



# *Split Gill*

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Introduction to genomics  
July 2021



# Outline

➤ Fun Facts

➤ Studied genome paper

➤ General genomic information

➤ Biological sample

➤ Sequencing strategy

➤ Sequencing methods

➤ Genome Assembly

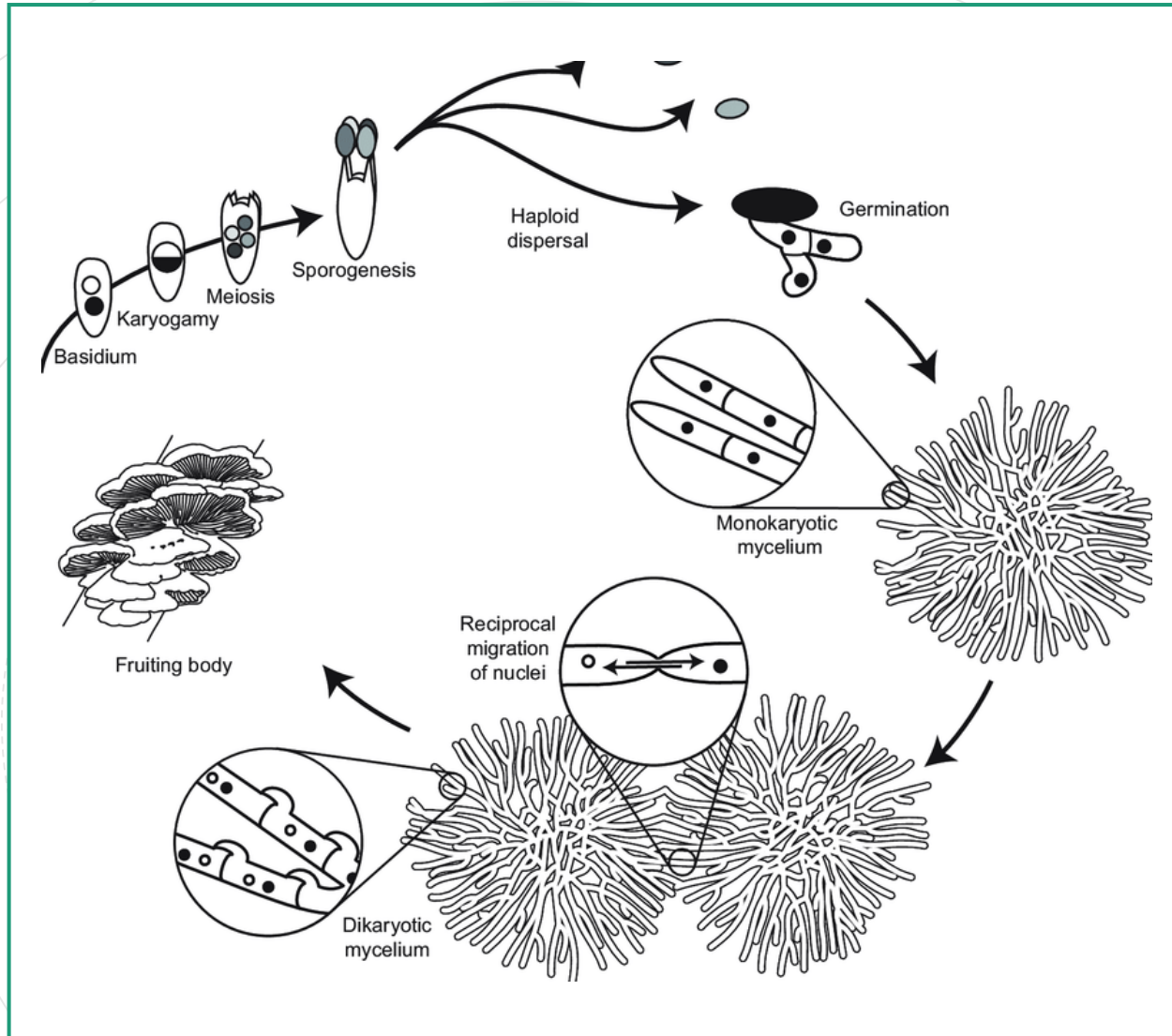
➤ Genome outcome



# *Fun facts*

- Split Gill it know as Schizophyllum Commune.





## *Fun facts*

- One of the most interesting things about *Schizophyllum Commune* is that its system of sexual reproduction.

# Fun facts



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Most of them are considered basidiomycetes, their fleshy fruiting bodies bearing spores.

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it grows on every continent except Antarctica.

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The mushrooms of *S. commune* are used as a food source in Africa and Asia.



# *Fun facts*

- Most of the mushroom-forming parasites can't be hereditarily changed, or even refined under lab conditions.



# genome paper



ARTICLES

**nature  
biotechnology**

## Genome sequence of the model mushroom *Schizophyllum commune*

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Ronald P de Vries<sup>1,5</sup>, Eric Record<sup>6,7</sup>, Anthony Levasseur<sup>6,7</sup>, Scott E Baker<sup>2,8</sup>, Kirk A Bartholomew<sup>9</sup>,  
Pedro M Coutinho<sup>10</sup>, Susann Erdmann<sup>3</sup>, Thomas J Fowler<sup>11</sup>, Allen C Gathman<sup>12</sup>, Vincent Lombard<sup>10</sup>,  
Bernard Henrissat<sup>10</sup>, Nicole Knabe<sup>3,18</sup>, Ursula Kües<sup>13</sup>, Walt W Lilly<sup>12</sup>, Erika Lindquist<sup>2</sup>, Susan Lucas<sup>2</sup>,  
Jon K Magnuson<sup>8</sup>, François Piumi<sup>6,7</sup>, Marjatta Raudaskoski<sup>14</sup>, Asaf Salamov<sup>2</sup>, Jeremy Schmutz<sup>2</sup>,  
Francis W M R Schwarze<sup>15</sup>, Patricia A vanKuyk<sup>16</sup>, J Stephen Horton<sup>17</sup>, Igor V Grigoriev<sup>2</sup> & Han A B Wösten<sup>1</sup>

ved.



# *General genomic information*

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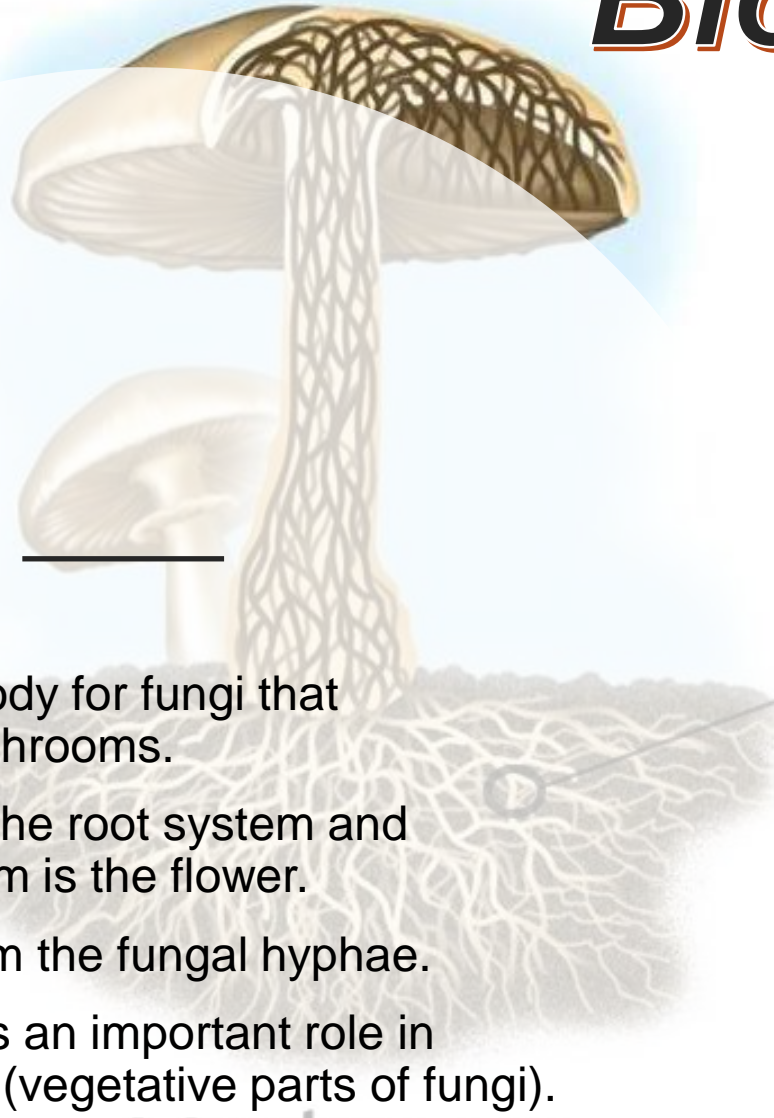
□ Size of S.Commune → 38.5

□ Number of chromosome → 11

□ Haploid →  $n$

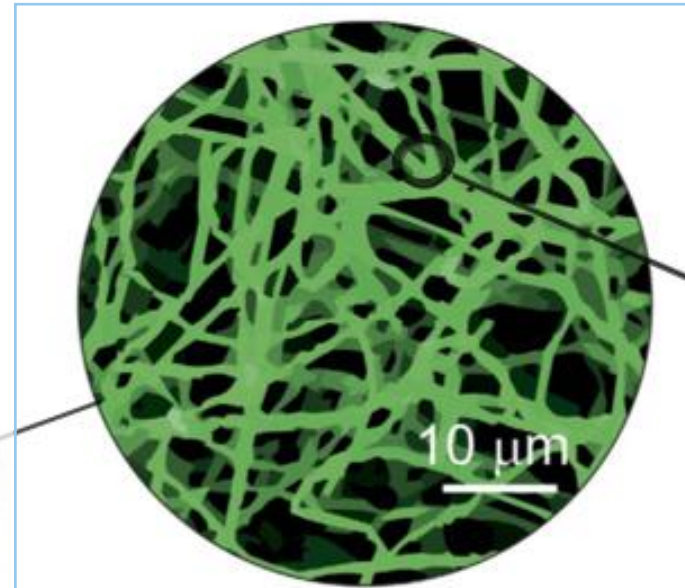


# *Biological sample*

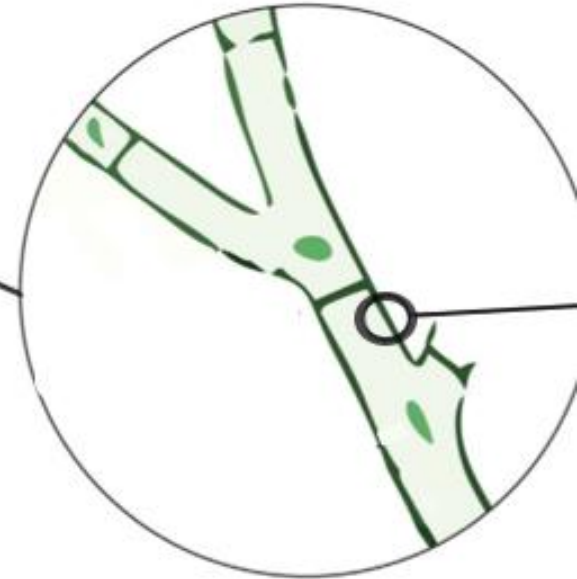


- mycelium:
- vegetative body for fungi that produce mushrooms.
- mycelium is the root system and the mushroom is the flower.
- develops from the fungal hyphae.
- mycelia plays an important role in reproduction (vegetative parts of fungi).

Mushroom



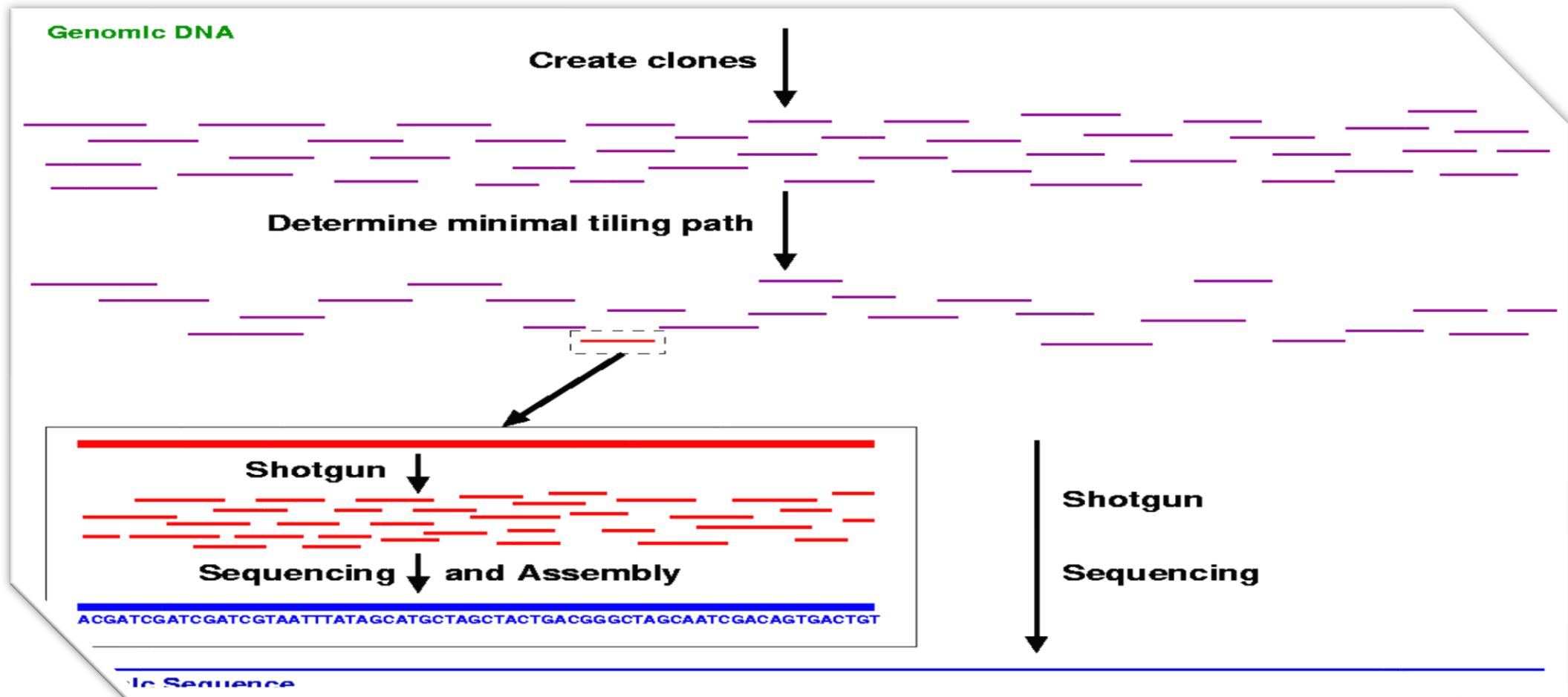
Mycelium



Hypha

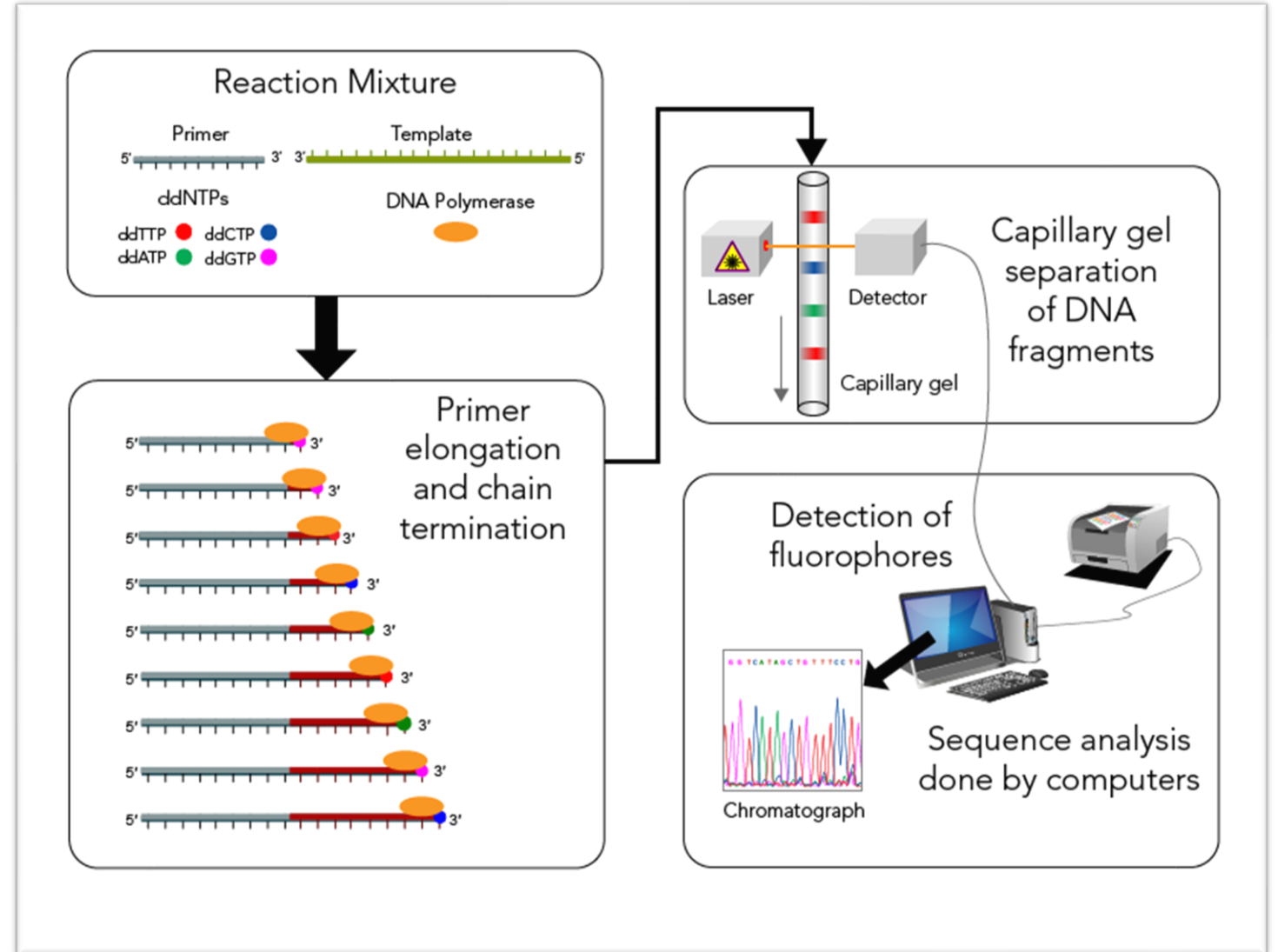
# Sequencing strategy

- using whole-genome shotgun strategy



# Sequencing methods

➤ They used sanger method:



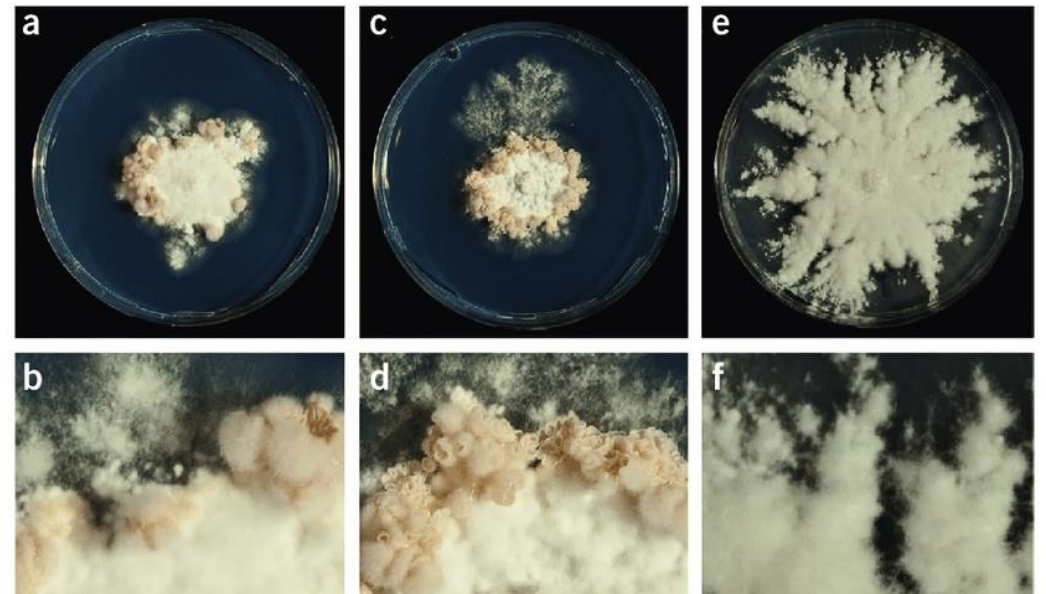
# *Genome Assembly*

- ❑ Genome coverage = 8.29X
- ❑ Number of contigs = 352
- ❑ L50 contig = 362.4KB
- ❑ N50 contig = 30
- ❑ Scaffold N50 = 5
- ❑ Scaffold L50 = 2.5 MB



# Genome Biological Outcome

- Transcription factors:
- The genome of *S. commune* reveals genes encoding 471 putative transcription factors.
- there are two factors that inhibit and induce mushroom development respectively are *fst3* and *fst4*.
- In the case of deletion of (*bri1* and *hom2*), the growth of the fungus will stop and its development will stop at the stage of morphogenesis



# ***Genome Biological Outcome***

- Wood degradation by *S. commune*:
- Fungi are major players in wood degradation.
- two types of rot fungus:
  - white-rot fungus *S. commune* degrades all woody cell wall components, while the brown-rotters efficiently degrade cellulose.
- The genome lacks genes encoding peroxidases of the LO2 family
- *S. commune* has the highest number of glycoside hydrolases and polysaccharide lyases.



## Questions:

- What are the different between monokaryon and dikaryon?
- What are functions of are fst3 and fst4?

