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► To cite this version:

Emmanuelle Morin, Eric C H Chen, Alan Kuo, Denis Beaudet, Igor V Grigoriev, et al.. Exploring genome diversity of 6 strains of the model arbuscular mycorrhizal symbiont *Rhizophagus irregularis*. JOBIM, Jul 2018, Marseille, France. hal-03324326

HAL Id: hal-03324326

<https://hal.science/hal-03324326v1>

Submitted on 23 Aug 2021

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Exploring genome diversity of 6 strains of the model arbuscular mycorrhizal symbiont *Rhizophagus irregularis*



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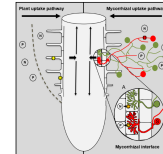
5 : Laboratoire de Recherche en Sciences Végétales, UPS, CNRS 24 Chemin de Borde Rouge-Auzeville, Université de Toulouse Castanet-Tolosan 31326, France



Background and data

Arbuscular mycorrhizal fungi (AMF) are members of the subphylum Glomeromycotina and are involved in a widespread symbiosis with the roots of most land plants. AMF are known to improve plant fitness through the establishment of mycorrhizal symbioses. Genetic and phenotypic variations among closely related AMF isolates can significantly affect plant growth, but are unclear.

To elucidate the genomic changes underlying this variability, we improved the genome assembly and gene annotation of the model strain *Rhizophagus irregularis* DAOM197198, and compared its gene content with five isolates of *R. irregularis* sampled in the same field.



In addition to plant uptake pathway, the mycorrhizal uptake pathway comprises:

- fungal transporters in the extraradical mycelium (red or green symbols)
- transport through the hyphae (mycorrhizal interface)
- mycorrhiza-inducible plant transporters in the periarbuscular membrane (orange symbols).

Genome annotation and portals

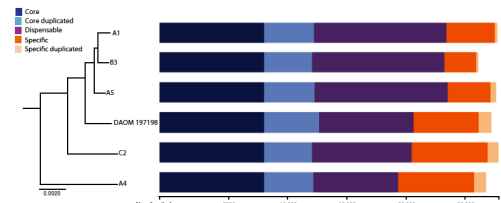
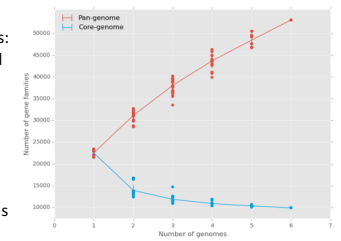
JGI Annotation Pipeline:

- integrates an array of tools for gene prediction : protein-coding gene models are predicted using a combination of gene predictors of three general kinds:
 - ab initio : Fgenesh and GeneMark
 - homology-based : Fgenesh+ and Genewise
 - transcriptome-based : models are predicted from assembled RNA-sequencing data derived from the cultured fungus
- for each genomic locus, the best representative gene model is selected based on a combination of protein homology and transcriptome support
- all predicted proteins are then functionally annotated :
 - protein alignments to the NCBI's NR, Swiss-Prot, KEGG and KOG DBs
 - detection of sequence motifs responsible for protein localization : signalP and TMHMM
 - prediction of functional domains from Pfam and other databases : InterProScan
 - expert annotation of different categories of proteins : CAZymes, proteases (MEROPS), secondary metabolism proteins

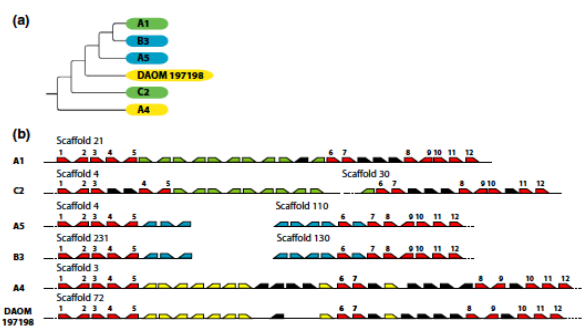
Pan and core genome curves

Prediction of secreted proteins was performed using combined characteristics:

- protein structure : presence of a signal peptide detected with SignalP and no transmembrane helix or one overlapping the signal peptide was found by TMHMM
- protein subcellular localization : subcellular localization assigned as secretory pathway using TargetP and as



Intraspecific genome diversity



A divergent region between the *Rhizophagus irregularis* isolates.

- (a) Phylogenetic relationships of the isolates based on rRNA sequences, mitochondrial genes, and most orthologous nuclear genes.
- (b) Gene order and sequence comparison along a 67 kb syntenic region present in all isolates investigated. The red color represents flanking syntenic genes that extend beyond what is presented in the figure, with the number indicating which genes are orthologs to each other; black represents genes showing no evidence of synteny; other colors represent the sequence conservation and synteny unique to pairs of isolates.

Conclusion

All isolates harbor striking genome variations, with large numbers of isolate-specific genes, gene family expansions, and evidence of interisolate genetic exchange. Overall, these findings indicate a substantial divergence in the functioning capacity of isolates harvested from the same field, and thus their genetic potential for adaptation to biotic and abiotic changes. Our data also provide a first glimpse into the genome diversity that resides within natural populations of these symbionts.

Chen E.C.H., Morin E. *et al.* High intraspecific genome diversity in the model arbuscular mycorrhizal symbiont *Rhizophagus irregularis* (2018) *New Phytologist*, doi: 10.1111/nph.14989

This work was also supported by the Laboratory of Excellence ARBRE (ANR-11-LABX-0002-01),

