

Genome sequence of *Podospora anserina* reveals unsuspected ability to use complex carbon sources

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The model fungus *Podospora anserina* (*P. anserina*) has undergone substantial evolution since its separation from *Neurospora crassa*, as revealed from the *Podospora* draft genome sequence published in BioMed Central's open access journal, *Genome Biology*. The study also shows that the *Podospora* genome contains a large, highly specialised set of genes potentially involved in the breakdown of complex carbon sources, which may have potential use in biotechnology applications.

P. anserina is a dung-inhabiting, saprophytic fungus used to study areas of eukaryotic and fungal biology, including ageing and sexual development. Eric Espagne, Olivier Lespinet and Fabienne Malagnac from the Institute of Genetics and Microbiology in Paris and a team of researchers from France and The Netherlands used a whole genome shotgun and assembly approach to produce a 10X draft sequence of the fungus.

The researchers found evidence that *P. anserina* has undergone dynamic evolution since it diverged from its close relative *N. crassa*. They found evidence of extensive gene loss and gene shuffling, as well as substantial gene duplication. In addition, the transcription machinery of *P. anserina* produced a large number of RNAs that could potentially have regulatory roles. Further investigation of these non-conventional transcripts is required and could lead to the discovery of novel regulatory mechanisms, specifically during mycelium growth or accompanying the

differentiation of the multicellular fructification produced during sexual reproduction.

The research team also discovered that *P. anserina* contains a large array of genes that may allow the fungus to use the natural carbon sources found wherever it grows. For example, the fungus carries genes potentially involved in the breakdown of the plant polymers cellulose and lignin, which may have future applications in biotechnology.

Espagne concludes: “As for other saprophytic fungi, the *P. anserina* genome sequence has opened new avenues in the comprehensive study of a variety of biological processes ... It also demonstrates how *P. anserina* is well adapted at the genome level to its natural environment, which was confirmed by the analysis of growth profiles. This result emphasizes the necessity to study several less well-tracked organisms in addition to those well known in the scientific community, as these may yield unexpected new insights into biological phenomena of general interest.”

Source: BioMed Central

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