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Towards a better understanding of the ecology of *Listeria monocytogenes* in pork processing facilities



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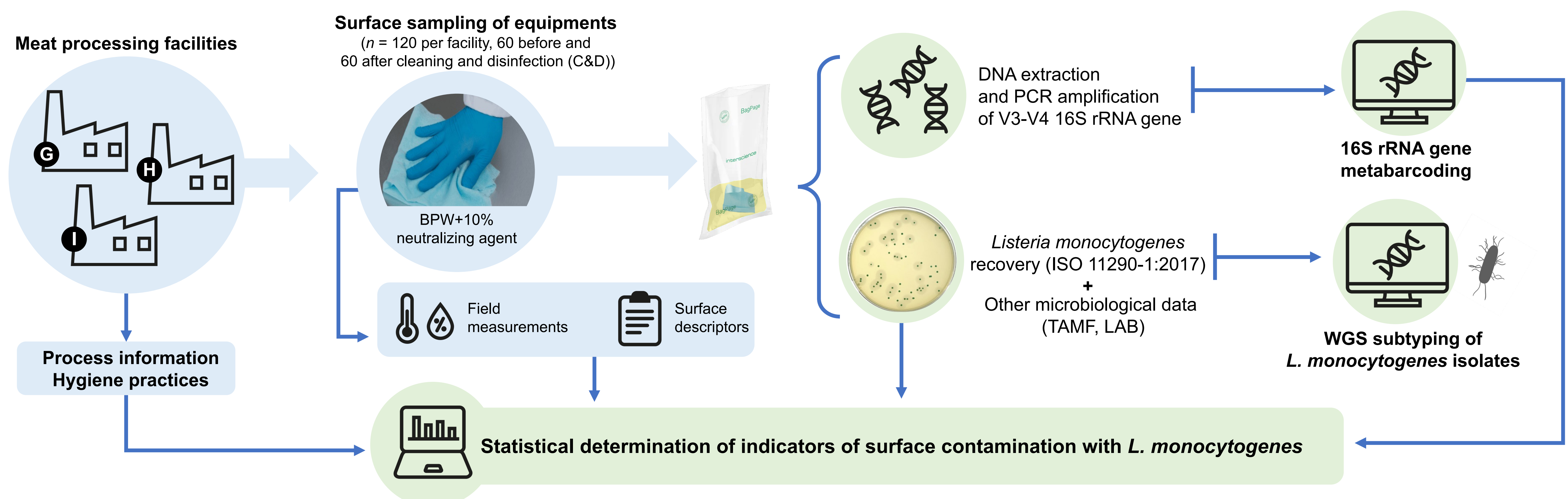


Introduction

Listeriosis is one of the most serious and severe foodborne diseases caused by the bacteria *Listeria monocytogenes*. A gradual increase in listeriosis cases was observed across all EU/EEA countries from 2019 to 2023, with 2 993 confirmed cases of listeriosis reported in 2023 (ECDC, 2025). This pathogenic bacterium is well-adapted to the adverse conditions encountered in the food processing environments and can survive for long periods on industrial surfaces.

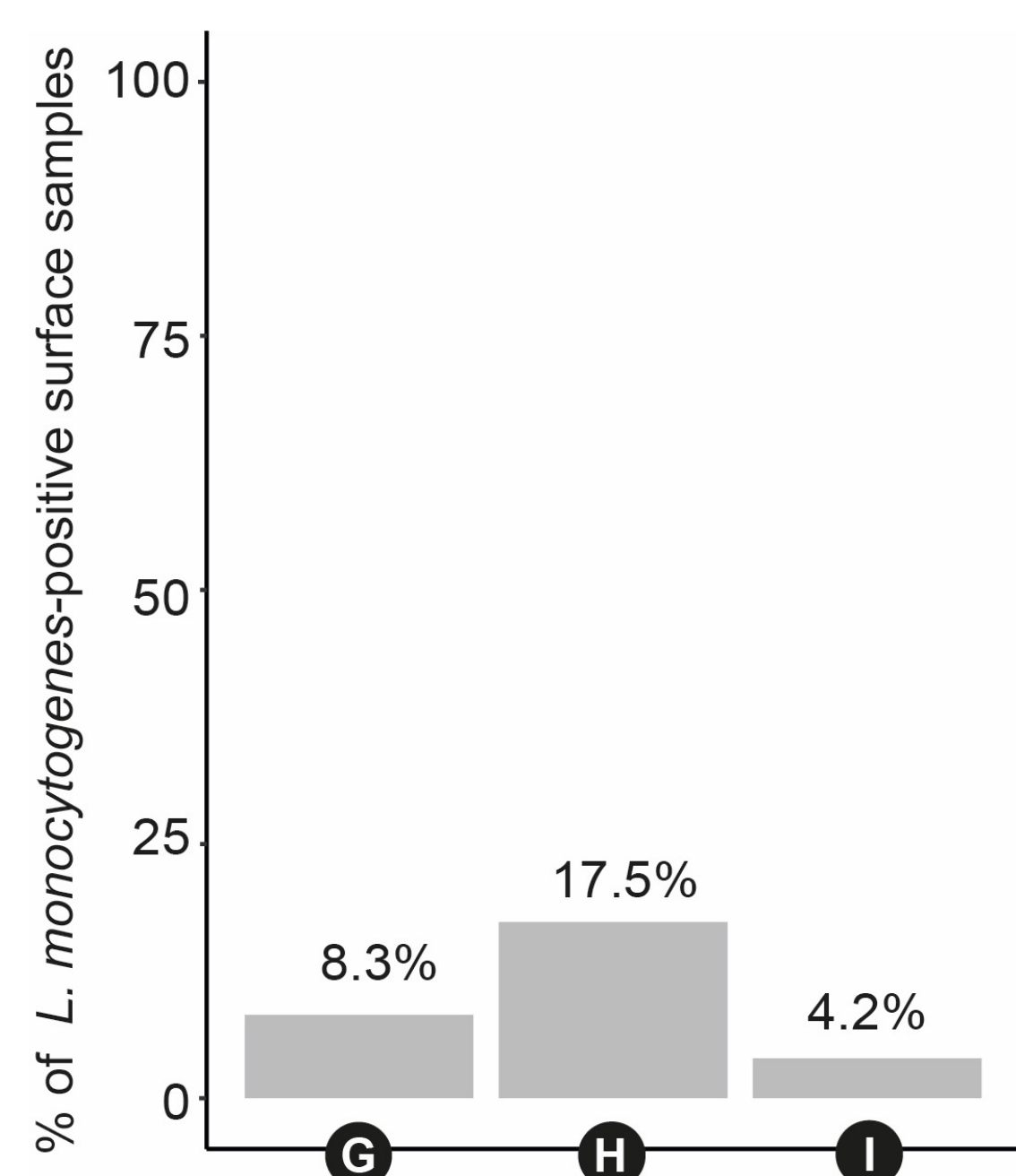
The French ANR SUBLIM Research program (ANR-22-CE21-0010-01) aims to develop an integrative approach to better understand the combined effects of multiple factors on the establishment of *L. monocytogenes* in various food processing environments, and to define reliable biological and environmental indicators of the presence of this pathogen on food processing surfaces.

Materials and methods



Results

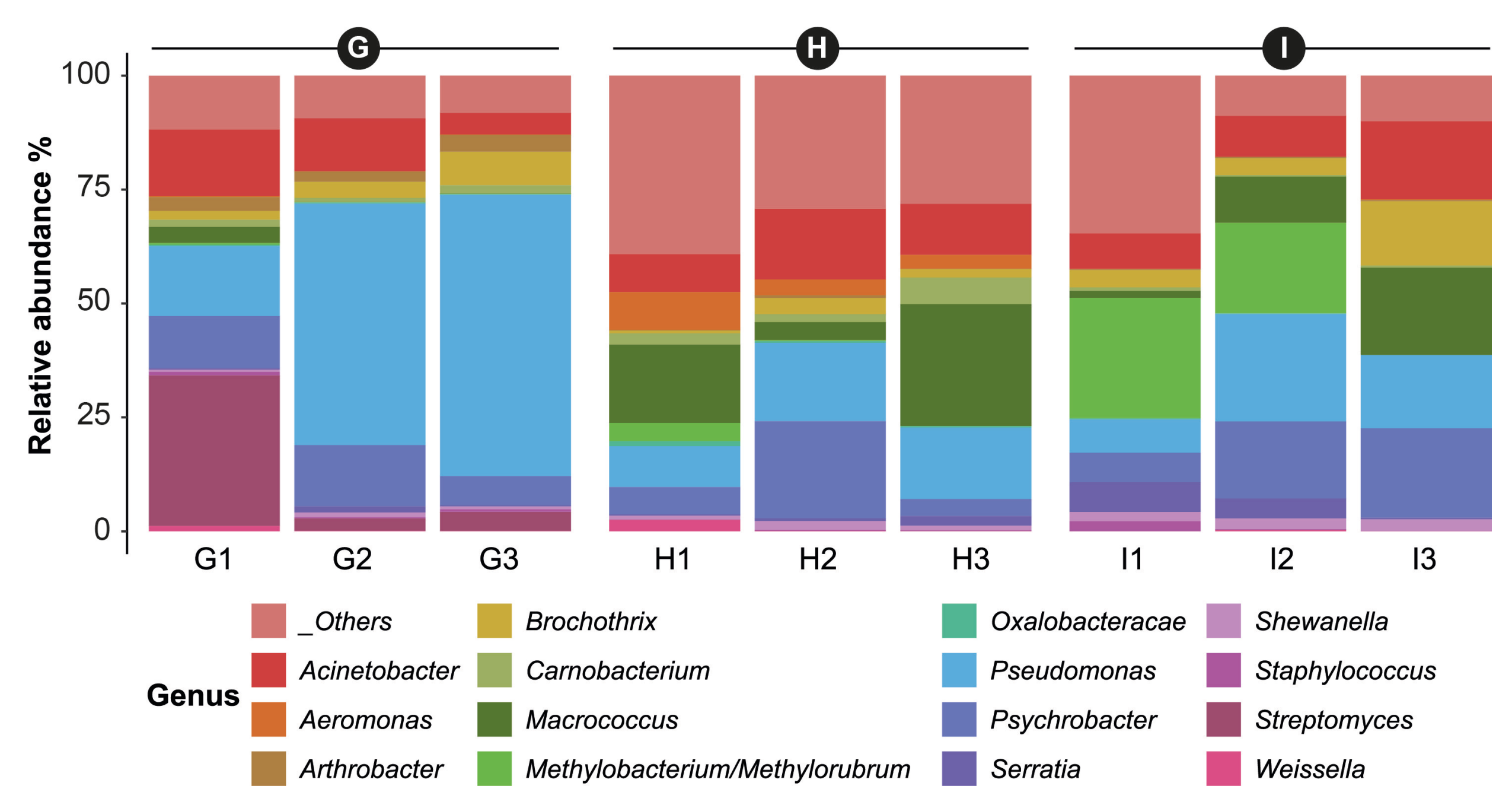
- Occurrence and diversity of *L. monocytogenes* in surface samples collected from the three pork processing facilities (noted G, H and I)



Clonal complexes	No. of isolates†	No. of positive locations		
		Total	After C&D only	High hygiene areas only
CC5	11	5 ^{(2)*}	3	0
CC9	5	5 ⁽²⁾	1	0
CC8	4	3 ⁽²⁾	1	1
CC1	3	3 ⁽²⁾	0	2
CC412	3	3 ⁽¹⁾	1	0
CC37	2	1 ⁽¹⁾	0	0
CC121	2	2 ⁽¹⁾	0	2
CC6	1	1 ⁽¹⁾	1	0
CC14	1	1 ⁽¹⁾	0	0
CC20	1	1 ⁽¹⁾	0	0
CC77	1	1 ⁽¹⁾	1	0
CC224	1	1 ⁽¹⁾	1	0

† One out of the 36 isolates cannot be recovered due to loss of cultivability
* () No. of facilities

- Mean relative abundances of bacterial communities obtained from all surface samples in each pork processing facility (noted G, H and I) at each sampling campaign (noted 1, 2 and 3)



Conclusion

L. monocytogenes was detected in 36 (10%) out of 360 surface samples collected from the three meat processing facilities. Most of the CCs recovered in this study were previously described in the French pork processing chain. Especially, CC1 and CC6 are known to include hypervirulent strains. *Acinetobacter*, *Pseudomonas* and *Psychrobacter* genera were part of the core microbiota occurring on the surfaces sampled from all the facilities. Based on the classification tree model generated from the 16S metabarcoding datasets, the probability that a sample tests positive for *L. monocytogenes* was approximately 79% when the relative abundance of the genus *Acinetobacter* spp. was greater than 379 sequences. Further analysis will permit to determine other factors co-occurring with the presence/absence of *L. monocytogenes*. This work will provide improved understanding of the ecology of *L. monocytogenes* in food processing environments that will help implement effective strategies to mitigate the risk of *L. monocytogenes* contamination.