

Nitrous Oxide Generation is Affected by Interactive Carbon Exchange between Ammonia Oxidizing Bacteria and Denitrifying Bacteria

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한국미생물학회 학술대회논문집 , 2019.4, 80-80(1 pages) 출처

(Source)

한국미생물학회 발행처

The Microbiological Society of Korea (Publisher)

http://www.dbpia.co.kr/journal/articleDetail?nodeId=NODE08756718 **URL**

Min Joon Song, Hyun Yoon, Hee Joo Han, Seokhwan Yoon (2019). Nitrous Oxide Generation is Affected by Interactive Carbon Exchange between Ammonia Oxidizing Bacteria and Denitrifying Bacteria. 한국미생물학회 학 APA Style

술대회논문집, 80-80

이화여자대학교 203.255.***.68 2020/05/18 04:01 (KST) 이용정보 (Accessed)

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B089

Changes in Microbial Community during Kimchi Fermentation Process by Carbon Dioxide Treatment Seung Woo Ahn¹, Se Hee Lee¹, Che Ok Jeon², and Seong Woon Roh^{1*}

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Kimchi is a traditional fermented food in Korea. Kimchi is made from kimchi cabbage, which is a main ingredient, and various ingredients. Fermentation takes place by microorganisms in well-mixed ingredients, and the process is mainly carried out by lactic acid bacteria (LAB). The taste and flavor of kimchi is determined mainly by the result of fermentation metabolism of LAB. During fermentation, the microbial community of kimchi changes due to various causes such as temperature, ingredients, and salinity. The amount and type of fermentation metabolites also change accordingly. Carbon dioxide (CO₂) is one of the final products of heterolactic fermentation of LAB in kimchi. Here, we studied the effect of CO₂ on the fermentation process of kimchi. The microbial communities and metabolites of kimchi with and without CO₂ treatment were analyzed. Metatranscriptomic analysis was also performed at each stage of fermentation. Bacterial community analysis showed that the Weissella koreensis (heterofermentative LAB) was dominant in CO₂ treated kimchi, while Lactobacillus sakei (homofermentative LAB) was the dominant species in kimchi without CO₂ treatment. The concentrations of lactate and ethanol were also different, and the results of metatranscriptomic analysis using RNA sequencing also supported bacterial community analysis results. Collectively, our results highlight that the pre-treatment of CO₂ in kimchi production is capable of affecting the microbial and metabolic profiles during the fermentation.

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Nitrous oxide (N₂O) is regarded as one of major greenhouse gases, due to its global warming potential ~298 times higher than that of carbon dioxide. Wastewater treatment plants (WWTP) have long been recognized as one of the major sources of nitrous oxide N₂O emission. 90% N₂O in WWTP is emitted from activated sludge compartment. Of these, nitrification process takes account for 58~83% of N₂O emission depending on dissolved concentration, suggesting that ammonia oxidizing bacteria (AOB) might play a key role in N₂O emission in oxic unit. Whole genome analysis of Nitrosomonas europaea revealed that the scant genes encoding the catabolism of organic compounds and transporters for organic molecules. However, its inorganic carbon cycle associated with Calvin-Benson-Bassham cycle has potential to produce organic carbon such as hexose. This implies that feasibility that organic carbon produced by Nitrosomonas europaea might be relevant to electron donor or carbon source for denitrifiers, thereby possibly enhancing denitrification potential. In this regard, this research was conducted to investigate how AOB's metabolites (organic C) affect denitrifying bacteria performance