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MAX-PLANCK-INSTITUT FÜR MULTIDISZIPLINÄRE NATURWISSENSCHAFTEN

Evolutionary Genomics: Consequences of Biodiverse Reproductive Systems (EvoReSt)

EvoReSt

A3

Heterothallic and homothallic genome evolution in the fungal genus *Sordaria*

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State of the art

- In fungi different sexes are referred to as mating types (MAT) [1]. In the Ascomycota, MAT exists in two alternative versions (MAT1-1 and MAT1-2) [2].
- Heterothallic species are self-sterile and homothallic are self-fertile.
- The MAT loci encode transcription factors [3]. Usually, these control the MAT-specific pheromone and pheromone-receptor genes located elsewhere in the genome [4].

Objectives

- MAT gene divergence in Sordariales
- Impact of Transposable Elements (TEs) on the mating-system
- Genomic reasons for lack of asexual spores and heterokaryon incompatibility in homothallic species
- Influence of UV-light on genome and on expression of genes active during sexual development

PhD 1 - Genome evolution of homothallic and heterothallic members of the genus *Sordaria*

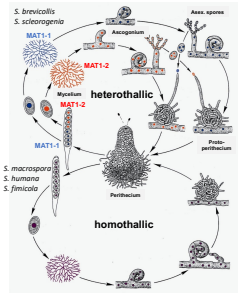

Fig. 1 Life cycle of heterothallic and homothallic members of the genus Sordaria.

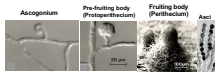

Fig. 2 Structures developed during sexual development of *S. macrospora*.

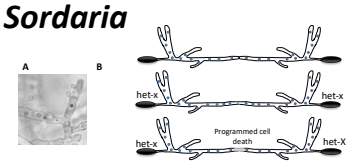

Fig. 3 Heterothallic species produce microconidia [5] (A) and undergo heterokaryon incompatibility (B). A *het* locus is a locus at which heteroallelism cannot be tolerated in a heterokaryon.

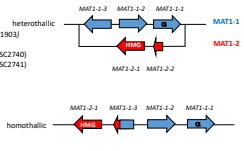

Fig. 4 MAT loci of homothallic and heterothallic members of Sordaria. Genes encoding transcription factors are combined in one genome in homothallic species. (HMG, High Mobility Group domain, α, α domain).
The annotated, chromosome assembled genome of *S. macrospora* is available and will be used as a reference genome [6,7]. Sequence of *S. humana* and *S. brevicollis* MAT1-2 are available at JGI.

- Generation of genomic sequence from heterothallic *S. brevicollis* MAT1-1 and *S. sclerogenia* (MAT1-1 and MAT1-2) and the homothallic *S. fimicola*.
- *dN/dS* ratios of protein coding genes and calculation of mutation accumulation in homothallic versus heterothallic genomes.
- *De novo* identification of repetitive TE sequences.
- Analysis of conidiation-associated genes and genes involved in heterokaryon incompatibility.

PhD 2 - Evolutionary aspects of heterothallism versus homothallism

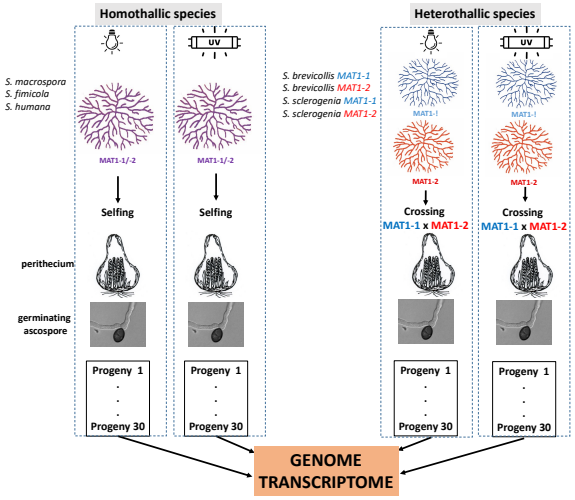

Fig. 5 Workflow: Influence of UV-light on sexual reproduction systems.:

- Assessment of optimal UV radiation dose.
- Preparation of ascospore progeny.
- Sequencing of genome and transcriptome.
- Determination UV-light induced changes of genes and expression of genes involved in sexual development.
- Hypotheses regarding UV-light induced changes will be verified by knock-out mutants.

References

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