

The First Whole Genome Sequence Discovery of the Devastating Fungus

Arthrinium rasikravindrae

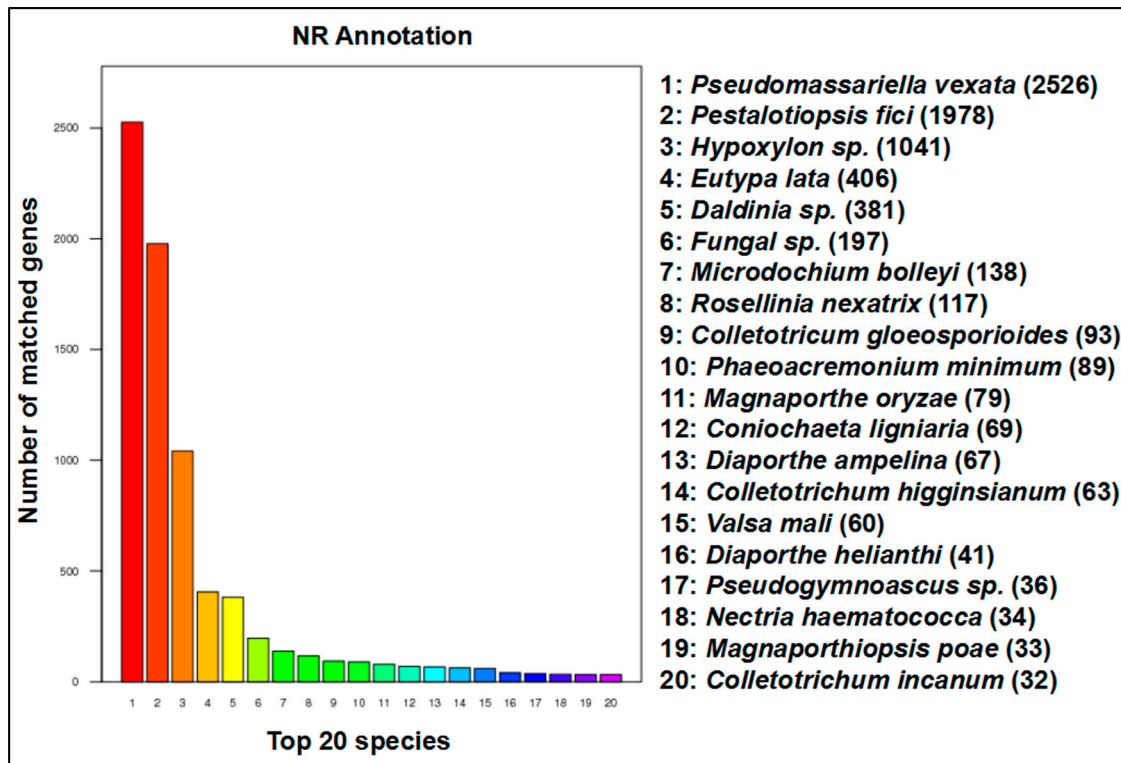
Supplementary data

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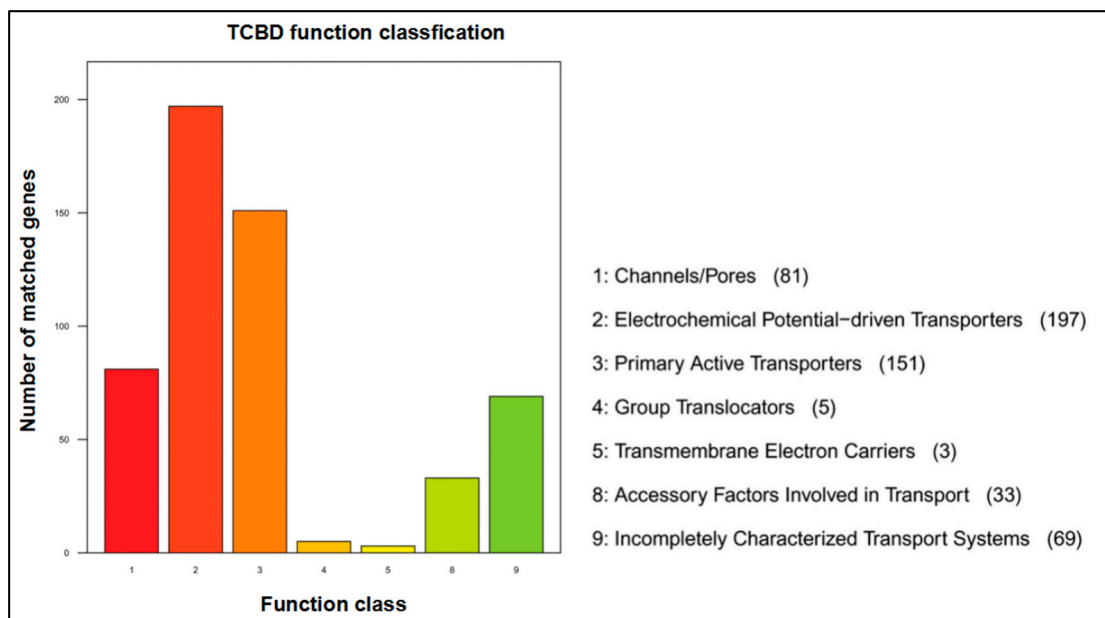
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Supplementary Table S1. Statistical assembly summary for comparative fungal genomes.

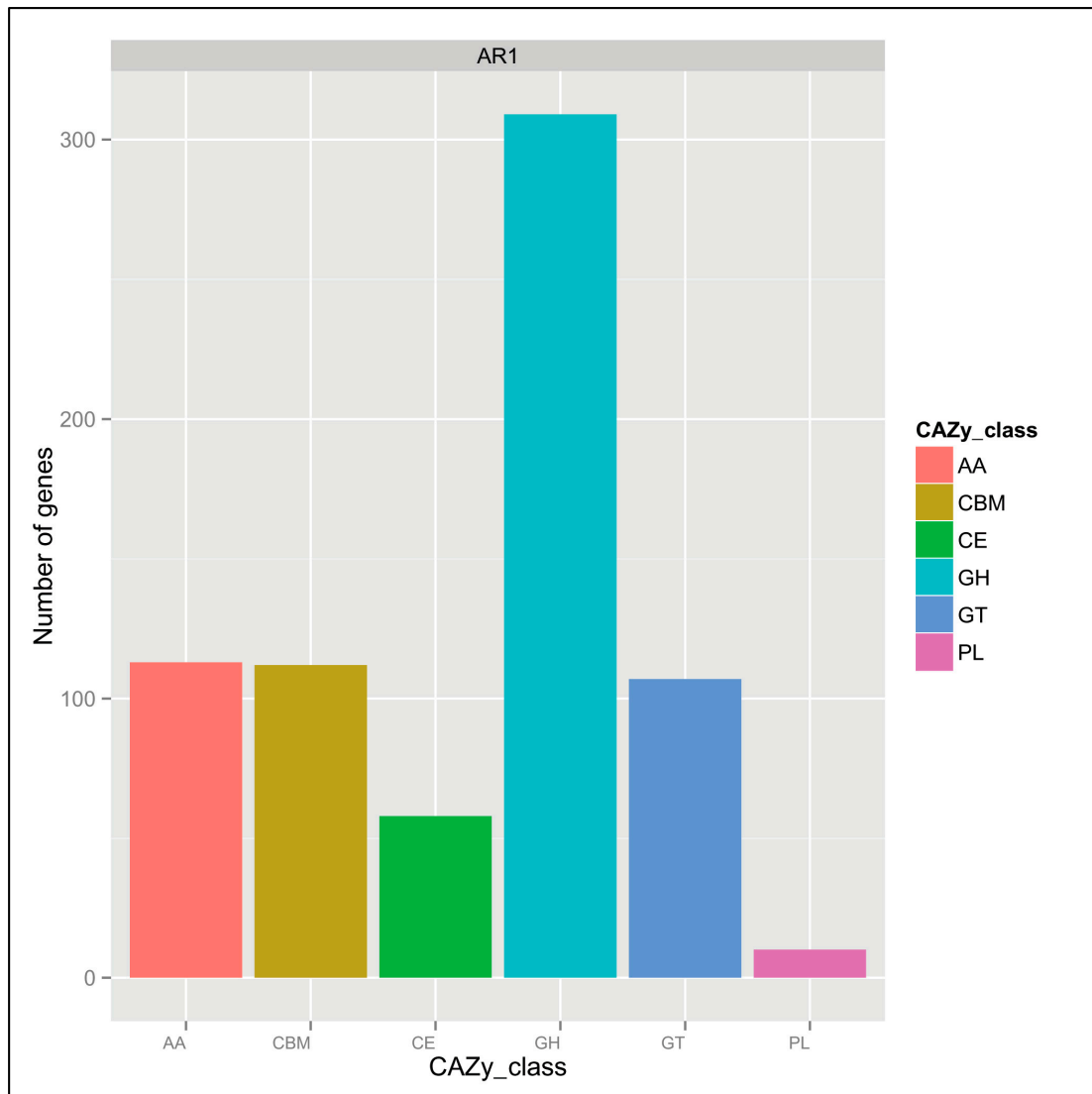
Species	Naming	Accession number in Gene Bank	Total Length (MB)	GC (%)	N50	Scaffolds	Contigs
<i>Arthrinium phaeospermum</i>	AP-Z13	QYRS000000000.1	48.45	53.05	3,733,262	19	19
<i>Arthrinium malaysianum</i>	STlab-iicb	QUSE000000000.1	46.11	52.50	336,634	43	266
<i>Fusarium proliferatum</i>	ET1	FJOF000000000	45.21	48.50	3,311,891	32	17
<i>Fusarium oxysporum</i>	FO2	AAXH000000000.1	61.38	48.42	95,416	114	1362



Supplementary Figure S1. NR annotation of species. In this figure, X-axis represents the top 20 species from 1-20, while the Y axis represents the number of matched genes between the species with a scale up to 2500. NR annotation is divided into 20 classes. Different colors depict top 20 species, their names, and values.



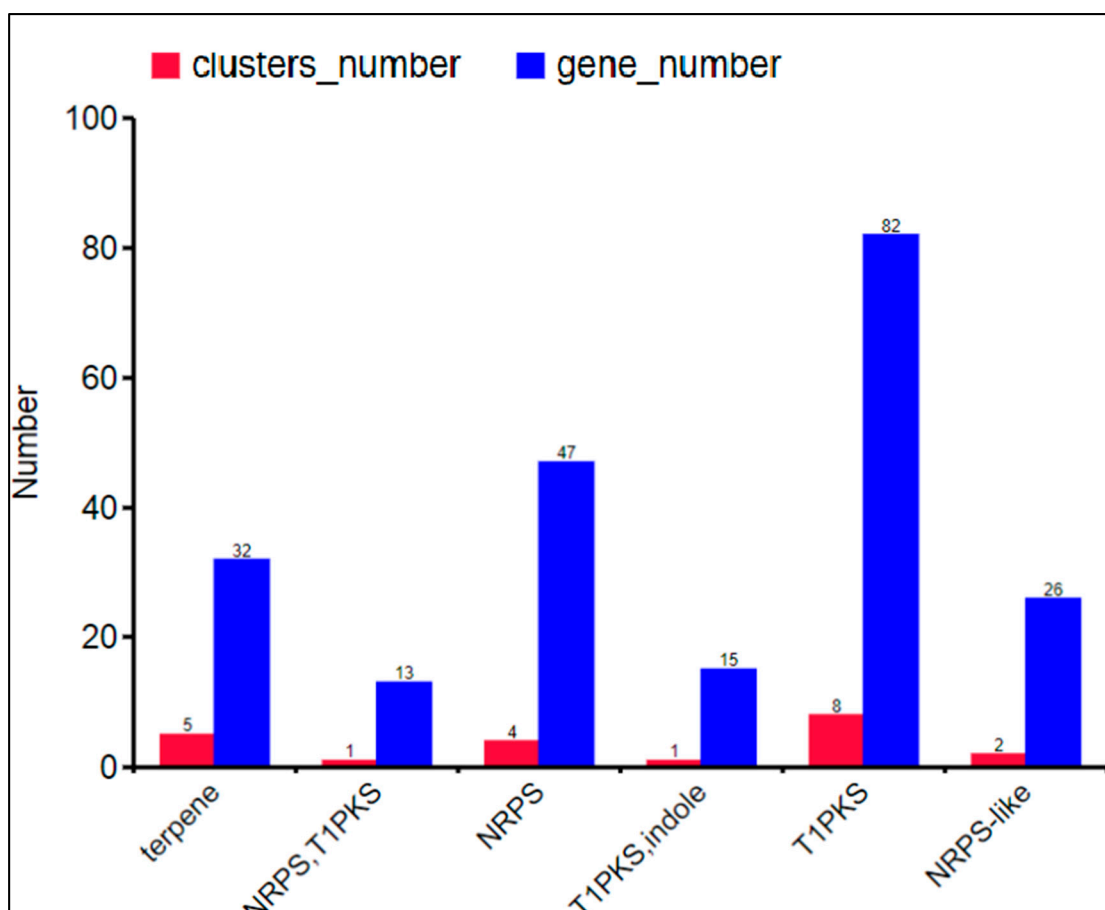
Supplementary Figure S2. TCBD functional classification. In this figure, X-axis represents the functional class & the Y-axis shows the number of matched genes, (a) TCBD functional classification 1-5, 8, and 9 class with different colors, functional class numbers, names, and values.



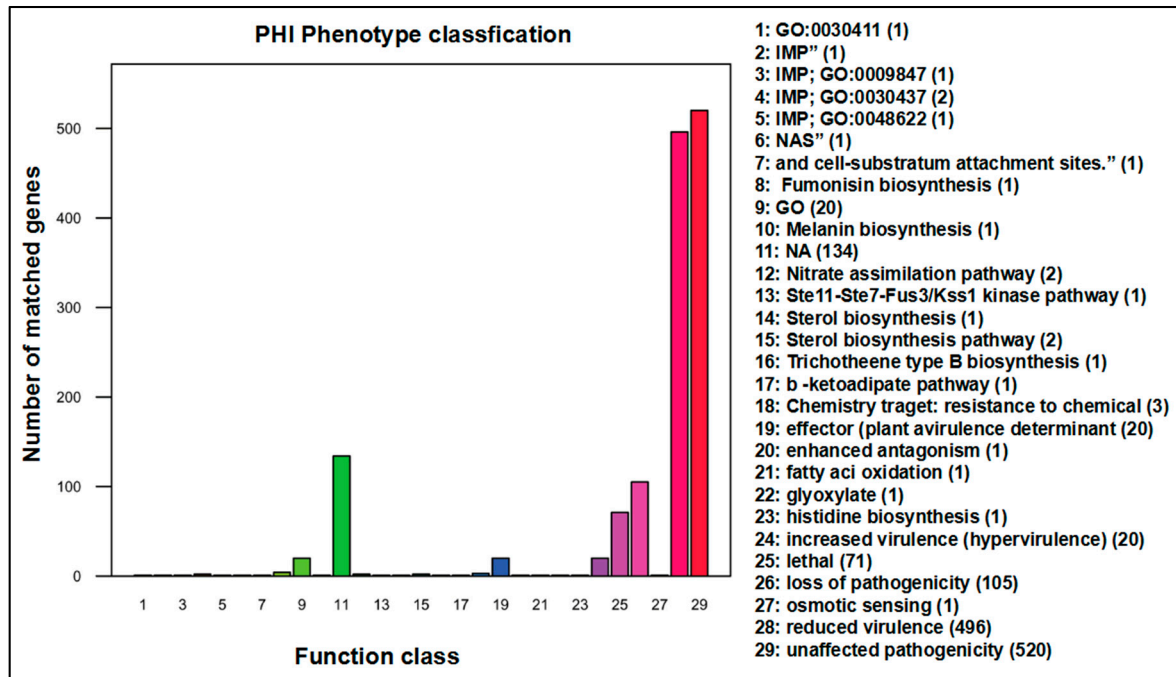
Supplementary Figure S3. Carbohydrate enzyme classification and annotation.

In this figure X-axis shows the CAZy_class with their names as shown in different colors and Y-axis denotes the genes number of genes with a scale of 300, while it is divided into 6 classes (AA), (CBM), (CE), (GH), (GT) and (PL).

Note: AR1= *Arthrinium rasikravindraae* 1.



Supplementary Figure S4. Secondary metabolic gene Cluster. In this figure two different colors are shown, red color indicates the cluster number and blue color represents the gene number, while the X-axis denotes the type of cluster and their names, and the Y-axis shows gene numbers with a scale from 0-100.



Supplementary Figure S5. PHI phenotype classification. In this figure, X-axis shows the function class with their class number and Y-axis shows the number of matched genes. PHI Phenotype classification shows 29 functional classes, functional class number and their names.