Phylogenomic analysis of secondary metabolism genes sheds light on their evolution in Aspergillus - DTU Orbit (04/12/2018)

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The World Health Organization is reporting a rising number of multiple drug resistant pathogens every year, increasing the need for new drug development. However, current methods for natural product discovery rely on time consuming experimental work, making them unable to keep up with this demand. In the aspMine project, we are sequencing and analyzing over 300 species of Aspergilli, a group of filamentous fungi rich in natural compounds. The vast amount of data obtained from these species challenges the way we were mining for products and requires new pipelines for secondary metabolite analysis. Natural products are encoded by genes located in close proximity, called secondary metabolic gene clusters, which makes them interesting targets for genomic analysis. We use a modified version of the Secondary Metabolite Unique Regions Finder (SMURF) algorithm, combined with InterPro annotations to create approximate maximum likelihood trees of conserved domains from secondary metabolic genes across 56 species, giving insights into the secondary metabolism gene diversity and evolution. In this study we can describe the evolution of non-ribosomal peptide synthetases (NRPS), polyketide synthases (PKS) and hybrids thereof, find possible common ancestors and detect horizontal gene transfer events. Finally, we have performed large scale analysis of gene cluster dynamics and evolution, which provides us with better understanding of speciation in Aspergilli. With this new insights into the evolution of natural products, an application in synthetic natural product assembly lies within our grasp.

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