Accepted Manuscript

Changes in the microbial communities in vacuum-packaged smoked bacon during storage

Xinfu Li, Cong Li, Hua Ye, Zhouping Wang, Xiang Wu, Yanqing Han, Baocai Xu

PII: S0740-0020(18)30179-5

DOI: 10.1016/j.fm.2018.08.007

Reference: YFMIC 3064

To appear in: Food Microbiology

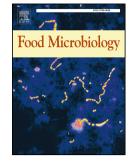
Received Date: 1 March 2018

Revised Date: 15 August 2018

Accepted Date: 16 August 2018

Please cite this article as: Xinfu Li, Cong Li, Hua Ye, Zhouping Wang, Xiang Wu, Yanqing Han, Baocai Xu, Changes in the microbial communities in vacuum-packaged smoked bacon during storage, *Food Microbiology* (2018), doi: 10.1016/j.fm.2018.08.007

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.



ACCEPTED MANUSCRIPT

1 Changes in the microbial communities in vacuum-packaged smoked

2 bacon during storage

3

4 Xinfu Li^{1a,b,d}, Cong Li^{a,b,d}, Hua Ye^{a,b}, Zhouping Wang^{a,b}, Xiang Wu^d, Yanqing Han^d,
5 Baocai Xu^{b,c,d*}

^a State Key Laboratory of Food Science and Technology, Jiangnan University, Wuxi 214122,
China

8 ^b School of Food Science and Technology, Jiangnan University, Wuxi 214122, China

^c School of Food Science and Engineering, Hefei University of Technology, Hefei, 230009, China

^d State Key Laboratory of Meat Processing and Quality Control, Yurun Group, Nanjing, 211806,

11 China

12 ABSTRACT

This study aimed to gain deeper insights into the microbiota composition and 13 population dynamics, monitor the dominant bacterial populations and identify the 14 specific spoilage microorganisms (SSOs) of vacuum-packed bacon during refrigerated 15 storage using both culture-independent and dependent methods. High-throughout 16 sequencing (HTS) showed that the microbial composition changed greatly with the 17 prolongation of storage time. The diversity of microbiota was abundant at the initial 18 19 stage then experienced a continuous decrease. Lactic acid bacteria (LAB) mainly Leuconostoc and Lactobacillus dominated the microbial population after seven days 20 of storage. A total of 26 isolates were identified from different growth media using 21 traditional cultivation isolation and identification method. Leuconostoc mesenteroides 22 23 and *Leuconostoc carnosum* were the most prevalent species since day 15, while Lactobacillus sakei and Lactobacillus curvatus were only found on day 45, 24 suggesting that they could be responsible for the spoilage of bacon. Serratia, Rahnella, 25 Fusobacterium and Lactococcus underwent a dramatic increase at some point in 26

E-mail address: baocaixu@163.com (B. Xu)

^{*} Corresponding author. School of Food Science and Technology, Jiangnan University, Wuxi, Jiangsu 214122, P.R. China

Download English Version:

https://daneshyari.com/en/article/8946042

Download Persian Version:

https://daneshyari.com/article/8946042

Daneshyari.com