



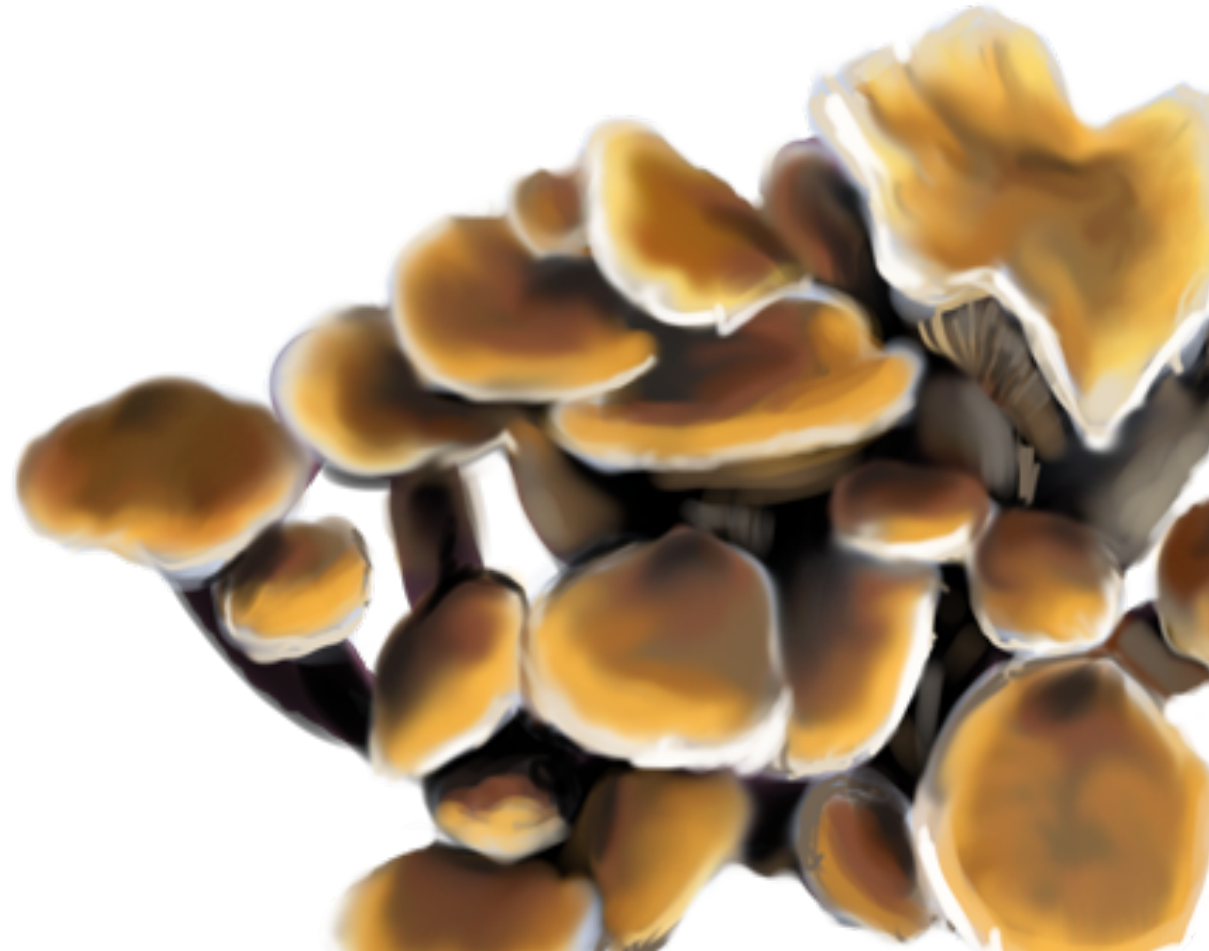
Sword-belt Mushroom Genome

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Introduction to Genomics (485)
July 2021



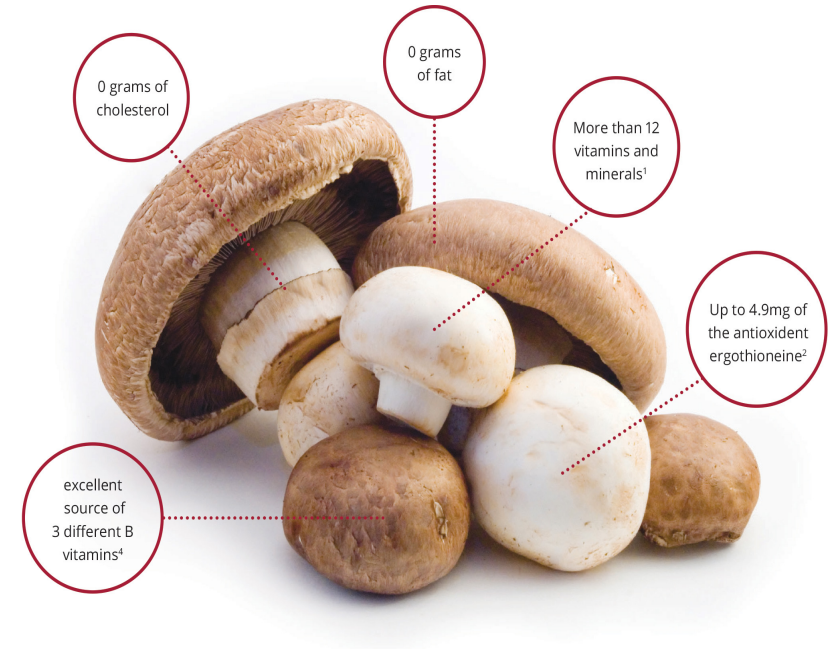
Outline

- Fun facts
- My genome paper
- General genomic informations
- Biological sample
- Sequencing strategy
- Sequencing method
- Genome assembly
- Genome biological outcome



Fun facts

- Sword-belt *agrocybe aegerita* known as black poplar
- In Italian known as pioppino
- They are very popular for their superb taste. Some say it even tastes like bacon!!
- Preferring hardwoods, cotton woods, willows and poplars
- In Asia, it is used fresh and rehydrated in various dishes, including stir-fry, soup, stew, and hot pot



Fun facts

- **Characteristics :**

They have large fruitbodies

- Also it's very smooth

- **Color :**

Yellowish and brown

- **Growing :**

United states and Southern Europe



My genome paper

Gupta et al. *BMC Genomics* (2018) 19:48
DOI 10.1186/s12864-017-4430-y

BMC Genomics

RESEARCH ARTICLE

Open Access



The genome sequence of the commercially cultivated mushroom *Agrocybe aegerita* reveals a conserved repertoire of fruiting-related genes and a versatile suite of biopolymer-degrading enzymes

Deepak K. Gupta^{1,3,5}, Martin Rühl^{4,5,7}, Bagdevi Mishra^{1,3,5}, Vanessa Kleofas^{4,5}, Martin Hofrichter⁶, Robert Herzog^{2,3,5}, Marek J. Pecyna⁸, Rahul Sharma^{1,3,5}, Harald Kellner⁶, Florian Hennicke^{2,3,5,9*} and Marco Thines^{1,3,5*}

General genomic informations

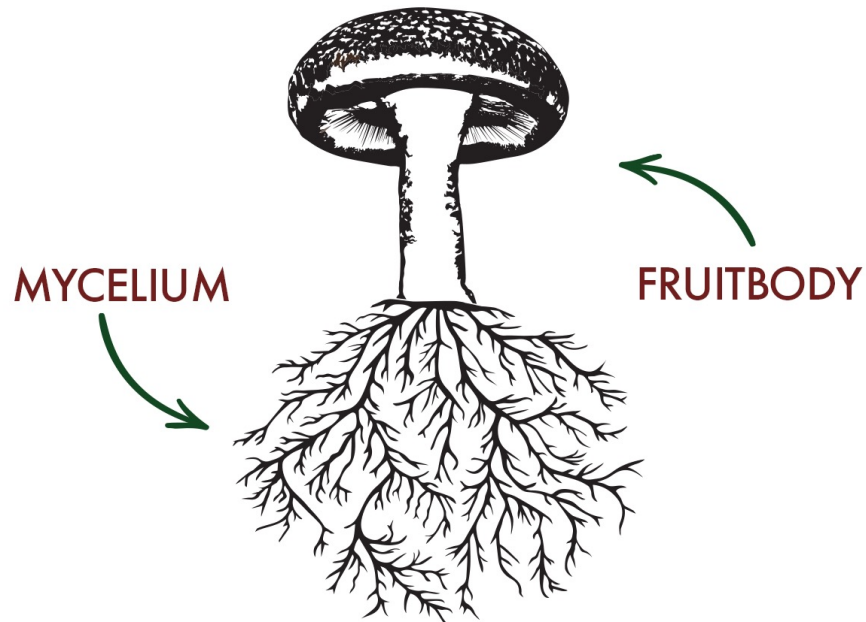
- Common name : Sword-belt mushroom
- Scientific name : *Agrocybe aegerita*
- 44 Mb in size
- Order : agaricales



Biological sample

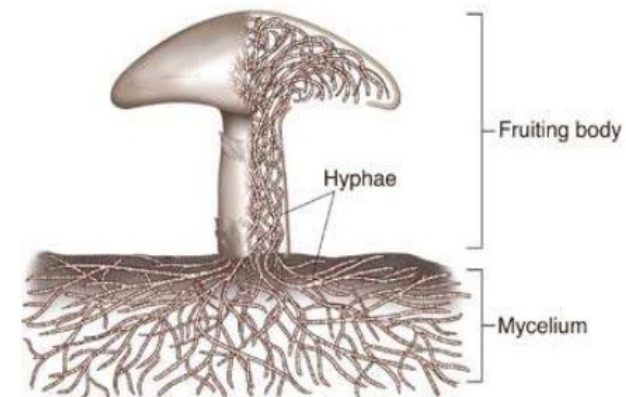
- Mycelium

- the vegetative part of a fungus ,
consisting of a network of fine white
filaments (hyphae)



Structure of Fungi

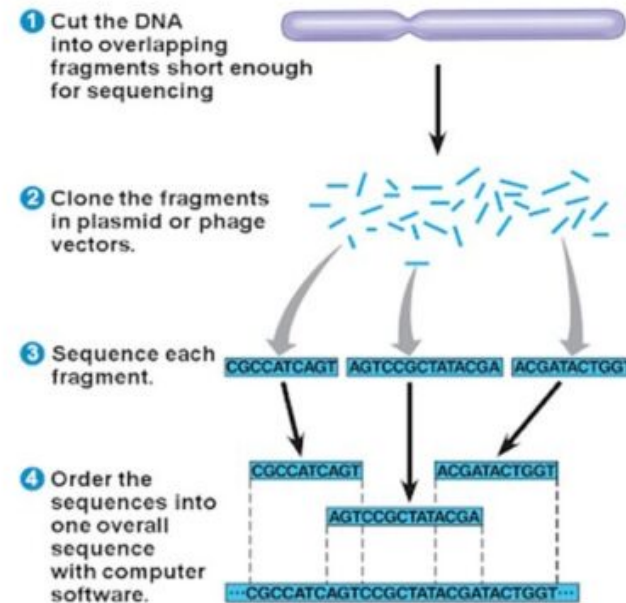
The bodies of multicellular fungi are composed of many hyphae tangled together into a thick mass called a *mycelium*



Sequencing strategy

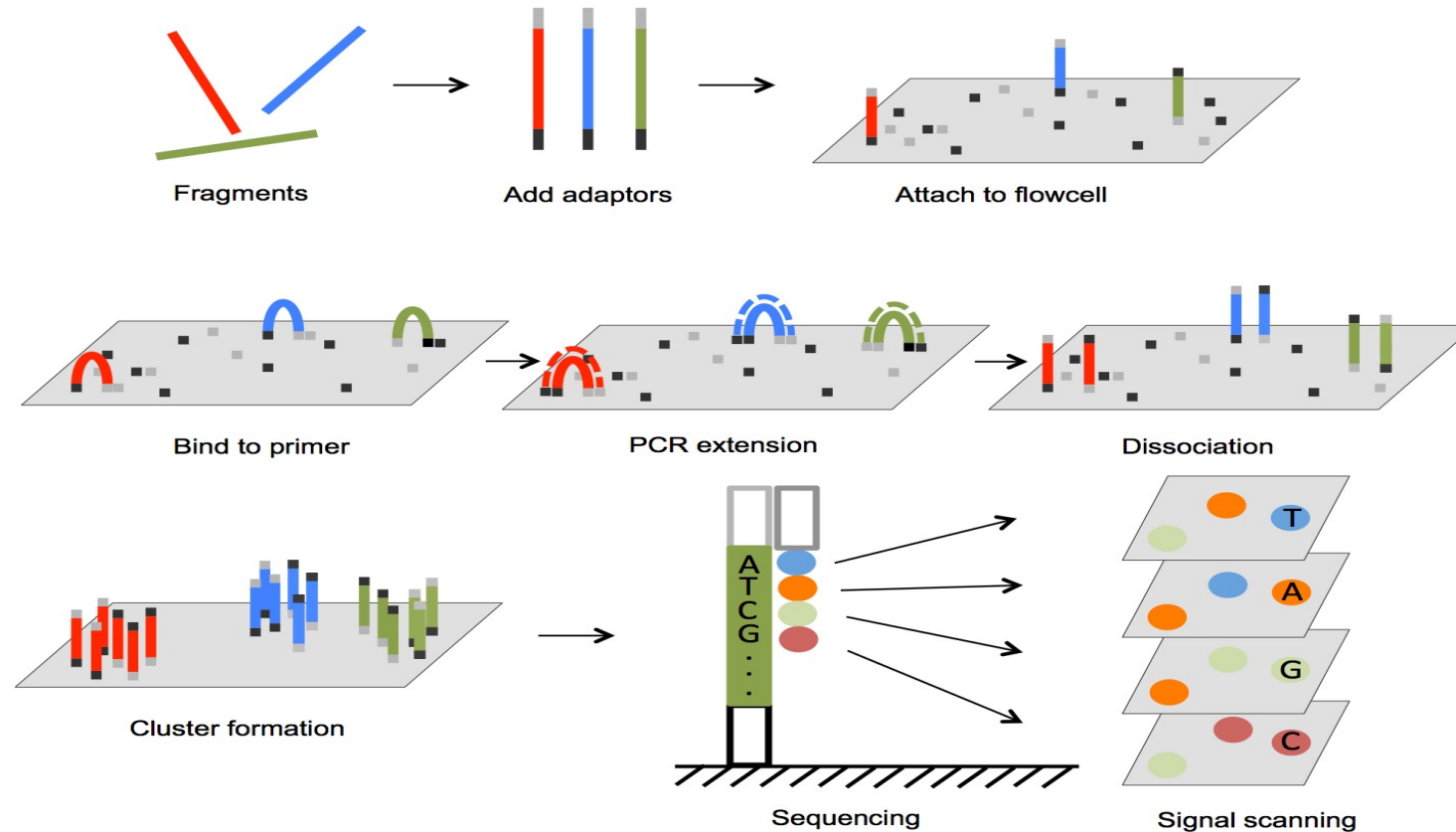
- They used whole genome shot-gon sequencing strategy

Whole-Genome Shotgun Sequencing overview, steps and achievements



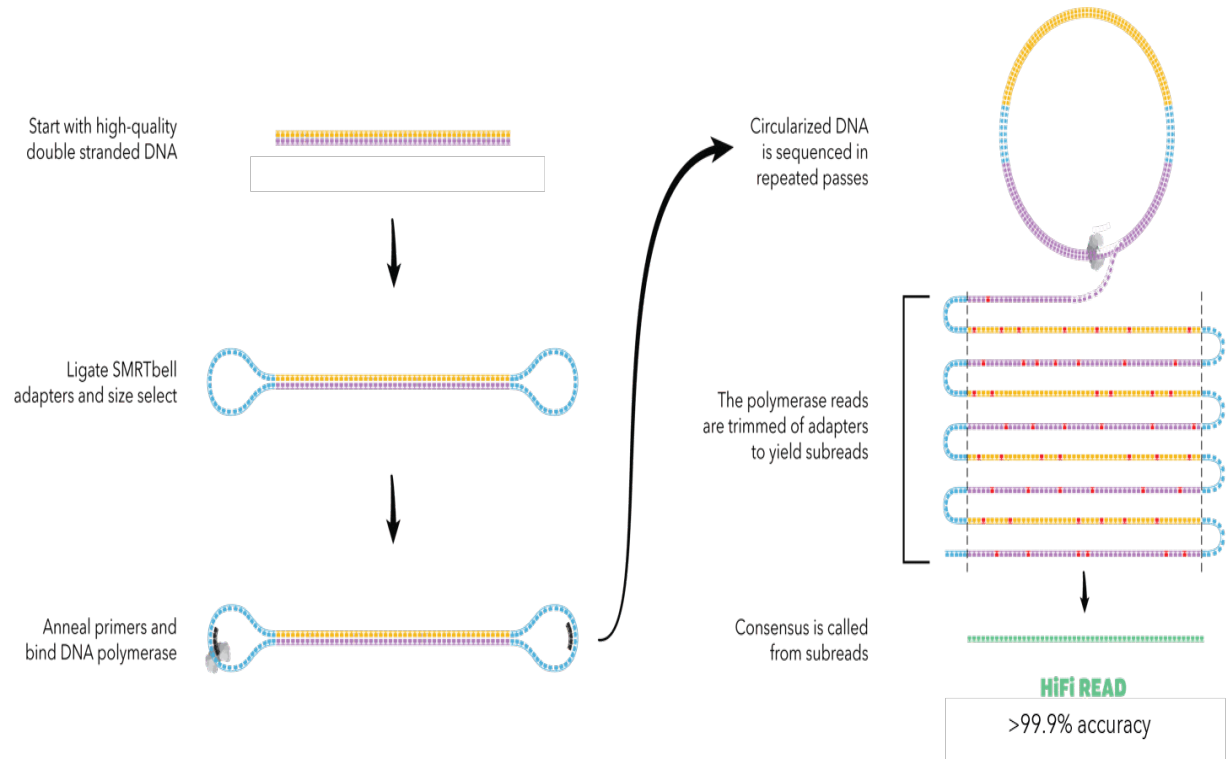
Sequencing method

- Quality analysis of genomic DNA and total RNA before sequencing, library construction, and sequencing on PacBio (RS II) and Illumina (HiSeq 2500) instruments
- Illumina sequencing method was used



Sequencing method

- PacBio sequencing was used
- PacBio have long reads



Genome assembly

- 127 scaffolds
- L50 scaffolds = 20
- Shortest scaffolds = 2417
- Genome coverage = 0.258 X
- N50 scaffolds length = 768,404



Genome biological outcome

- ✓ *Agrocybe aegerita* able to complete its life cycle by the formation of typical agaric fruit bodies on agar medium after three weeks, depending on light. In the absence of light, a 'dark stipe' phenotype occurs.
- ✓ It shows more similarity to white-rot fungi than to litter decomposers, including 18 genes coding for unspecific peroxygenases and three dye-decolourising peroxidase genes expanding its lignocellulolytic machinery.
- ✓ In nature, it is a saprotrophic or facultative pathogenic fungus causing a white-rot of hardwood in forests of warm and mild climate.
- ✓ For some genes involved in fruit body formation, paralogisation was observed, but not all fruit body maturation-associated genes known from other agaricomycetes seem to be conserved in the genome sequence of *A. aegerita*.

Questions

- What is the sequencing method was used? Explain it
- Why the organism is called black poplar?

