Unravelling the genetic mechanisms of unisexual reproduction in *Huntiella moniliformis*

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Unisexuality, the phenomenon that allows a fungus of a single mating type to sexually reproduce in isolation has been described in only three genera of filamentous ascomycetes, Neurospora, Huntiella and Thermoascus. Huntiella is the only genus whereby MAT 1-2 isolates are able to undergo a unisexual reproduction. This genus is a member of the family Ceratocystidaceae, a group of well-known pathogenic fungi that infect a wide variety of economically important plants including Eucalyptus, Acacia and Pinus species, as well as sweet potato, cacao and pineapple. The underlying molecular mechanisms that are responsible for unisexuality in filamentous fungi are poorly understood. Using a comparative genomics, transcriptomics and gene knock out approach, we thus aimed to elucidate the molecular mechanism responsible for unisexuality in Huntiella. We compared the genomes of two Huntiella species, the unisexual H. moniliformis and the heterothallic H. omanensis. In addition, we sequenced and compared the transcriptomes of vegetative and sexually-competent cultures of both species. In this way we were able to determine some of the genes which are important for sexual reproduction in these fungi. Firstly, we showed that the MAT 1-2-7 gene in the H. moniliformis mating type locus is truncated, unlike the full-length gene from H. omanensis. We also noted that MAT1-1 individuals of H. omanensis produce the α-factor pheromone and MAT1-2 individuals the a-factor pheromone, as expected from a typically heterothallic species. In contrast MAT1-2 individuals of H. moniliformis express both pheromones at significant levels. We hypothesized that the MAT1-2-7 truncation in H. moniliformis has resulted in the mating-type independent expression of both pheromones. We have deleted the MAT 1-2-7 gene in H. omanensis and preliminary results suggest that these mutants share some unisexual characteristics with H. moniliformis. Further studies will be aimed at determining the expression profile of these deletion strains to assess whether a similar pheromone expression pattern is observed.