Development of novel method for detection of low-abundant microorganisms during fermentation process

The information about low-abundant microorganisms during fermentation process is very important for ensuring microbial safety and stabilization of the quality of the product. Recently, polymerase chain reaction (PCR), which amplifies a small amount of DNA millions of times, is in use for detection of microorganisms. However, it is difficult to detect low-abundant microorganisms during fermentation process by PCR, because there are large quantities of microorganism (yeast).

To resolve this problem, we focused on COLD-PCR method and developed a novel method (modified COLD-PCR) which inhibits the amplification of DNA derived from the overwhelming majority species (yeast) and amplifies the DNA of low-abundant microorganisms preferentially.

Modified COLD-PCR enables the detection of low-abundant microorganisms that we could not otherwise detect. Using this method, we will be able to identify the microbial community besides yeast during the fermentation process in more detail and to perform advanced microorganism management, and it is expected to contribute to ensuring microbial safety and improving product quality.

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The problem with the conventional method: It is difficult to detect low-abundant microorganisms coexisting with overwhelming majority species (e. g. yeast during fermentation) by PCR-based methods. Novel method: The DNA derived from low-abundant microorganisms is amplified preferentially by inhibiting the amplification of DNA derived from the overwhelming majority species (yeast).

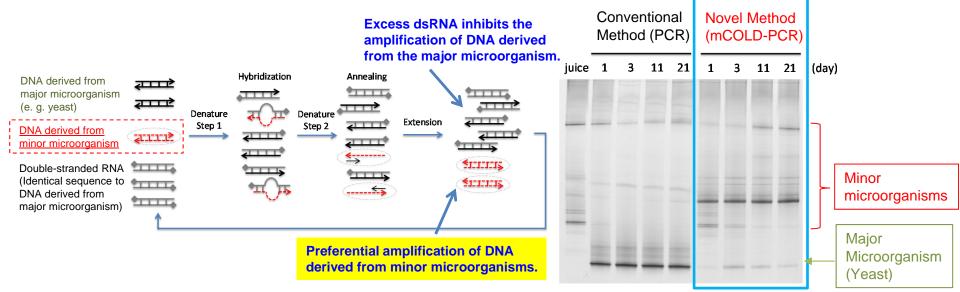


Figure 1. Principle of novel method.

Figure 2. Comparison between microbiota analyzed by the conventional method and those by the novel method.

The novel method enables advanced microorganism management during fermentation!

It is expected to contribute to ensuring the microbial safety and improving the quality of the product!