Growth patterns of luminous Photobacterium on chilled chicken meat and genotypic characterization of individual isolates

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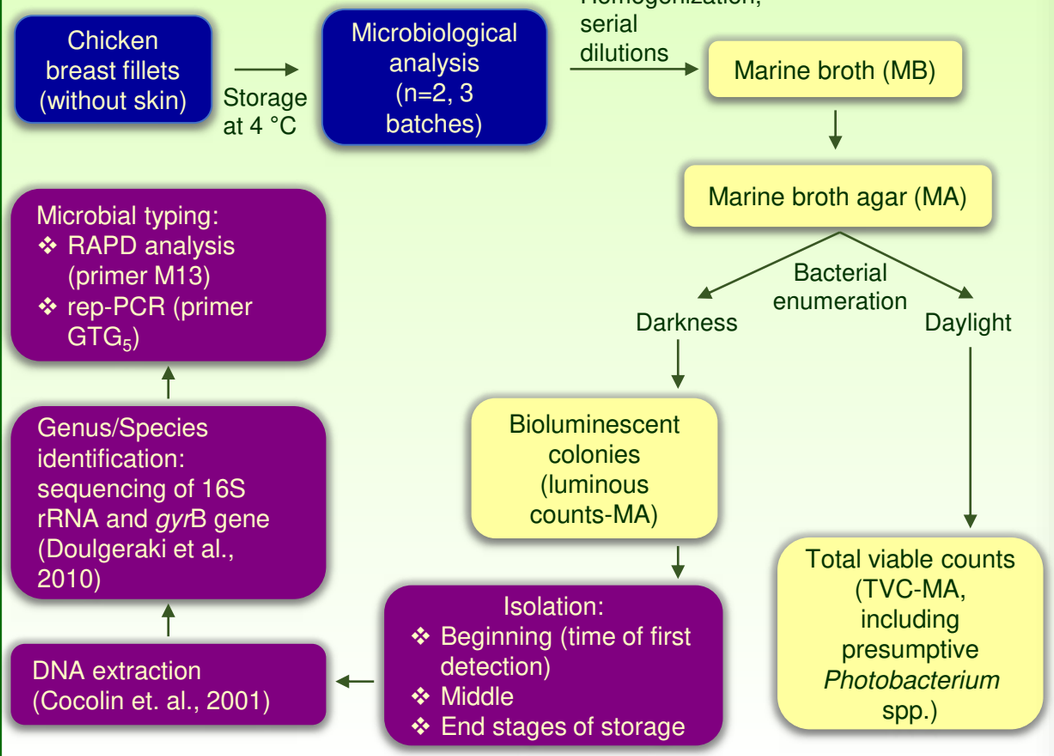
INTRODUCTION

Chicken meat spoilage is caused by a dominant fraction of the initial microbial association that consists mainly of *Pseudomonas*, *Brochothrix thermosphacta*, *Enterobacteriaceae* and lactic acid bacteria (LAB). The recent application of next generation sequencing technologies on spoiled chicken meat has revealed the presence of *Photobacterium* genus at significantly high abundances.

AIM

This study aimed to: a) assess the presence and growth patterns of luminous *Photobacterium* on chicken breast fillets during refrigerated (4°C) storage and b) estimate their genotypic biodiversity.

MATERIALS AND METHODS



CONCLUSION

The relatively high numbers of luminous *Photobacterium* along with the genotypic differentiation suggest this genus as potential chicken meat spoiler with high genetic diversity.

Acknowledgment

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RESULTS AND DISCUSSION

- Luminous bacteria were scarcely encountered at the beginning of storage in one out of three batches at *ca*. 2.0 log CFU/g (Figure 1).
- They were found at significantly higher populations, ranging from 5.3 to 7.0 log CFU/g, at later stages of storage in samples from two batches.
- In the third batch, they were only occasionally enumerated throughout storage at populations of up to 3.9 log CFU/g.
- Ninety luminous *Photobacterium* isolates were recovered from chicken breast fillets during storage (Figure 2).
- Pattern similarity based on RAPD-PCR and REP-PCR fingerprint profiles allowed the discrimination of bacterial isolates in 18 clusters when a coefficient of similarity of 85% was used (Figure 3).
- So far, the sequence of the two genes assigned representative number of isolates to *Photobacterium phosphoreum*.

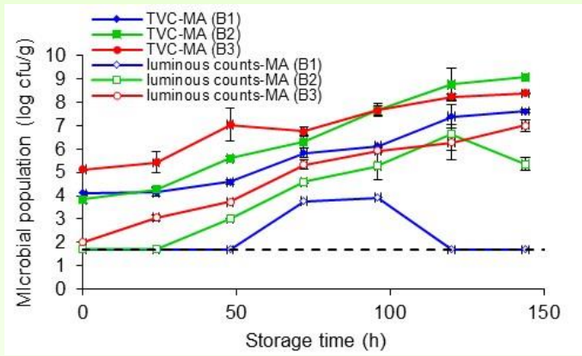

Figure 1. Evolution of TVC (bold symbols) and luminous bacteria (open symbols) on chicken breast fillets stored at 4°C for each of the three experimental batches (B1-B3), as enumerated on MA medium (mean ± standard deviation, n=2). The detection limit (- - - - -) of the enumeration method was 1.7 log CFU/g.

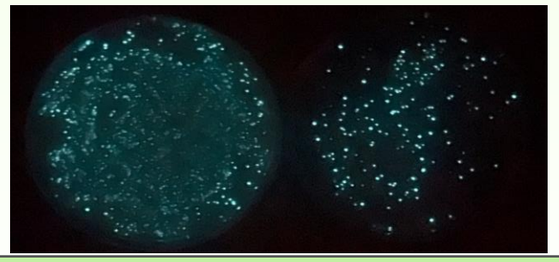

Figure 2. Luminous *Photobacterium* on chicken breast fillets stored for 6 days at 4 °C as enumerated on MA.

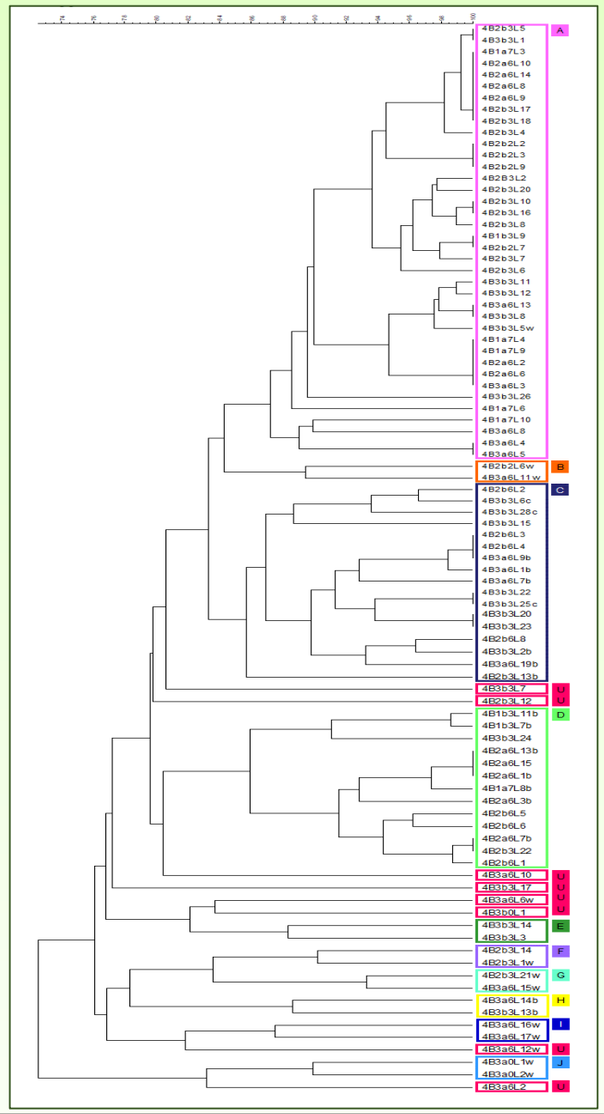

Figure 3. Cluster analysis of RAPD-/REP-PCR patterns obtained with primers M13 and GTG_5 of the 90 bacterial isolates applying combined analysis of fingerprint data, the Pearson coefficient and the unweighted pair group method using arithmetic averages (UPGMA). Genotype clusters appear on the right with different letters in colored rectangles. U letter represents unique isolates.