

**Keywords** mixed bacteria; biofilm; extracellular polymorphs

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## 新疆发酵辣椒酱中关键产香微生物的筛选及验证

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**摘要** 微生物代谢是影响发酵食品风味品质的重要因素。为了明确微生物在发酵辣椒酱关键香气形成中的作用,本研究借助高通量测序技术解析了发酵辣椒酱的微生物组成,利用气相色谱-嗅觉分析技术结合香气活性值识别出关键香气化合物,基于统计学分析和回接验证实验阐明了微生物与关键香气化合物的关系。结果表明,*Lactobacillus* 是新疆发酵辣椒酱主要的细菌属,*Alternaria*、*Kazachstania* 和 *Debaryomyces* 等是主要的真菌属;芳樟醇、苯乙醇、水杨酸甲酯等 11 种物质被确定为发酵辣椒酱的关键香气化合物;相关性分析结果表明,*Kazachstania* 和 *Zygosaccharomyces* 与绝大多数的关键香气物质呈显著正相关,而优势菌属 *Lactobacillus* 与大部分香气物质呈显著负相关;回接验证结果证明,*Zygosaccharomyces bisporus* 产香能力最为突出,与乙酸酯类关键香气物质的形成密切相关,*Kazachstania humilis* 产香能力次之,与短链羧基化合物的形成密切相关,而 *Lactiplantibacillus plantarum* 产香能力最弱。以上研究结果可为揭示发酵辣椒风味形成机制和发酵食品品质的科学调控提供参考。

**关键词** 发酵辣椒酱;微生物多样性;香气化合物;相关性分析;验证

## Identification and validation of vital microbes that promote aroma formation in fermented pepper pastes from Xinjiang

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**Abstract** Microbial metabolism is an essential factor affecting the flavor quality of fermented foods. To clarify the roles of microbes in aroma formation, this study analyzed the microbial composition of fermented pepper pastes with high-throughput sequencing technology and identified key aroma compounds using gas chromatography-olfactory analysis combined with aroma activity values. Then, statistical analysis and validation experiments were used to clarify the relationships between microbes and key aroma compounds. The results showed that *Lactobacillus* was the dominant bacterial genus and *Alternaria*, *Kazachstania*, and *Debaryomyces* were the main fungal genera of fermented pepper pastes. Eleven substances (e.g., linalool, phenylethyl alcohol, and methyl salicylate) were identified as key aroma compounds. Correlation analysis showed that *Kazachstania* and *Zygosaccharomyces* were significantly positively correlated with most key aroma substances, while the dominant genus *Lactobacillus* was significantly negatively correlated with them. The validation results demonstrated that *Zygosaccharomyces bis-*

porus was the most prominent aroma producer, closely related to the formation of acetates. *Kazachstania humilis* was the second most important aroma producer, closely related to form short-chain carbonyl compounds, while *Lactiplantibacillus plantarum* was the weakest in aroma production. These results can provide references to reveal the aroma formation mechanism of fermented peppers and the scientific regulation of fermented food quality.

**Keywords** fermented pepper paste; microbial diversity; aroma compounds; correlation analysis; validation

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### 鲛鱼香肠发酵过程中凝胶特性、微生物群落和风味物质的演替规律

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**摘要** 本研究旨在探究以植物乳杆菌(*L. plantarum*)CY1-2为发酵剂的鲛鱼香肠,在不同发酵时间凝胶强度、TVB-N、氨基酸、微生物多样性以及挥发性风味物质的演替规律。并利用双向正交偏最小二乘法(O2PLS)分析了微生物与挥发性化合物之间的相关性。结果表明,鲛鱼鱼肠发酵40 h后,与自然发酵组相比,接种植物乳杆菌组的凝胶强度提高了207.7%、TVB-N降低了54.2%、游离氨基酸总量增加了37.49%。风味物质共检测出36种化合物,包括醛类9种、烃类9种、醇类7种、酸类4种、酮2种和酯类5种。发酵过程中出现了不同的微生物种类。发酵初期水栖菌属(*Enhydrobacter*)为优势属,发酵8 h后迅速被巨型球菌属(*Macroccoccus*)取代,发酵40 h后乳杆菌属成为优势属。相关性分析表明,溶酪巨型球菌和植物乳杆菌在挥发性化合物的形成中起重要作用。植物乳杆菌与烷烃、醇类、酯类、醛类和酸类呈正相关。这些发现为研究微生物与发酵食品的品质及风味的相关性提供了理论依据。

**关键词** 细菌群落;挥发性化合物;双向正交偏最小二乘法(O2PLS)

### The succession law of gel characteristics, microbial community and flavor substances during fermentation of Spanish mackerel sausage

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**Abstract** This study aims to explore the succession rules of gel strength, TMB-N, amino acids, microbial diversity and volatile flavor substances of Spanish mackerel sausage with *Lactobacillus plantarum* CY1-2 as starter at different fermentation times. The correlation between microorganisms and volatile compounds was also analyzed by using the bidirectional orthogonal partial least squares method (O2PLS). The results showed that after 40 h of Spanish mackerel sausage fermentation, compared with the natural fermentation group, the gel strength of *L. plantarum* inoculated group was increased by 207.7%, TVB-N was decreased by 54.2%, and the total amount of free amino acids was increased by 37.49%. A total of 36 compounds were detected in flavor substances, including 9 aldehydes, 9 hydrocarbons, 7 alcohols, 4 acids, 2 ketones and 5 esters. Different microbial species have emerged during the fermentation process. At the early stage of fermentation, *Enhydrobacter* was the dominant genus, which was quickly replaced by *Macroccoccus* after 8 h of fermentation, and after 40 h of