

How *Aspergilli* rearrange Secondary Metabolic Gene Clusters to Generate New Compounds

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The WHO is reporting a rising number of multidrug resistant strains every year, increasing the need for new drug development. However, the current methods for natural product discovery rely on a large amount of experimental work, making them unable to keep up with this demand.

In the aspMine project, we are sequencing and analyzing more than 300 genomes of *Aspergillus* species, partially to tackle this problem and increase the speed of natural product discovery using comparative genomics.

Our comparative approach relies on a database setup (MySQL), the Secondary Metabolite Unique Regions Finder (SMURF) algorithm, BLASTP and clustering analysis to process the huge amount of data. Finally, the analysis of this large dataset enables us to examine gene cluster diversity and dynamics in *Aspergilli*. In the previous studies we have shown that *Aspergilli* harbour up to 60 secondary metabolic gene clusters (SMGC), many of them of unknown function, promising possible solutions for the demand in natural products.

In this study we are focusing on the SMGCs that have been combined and rearranged into larger SMGC. We use knowledge based filtering on tailoring domains of SMGCs to define their borders in syntenic block analysis and detect cases of SMGC insertion. Verification of rearrangement events is done by analysis of tailoring domains. With this study, we describe SMGC dynamics throughout the *Aspergillus* genus and give insights into rearrangement of SMGC for new natural products. Our results will be helpful in the development of new natural compounds and tackle the problem of antibiotic resistance.