

Gene cluster dynamics throughout the *Aspergillus* genus

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The genus *Aspergillus* has an enormous biosynthetic potential, which makes them excellent organisms for synthesis of natural compounds. However, it is proposed that industry has not yet revealed their full biosynthetic potential, especially in regard to non-ribosomal peptide and polyketide synthesis. At the same time, the demand for new pharmaceuticals is rising, making natural product discovery an important task in research and industry. Unfortunately, current methods rely on a vast amount of experimental work and cannot keep up with this demand.

In the aspMine project we are sequencing and analyzing 300 *Aspergillus* genomes to tackle this problem and increase the speed of natural product discovery using comparative genomics. Focusing on the section *Nigri*, we identified 3105 secondary metabolite biosynthetic gene clusters which we grouped together to find their distribution pattern throughout *Aspergilli*. Finally, we identified the gene cluster coding for Aurasperone B using this distribution pattern.

We think that we can greatly accelerate natural product discovery and provide insights into the gene cluster dynamics throughout the *Aspergillus* genus.