

STUDY ON MICROORGANISMS FLORA DURING JINHUA HAM FERMENTATION

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Introduction

Jinhua ham belongs to dry-cured meat products, originating in the end of Northern Song Dynasty, that was 900 years ago. It is the most famous traditional meat product home and abroad, which ranks with Xuan Wei ham and Ru Gao ham as “three hams” in China. which make them become meat products with distinct flavour. Typical dry-cured hams all become meat products with characteristic flavour after curing, seasoning and dehydration, fermentation and ripening.

Material and methods

Studied ham which produced by traditional processing technology of Zhejiang Lanxi City Yongxin Limitid Company.

proteose peptone, beef sream yeast decoction, Ammonium, glucose, K_2HPO_4 , $MgSO_4 \cdot 7H_2O$, $MnSO_4 \cdot 4H_2O$, ect. All other chemicals and glass were purchased from Chongqing Glass and Chemical Reagent Company.

Main Equipment: OLYMUPUS Microscope (Olympus Co.LTD), MotiC-AE31 Microscope Photo (MotiC China Group Co.LTD).

Flora count determination was referred to methods of GB-T4789.2-2003. Bacterier identification was referred to Microbiology Exprimantal Handbook (Deqing Zhou, Fudan University). Make classical determination of morphologic characteristics, physiological and biochemical characteristics, ecological characteristics and so on.

Results and discussion

Change of microbial counts in pre-fermentation. Pre-fermentation was the stage that hams hung to dry, entering to fermentation room, then after “repairing with knife”. Temperature and humidity were proper at this time, water content of hams was still higher. So the surface and interior microorganisms of ham were most at the stage.

Microbial change in post-fermentation. Temperature gradually increased in post-fermentation, microbial counts would steadily decreased.

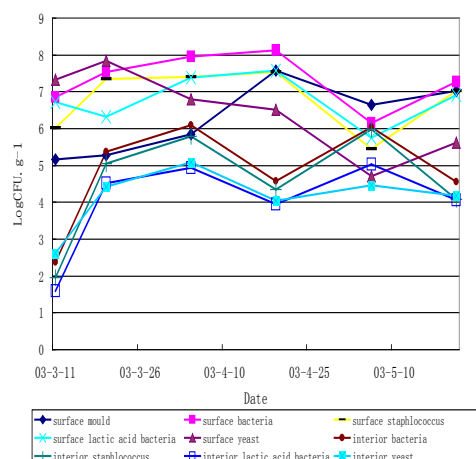


Figure 1 Change of microbial counts in pre-fermentation

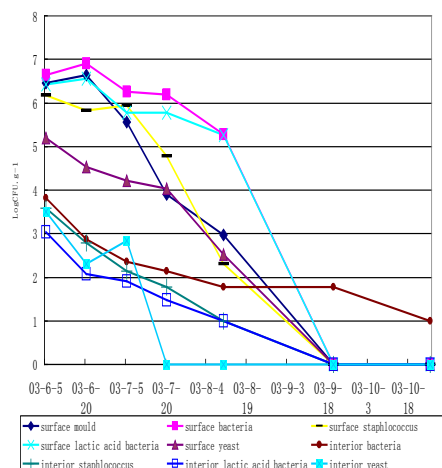


Figure 2 Change of microbial counts in post-fermentation

Conclusions

Maximum of microbe interior ham get 10^6 cfu/g, which was enough to influence flavour of ham. But the count decreased to low values ($<10^3$ cfu/g) in the ripening period(June to August), so we deduced that the aroma of ham produced by both Microbacterial enzymes and interior enzymes of ham in the later ripening period.

The microflora on the surface of Jinhua ham influenced each other, but moulds on the surface really affected interior microbial counts. In the early stage, both increased, when mould counts increased to a certain level, it would inhibit growth of interior microbe, so the counts dropped; but when mould counts dropped, interior bacteria counts increased.

Micrococcaceae predominated in bacteria throughout the curing and maturation processes, Lactic acid bacteria also had a large mount. The predominant spp. were *Staphylococcus xylosus*, *Staphylococcus lugunensis* and *Micrococcus varians*. *Pediococcus pentosaceus*, *P. urinaeequi* and *Lactobacillus alimentarius* predominated in Lactic acid bacteria.

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