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Genome Sequencing and Comparative Analysis of the Biocontrol Agent Trichoderma harzianum sensu stricto TR274:

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Genome Sequencing and Comparative Analysis of the Biocontrol Agent *Trichoderma harzianum sensu stricto* TR274

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Genome sequencing and comparative analysis of the biocontrol agent *Trichoderma harzianum sensu stricto* TR274

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**Abstract**

Biological control is a complex process which requires many mechanisms and a high diversity of biochemical pathways. The species of *Trichoderma harzianum* are well known for their biocontrol activity against many plant pathogens. To gain new insights into the biocontrol mechanism used by T. harzianum, we sequenced the isolate TR274 genome using Illumina. The assembly was performed using AllPaths-LG with a maximum coverage of 100x. The assembly resulted in 2282 contigs with a N50 of 3703bp. The genome size generated was 40.8 Mb and the GC content was 47.7%, similar to other *Trichoderma* genomes. Using the JGI Annotation Pipeline we predicted 100% genome completeness and 97.9% of RNA-SEQ reads were covered. CEGMA tests suggested 100% genome content for all genomes sequenced at JGI, similarly divided in virtually all categories analyzed compared with the reference genomes.

**Objectives**

- Perform assembly and annotation of the *T. harzianum* TR274 genome.
- Compare all *Trichoderma* genomes available on JGI structural and functionally.
- Analyze the expansions and contractions of protein families involved in their respective lifestyles.
- Narrow possible variations between two isolates of *Trichoderma harzianum* stricto sensu.

**Conclusions**

- Corroboration of the ancestral mycoparasite lifestyle idea previously described by Kubicek et al. 2011.
- *Trichoderma* and Pachybasiomycetes sections have different mycoparasite approaches reflected by the gene composition (i.e. Secondary metabolism expansions on Pachybasiomycetous sections).
- Longibrachiatum section lost a high number of gene families leading to a different lifestyle.
- Even close related strains like *T. harzianum* TR274 and CBS228.95, have consistent differences (i.e. secondary metabolites clusters).

**References**


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**Results**

**Trichoderma Phylogeny and Genome Features**

<table>
<thead>
<tr>
<th>Trichoderma Sections</th>
<th>T. harzianum (Trihar1)</th>
<th>T. virens (Triru1)</th>
<th>T. atroviride (Tratru1)</th>
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**Graphs and Data**

- Phylogenetic tree showing the relationship between different *Trichoderma* species.
- Comparative analysis of genome features and synteny blocks.
- Distribution of orthologs based on Best Bidirectional Blast hits.

**Orthologs Distribution**

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**Synteny**

- Distribution of PFAM domains on two synteny graphs with gene families.
- Comparison of gene families distribution across different *Trichoderma* species.

**Figures**

- Gene family distribution among different *Trichoderma* species.
- Genome synteny analysis showing expansions and contractions on *Trichoderma* genus.

**Acknowledgments**

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