

Genomic Analysis of Mitochondria of *Metschnikowia*

Background

Our current understanding of mitochondrial genomes is biased toward metazoans, which represent the majority of sequenced mitochondrial DNAs (mtDNAs). The high diversity in size, shape, and gene synteny among yeast mitochondrial genomes make them an appealing alternative to those of metazoans for studying genomic diversity and evolution. Recently, more than 60 draft-genome assemblies of large-spored *Metschnikowia* species have been determined. Complete mitochondrial genomes of these yeasts, however, are yet to be constructed and characterized. Therefore, I propose to construct and analyze the mitochondrial genomes of all 61 strains of large-spored *Metschnikowia* species.

Hypothesis

The initial hypothesis is that the features of the mitochondrial genomes will follow species relatedness.

Methods

I have found that the sequencing read databases of these species are highly enriched in mitochondrial sequences with a high adenine and thymine content. These properties will be used to help isolate mitochondrial reads and assemble them into intact and complete genome sequences.

Results

The preliminary analyses showed that the mtDNAs from *Metschnikowia* can be circular or linear, and it will be of interest to find out whether the distribution of circular and linear forms follows phylogenetic lines. Also, genome sizes have shown a four-fold range so far, but it is not yet known if the size distribution will be consistent with the phylogeny. Similarly, patterns of both gene synteny and genome topology varies between early and late emerging species. Furthermore, *cox1* and *cob* contain multiple introns that varies extensively in numbers and can be incredibly high (≈ 20).