

Genome sequencing and Annotation of *Lentinus* Section *Tigrini*

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Introduction

Lentinus tigrinus (Bull.) Fr. is a white rot fungus commonly found across Europe and parts of North America, growing on riverbeds and partially submerged logs. *L. tigrinus* exhibits an enigmatic phylogenetic divergence between North American and European populations. This study presents preliminary genomic analysis of *L. tigrinus* from both groups in addition to two other species within the section *Tigrini*, including a possibly novel species of *Lentinus* in the section *Tigrini* from Guyana, offering further insights into the diversity of this clade.

Methodology

Genetic Analysis

Genome sequencing for eight specimens from section *Tigrini*, two *L. tigrinus* from the Global West group, two from the Global East group, two *L. glabratu*s, and two possibly novel *Lentinus* sp. collected from Guyana in South America, was performed using 150x150 Illumina Novoseq6000. Genomes were assembled using MegaHit v1.2.9. We used Funannotate v1.8.17 to perform genome annotations. COGs from the annotations were compared between the cryptic *L. tigrinus* populations.

Phylogenetic Analysis

Curated ITS dataset from UNITE species hypotheses and GenBank accessions across the genus *Lentinus*. Dataset was modeled around the genus-level *Lentinus* analysis performed in Seelan et al. 2015. Alignments were done in MAFFT v7.525; phylogenetic tree was constructed and bootstrapped in IQ-TREE v2.3.6.

Works cited

Li, D., Liu, C.-M., Luo, R., Sadakane, K. & Lam, T.-W. MEGAHIT: an ultra-fast single-node solution for large and complex metagenomics assembly via succinct de Bruijn graph. *Bioinformatics* 31, 1674–1676 (2015).

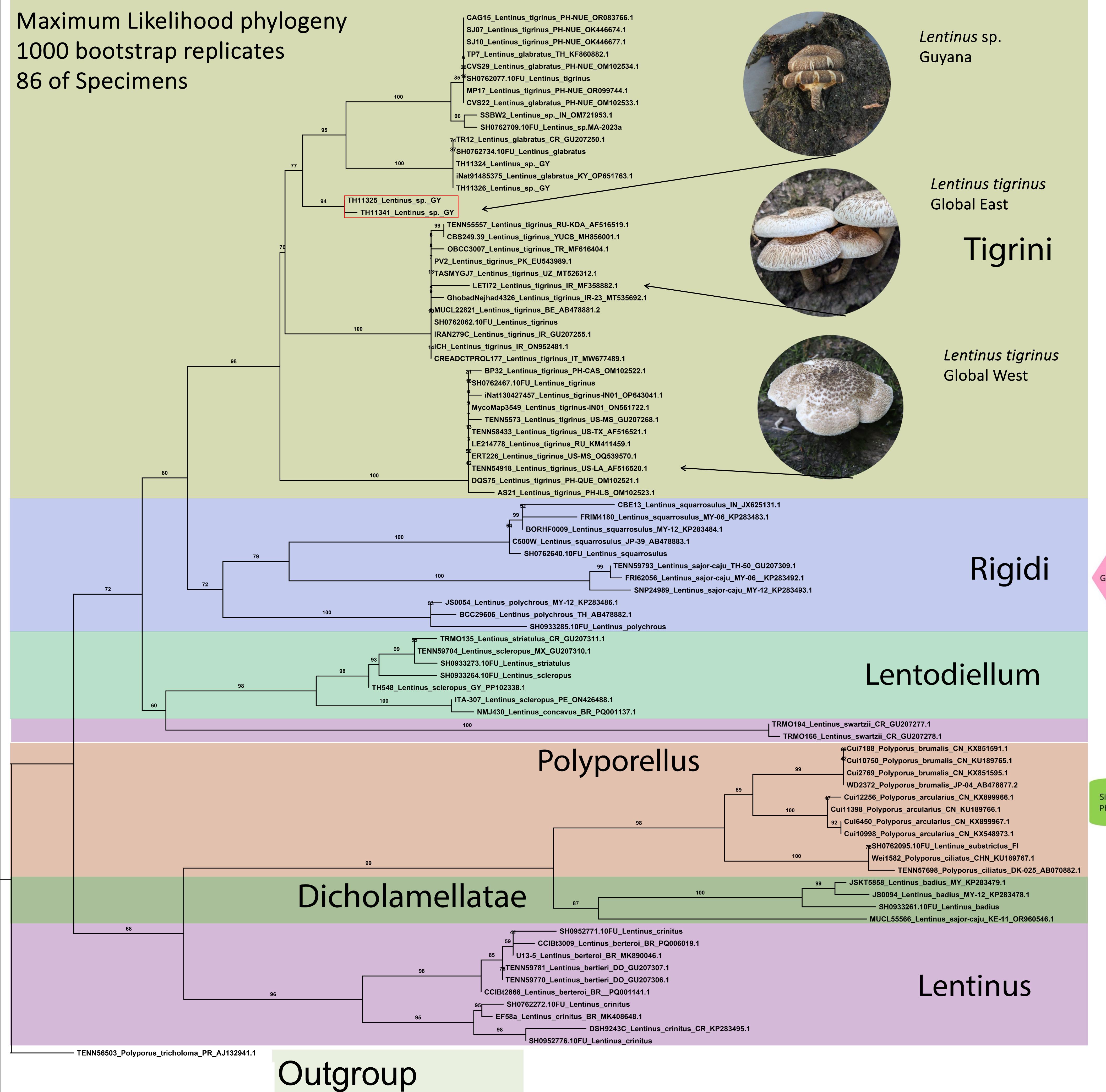
Funannotate: github.com/nextgenus/funannotate?tab=readme-ov-file

Abarenkov, K. et al. The UNITE database for molecular identification of fungi – recent updates and future perspectives. *New Phytologist* 186, 281–285 (2010).

Seelan, J. S. S. et al. Phylogenetic relationships and morphological evolution in *Lentinus*, *Polyporellus* and *Neofavolus*, emphasizing southeastern Asian taxa. *Mycologia* 107, 460–474 (2015).

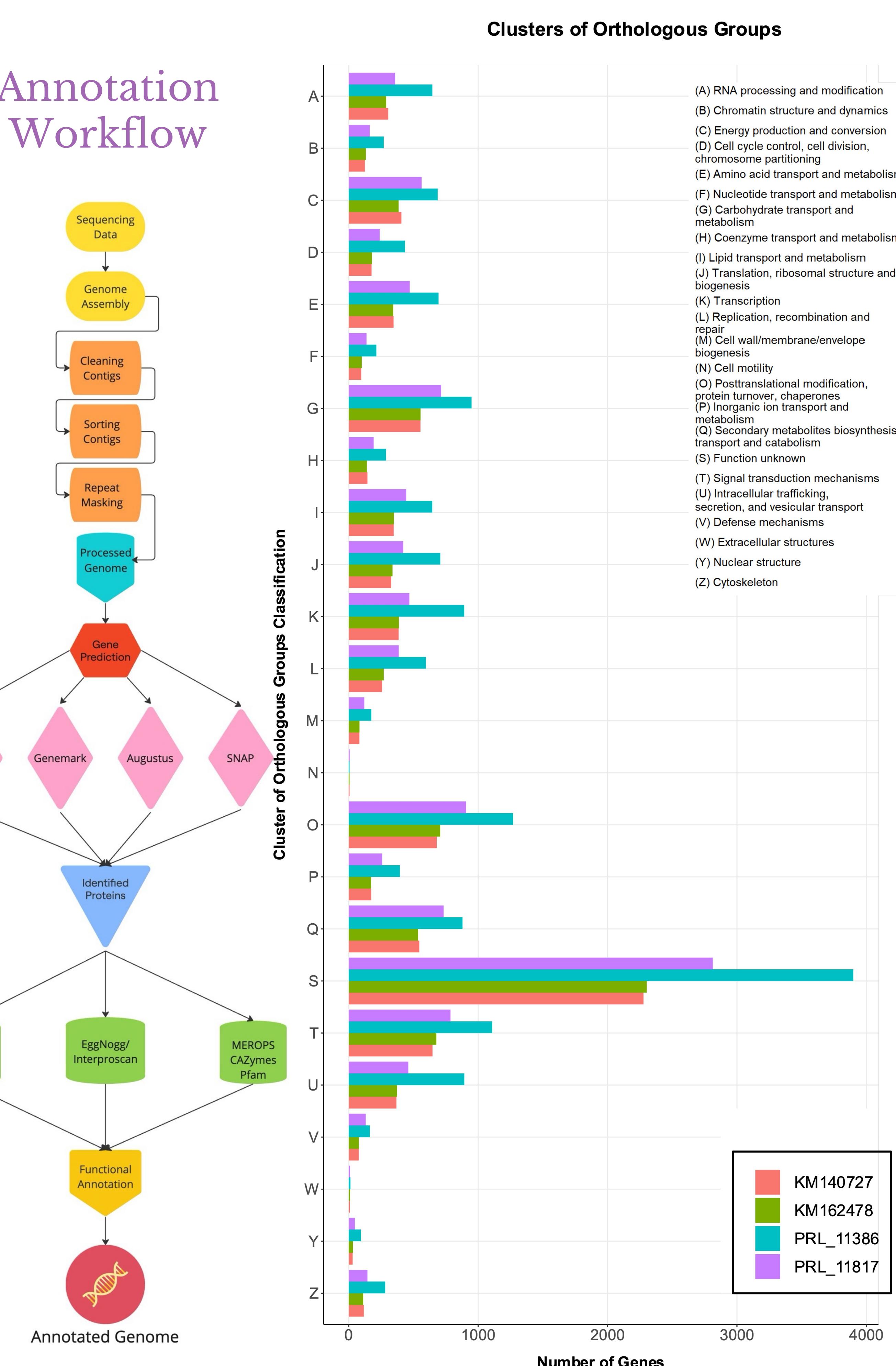
Katoh, K. MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. *Nucleic Acids Research* 30, 3059–3066 (2002).

Minh, B. Q. et al. IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. *Molecular Biology and Evolution* 37, 1530–1534 (2020).

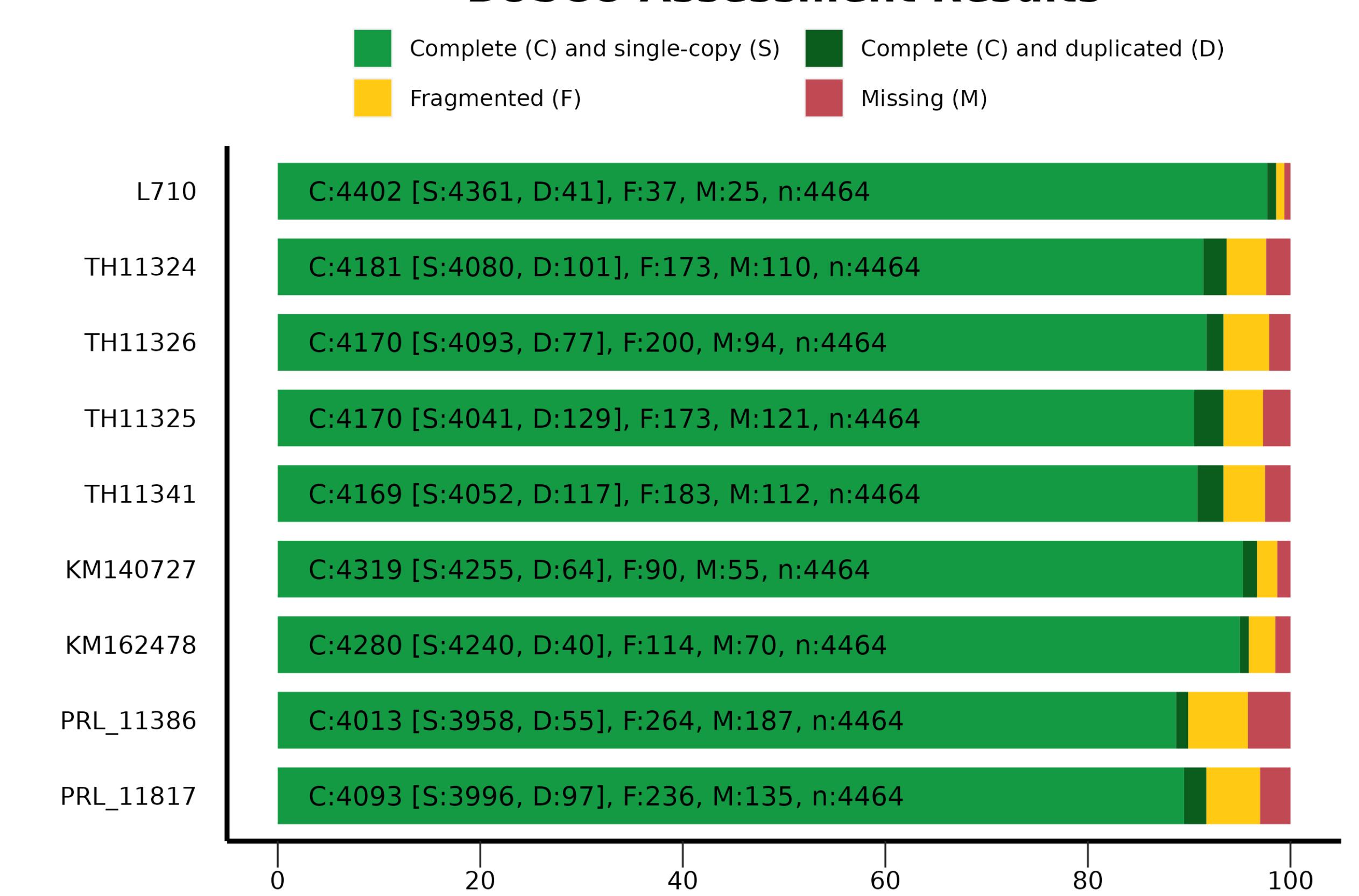


Genome Assembly Statistics

Sample	Taxa	Locality	Read Count	N50	Contig Number	Max Contig	Total Length	Average Contig
L710	<i>Lentinus tigrinus</i>	United States	24082486	94823	3901	998414	39864871	10219
Lentinus_TH11324	<i>Lentinus glabratu</i> s	Guyana	19505684	8089	22119	228275	55631820	2515
Lentinus_TH11326	<i>Lentinus glabratu</i> s	Guyana	8454050	7679	23672	205489	54886674	2319
Lentinus_TH11325	<i>Lentinus</i>	Guyana	16305726	8445	20733	193278	54081389	2608
Lentinus_TH11341	<i>Lentinus</i>	Guyana	20406124	8479	20387	193678	54057341	2652
Lentinus_tigrinus_KM140727	<i>Lentinus tigrinus</i>	England	21074114	26779	10809	516705	41038384	3797
Lentinus_tigrinus_KM162478	<i>Lentinus tigrinus</i>	Italy	7260958	19519	10570	250723	40808936	3861
Lentinus_tigrinus_PRL_11386	<i>Lentinus tigrinus</i>	United States	6488712	4330	30122	145743	61017301	2026
Lentinus_tigrinus_PRL_11817	<i>Lentinus tigrinus</i>	United States	6628646	6270	24423	198022	52761029	2160



BUSCO Assessment Results



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