Draft Genome Sequence of the Plant-Pathogenic Fungus
Stemphylium lycopersici Strain CIDEFI-216

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INTRODUCTION

The genus *Stemphylium* Wallr. was established in 1833 (1) , currently the estimated number of species vary from 30 to more than 150 (2, 3). In those species with known teleomorphs, *Stemphylium* is the anamorphic stage of the ascomycete *Pleospora* (Pleosporaceae, Pleosporales, Dothideomycetes, Ascomycetes, 2). Fungi within this genus are widely distributed and have a broad plant-host range, establishing with their hosts a pathogenic, saprotrophic or entophytic relationship (4-7). Pathogenic forms cause severe yield reductions and economic losses in horticultural and fruit tree crops (2, 8). Since *Stemphylium lycopersici* was described on tomato (*Solanum lycopersicum* L.) in 1931 (9, 10), it has been considered the causal agent of leaf spot in more than 30 hosts genera worldwide (8, 11).

OBJETIVE

The aim of this work was to produce an annotated *Stemphylium lycopersici* draft genome.

MATERIALS AND METHODS

S. lycopersici strain CIDEFI-216 was isolated from a tomato plant affected by gray leaf spot disease collected at the tomato-growing area of Bella Vista, Corrientes, Argentina. Genomic DNA from a monosporic culture was isolated by using the DNeasy Plant Mini Kit (Qiagen). DNA quality and quantity was assessed by both gel electrophoresis and spectrometry. Libraries were prepared with the TruSeq Nano DNA Library Preparation Kit, 2 x 100-bp paired-end sequencing was performed using an Illumina HiSeq 2000 sequencing system. Reads were assembled with the SOAPdenovo2 assembler software (12) at Macrogen Co. (Seoul, South Korea). *Ab initio* gene prediction was performed using Fgenesh 2.6 (13), trained on an algorithm optimized for *Alternaria brassicicola*. tRNAs and rRNAs were predicted using tRNAscan-SE (14) and hmmsearch 3.0 (15-18) tools from WebMGA server (19). An homology-based automatic annotation of the predicted open reading frames (ORFs) was carried out using Blast2GO Basic (20) and InterProScan (21).

RESULTS
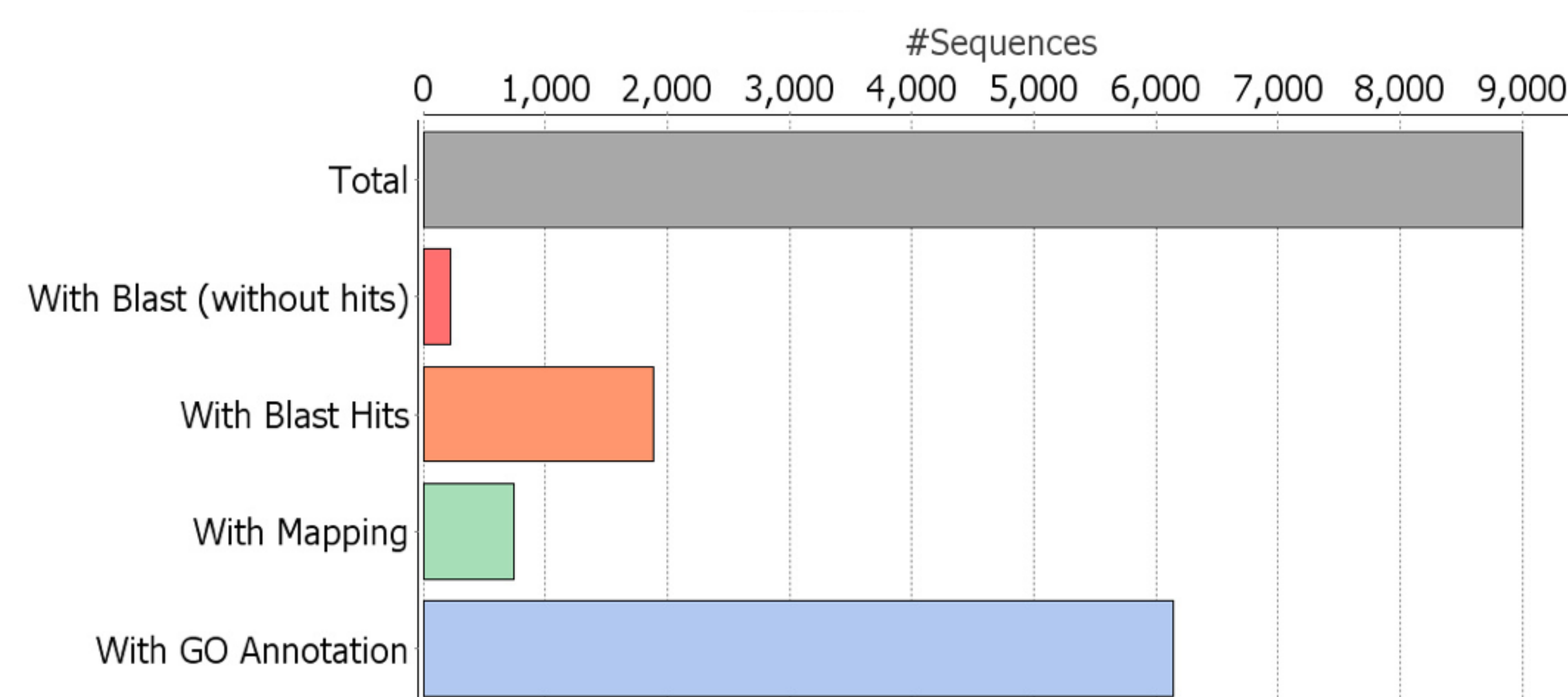
Data distribution from the annotation process.

|	Scaffolds	Contigs
Number of sequences	419	5,588
Sequence sum	35,187,764	35,011,709
N50	498,048	36,073
Longest sequence	1,567,143	171,373
Shortest sequence	1,004	8
Average length	83,98	6,265
Assembled bases	35.18 Mbp	
GC (%)	50.5	
Estimated Genome size	40.60 Mbp	
Average Coverage	77.39 X	
ORF predicted	8998	
tRNAs predicted	94	
rRNA predicted	44	
GenBank Accession	LGLR01000000	

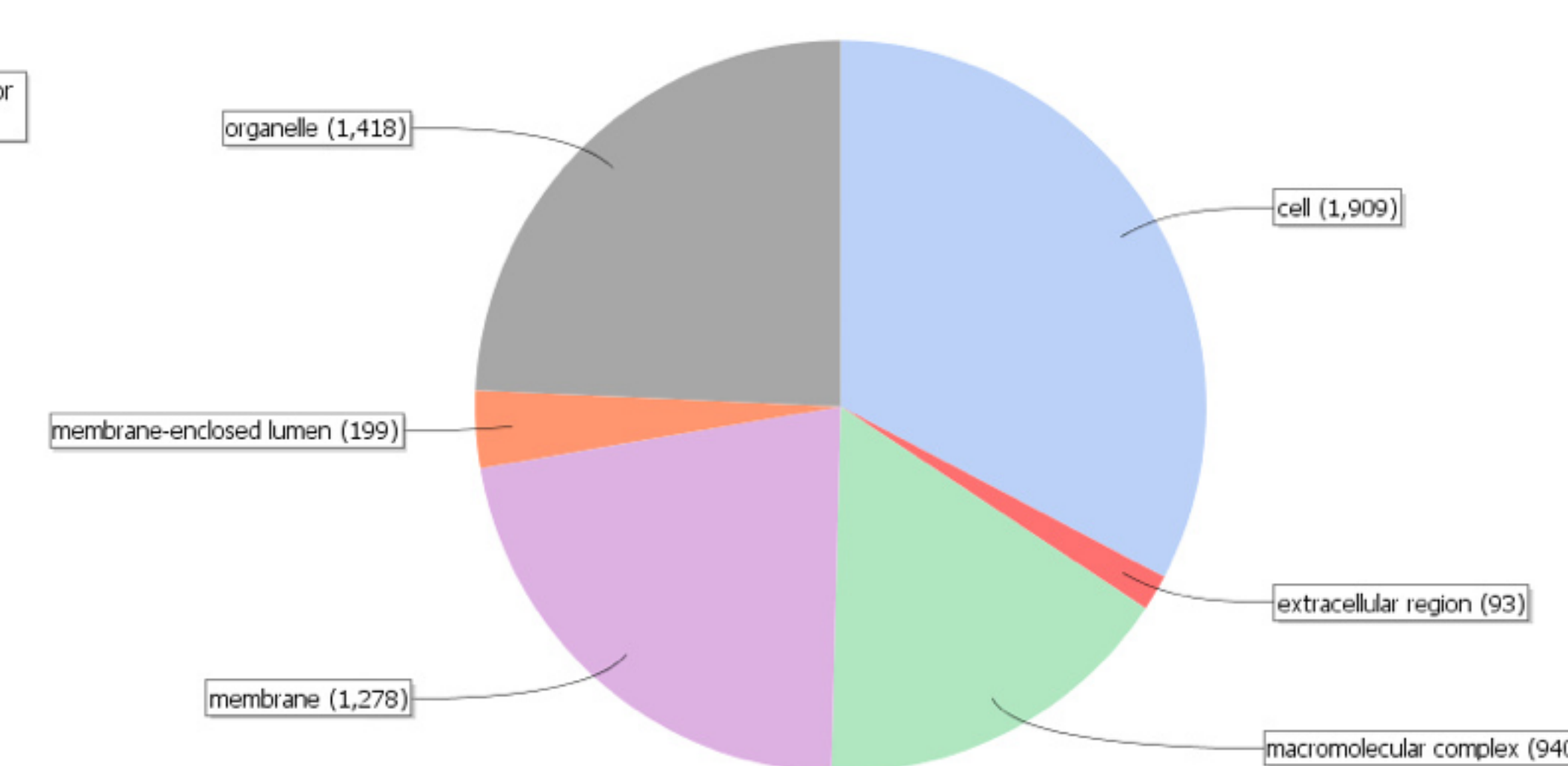*S. lycopersici* draft genome general features.
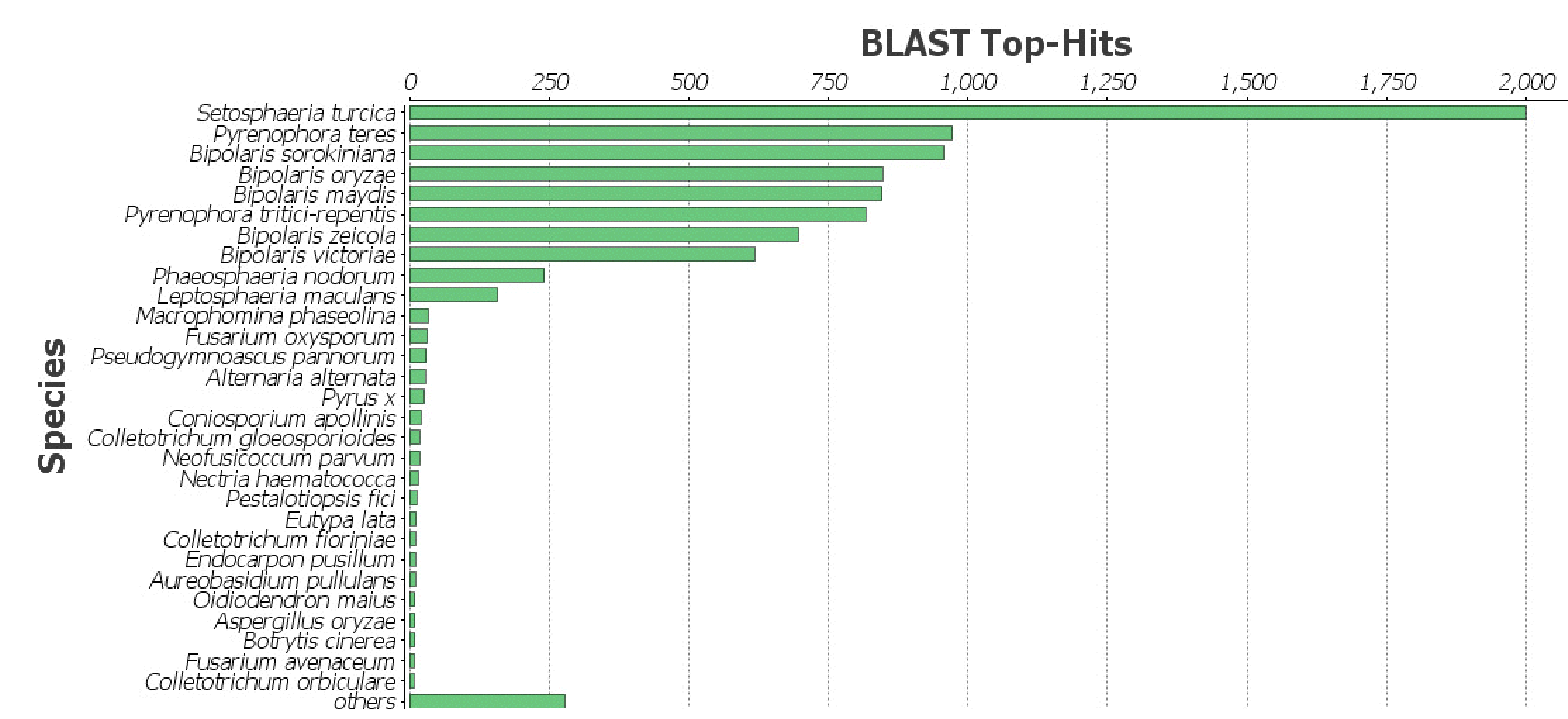
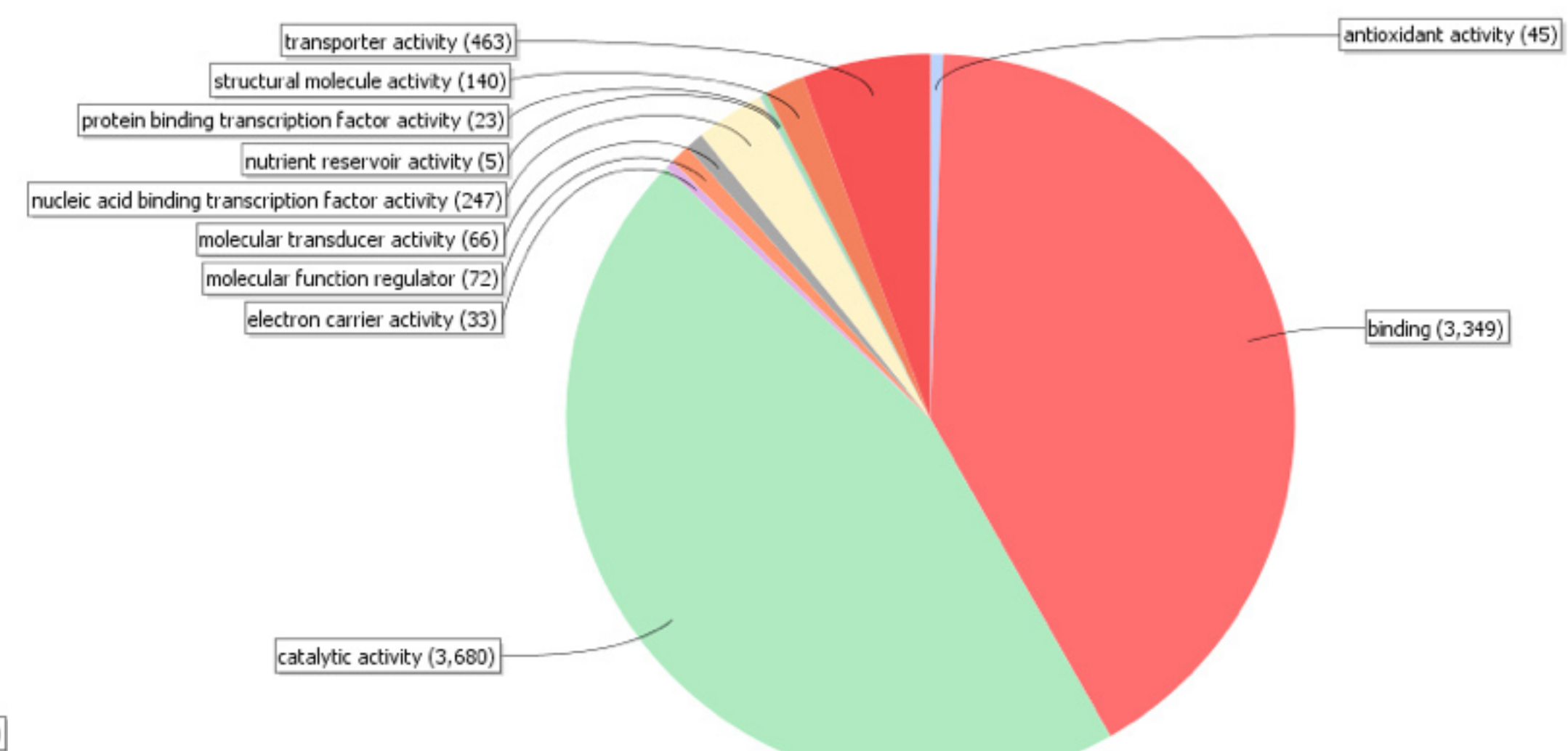BLAST top-hits species distribution of gene annotation.
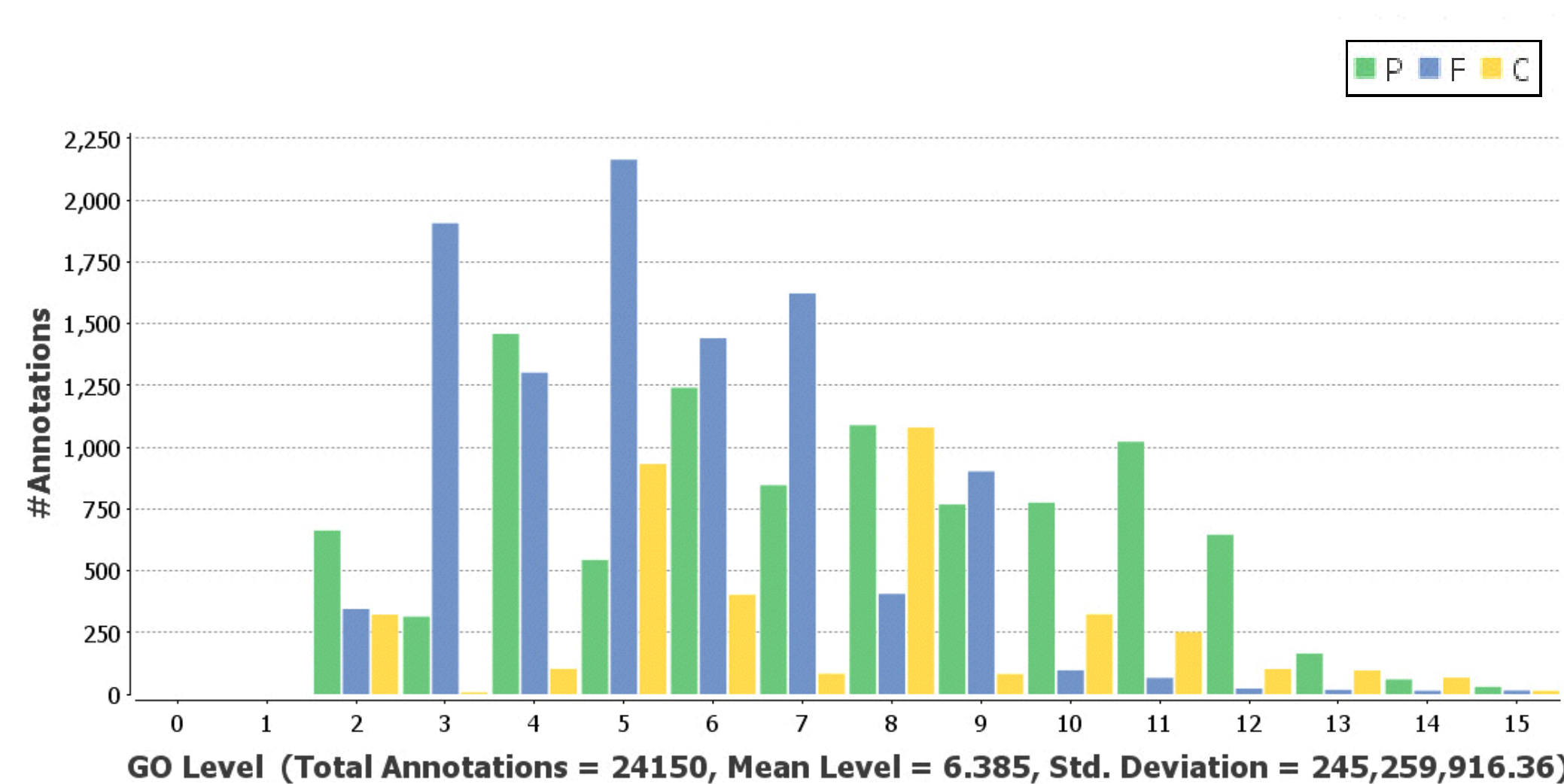
Gene Ontology (GO) level distribution.
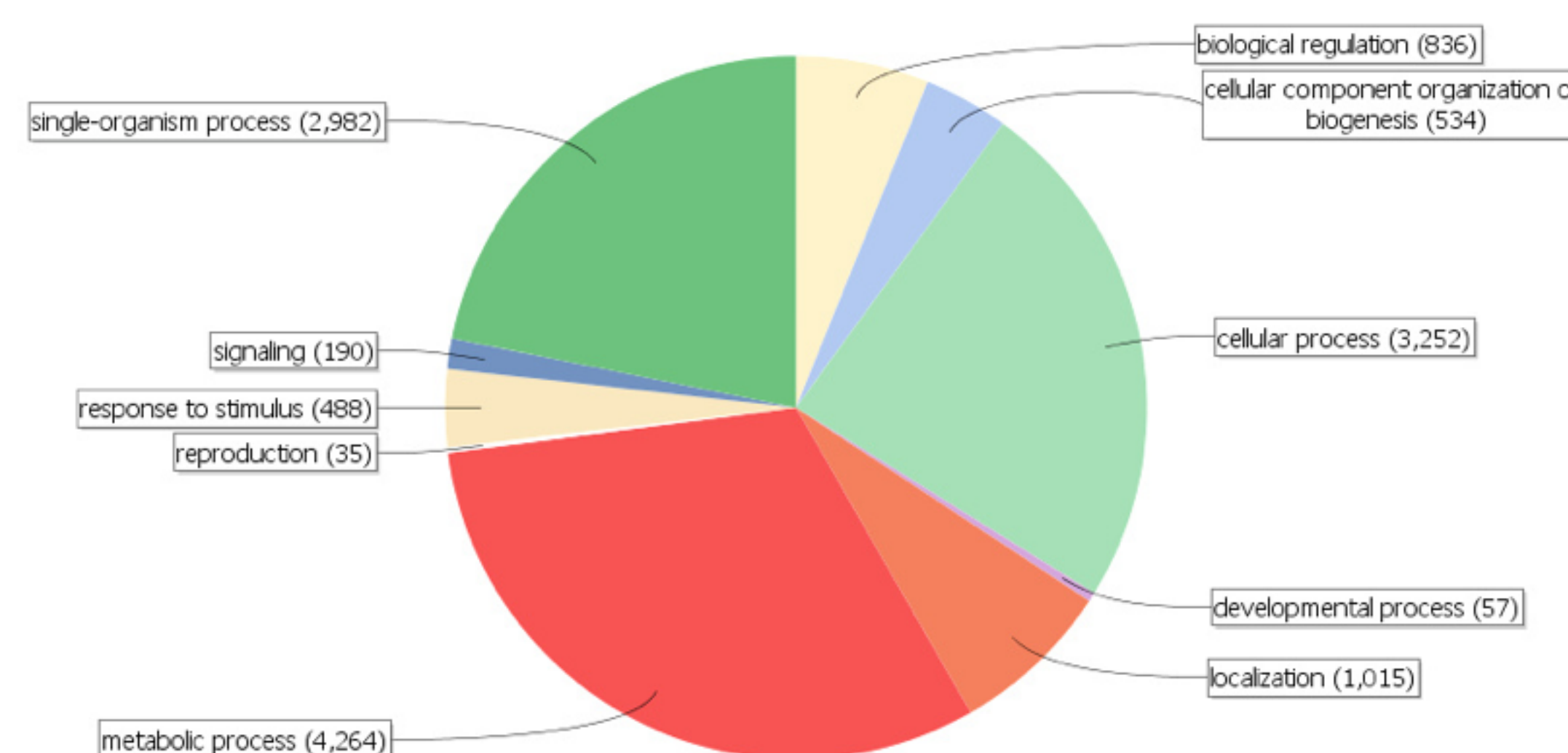
GO graph of 2nd level GO terms for the **biological process** category. The number of GOs in each class is shown.

GO graph of 2nd level GO terms for the **cellular component** category. The number of GOs in each class is shown.

GO graph of 2nd level GO terms for the **molecular function** category. The number of GOs in each class is shown.

CONCLUSION

This draft genome sequence represents the first available for *S. lycopersici* and is a new resource for future research on the basis the pathogenic behavior as well as its lifestyle. Furthermore, the sequence will shed light into the taxonomy of this fungus.

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