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Authors

Li, Runze
Goswami, Umang
King, Maria
et al.

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In situ detection of live-to-dead bacteria ratio after inactivation by means of synchronous fluorescence and PCA

Runze Li^a, Umang Goswami^a, Maria King^b, Jie Chen^c, Thomas C. Cesario^d, and Peter M. Rentzepis^{a,1}

^aDepartment of Electrical and Computer Engineering, Texas A&M University, College Station, TX 77843; ^bDepartment of Biological and Agricultural Engineering, Texas A&M University, College Station, TX 77843; ^cCenter for Ultrafast Science and Technology, Key Laboratory for Laser Plasmas (Ministry of Education), School of Physics and Astronomy, Collaborative Innovation Center of Inertial Fusion Sciences and Applications (CICIFSA), Shanghai Jiao Tong University, Shanghai 200240, China; and ^dSchool of Medicine, University of California, Irvine, CA 92697

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The determination of live and dead bacteria is of considerable significance for preventing health care-associated infection in hospitals, field clinics, and other areas. In this study, the viable (live) and nonviable (dead) bacteria in a sample were determined by means of their fluorescence spectra and principal component analysis (PCA). Data obtained in this study show that it is possible to identify bacteria strains and determine the live/dead ratio after UV light inactivation and antibiotic treatment, in situ, within minutes. In addition, synchronous fluorescence scans enable the identification of bacterial components such as tryptophan, tyrosine, and DNA. Compared with the time-consuming plating and culturing methods, this study renders a means for rapid detection and determination of live and dead bacteria.

bacteria inactivation | fluorescence spectroscopy | PCA

The determination of live and dead bacteria is of considerable significance in preventing health care-associated infection (HAI) in hospitals, field clinics, and other pathogen-containing areas. HAI is one of the top 10 causes of death in the United States (1) and up to 10% of hospital patients may develop HAI, which adds \$5.5 billion extra per year for patient treatment, as estimated by the National Center for Disease Control and Prevention (CDC). These infections transmitted in the hospital environments are especially important because they often are caused by antibiotic-resistant organisms such as methicillin-resistant *Staphylococcus aureus*, vancomycin-resistant *Enterococcus faecium*, *Pseudomonas aeruginosa*, and *Acinetobacter spp* (2). Hospitals cannot continuously search for contamination by these organisms because the monitoring of pathogenic bacteria presented in the environments is a time-consuming process that requires culturing such organisms. Therefore, a rather strong need exists for new surveillance methods that can detect microbial contamination before it causes HAI and continuously monitor for the presence of these bacterial strains and similar populations that cause infections. Likewise, a method to detect immediately bacteria found in wounds, particularly those occurring in remote areas, where neither time nor resources are available to adequately diagnose infection, and to determine if the bacteria were living or dead, would be very useful in initiating early appropriate therapy. In addition, illnesses caused by food-borne bacteria are a global concern that demands rapid detection of pathogens present in food to prevent epidemics of gastrointestinal disease. Early detection of these organisms and knowledge of their viability would be extremely beneficial in preventing outbreaks.

Furthermore, the rapid determination of the evolution of live-to-dead bacteria ratio over time may also be a critical means to determine antibiotic efficacy in treating a specific organism. The CDC has recently estimated that there are 2 million infections and 23,000 deaths a year caused by antibiotic-resistant organisms (3). These resistant organisms commonly found in health care facilities (4, 5) can be resistant to multiple drugs (6–9) and associated with higher mortality rates (10). The need to

accurately select the correct antibiotic therapy in this era has been made more acute because of the misuse of currently available antibiotics by inappropriate applications (11) and the fact that new antibiotic development has slowed (11, 12). However, patients currently being treated for an infection typically undergo a rather time-consuming process, which includes specimen collection, empiric initial antibiotic selection, and then waiting while the laboratory processes the specimen, cultures the organism, and completes antibiotic sensitivity testing (13). This traditional process can take a number of days in an era where timely (14) and effective treatment of severe infections can be lifesaving (15). Any method which would accelerate the assessment of antibiotic efficacy could permit essential changes in patient management before the septic process evolves to an irreversible state. Overall, the ability to determine rapidly antibiotic sensitivity and effectiveness is increasingly important as antibiotic resistance becomes a major threat.

Several methods have been proposed for the rapid identification of bacteria, including Raman and fluorescence spectroscopy (16). Three different genera of bacteria: *Escherichia*, *Salmonella*, and *Campylobacter* (all can cause gastrointestinal infections), have been also identified by means of synchronous fluorescence coupled with principal component analysis (PCA) (17). *Lactobacillus* and *Saccharomyces* have been characterized using autofluorescence (18). It may also be possible to classify bacteria strains by excitation at wavelengths that are different for each strain studied. For example, the most appropriate

Significance

The in situ and rapid detection of live and dead bacteria is crucial for preventing health care-associated infection in hospitals, field clinics, and other areas such as monitoring wound healings. Traditionally, determining the number of pathogenic organism involves specimen collection, appropriate culture on agar plates within laboratory environments, and counting the colony-forming units. These are very time-consuming procedures and could therefore increase the risk of infection or even death. In this paper, we demonstrate that the live/dead bacteria ratio after UV radiation and antibiotic treatment may be obtained easily, through a handheld spectrophotometer integrated with principal component analysis. Such procedures may provide a new way for the rapid detection and classification of live and dead bacteria in situ within minutes.

Author contributions: R.L., J.C., T.C.C., and P.M.R. designed research; R.L., U.G., and J.C. performed research; M.K. and J.C. contributed new reagents/analytic tools; J.C., T.C.C., and P.M.R. analyzed data; and R.L., U.G., J.C., and P.M.R. wrote the paper.

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¹To whom correspondence should be addressed. Email: prentzepis@tamu.edu.

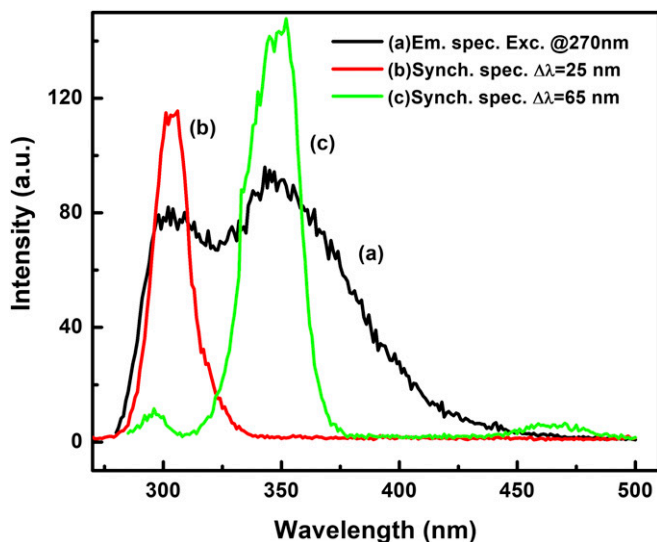


Fig. 1. (a) Conventional fluorescence spectrum of a tryptophan and tyrosine mixture in saline excited with 270-nm light. (b) The synchronous spectra of the same mixture scanned at $\Delta\lambda = 25$ nm show the tyrosine band with a maximum at 310 nm. (c) The synchronous spectra of the same mixture scanned at $\Delta\lambda = 65$ nm shows the tryptophan band with a maximum at 350 nm.

excitation wavelengths for *Escherichia coli* were found to be 410 and 430 nm, while for bacteria found in meat the best excitation wavelength was found to be 250 nm (19). Therefore, it is possible that those methods could provide an essential answer long before the more traditional method has been completed by reporting a decreased ratio of live-to-dead bacteria.

However, the devices used in previous studies are generally not portable and prolonged operations may be required before obtaining the results. The proper fluorescence recording device should be able to detect and identify in situ within a very short period of time for pathogens in clinics and remote areas and preferably be able to determine the ratio of live over dead bacteria at any time during treatment or after an inactivation process. This information will allow physicians to determine timely, more accurate treatment of infected patients. In this study, we present the design of a handheld fluorescence spectrometer, which coupled with PCA, demonstrates capability of in situ measuring live/dead bacteria ratio. This study renders a means for the rapid detection and classification of live and dead bacteria in situ within a few minutes.

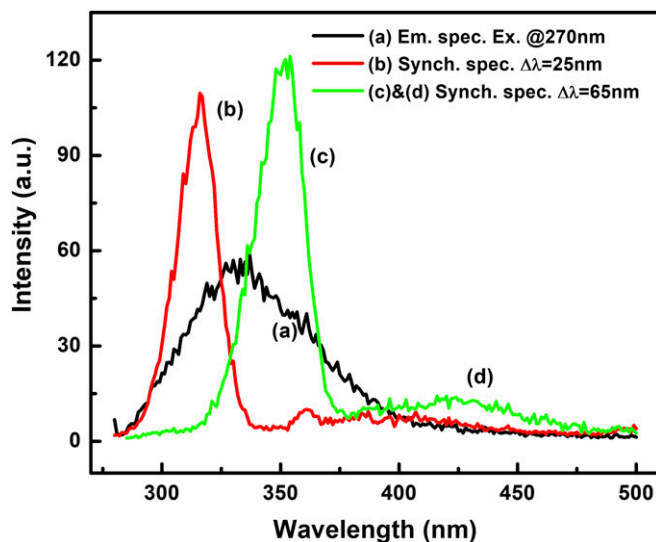


Fig. 2. (a) Fluorescence spectrum of *Bacillus* at 270-nm excitation wavelength. (b) *Bacillus* synchronous spectra scanned at $\Delta\lambda = 25$ nm show the tyrosine band at 310 nm. (c) *Bacillus* synchronous spectra scanned at $\Delta\lambda = 65$ nm show the tryptophan band at 350 nm and (d) the broad (410–470 nm) low-intensity DNA band.

Experimental

Synchronous Fluorescence. Synchronous fluorescence is often chosen as the method for bacteria and mixture components identification because it provides a means for selecting the most appropriate excitation (λ_{exc}) and emission (λ_{em}) wavelengths for their detection (20). In conventional fluorescence, the intensity of the emission spectrum depends on the excitation wavelength even though the general spectral features remain the same. However, in the synchronous fluorescence, the intensity I_s is a function of the intensity distribution E of both excitation and emission spectra:

$$I_s = kclE_{exc}(\lambda - \Delta\lambda)E_{em}(\lambda),$$

where k is a sample-dependent constant, c is the concentration of the fluorophore in the sample, and l is the optical beam path length.

While scanning the excitation and emission wavelengths simultaneously, the synchronous technique keeps a constant wavelength offset $\Delta\lambda = \lambda_{em} - \lambda_{exc}$, as shown in the above equation. By properly selecting $\Delta\lambda$, usually matching the difference between the absorption and fluorescence band maxima of the fluorophore of interest, the synchronous method could result in simplified fluorescence spectra with sharper peaks and narrow profiles compared with the conventional method. A rather typical illustration of the conventional and synchronous techniques relevant to bacteria-fluorescing components, tryptophan (Trp) and tyrosine (Tyr), is shown in Fig. 1. The normal fluorescence spectrum of a Trp and Tyr mixture in saline excited with 270 nm is depicted in Fig. 1A, which is composed of a

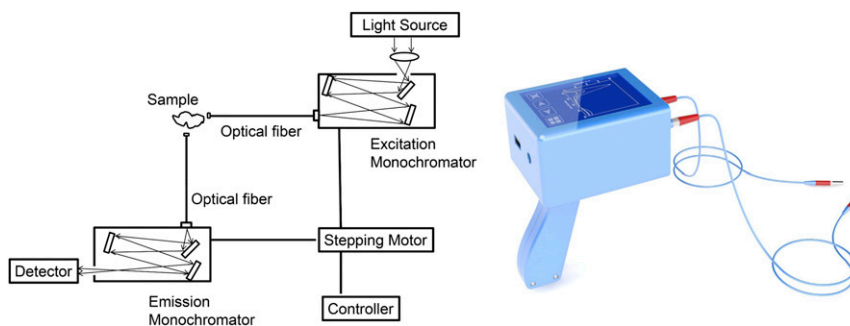


Fig. 3. (Left) Handheld spectrometer schematic. (Right) Conceptual design of the handheld spectrometer appearance with two optical fibers attached to the excitation and emission monochromators. When the two monochromators are coupled together, it allows for the recording of synchronous spectra at a preselected wavelength interval $\Delta\lambda$.

Table 1. *Bacillus* bacteria cell viability lost as a function of irradiation time

Irradiation time, min	Alive (viable)	Dead (nonviable)
0	○ ○ ○ ○ ○ ○ ○ ○	—
5	○ ○ ○ ○	× × ×
22	○	× × × × × ×

Each O and X corresponds to log₁₀ bacteria. Irradiation was performed with 5.5-mW/cm², 230–280-nm UV light.

minute of UV irradiation and then decreased continuously as a function of UV irradiation time. Similar results were also observed with *E. coli* bacteria. Because the fluorescence intensity is a measure of the concentration of the bacteria in the sample, a decrease in intensity designates a decrease in the number of bacteria per milliliter. The 330-nm peak displayed in the fluorescence spectra of *Bacillus* and *E. coli* is most probably due to tryptophan and therefore the initial increase and subsequent decrease in this fluorescence band intensity may correspond to an increase and subsequent decrease in tryptophan concentration. We performed similar experiments with Trp alone and mixtures of Trp and Tyr in water and saline solutions and did not observe any initial increase in the emission intensity, but only a continuous decrease of both the 330-nm intensity and the entire fluorescence spectrum as a function of irradiation time. We propose that some tryptophan, which was bonded to the bacteria membrane and therefore did not exhibit the same tryptophan emission maximum, was cleaved by the UV radiation, providing an additional amount of free tryptophan and thus the small initial increase in the 330-nm band intensity of *Bacillus* and *E. coli* spectra. We are performing additional experiments aimed at identifying the mechanism of the increase of the 330-nm bacterial fluorescence band during the first minute of UV irradiation. In addition, we are using Raman and coherent anti-Stokes Raman spectroscopy for the study of the Trp-membrane bond dissociation which may result in free Trp and thus help explain the observed increase in the 330-nm bacterial fluorescence band intensity maximum. Increasing the UV radiation time, or dose, results in the well-known degradation of Trp and consequently the decrease in the band intensity.

As noted above, plating data shown in Table 1 reveal that *Bacillus* viability is lost for 90% of the bacteria during the first 5 min of UV irradiation, which is similar to that found in *E. coli* under the same experimental condition. This is consistent with the bacterial membrane-Trp bond cleavage result, which generates some free Trp and forms a “hole” in the membrane that allows the UV radiation to penetrate through the bacteria wall, react with nucleic acid(s), and dimerize DNA. The measured inactivation response of both bacteria strains essentially suggests that only 100–500 cells per milliliter live bacteria remained, from the original 10⁷ cells per milliliter after about 10–20-min irradiation with 5.5-mW/cm² UV light. It has been proposed (26, 27) that a larger amount of respiratory bacteria survived after an equal irradiation dose. Microscopic examination of the bacteria samples we used indicated that before UV irradiation, the bacteria were single, or possibly in some cases paired; therefore, we consider the UV light interacts with nonaggregated bacteria. It

has been reported that at higher UV doses a small fraction remains unaffected, such as the 100–500 viable bacteria found in our studies after 20 min of UV irradiation. A possible reason is the formation of dead bacteria aggregates which envelop live bacteria and shield them from the destructive effects of UV irradiation. Microscopic studies suggest that aggregation does develop after prolonged irradiation. It is interesting to note that the resistance to inactivation observed in aggregated bacteria, which is widely believed to be dimerization of cellular nucleic acid, DNA, is not transmitted to successive generations. Therefore, we consider aggregation as a bacterial defense mechanism against radiation damage and other forms of stress which may also result in aggregation (28, 29).

Owing to the fact that treatment with antibiotics is a preferable means for bacteria disinfection, we treated 10⁸ cells per milliliter *E. coli* with 100 µg/mL Ampicillin for 5 min, 22 min, 4 h, and 24 h. Plating and overnight incubating show that after 5 and 22 min of Ampicillin treatment, the bacteria population did not change; however, about 10⁵ cells per milliliter bacteria were killed after 4 h of treatment and all bacteria were killed after 24 h of treatment. Using the same synchronous fluorescence and PCA method described above, the separation of live and dead bacteria after each treatment period were clearly displayed on plot. We are performing experiments with Ampicillin and other antibiotics to establish the value of this method in determining the identity and ratio of live/dead bacteria in situ within minutes.

The handheld synchronous spectrometer may also record normal and synchronous fluorescence spectra of bacteria mixtures of different strains. The characteristic spectra of each strain may be distinguished by the synchronous fluorescence, and the live/dead bacteria ratio could be revealed by PCA. In addition, this device may also make possible the identification of the components such as tryptophan, tyrosine, and DNA of many strains of bacteria.

Conclusion

The data presented in this paper show that it is possible to record in situ the normal and synchronous fluorescence spectra of bacteria and mixtures. Our data also show that by such techniques we may identify the components of bacteria and chemical mixtures and clearly display the fluorescence bands of the individual components. In addition, it is possible to distinguish between live and dead bacteria and determine the ratio of live/dead bacteria as a function of UV irradiation dose and antibiotic treatment that result in bacteria inactivation. It may even be possible to perform such assays directly on patient samples such as urine, cerebrospinal fluid, pleural fluid, or other body fluids either by adding antibiotics directly to these fluids and assessing the change in the ratio of live-to-dead bacteria or after the initiation of the treatment by determining the increasing proportion of dead bacteria.

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