



Characterization of Transposable Elements in the Ectomycorrhizal Fungus *Laccaria bicolor*

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Background

- The publicly available *Laccaria bicolor* genome sequence has provided a rich genomic resource allowing systematic identification of transposable elements (TEs) in this symbiotic ectomycorrhizal fungus. Using a TE-specific annotation pipeline, we have characterized and analyzed TEs in the *L. bicolor* S238N-H82 genome.

Science

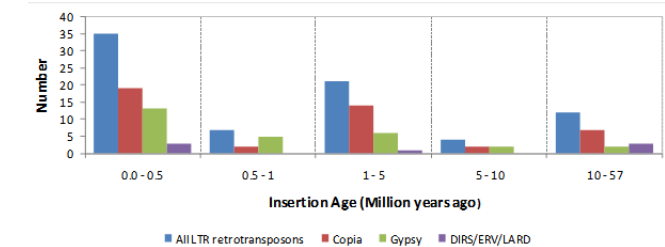
- TEs occupy 24% of the 60 Mb *L. bicolor* genome and represent 25,787 full-length and partial copy elements distributed within 171 families. Moreover, TEs are not randomly distributed across the genome, but are tightly nested or clustered. The majority of TEs exhibits signs of ancient transposition, with the exception of some intact copies of terminal inverted repeats (TIRS), long terminal repeats (LTRs) and a large retrotransposon derivative (LARD) element.
- There were three main periods of TE expansion in *L. bicolor*: the first from 57 to 10 Mya, the second from 5 to 1 Mya and the most recent from 0.5 Mya ago until now.

Significance

- This analysis 1) provides insight into evolution of *Laccaria* from a saprophytic to a symbiotic lifestyle; 2) improves genome annotation; and 3) provides a valuable resource for understanding the role of TEs in genome evolution, organization, and function.

Number of LTR retrotransposon families relative to their insertion age expressed in million years.

a) the *Laccaria bicolor* genome



Density of transposable elements (TE) along the five first linkage groups of *L. bicolor*. Lane 2 to 5 correspond to various TE classes.

