

## Genome mining of the genetic diversity in the *Aspergillus* genus - from a collection of more than 30 *Aspergillus* species - DTU Orbit (08/11/2017)

### Genome mining of the genetic diversity in the *Aspergillus* genus - from a collection of more than 30 *Aspergillus* species

In the era of high-throughput sequencing, comparative genomics can be applied for evaluating species diversity. In this project we aim to compare the genomes of 300 species of filamentous fungus from the *Aspergillus* genus, a complex task. To be able to define species, clade, and core features, this project uses BLAST on the amino acid level to discover orthologs. With a potential of 300 *Aspergillus* species each having ~12,000 annotated genes, traditional clustering will demand supercomputing. Instead, our approach reduces the search space by identifying isoenzymes within each genome creating intragenomic protein families (iPFs), and then connecting iPFs across all genomes. The initial findings in a set of 31 species show that ~48% of the annotated genes are core genes (genes shared between all species) and 2-24% of the genes are redefining the individual species. The methods presented here will allow for detailed investigation into mapping of genotype to phenotype across a very large set of genomes without losing information.

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