

### 糸状菌における二次代謝関連遺伝子群の発現調節

糸状菌はペニシリンをはじめとする抗生物質や様々な天然生理活性物質の生産菌として知られている。近年、糸状菌のゲノム解析が急速に進められる中、興味深いことに、糸状菌ゲノム中には予想以上に膨大な数の二次代謝関連遺伝子群が存在することが明らかになった。しかし、そのほとんどは一般的な実験室培養条件下では休眠状態であることも明らかになっている。糸状菌においてこれらの二次代謝関連遺伝子群がどのように発現調節されているかは非常に興味深いテーマである。今日は糸状菌において複数の二次代謝遺伝子群を同時に調節している新規転写因子の発見に関する論文を紹介する。

#### 紹介論文

##### Discovery of *McrA*, a master regulator of *Aspergillus* secondary metabolism

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#### Summary

Fungal secondary metabolites (SMs) are extremely important in medicine and agriculture, but regulation of their biosynthesis is incompletely understood. We have developed a genetic screen in *Aspergillus nidulans* for negative regulators of fungal SM gene clusters and we have used this screen to isolate mutations that upregulate transcription of the non-ribosomal peptide synthetase gene required for nidulanin A biosynthesis. Several of these mutations are allelic and we have identified the mutant gene by genome sequencing. The gene, which we designate *mcrA*, is conserved but uncharacterized, and it encodes a putative transcription factor. Metabolite profiles of *mcrA* deletant, *mcrA* overexpressing, and parental strains reveal that *mcrA* regulates at least ten SM gene clusters. Deletion of *mcrA* stimulates SM production even in strains carrying a deletion of the SM regulator *laeA*, and deletion of *mcrA* homologs in *Aspergillus terreus* and *Penicillium canescens* alters the secondary metabolite profile of these organisms. Deleting *mcrA* in a genetic dereplication strain has allowed us to discover two novel compounds as well as an antibiotic not known to be produced by *A. nidulans*. Deletion of *mcrA* upregulates transcription of hundreds of genes including many that are involved in secondary metabolism, while downregulating a smaller number of genes.