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Genomic landscape of secondary metabolism in *Aspergillus* species

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Purpose: Filamentous fungi produce a broad range of secondary metabolites such as penicillin, aflatoxin, and gliotoxin. Increasing numbers of sequenced fungal genomes revealed their potentials to produce more diverse metabolites than previously discovered. However, most of the biosynthetic genes are hardly expressed under laboratory conditions. Although fungal genome sequences are accumulated, transcriptomic view for evolution of SM biosynthesis was sparse. To gain deeper insight into fungal secondary metabolism (SM), here we conducted comparative genomics and transcriptomics analyses using strains of closely related *Aspergillus* species.

Methods: Genomes of *Aspergillus fumigatus*, *A. lentulus*, *A. udagawae*, *A. fischeri*, and *A. pseudoviridinutans* were compared with regard to SM genes. Transcriptomic data were obtained from 4 different cultures such as potato dextrose broth, Sabouraud broth, Czapek-Dox, potato dextrose agar.

Results and conclusions: The 5 *Aspergillus* species possess 34-75 SM core genes for polyketide synthase and non-ribosomal peptide synthase, and 13 types of the SM gene cluster are evolutionarily conserved in all species tested. Transcriptome analysis revealed that rate of active (expressed) genes for the lineage-conserved SM core genes was higher than that for species-specific SM core genes. This finding is suggestive of evolutionary diversification at transcriptional level besides genomic rearrangement or cluster gain and loss event.