Improvement of Filamentous Fungi Using TAQing System

Production of secondary metabolites derived from fungal dormancy genes

【 The Case before publication of patent publications 】

Details of TAQing system can be disclosed after contract

Overview

Many drugs have been developed from natural products produced by filamentous fungi. On the other hand, it has been reported that many biosynthetic genes of unexplored natural products that can be candidates for drugs are dormant on the genome of filamentous fungi. Using a large-scale genome rearrangement technology "TAQing system (A technique in which the restriction enzyme TAQI is introduced into a cell to simultaneously and multiply break DNA double strands, followed by recombination repair to produce a variety of genomic rearrangements)," the inventors generated a number of mutant strains of filamentous fungi in which dormant biosynthetic genes were activated, and succeeded in remarkably inducing the production of natural products not produced by wild strains.

The development of a secondary metabolic activation method using the TAQing system has been investigated using the model filamentous fungus Aspergillus nidulans.

Product Application

☐ Acquisition of a filamentous fungus having a new useful character
☐ Search for new natural products

IP Data

IP No.	:	JP2023-121930
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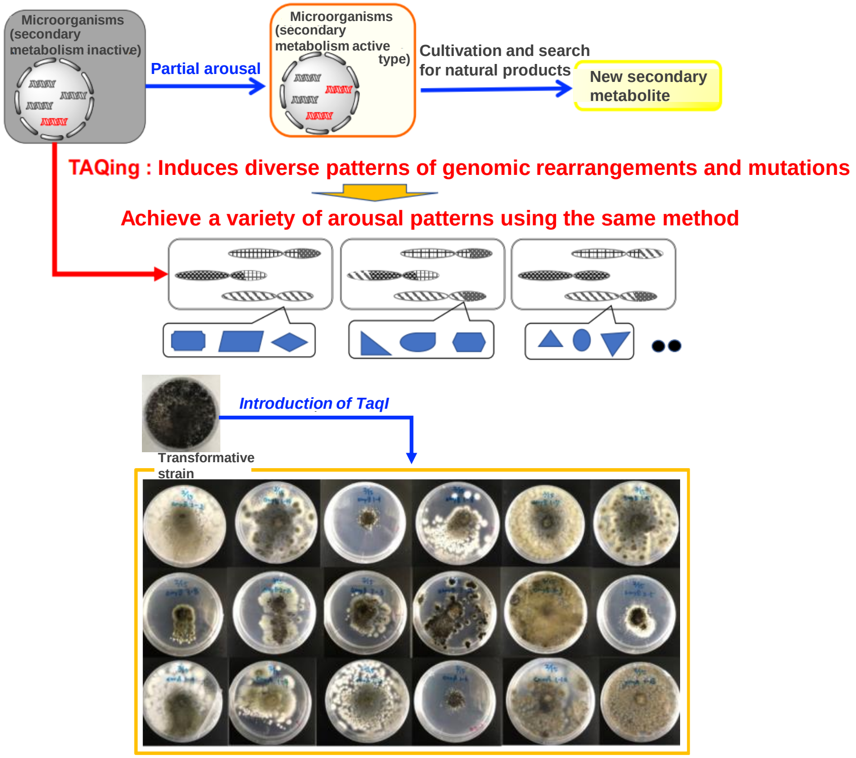
Admin No.	:	T22-154

Features･Outstandings



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