

Table S3. Analysis of non-ribosomal peptide synthetase (NRPS) genes and polyketide synthase (PKS) genes in *Ascodesmis nigricans*.

Putative NRPS and PKS genes were identified among the *A. nigricans* predicted proteins by BLASTP analyses versus corresponding genes from other ascomycetes. Initial BLASTP hits were further characterized by more detailed BLASTP and CD (conserved domain) searches. Overall, there was no homolog to any PKS, and no protein with a domain structure that would be indicative of PKSs. Thus, in contrast to *P. confluens*, where there is a single PKS gene (encoding a type I PKS), *A. nigricans* does not seem to encode PKS genes. Five putative NRPS genes were identified and are given in the table below. proteinId340667 is a candidate for a siderophore biosynthesis NRPS (homologous to *P. confluens* PCON_02859), it has same domain structure as the corresponding *P. confluens* gene (given in the table, A: adenylation domain, C: condensation domain, T: thiolation domain = peptidyl carrier protein of NRPSs). proteinId396591 is most likely also a NRPS, but without a clear ortholog in *P. confluens*. There are three putative alpha-aminoadipate reductase (AAR) NRPSs, which are typical fungal NRPSs involved in amino acid biosynthesis. Most fungi have only one AAR gene, *P. confluens* with five genes is an exception (Traeger et al. 2013). The AAR gene family expansion also can be observed in *A. nigricans*, but to a lesser degree.

| locus_tag | Putative function based on conserved domain search | peptide length |
|-----------------|---|----------------|
| proteinId340667 | siderophore-synthesizing NRPS, domain structure ATCATCATCATCTCTC | 5638 |
| proteinId396591 | NRPS protein, domain structure ATCATC, the second A domain is partial | 1951 |
| proteinId28293 | alpha-aminoadipate reductase (AAR) | 1438 |
| proteinId195633 | similar to alpha-aminoadipate reductase (AAR) | 1018 |
| proteinId393348 | similar to alpha-aminoadipate reductase (AAR) | 1044 |