



French black truffle and its genome

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Introduction to genomics (485)
July 2021



Outline



Outline

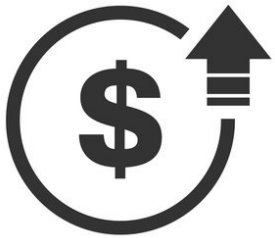


- Fun facts
- My genome paper
- General genomic information
- Biological sample
- Sequencing strategy
- Sequencing method
- Genome assembly
- Genome biological outcome



Fun facts

- Valuable
- Called in French 'Diamant Noir' means black diamond



COST



Fun facts

- Geographic distribution
- Southern Europe



Fun facts

- Cultivaion
- Using dogs and pigs



Fun facts

- Nutritional value
- Source of antioxidants
- Vitamin C
- Provide fiber, calcium, phosphorus, iron, manganese and magnesium

Nutrition Facts	
Serving size	
<hr/>	
Amount per serving	
Calories	
<hr/>	
	% Daily Value*
Vitamin C	
Fiber	
Calcium	
Phosphorus	
Iron	
Manganese	
Magnesium	
<hr/>	
<small>* The % Daily Value (DV) tells you how much a nutrient contributes to a daily diet.</small>	

My genome paper

Vol 464 | 15 April 2010 | doi:10.1038/nature08867

nature

LETTERS

Périgord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis

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The Périgord black truffle (*Tuber melanosporum* Vittad.) and the Piedmont white truffle dominate today's truffle market^{1,2}. The hypogeous fruiting body of *T. melanosporum* is a gastronomic delicacy produced by an ectomycorrhizal symbiont³ endemic to calcareous soils in southern Europe. The worldwide demand for this truffle has fuelled intense efforts at cultivation. Identification of processes that condition and trigger fruit body and symbiosis formation, ultimately leading to efficient crop production, will be facilitated by a thorough analysis of truffle genomic traits. In the ectomycorrhizal *Laccaria bicolor*, the expansion of gene families may have acted as a 'symbiosis toolbox'⁴. This feature may however reflect evolution of this particular taxon and not a general trait shared by all ectomycorrhizal species⁵. To get a better understanding of the biology and evolution of the ectomycorrhizal symbiosis, we report here the sequence of the haploid genome of *T. melanosporum*, which at ~125 megabases is the largest and most complex fungal genome sequenced so far. This expansion results from a proliferation of transposable elements accounting for ~58% of the genome. In contrast, this genome only contains ~7,500 protein-coding genes with very rare multigene families. It lacks large sets of carbohydrate cleaving enzymes, but a few of them involved in degradation of plant cell walls are induced in symbiotic tissues. The latter feature and the upregulation of genes encoding for lipases and multicopper oxidases suggest that *T. melanosporum* degrades its host cell walls during colonization. Symbiosis induces an increased expression of carbohydrate and amino acid transporters in both *L. bicolor* and *T. melanosporum*, but the comparison of genomic traits in the two ectomycorrhizal fungi showed that genetic predispositions for symbiosis—the 'symbiosis toolbox'—evolved along different ways in ascomycetes and basidiomycetes.

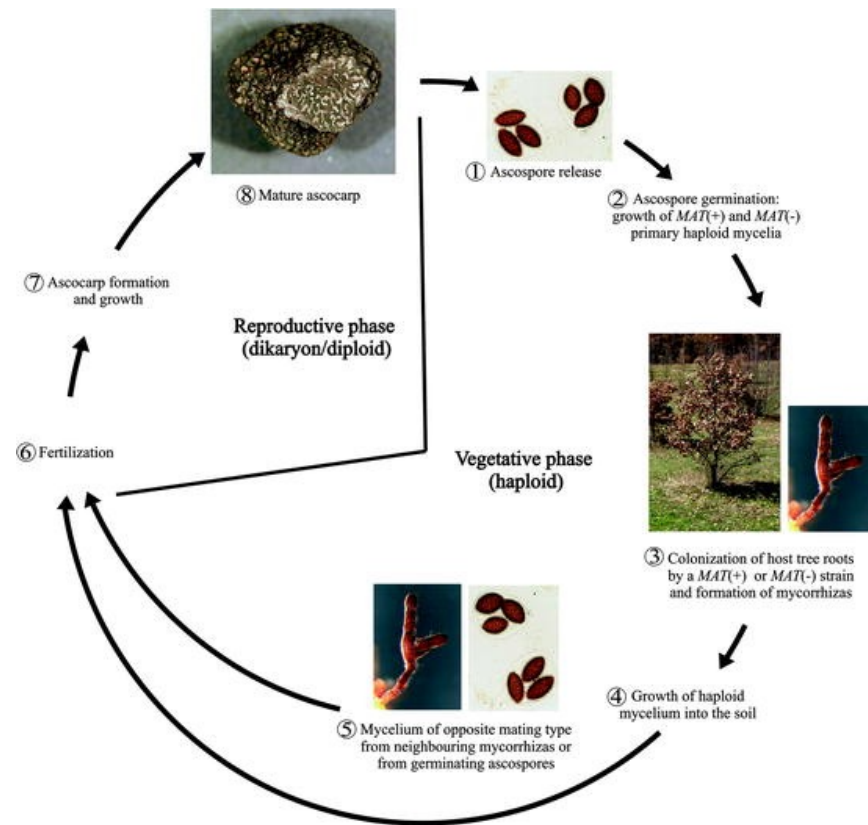
The 125-megabase (Mb) genome of *T. melanosporum* is the largest sequenced fungal genome to date⁶, but no evidence for whole-genome duplication or large scale dispersed segmental duplications was observed (Supplementary Table 1 and Supplementary Information section 2). The approximately fourfold larger size of the truffle genome compared with other sequenced ascomycetes is accounted for by multi-copy transposable elements (TE) which constitute about 58% of the assembled genome (Fig. 1, Supplementary Figs 5, 6 and 8, Supplementary Information section 3). Estimated insertion times suggest a major wave of retrotransposition at <5 million years ago (Supplementary Fig. 7). TEs are not uniformly spread across the genome, but are clustered in gene-poor or gene-lacking regions (Fig. 1 and Supplementary Fig. 8). The expansion of regions between blocks of protein-coding genes results from an increased density of TEs. The proliferation of TEs within the truffle genome may result from its low effective population size⁷ during postglaciation migrations⁸ (Supplementary Information section 2.5).

The predicted proteome is in the lower range of sequenced filamentous fungi⁹, as only 7,496 protein-coding genes were identified (Supplementary Information section 4). They are mainly located in TE-poor regions and the gene density is heterogeneous when compared with that of other ascomycetes (Fig. 1, Supplementary Figs 8 and 9). Among the predicted proteins, only 3,970, 5,596 and 5,644 showed significant sequence similarity to proteins from *Saccharomyces cerevisiae*, *Neurospora crassa* and *Aspergillus niger*, respectively (Supplementary Fig. 10). This agrees with the predicted ancient separation (>450 Myr ago) of the Pezizomycetes from the other ancestral fungal lineages (Supplementary Fig. 4)⁸. Of the ~5,650 *T. melanosporum* genes that have an orthologue, very few show conservation of neighbouring orthologues (synteny) in at least one of the other species (Supplementary Fig. 11, Supplementary

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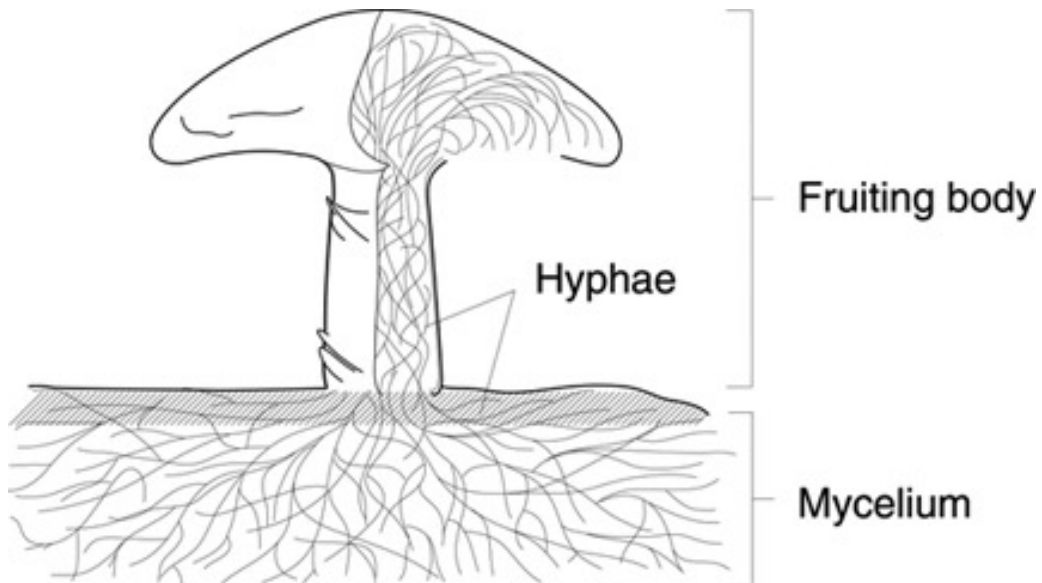
General genomic information

- Chromosome number ≥ 8
- Genome size ~ 125 Mb
- Level of ploidy (predominant haploid)



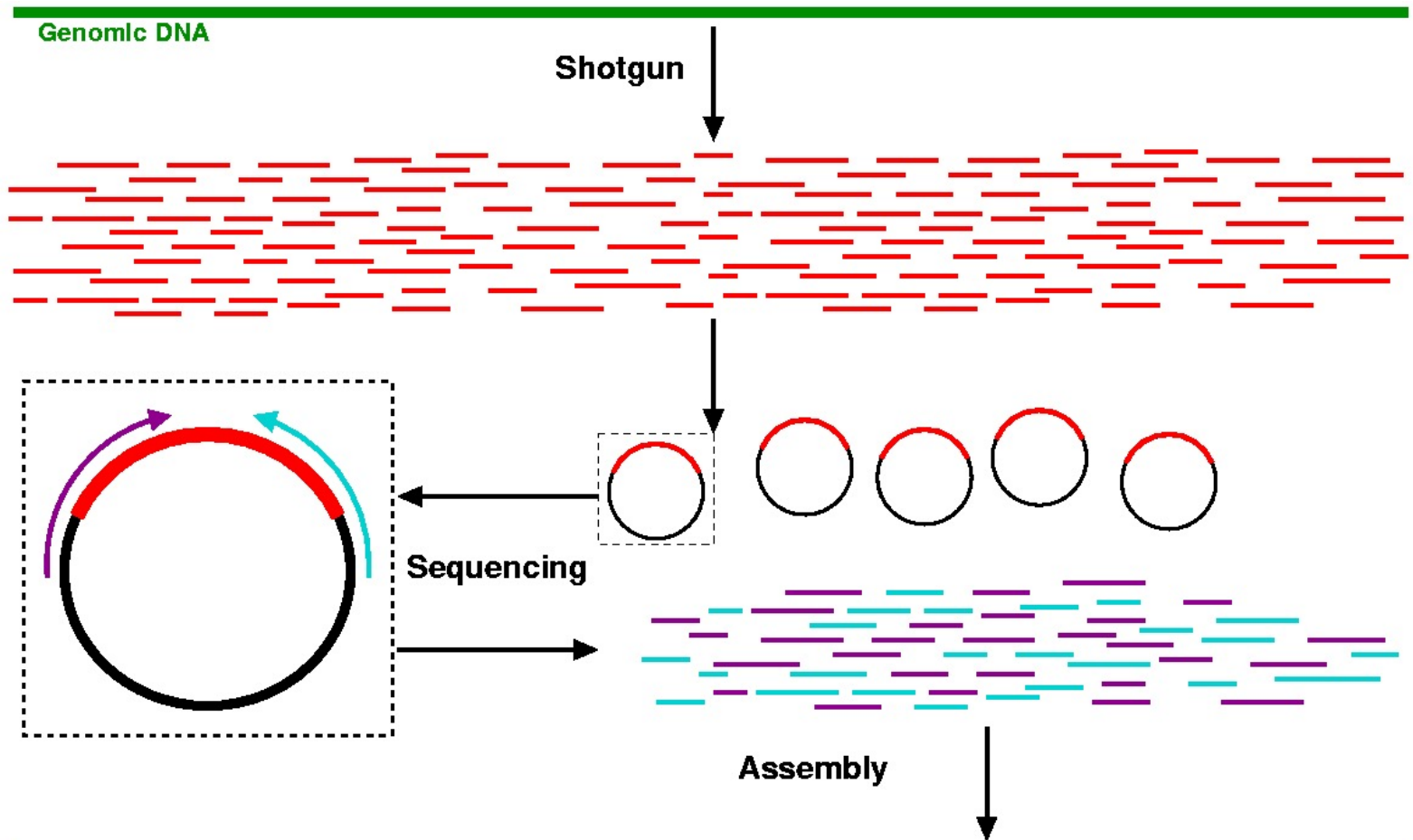
Biological sample

- Vegetative mycelium (Mel28)



Sequencing strategy

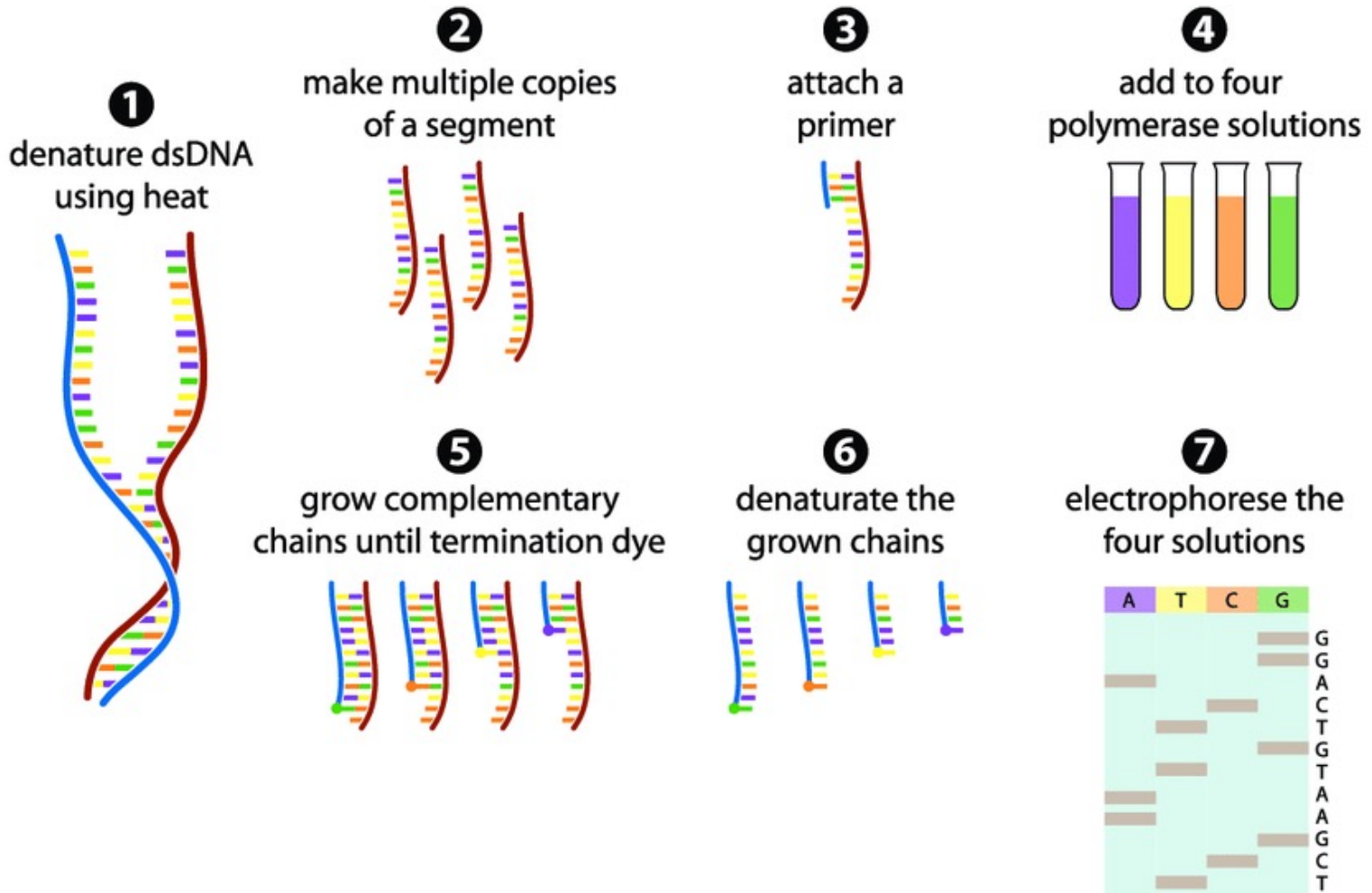
- Whole genome shotgun



ACGATCGATCGATCGTAATTTATAGCATGCTAGCTACTGACGGGCTTTTACGGCGTTAGATATATATCGATCGATCGATGCTATATAGCGTGACTGATCGTAGCTGTAGCTAGCTGTAGCTAGCT
Genomic Sequence


Sequencing method

- Sanger technique




Genome assembly

- Coverage 10x
- Contig description

Type	N°	<i>N50</i> (Kb)	Longest (Kb)
Contigs	4464		
Supercontigs	398	638	2785

Genome assembly

- Contigs description

Type	N°	N50 (Kb)	Longest (Kb)
Contigs	4464	62	
Supercontigs	398	638	2785

Genome assembly


- Contigs description

Type	N°	<i>N50</i> (Kb)	Longest (Kb)
Contigs	4464	62	918
Supercontigs	398	638	2785

Genome assembly

- Scaffold description


Type	N°	<i>N50</i> (Kb)	Longest (Kb)
Contigs	4464	62	918
Supercontigs	398		



Genome assembly

- Scaffold description

Type	N°	<i>N50</i> (Kb)	Longest (Kb)
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Genome assembly

- Scaffold description

Type	N°	<i>N50</i> (Kb)	Longest (Kb)
Contigs	4464	62	918
Supercontigs	398	638	2785

Genome biological outcome

- Complete absence of highly similar gene pairs.
- Of the predicted 7,500 protein coding genes, only seven pairs share >90% amino acid identity in their coding sequence.
- Whereas 30 pairs share >80% identity.

Genome biological outcome

- The volatiles that is released by the truffles attract rodents and truffle flies, which disperse their spores.
- It's not attractive only for rodent and flies but also humans who consider this elusive mushroom a delicacy.
- *T.melanosporum* is the first sequenced fungus producing highly flavoured fruiting bodies.

Questions

- What is the level of ploidy of *Tuber melanosporum*?
- Long reads are better than short reads for genome assembly (true or false)
- Why is paired end sequencing better than single end?



Thank you for listening

