



## Co-evolution of secondary metabolite gene clusters and their host

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## ABSTRACT FOR ECCB2016 (European Conference on Computational Biology 2016)

**Title:** Co-evolution of secondary metabolite gene clusters and their host

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Secondary metabolite gene cluster evolution is mainly driven by two events: gene duplication and annexation and horizontal gene transfer. Here we use comparative genomics of *Aspergillus* species to investigate the evolution of secondary metabolite (SM) gene clusters across a wide spectrum of species. We investigate the dynamic evolutionary relationship between the cluster and the host by examining the genes within the cluster and the number of homologous genes found within the host and in closely related species.

Our strategy is to investigate annotated SM genes (SMURF) and through homology (based on BLAST) identify homologs in the genome and their location (inside or outside of clusters). An example case is the analysis of SM cluster families found across several species where the number of orthologs vary. Depending on the phylogenetic distribution of the SM clusters, this case illustrates horizontal gene transfer (HGT) and gene duplication events.

Another case is clusters where one gene has one homolog outside the cluster and the rest of the cluster genes are unique to the cluster. This type of case would indicate a recent or ancestral gene duplication event or HGT. The analysis has been performed on 15 genomes (930 gene clusters) and 79 cases were identified. Comparative genomics based on clusters from 50 new *Aspergillus* genomes will be applied to get an understanding of which cluster evolution occurs in association with the host and which happens within the gene cluster.