Supplement A, October 2020
Volume 83
Pages 1–288
ISSN: 0362-028X

JFP

Journal of Food Protection®

Protecting the Global Food Supply

International Association for Food Protection®

jfoodprotection.org foodprotection.org

Significance: These data demonstrate that although SICs of these antimicrobials may not inhibit biofilm formation, HP and LAE are promising strategies to combat mature *Lm* biofilms.

T7-03 Development of a Dry Surface Biofilms Rapid Model for Disinfectant Testing

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❖ ***Developing Scientist Entrant***

Introduction: EPA-registered disinfectants are tested against planktonic bacteria or wet surface biofilms (WSB) although under actual use conditions, bacteria mainly exist as dry biofilms (DB) which are harder to inactivate than WSB.

Purpose: This study aimed to develop dry surface biofilm models of *Staphylococcus aureus* and *Pseudomonas aeruginosa* for subsequent use in EPA disinfectant testing, which requires six log CFU per coupon.

Methods: *S. aureus* ATCC-6538 and *P. aeruginosa* ATCC-15442 WSB were grown on glass coupons following EPA MLB SOP MB-19. Rods holding coupons were harvested from a CDC bioreactor and dried at 25°C or 30°C for *S. aureus* and at 16°C or 21°C for *P. aeruginosa* for 24 to 120 h. Three coupons with DB were harvested every 24 h for five days, processed to release DB from glass coupons, and grown on TSA or R2a agar for 48 ± 4h at 36°C following EPA MLB SOP MB-20. Scanning electron microscopy was used to visualize biofilm matrixes on coupons (N = 100) pre- and post-DB development.

Results: Overall, we achieved an average ≥6 log CFU per coupon biofilm post-drying regardless of temperature and dry time for both organisms. For *S. aureus,* significantly higher mean log densities per coupon were achieved after 24 h compared to 96 h and 120 h of drying (P < 0.05). For *P. aeruginosa* grown at 21°C, there were no significant differences in DB CFU density irrespective of time, (P > 0.05). Overall, 86% of coupons (86/100) with DB had a visible biofilm matrix.

Significance: The developed method is a viable *in vitro* model for disinfectant testing against DB, which represent a systematic challenge to the food industry.

T7-04 Meta-regression Models Describing the Effects of Essential Oils and Added Lactic Acid Bacteria on *Staphylococcus aureus* Inactivation in Cheese

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Introduction: Biopreservation methods based on the use of natural extracts and starter cultures have been proposed as hurdles to increase the microbiological safety of many food products, including cheese.

Purpose: This study's objective was to extract all published findings on *Staphylococcus aureus* (SA) inactivation in cheese containing essential oils (EOs) and added lactic acid bacteria (LAB) and unify them by constructing two separate meta-regression models.

Methods: Suitable primary studies were identified through exhaustive literature search. Twenty studies were considered appropriate for inclusion (N = 299), and the following information was extracted: antimicrobial class (EO or LAB) and name, mean log reduction, storage temperature, exposure time, antimicrobial application (i.e., cheese mixture, cheese surface, milk, or film), and antimicrobial and pathogen's inoculum concentrations. Studies were assigned weights according to the sample size (n) used along the experiment to evaluate microbial inactivation.

Results: The EOs model revealed the significant impact of application type (P < .0001), storage temperature (P < .0001) and inoculum concentration (P = 0.019) on SA microbial reduction. Additionally, exposure time and antimicrobial concentration affected SA inactivation, although those effects were dependent on the type of application (P < .0001). Cheese mixture and milk were found to be the matrices promoting the highest microbial reduction, whereas incorporation in films presented the lowest inhibitory effect. Among the types of EOs meta-analyzed, lemon balm and sage produced the greatest mean bactericidal effects. The LAB model did not show differences (P = 0.091) in the inhibitory effect achieved by different applications (milk or cheese mixture), but revealed the interaction between this term and exposure time (P = 0.040). Heterogeneity analysis showed that the moderators of the EO and LAB models explain >95% and 11.80% of the between-antimicrobial variability, respectively.

Significance: The meta-regression models produced provide valuable insight on the main causes of variability in microbial reduction, which is vital when implementing and optimizing biopreservation hurdle technologies for pathogen control in foods.

T8-01 GenomeTrakr Best Practices for Uploading Sequence Data to NCBI: Assuring Good Sequence Quality and Proper Data Curation

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Introduction: The GenomeTrakr surveillance network of laboratories collects genomic data for foodborne pathogens isolated from non-clinical sources (e.g., food, environmental, water). These data are submitted to NCBI's pathogen surveillance platform called NCBI Pathogen Detection (NCBI-PD) to aid in traceback and regulatory actions. Until 2019, the FDA brokered most of these submissions for nearly 50 GenomeTrakr laboratories, receiving genomic data and metadata, performing quality control, and submitting to NCBI.

Purpose: As founders of GenomeTrakr, with extensive experience in managing an open genomic surveillance platform for foodborne pathogens, we are pleased to share our Best Practice guidelines here.

Methods: In 2019 GenomeTrakr released an SOP for PulseNet laboratories to independently submit their GenomeTrakr isolates to NCBI-PD through the software platform, BioNumerics. With the release of "Optimizing open data to support One Health: Best practices to ensure interoperability of genomic data from microbial pathogens" (2020), GenomeTrakr laboratories, or any laboratory interested in participating in open genomic pathogen surveillance, will find detailed guidance for directly contributing sequence and metadata to NCBI-PD.

Results: These Best Practices include four new protocols, hosted on a version-controlled web platform, protocols.io. They include detailed step-by-step protocols to assess sequence quality, to populate the metadata template using standardized vocabulary, to submit genomic data and metadata to NCBI, and to maintain and curate public data submitted by your laboratory.

Significance: The best practices document will improve workflow efficiency by eliminating the FDA as a data broker as well as assure that acceptable quality standards are preserved as the process becomes decentralized. Importantly, these tools and SOPs are written for *any* laboratory wishing to submit microbial pathogen data to NCBI, which, we hope, will democratize the process, increasing participation for all open genomic pathogen surveillance efforts.