



# Conservation of Divergent Transcript in Fungi



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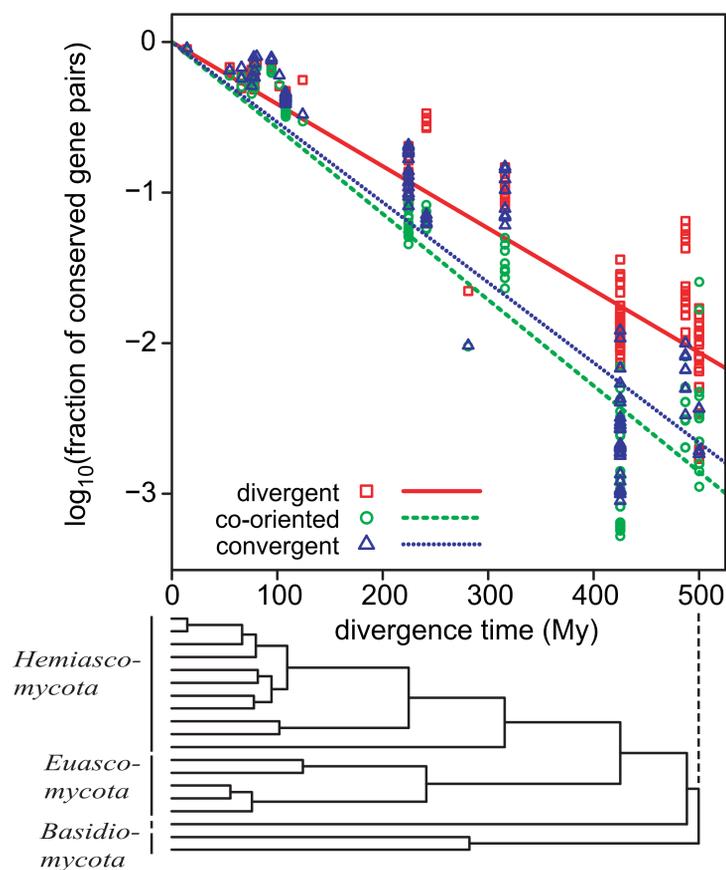
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## Introduction

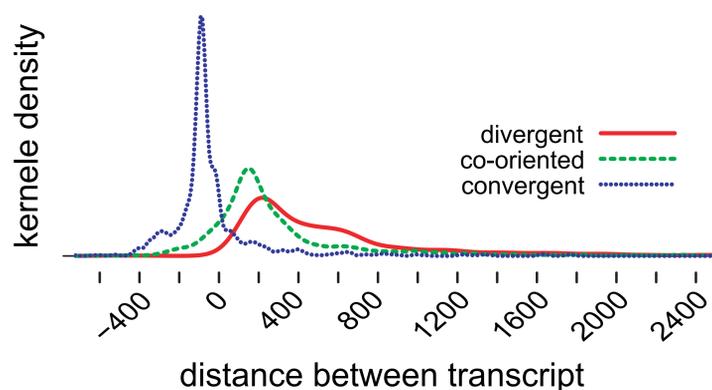
We quantified the conservation of divergent ( $\leftarrow\rightarrow$ ), co-oriented ( $\rightarrow\rightarrow$ ) and convergent ( $\rightarrow\leftarrow$ ) genes in the genomes of 19 asco- and basidiomyceteous fungi. Divergent gene orientation is most conserved, which suggests an abundance of bidirectional promoters.

## Divergent gene pairs are more conserved in orientation ...



## ... although they have longer intergenic spacers.

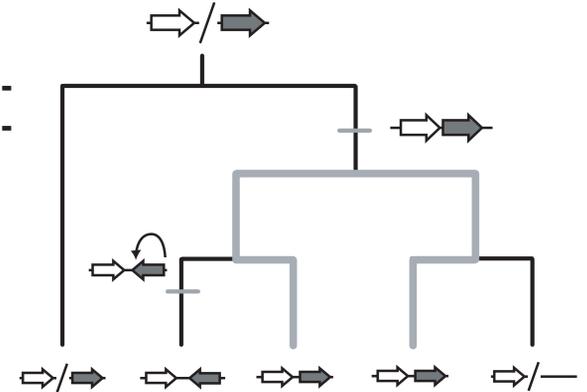
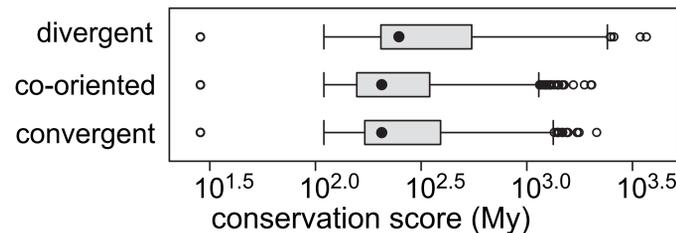
If separation of genes was only dependent on intergenic distance (neutral model), then the more conserved divergent gene pairs should have shorter intergenic spacers.



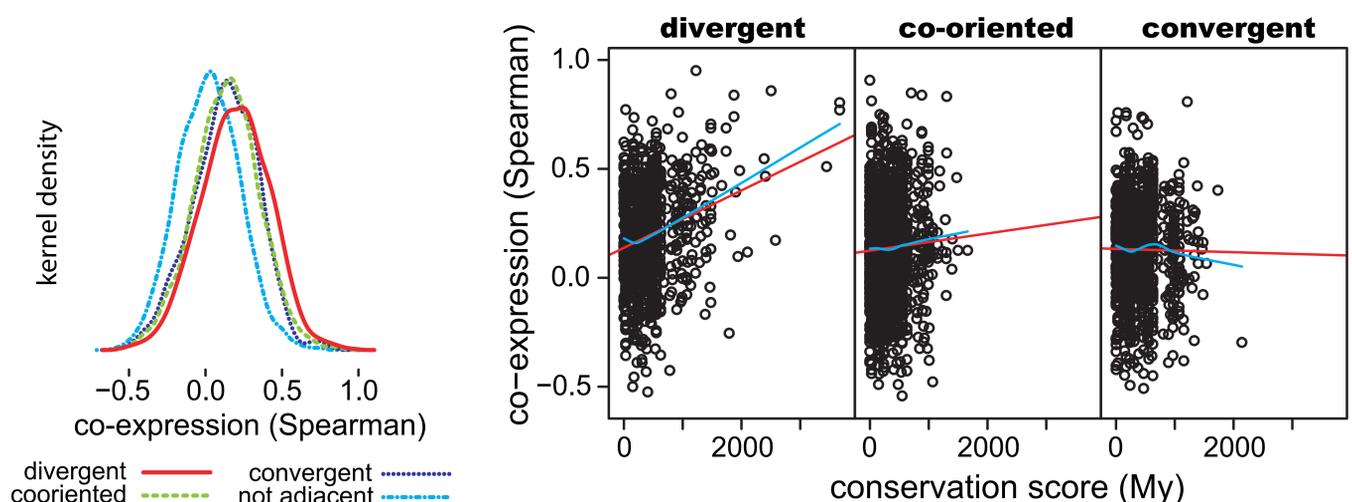
## Quantify the conservation of individual gene pairs

Gene pairs were scored by how long their orientation was maintained during fungal evolution.

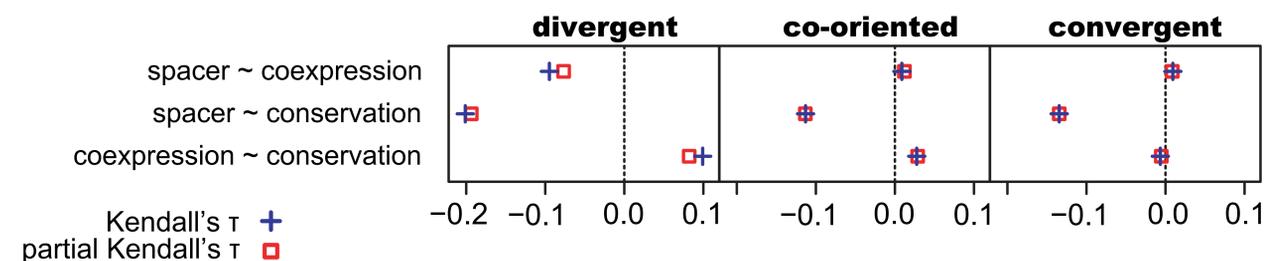
We assumed that a gene pair gained its orientation exactly once during this time (Dollo parsimony).



## Conservation of orientation correlates with co-expression ...



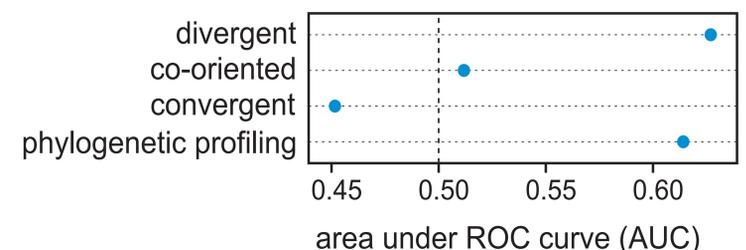
## ... independent of spacer length.



## Conserved divergent gene pairs are functionally related!

Interactions from KEGG, MIPS, and Yeast GRID.

Higher conservation of functionally related gene pairs only for divergent gene pairs (one-sided U-test,  $p=1.65 \times 10^{-2}$ ).



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