Genes Linked to Production of Secondary Metabolites in Talaromyces atroroseus Revealed Using CRISPR-Cas9

The full potential of fungal secondary metabolism has until recently been impeded by the lack of universal genetic tools for most species. However, the emergence of several CRISPR-Cas9-based genome editing systems adapted for several genera of filamentous fungi have now opened the doors for future efforts in discovery of novel natural products and elucidation and engineering of their biosynthetic pathways in fungi where no genetic tools are in place. So far, most studies have focused on demonstrating the performance of CRISPR-Cas9 in various fungal model species, and recently we presented a versatile CRISPR-Cas9 system that can be successfully applied in several diverse Aspergillus species. Here we take it one step further and show that our system can be used also in a phylogenetically distinct and largely unexplored species from the genus of Talaromyces. Specifically, we exploit CRISPR-Cas9-based genome editing to identify a new gene in T. atroroseus responsible for production of polyketide-nonribosomal peptide hybrid products, hence, linking fungal secondary metabolites to their genetic origin in a species where no genetic engineering has previously been performed.

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