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### **Studying the pathogenic and allergic phenotype of *Aspergillus fumigatus***

*Aspergillus fumigatus* is a unique microorganism, because it is an opportunistic pathogen in immunocompromised patients with additional allergic potential in immunocompetent patients. Due to the excessive production of conidia the human respiratory tract is constantly being exposed to this fungus. *A. fumigatus* can be part of 50% respiratory infections and cause a mortality rate of 50%. We know the impact in human health of *A. fumigatus*, but the actual biological factors of its phenotype and functions are not yet fully understood.

With the advantages of NGS, we can dive in the genotypic information and provide a link with the related physiology. The genome is around 29 Mbp and since the fungal life cycle also contains a sexual stage, two mating types are recognized. Possibly also a parasexual recombination cycle is involved. A well-established genomic analysis and comparison of *A. fumigatus* is still challenging. We aim to use all available public sequences of *A. fumigatus* in a combination with the latest advantaged tools to perform complete whole genomic comparisons and unravel the key-mechanisms that may explain the pathogenic and allergic phenotype.

### **Experimental Design**

There are more than 30 whole genome sequences (with the possibility of obtaining more) which can be used for the analysis. A high number of these sequences is raw data therefore an assembly process should be applied.

- ❖ Assemble raw data from *A. fumigatus* and perform QC for all the available and assembled genomes
- ❖ Use multiple annotation pipelines to perform an accurate functional annotation
- ❖ Perform comparison analysis on sequence, genes and domains level
- ❖ Perform typing of the genomes on the basis of allelic differences
- ❖ Connect interesting genotypes with phenotypes and identify important pathways

### **Techniques**

- ❖ Use of assemblers optimized or need for optimization for *A. fumigatus*
- ❖ Use of multiple annotation pipelines and manual biocuration
- ❖ Use of mining techniques for public databases for functional genes and metabolic pathways
- ❖ Application of MLST methods for standardization of typing of *A. fumigatus*