

To better reveal the relationship between the kinetics of metabolite production and bacterial growth, a sigmoidal curve (or 4-parameter logistic model) expressed as $y = m_2 + \frac{m_1 - m_2}{1 + (t / m_3)^{m_4}}$ was used to fit the time dependent data.⁶³ m_1 and m_2 are the responses (y values) at $t=0$ and $t=\infty$, respectively, m_3 is the curve inflection point (the point where bacteria have the maximum growth rate), m_4 is the Hill's slope of the curve (slope that defines the steepness of the curve), and t is the time (min). For DMDS, I_{680}/I_{77} was the dependent variable. For non-volatile substances, the ratio of the peaks at 733 and 658 cm^{-1} (I_{733}/I_{658}) was used since the dynamic change in this ratio was larger than the measured change in the I_{658}/I_{77} or I_{733}/I_{77} ratios (**Figure S7**). Accordingly, I_{733}/I_{658} reflects both non-volatile metabolite production and nutrient consumption. To simplify the calculation, we ignored the peak shift at $\sim 733\text{ cm}^{-1}$ and I_{733} represents the intensity of the peak in the range between 725 and 733 cm^{-1} . The fitted parameters are listed in **Table S2**. As shown in **Figures 3D** and **3E**, both I_{680}/I_{77} for DMDS and I_{733}/I_{658} for non-volatile substances were well fitted by the logistic growth model ($R^2=0.972$ and 0.992 , respectively) and are consistent with the bacterial growth curve ($R^2=0.999$). The logistic curves indicate that the detected SERS signals can be directly related to bacterial

growth. By tracking the rate of change in the signal ($r=dy/dt$; **Figure 3F**), where y is I_{680}/I_{77} or I_{733}/I_{658} for the SERS signals or OD_{600} for bacterial growth, we can see that the rate of change in I_{733}/I_{658} reached a maximum at ~ 6 h, followed later by the maximum in OD_{600} and then I_{680}/I_{77} . This trend is reflected by the respective m_3 values (**Table S2**). $r(I_{733}/I_{658})$ reflects the synergy between nutrient consumption and the production of non-volatile metabolites. The temporal trends in the rate measurements are consistent with nutrient consumption followed by bacterial growth and metabolite production. DMDS diffusion into the plate headspace may also contribute to the lag in its rate curve.

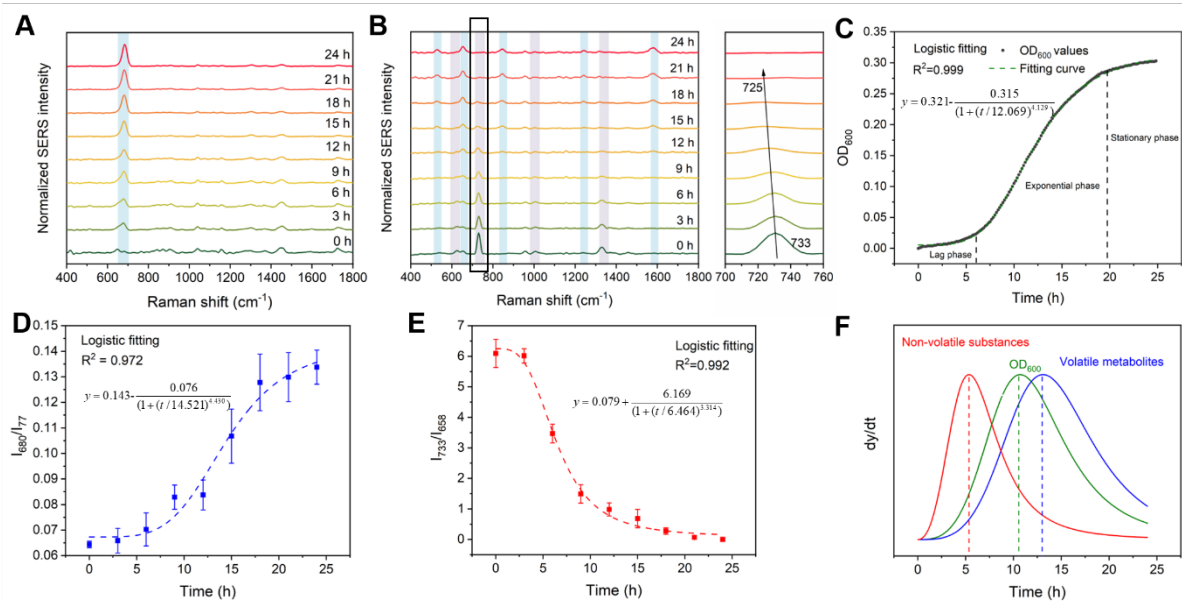


Figure 3. (A) SERS spectra collected for volatile metabolites at 3 h intervals with the intensities normalized by I_{77} ; (B) SERS spectra collected for non-volatile substances at 3 h intervals with the intensities normalized by I_{77} , the right panel highlights the shift of peak 733 cm^{-1} to 725 cm^{-1} ; The light blue bars indicate the characteristic peaks of bacterial metabolites while the light red bars refer to the LB medium peaks that decrease; (C) bacterial OD_{600} measured at 10 min intervals and fitted with logistic growth model; (D) kinetics data of I_{680}/I_{77} for volatile metabolites fitted with logistic growth model; (E) kinetics data of I_{733}/I_{658} for non-volatile substances fitted with logistic growth model; (F) signal change rate (dy/dt) of each curve, y reflects I_{680}/I_{77} (DMDS), I_{733}/I_{658} (non-volatile metabolites), or OD_{600} (bacterial growth), respectively.

Bacterial quantification. Following demonstration that the SERS signals of both volatile and non-volatile metabolites can be related to bacterial growth, we next used them to determine the

bacterial concentration. We first cultivated different starting concentrations of *P. syringae* within the LB agar plate, measured the OD₆₀₀, and recorded the SERS signals. As shown in **Figure S8A**, there was an obvious increase in OD₆₀₀ when the concentration was above 10⁶ CFU/mL following 24 h cultivation. For lower starting concentrations, the OD₆₀₀ signal could not be differentiated from the control. For the DMDS SERS signal, the concentration where there was a significant change in I_{680}/I_{77} was at 10⁷ CFU/mL (**Figure S8B**), which was 10× higher than that based on OD₆₀₀. We infer that the relatively low concentration of DMDS (<5 nM) when diluted within the headspace increased the detection limit. Compared to OD₆₀₀ and the DMDS signal, quantification of non-volatile metabolites (I_{733}/I_{658}) was improved over a lower initial concentration range (10⁵ to 10⁸ CFU/mL). When the concentration of *P. syringae* exceeded 10⁸ CFU/mL, I_{733}/I_{658} plateaued. In this case, I_{733}/I_{658} no longer changed due to the complete consumption of nutrients within LB. The combined SERS signals for both DMDS and nonvolatile substances can be used for bacterial quantification with good performance.

Diagnosis of viral infections. In real-world systems, bacterial metabolism can be affected by environmental conditions, especially following viral infection.^{64,65} The resulting alteration of bacterial metabolism may result in changes in the SERS signal. *P. syringae* was exposed to lytic bacteriophage Phi6 for 24 h and SERS spectra were collected. As shown in **Figure 4A**, following incubation with Phi6, no peaks arose for the volatile metabolites of *P. syringae*. Instead, the normalized intensities of the original peaks (e.g., I_{680}/I_{77}) decreased. The higher the initial Phi6 concentration, the greater the decline in the I_{680}/I_{77} ratio. This result suggests that Phi6 infection impedes DMDS production. The relative decrease in the DMDS SERS intensity can be used for Phi6 quantification. **Figure 4B** depicts the plot of I_{680}/I_{77} versus the initial Phi6 concentration. When the concentration ranged from 500 PFU to 50,000 PFU, I_{680}/I_{77} exhibited a good linear relationship versus the logarithm of the bacterial concentration.

The relationship between the SERS signal and phi6 concentration was more complicated

for non-volatile substances. As discussed previously, LB agar had a strong peak at $\sim 733\text{ cm}^{-1}$, which gradually shifted to $\sim 725\text{ cm}^{-1}$ and diminished during *P. syringae* cultivation. After 24 h, this peak completely disappeared and the peak at 658 cm^{-1} dominated. In the presence of Phi6, the SERS spectrum reflects an intermediate state between the fresh LB agar plate and 24 h incubated *P. syringae* (**Figure 4C**). Both peaks at $725\text{--}733\text{ cm}^{-1}$ and 658 cm^{-1} had strong intensities in the presence of Phi6. The peak ratio (I_{733}/I_{658}) changed with the initial Phi6 concentration and can be used for quantification. A linear relationship between I_{733}/I_{658} and the logarithm of Phi6 concentration was observed between 1,200 PFU and 50,000 PFU (**Figure 4D**).

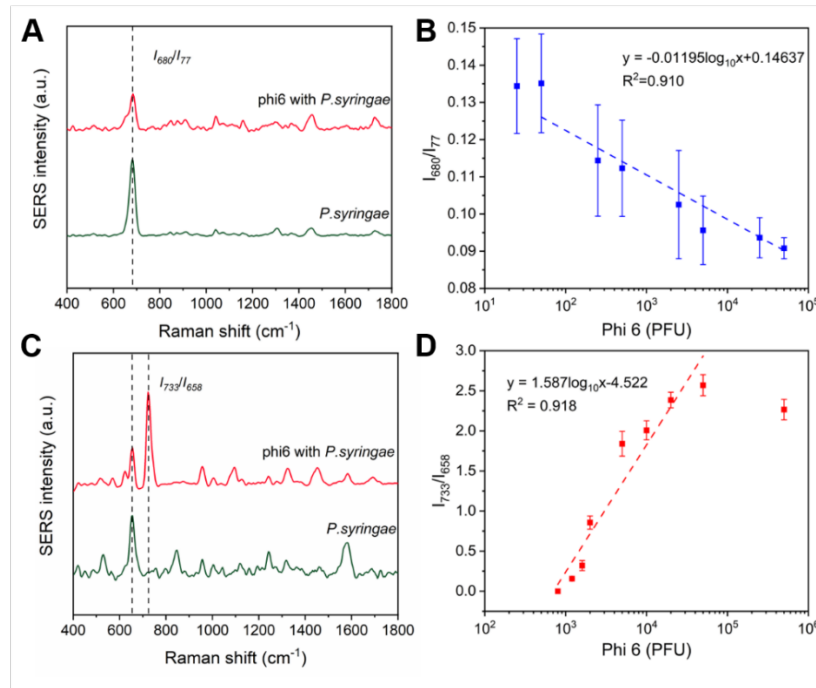


Figure 4. (A) SERS spectra of volatile metabolites of uninfected *P. syringae* and Phi6 (50,000 PFU) infected *P. syringae*; (B) the linear relationship between I_{680}/I_{77} and logarithm of Phi6 concentration (500-50,000 PFU); (C) SERS spectra of nonvolatile substances of *P. syringae* and Phi6 (10,000 PFU) infected *P. syringae*; (B) the linear relationship between I_{733}/I_{658} and logarithm of Phi6 concentration (1,200-50,000PFU).

It should be noted that the peak ratio changes detected for the non-volatile substances are do not uniquely reflect Phi6 infection. As discussed previously, both the cultivation time and the concentration of *P. syringae* can alter the ratio. For example, Phi6 ($\sim 10^4$ PFU) infected *P.*

354 *syringae* ($\sim 10^9$ CFU/mL) (**Figure 5A, curve a**) and *P. syringae* with a lower concentration
 355 ($\sim 10^7$ CFU/mL) (**Figure 5A, curve b**) had similar I_{733}/I_{658} ratios. It is possible, however, to
 356 use the entire SERS spectrum for viral infection diagnosis and unknown sample classification.
 357 To illustrate, we identified the 18 peaks present in both the *P. syringae* sample and in the Phi6
 358 infected *P. syringae* sample and normalized the spectra using I_{733} . Assignments of these peaks
 359 are listed in **Table S3**. Compared with *P. syringae* alone, the Phi6 infected *P. syringae* sample
 360 had an increased peak intensity at 957 cm^{-1} (phosphate or C=C deformation), but lower peak
 361 intensities at 526 cm^{-1} (S-S disulfide stretch in proteins), 842 cm^{-1} (glucose), 1092 cm^{-1} (C-C skeletal and C-
 362 O-C stretching from glycosidic link), and 1582 cm^{-1} (phenylalanine). Previous studies have
 363 shown that compared with uninfected controls, extracellular metabolites in phage infected
 364 bacterial samples have decreased concentrations.⁶⁴ The decrease suggests that surviving cells
 365 in the virus-infected cultures consumed materials from the lysed cells to support their
 366 metabolism, consequently depleting the selected metabolites and resulting in lower SERS
 367 intensities. Such subtle discrepancies cannot be differentiated by visual inspection of the SERS
 368 spectra. To achieve improved statistical classification, multivariate analysis was used to
 369 analyze the spectroscopic data.⁶⁶⁻⁶⁸ We used PCA to reduce the dimensionality of the 3600
 370 spectra collected from Phi6 infected samples and uninfected controls (2000 spectra for Phi6
 371 infected samples and 1600 spectra for uninfected controls). The first nine principal PCs ($\approx 95\%$
 372 of total spectral variance) were used for SVM classification. The classification results are
 373 summarized in **Figure 5B** in a confusion matrix form that indicates an overall accuracy of 93%
 374 can be achieved using SVM with a quadratic kernel. The sensitivity and specificity were 92.8%
 375 and 93.3%, respectively, as calculated from the PCA-SVM confusion matrix (**Table S4**).

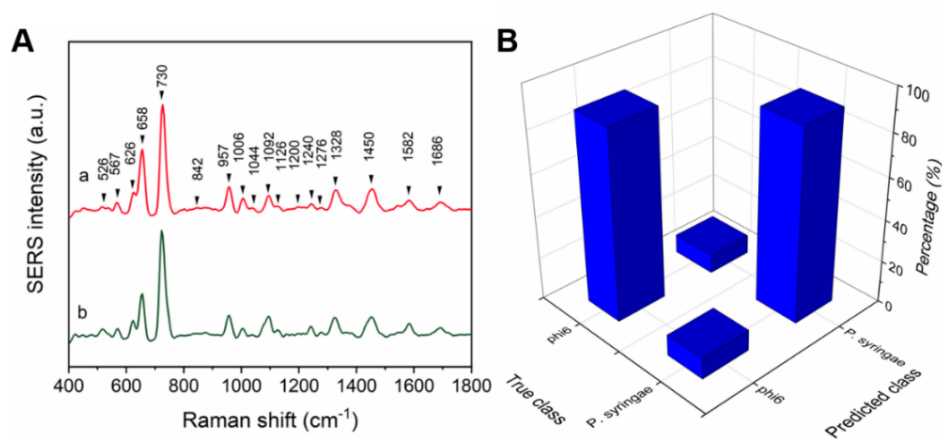


Figure 5. (A) SERS spectra of non-volatile substances of a) 10^4 PFU Phi6 infected 10^9 CFU/mL *P. syringae*; b), 10^7 CFU/mL *P. syringae*; (B) Histograms of confusion matrix for PCA-SVM ($n = 2000$ for 10^4 PFU Phi6 infected 10^9 CFU/mL *P. syringae* and $n = 1600$ for 10^7 CFU/mL *P. syringae*).

Environmental Implications. This study demonstrates the application of SERS detection of bacterial metabolites for both monitoring bacterial growth and diagnosis of viral infection. This method integrates the SERS signals of volatile metabolites in the headspace above a culture plate and non-volatile substances in the plate, thus providing detailed information about nutrient consumption, metabolite production, and bacterial growth. Compared with other conventional analytical methods, the present approach is especially promising for environmental analysis. Firstly, it can enable precise and rapid identification of bacteria without labor-intensive pretreatment work. Bacteria are ubiquitous and different sampling techniques as well as pretreatment methods are often required when sampling each matrix (e.g., water, soil, and air). The reported method is based on bacterial culturing and metabolic sensing and therefore, minimal pretreatment was required. The SERS results show comparable quantitative performance to classic culture based optical density measurements. Furthermore, the SERS tape is readily field-deployable, which can overcome sampling difficulties and minimize disturbances caused by the sampling process, especially in confined environments. We applied the same methodology to monitor another bacterium (*E. coli*) and its bacteriophage MS2. As expected, *E. coli* exhibits a different SERS pattern from *P. syringae* (Figure S9A).

Such spectral variation suggests that the fingerprint SERS profiles of these metabolites can enable accurate identification of bacterial species. When infected by bacteriophages, the host bacterial metabolism was altered in favor of viral replication and the alterations in the SERS signal, when coupled with multivariate analysis, can be used to diagnose viral infections. Our method could be successfully extended to diagnose MS2 infection by monitoring the metabolism of its host bacterium *E. coli* (**Figure S9B**). The results for both Phi6 and MS2 suggest that we can potentially apply this approach to measure other virus-cell interactions. Compared with traditional PCR, this method is capable to detect viable viruses and the SERS spectra can be collected on-site with the help of a portable Raman spectrometer. The results not only provide an alternative viral sensing method, but also suggest a feasible pathway to examine how environmental stimuli (pH, salinity, temperature, nutrients, antibiotics etc.) affect bacterial growth.

ASSOCIATED CONTENT

Additional information of SERS substrate characterization, Optical images with SERS results of *P. syringae* in a scan area, SERS results for DMDS quantification, PCA results, SVM results, SERS intensities of featured peaks, bacterial quantification results, SERS results for *E. coli* and MS2, bacterial metabolite list, kinetics fitting results, and SERS peak assignments (Figures S1-S9 and Tables S1-S4).

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