**Porecamp fungal strains:**

**Introduction:**

We have several strains of fungi which have been obtained by the [1000 fungal genomes](http://1000.fungalgenomes.org/home/) project. Our aim during this course will be to sequence several of these strains using Oxford Nanopore MinIon to improve or replace the existing draft assemblies which we have summarised below.

Data for these assemblies can be found on the VM image at /home/ubuntu/fungal\_strains\_porecamp

**Hanseniaspora vineae (Wine yeast):**

Tends to result in fruity/flowery flavours in wine due to a strong presence of phenyl/ethyl acetate. Approximately 50x more so than in wines fermented with *S.cerevisiae*.

Reference: <http://www.ncbi.nlm.nih.gov/pubmed/27014252>

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| **Statistics** | |
| Scaffold number | 305 |
| Scaffold N50 | 83kb |
| Assembly length | 11,383,302 bp |
| Illumina coverage | 212x |
| Platform | Illumina GAIIx |
| Expected number of chromosomes | Unknown |
| GC content | 37% |

Illumina assembly download: <http://www.ebi.ac.uk/ena/data/view/JFAV02000001-JFAV02000305>

N.B. Raw reads not available

**Debaryomyces fabryi:**

This is an extremely halophilic (salt-tolerant) species of fungus which is responsible for considerable for a considerable amount of food-spoilage. *D.fabryi* although considered non-pathogenic, grows optimally at 36-39C and has been isolated from human lesions.

Reference: <http://femsyr.oxfordjournals.org/content/13/2/180>

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| **Statistics** | |
| Scaffold number | 540 |
| Scaffold N50 | 59kb |
| Assembly length | 11,700,921 bp |
| Illumina coverage | 112x |
| Platform | Ion Proton |
| Expected number of chromosomes | Unknown |
| GC content | 35% |

Ion Proton assembly download: <http://www.ncbi.nlm.nih.gov/Traces/wgs/wgsviewer.cgi?val=LMYN01&search=LMYN01000000&display=contigs>

N.B. Raw reads not available

**Candida sojae:**

A xylose consuming yeast capable of producing xylitol (a sugar alcohol). Xylitol is often used as an artificial sweetener as it is not fermentable and tends to inhibit the growth of bacteria. This strain was isolated from a *Diatraea saccharalis,* a plague-insect of sugar cane.

Reference: <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4714119/>

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| **Statistics** | |
| Scaffold number | 511 |
| Scaffold N50 | 56kb |
| Assembly length | 11,747,307 bp |
| Illumina coverage | 48x |
| Platform | Illumina HiSeq 2000 |
| Expected number of chromosomes | Unknown |
| GC content | 32% |

Illumina assembly download: <http://www.ncbi.nlm.nih.gov/Traces/wgs/?val=LMTL01#contigs>

N.B. Raw reads not available

**Candida boidinii:**

This is also a xylose consuming yeast capable of producing xylitol. *C.boidinii* can also utilise methanol or methane as their carbon source for growth. This makes the organism potentially useful for the production of amino acids, co-enzymes and cytochromes as well as for the degradation of methane.

Reference: <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4714119/>

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| **Statistics** | |
| Scaffold number | 428 |
| Scaffold N50 | 122kb |
| Assembly length | 19,111,858 bp |
| Illumina coverage | 144x |
| Platform | Illumina HiSeq 2000 |
| Expected number of chromosomes | Unknown |
| GC content | 30% |

Illumina assembly download: <http://www.ncbi.nlm.nih.gov/Traces/wgs/?val=LMZO01#contigs>

N.B. Raw reads not available

**Lachancea waltii:**

This is a representative *Saccharomycetaceae* species which diverged from the *S.cervisiae* lineage prior to a whole genome duplication event. As such it is an important representative from a phylogenetic perspective. An improved assembly will enable better synteny comparison and identification of paralogous genes.

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| **Statistics** | |
| Scaffold number | 713 |
| Scaffold N50 | 63kb |
| Assembly length | 10,912,112 bp |
| Illumina coverage | 144x |
| Platform | Illumina HiSeq 2000 |
| Expected number of chromosomes | Unknown |
| GC content | 44% |

Reference: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2765284/> , <http://femsyr.oxfordjournals.org/content/4/3/233.long>

Illumina assembly download:

Illumina read files download:

**Sporopachydermia lactativora:**



Sporopachydermia lactativora, originally named Cyptococcus lactativorous, was isolated from Antartic seawater in 1966 and is named for its ability to utilize lactic acid. The lack of a visible capsule, inability to assimilate disaccharides and the trisaccharide raffinose was used to separate this from other Cyptococcus.

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| **Statistics** | |
| Scaffold number | 366 |
| Scaffold N50 | 85kb |
| Assembly length | 15,566,190 bp |
| Illumina coverage | Unknown |
| Platform | Illumina HiSeq 2000 |
| Expected number of chromosomes | Unknown |
| GC content | 45% |

Illumina assembly download: <http://genome.jgi.doe.gov/pages/dynamicOrganismDownload.jsf?organism=Spola1>

N.B. Raw reads not available

**Starmerella bombicola:**

Typically associated with insect hosts, this species is capable of producing sophorolipids which are often used as bio-surfactants. Surfactants are usually synthesized from petrochemicals so these could prove to be a useful substitute.

Reference: <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4384140/>

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| **Statistics** | |
| Scaffold number | 16 |
| Scaffold N50 | 2.89Mb |
| Assembly length | 9,561,028 bp |
| Coverage | 330x |
| Platform | Illumina HiSeq 2500 and MiSeq |
| Expected number of chromosomes | Unknown |
| GC content | 48% |

Illumina assembly download: <http://www.jcm.riken.jp/cgi-bin/nbrp/nbrp_download.cgi?JCM=9596>

Illumina raw reads: <http://www.ncbi.nlm.nih.gov/sra/?term=Starmerella+bombicola>

**Wickerhamomyces ciferrii:**

Wickerhamomyces ciferrii is a microorganism characterized by the production and secretion of large amounts of acetylated sphingoid bases, in particular tetraacetyl phytosphingosine. These can be converted into ceramides which have importance for the maintenance of epidermal skin permeability. These compounds are also valuable in the pharmaceutical and cosmetics industry since they provide antimicrobial and anti-inflammatory functions.

Reference: <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3536291/>

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| **Statistics** | |
| Scaffold number | 354 |
| Scaffold N50 | 98kb |
| Assembly length | 15,901,152 bp |
| Coverage | 15x |
| Platform | Roche/454 |
| Expected number of chromosomes | Unknown |
| GC content | 30% |

454/Roche assembly download: <http://www.ncbi.nlm.nih.gov/Traces/wgs/?val=CAIF01#contigs>

N.B. No raw data available

**Kluyveromyces wickerhamii:**

This yeast produces antimicrobial toxins which can be used for wine ageing and storage.

Reference:[**http://www.ncbi.nlm.nih.gov/pubmed/15336427**](http://www.ncbi.nlm.nih.gov/pubmed/15336427)

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| **Statistics** | |
| Scaffold number | 510 |
| Scaffold N50 | 37kb |
| Assembly length | 9,807,744 bp |
| Coverage | 12x |
| Platform | Roche/454 |
| Expected number of chromosomes | Unknown |
| GC content | 41% |

Roche/454 assembly download: <http://www.ncbi.nlm.nih.gov/nuccore/300516792>

**Candida maltosa:**

This species can be used to degrade phenols and other hydrocarbons.

Reference: <http://www.pjoes.com/pdf/15.1/Pol.J.Environ.Stud.Vol.15.No.1.47-51.pdf>

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| **Statistics** | |
| Scaffold number | 2,947 |
| Scaffold N50 | 11kb |
| Assembly length | 12,826,280 bp |
| Coverage | 130x |
| Platform | Illumina HiSeq |
| Expected number of chromosomes | Unknown |
| GC content | 34% |

Illumina assembly download: <http://fungi.ensembl.org/Candida_maltosa_xu316/Info/Index>

N.B. No raw data available