Characterization of unknown

t

Rhizophagus irregularis





Jordana Oliveira, PhD Postdoc at University of Ottawa Nicolas Corradi lab



Kokkoris et al., 2020

Where is the origin of AMF variability? How did they escape the extinction?

"Despite the long time frame of coevolution with highly divergent host plants of the green plant lineage, AMF exhibit surprisingly low morphological diversity and no obvious signs of plant specificity.[...] As a result, these fungi are still considered by many as being 'evolutionary scandals' that should have become extinct long ago."



TE landscape of *R. irregularis*

• A third part of TEs is composed of unknown families: based on homology





Genome Fraction

Kimura substitution level (CpG adjusted)

Bioinformatics, 37(17), 2021, 2529–2536 doi: 10.1093/bioinformatics/btab146 Advance Access Publication Date: 3 March 2021 Original Paper

OXFORD

Genome analysis ClassifyTE: a stacking-based prediction of hierarchical classification of transposable elements

Manisha Panta^{1,†}, Avdesh Mishra^{2,†}, Md Tamjidul Hoque 💿 ^{1,*} and Joel Atallah 💿 ^{3,*}

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Interspersed Repeat Landscape

DAOM

A1

B3

C2

4401

Unknown

RepModeler

A4

A5

G1

SL





SUPERFAMILIES and FAMILIES: Phylogenetic relationships

learning classification



• Transposase and TIRS presence





Cut-and-Paste Transposons in Fungi with Diverse Lifestyles

Anna Muszewska^{1,*,†}, Kamil Steczkiewicz^{2,†}, Marta Stepniewska-Dziubinska¹, and Krzysztof Ginalski² ¹Institute of Biochemistry and Biophysics, Polish Academy of Sciences, Warsaw, Poland ²Laboratory of Bioinformatics and Systems Biology, CeNT, University of Warsaw, Poland

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Accepted: December 7, 2017







TE families among the strains





Hybrid dysgenesis in animals



RESEARCH

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Hybrid dysgenesis in *Drosophila virilis* results in clusters of mitotic recombination and loss-of-heterozygosity but leaves meiotic recombination unaltered

Lucas W. Hemmer^{1,2*}, Guilherme B. Dias³, Brittny Smith⁴, Kelley Van Vaerenberghe¹, Ashley Howard¹, Casey M. Bergman³ and Justin P. Blumenstiel¹

"Hybrid dysgenesis is a phenomenon of sterility that arises during intraspecific hybridization when TE families are absent in one strain but abundant in another."

Final remarks

- The unknown and putative AMF superfamilies were identified.
- The strains carry >70% of shared families. But, some families are strains specific.
- TEs into A and B compartments seems to have different behaviors: degeneration and mobilization
- The dikaryon haplotypes are homogenous
- FUTURE QUESTIONS: How this differences can contribute to strain expression? Can TE specific families to sign/represent the strain?

REVIEW



CrossMark

Ten things you should know about transposable elements

Guillaume Bourque^{1,2*}, Kathleen H. Burns³, Mary Gehring⁴, Vera Gorbunova⁵, Andrei Seluanov⁵, Molly Hammell⁶, Michaël Imbeault⁷, Zsuzsanna Izsvák⁸, Henry L. Levin⁹, Todd S. Macfarlan⁹, Dixie L. Mager¹⁰ and Cédric Feschotte^{11*}



Genome Biology















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