Exploring Persistence Markers through Fatty Acid Profiles of *Listeria monocytogenes* under Distinct Temperature Conditions

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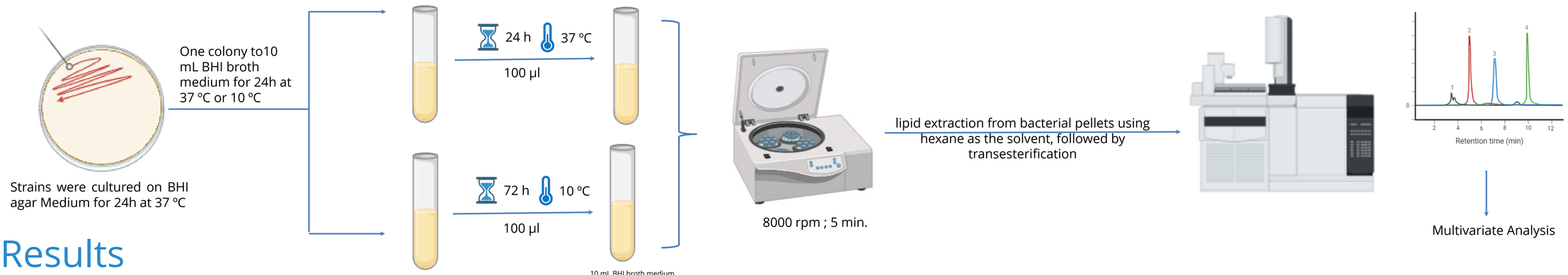
Introduction

Listeria monocytogenes, the causative agent of listeriosis, is a major foodborne pathogen. It is a ubiquitous, facultative anaerobic, gram-positive bacterium. Listeriosis can be a severe illness particularly affecting vulnerable groups: the elderly, immunocompromised individuals, pregnant women and neonates. *Listeria monocytogenes* exhibits remarkable adaptability to diverse and challenging environments, demonstrating an exceptional capacity to thrive in conditions such as refrigeration temperatures or high salt concentrations or other factors found in food processing environments (FPE). This resilience is a key factor in its ability to persist within food processing facilities and proliferate in various food products. Only certain strains are routinely isolated from these FPEs (persistent strains) while others are isolated sporadically (non-persistent strains).

Objectives

This study aimed to identify fatty acids that could serve as persistence markers in isolates from the GenoPhenoTraits4Persistence collection, classified as persistent (P) or non-persistent (NP)

Methods



Results

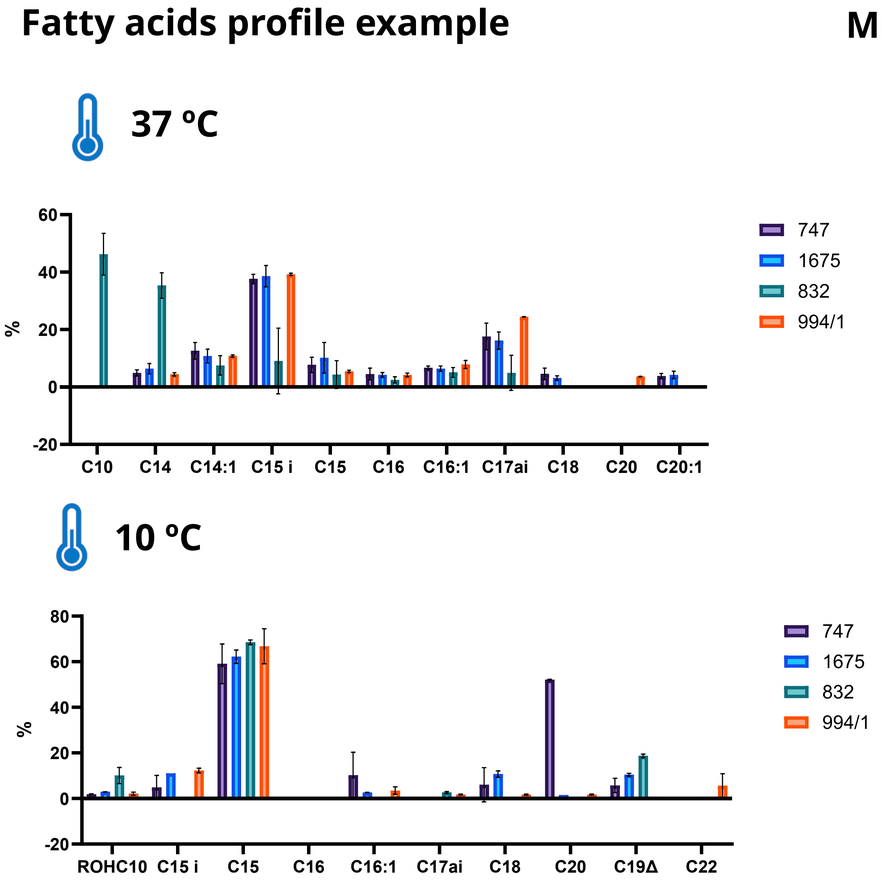


Figure 1– Fatty acids profile.

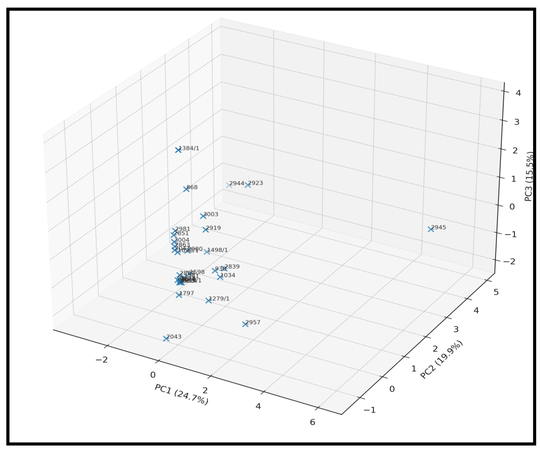


Figure 2– 3D PCA displaying global variance structure (PC1, PC2, PC3) of fatty acid profiles among all isolates.

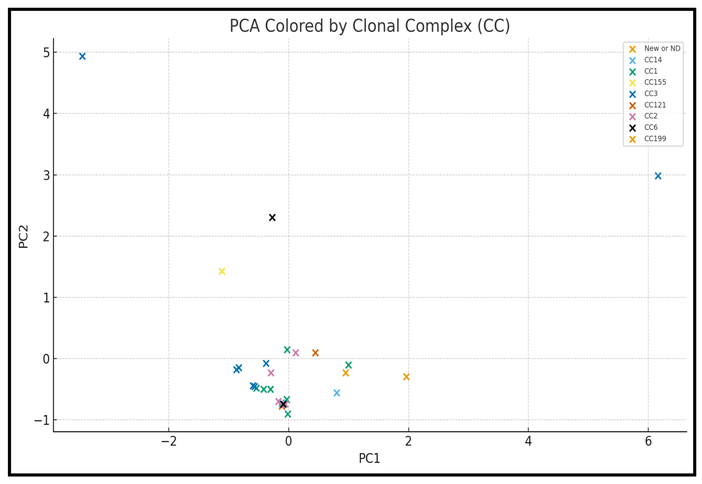


Figure 3 – PCA according to Clonal Complex, highlighting genetic lineage-specific clustering patterns.

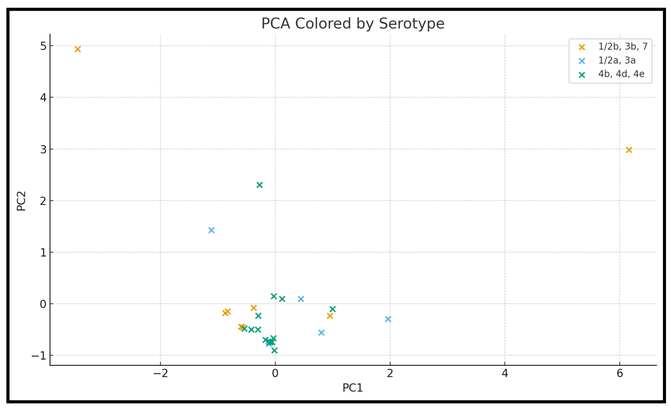


Figure 4 - PCA by serotype groups 1/2a, 1/2b, and 4b distribution.

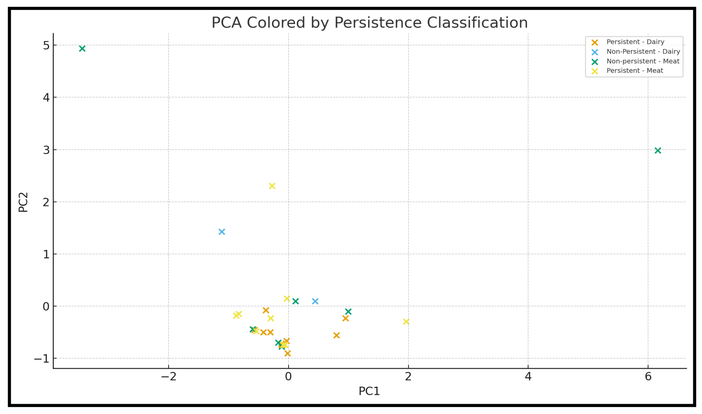


Figure 5- PCA according to persistence status in dairy or meat processing environments.

Conclusions

Fatty acid profiles at 10 ˚C demonstrate clear clustering according to clonal complex, indicating that membrane lipid composition is predominantly influenced by genetic lineage. Variations in persistence status do not account for differences in lipid profiles, implying that persistence in food-processing environments is governed by factors beyond membrane fatty acid composition. The detection of branched-chain fatty acids iso-C15 and iso-C17, along with ΔC19 at low temperatures, underscores their significance in *L. monocytogenes* adaptation to environmental stresses, particularly temperature changes and membrane fluidity regulation. Principal component analysis (PCA) confirmed strong clustering of fatty acid profiles by clonal complex, reinforcing the role of genetic background in shaping membrane lipid composition. Persistence status failed to explain the variability observed, suggesting that survival in food-processing settings depends on mechanisms other than fatty acid makeup. These lipid markers will be further investigated to determine their potential role in the adaptation and resilience of these strains under challenging conditions.

Acknowledgements

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