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**SMRT sequencing analysis of bacterial community in home-made paocai brine with different salt concentration****Jialu Cao and Liebing Zhang**

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Salt concentration is crucial to paocai saline taste and microflora, which have marked effects on paocai quality and flavor. This paper discusses the bacterial community of aged, home-made paocai brine with different salt concentration using single-molecular, real-time (SMRT) sequencing. Thirty-seven samples were divided into low (<8%, LS) and high (>8%, HS) salt concentration groups based on the common salt concentration. Our results revealed significant differences in bacterial compositions between LS and HS groups. Most samples from the LS group had higher relative abundance of lactic acid bacteria (LAB) species such as *Lactobacillus (Lb.) acetotolerans*, *Pediococcus ethanolidurans*, *Lb. buchneri*, and *Lb. verismoldensis*, whereas those from the HS group housed more *Ochrobactrum (O.) lupini*, *Lb. brevis*, a few opportunistic pathogens (*Enterobacter (E.) cloacae*, *Serratia (Ser.) marcescens* and *Klebsiella (Kle.) pneumoniae*) and some other low-abundance bacteria. Salt concentration was also positively correlated to *Lb. brevis*, *Lb. namurensis*, *O. lupini*, *Ser. marcescens* and *Kle. pneumoniae*, but negatively linked to *Lb. acetotolerans* and *Lb. buchneri*. The variations in bacterial community structure between LS and HS groups were also confirmed by multivariate statistical analyses. These results indicated that high salt concentration (>8%) did not decrease but even favored the survival or growth of certain undesired bacteria and inhibited some LAB in the aged, home-made paocai brine.

**Biography**

Jialu Cao is a PhD student in China Agricultural University, Beijing, China. Her PhD project is bacterial diversity and lactic acid bacteria in home-made paocai. In her study, she applied single molecular real time (SMRT) sequencing technology to analysis the bacterial community of paocai (traditional fermented vegetables in southwest area of China) for the first time. This approach provides accurate taxonomic classification at species level.

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