



# Analysis of the Role of Coevolution between Fungi of the *Trichophyton* Genus and their Various Hosts by Co-phylogenetic Methods



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## Introduction

Dermatophytoses are diseases caused by dermatophyte fungi including those of the genus *Trichophyton*. The systematics and taxonomy of this genus have been developed through constant changing criteria that have resulted in a confusing and complex-based taxonomy with some species indistinguishable from each other. One way to distinguished between these has been by the host from which it is isolated, considering the existence of anthropophilic and zoophilic species (1). For this reason, this study aimed to establish the role of co-speciation between *Trichophyton* and their different hosts in their phylogeny through cophylogenetic methods.

## Methods

A total of 60 *ITS* sequences of *Trichophyton* specimens and their respective *cytb* host sequences were obtained from GeneBank and subjected to phylogenetic analysis using Mega X with the Muscle algorithm. Bayesian phylogenetic reconstructions for both fungi and hosts were conducted using BEAST v1.10.4. The jModelTest v2.1.10 determined the generalized time reversible substitution model. Prior distributions were defined in Beauti v1.10.4, followed by Markov chain Monte Carlo simulations with a chain length of 10,000,000 and a 10% burn-in. A maximum clade credibility tree was generated using Tree Annotator v1.10.4. To assess congruence between host and fungi phylogenies, both the ParaFit function in CopyCat and the PACo function in 'paco' within R 3.5.2 were employed. An event-based tree-reconciliation co-phylogenetic analysis was performed using eMPress software (2, 3).

## Results

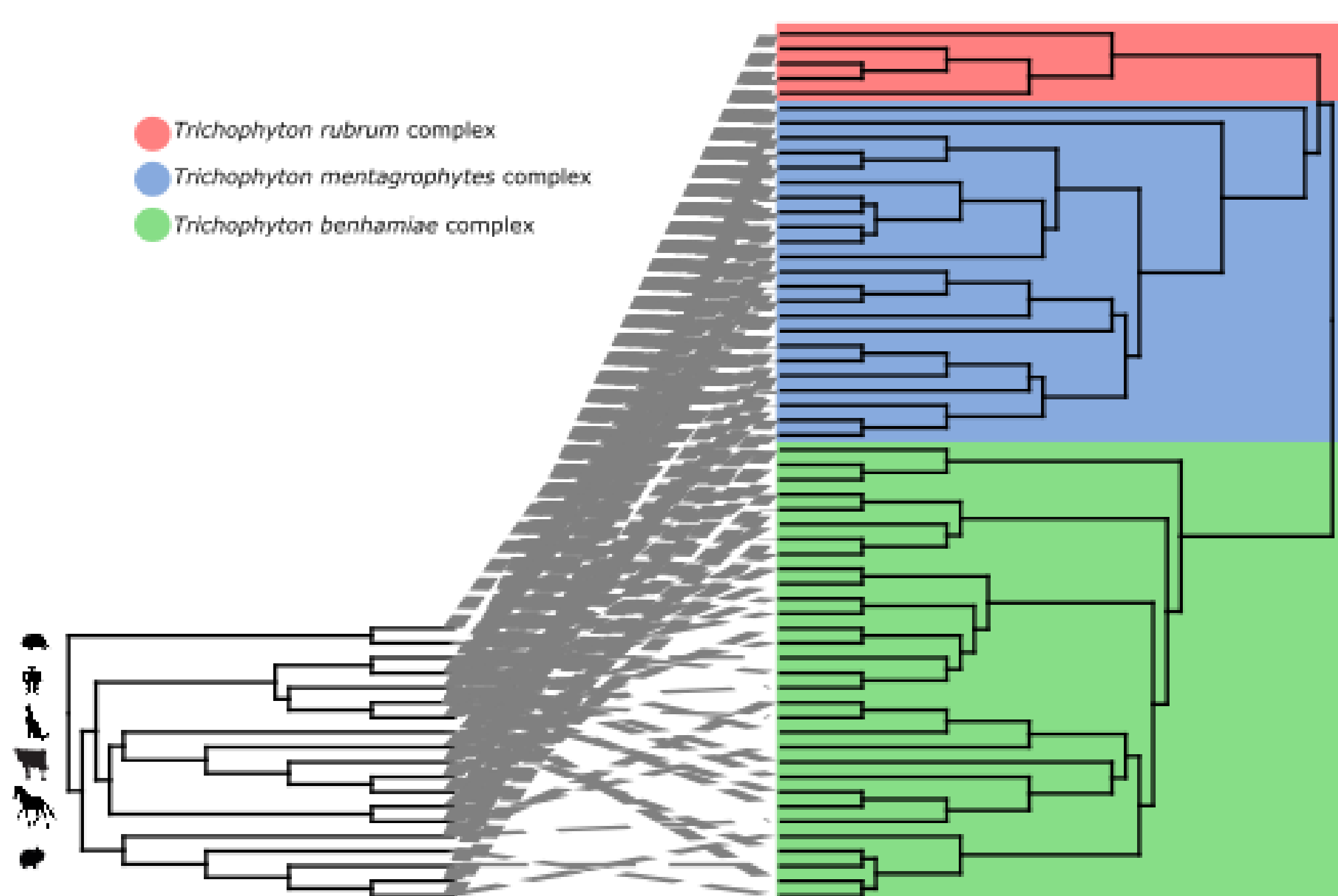


Fig. 1. Tanglegram of hosts (left) and *Trichophyton* (right) phylogenies with association lines and posterior probabilities.

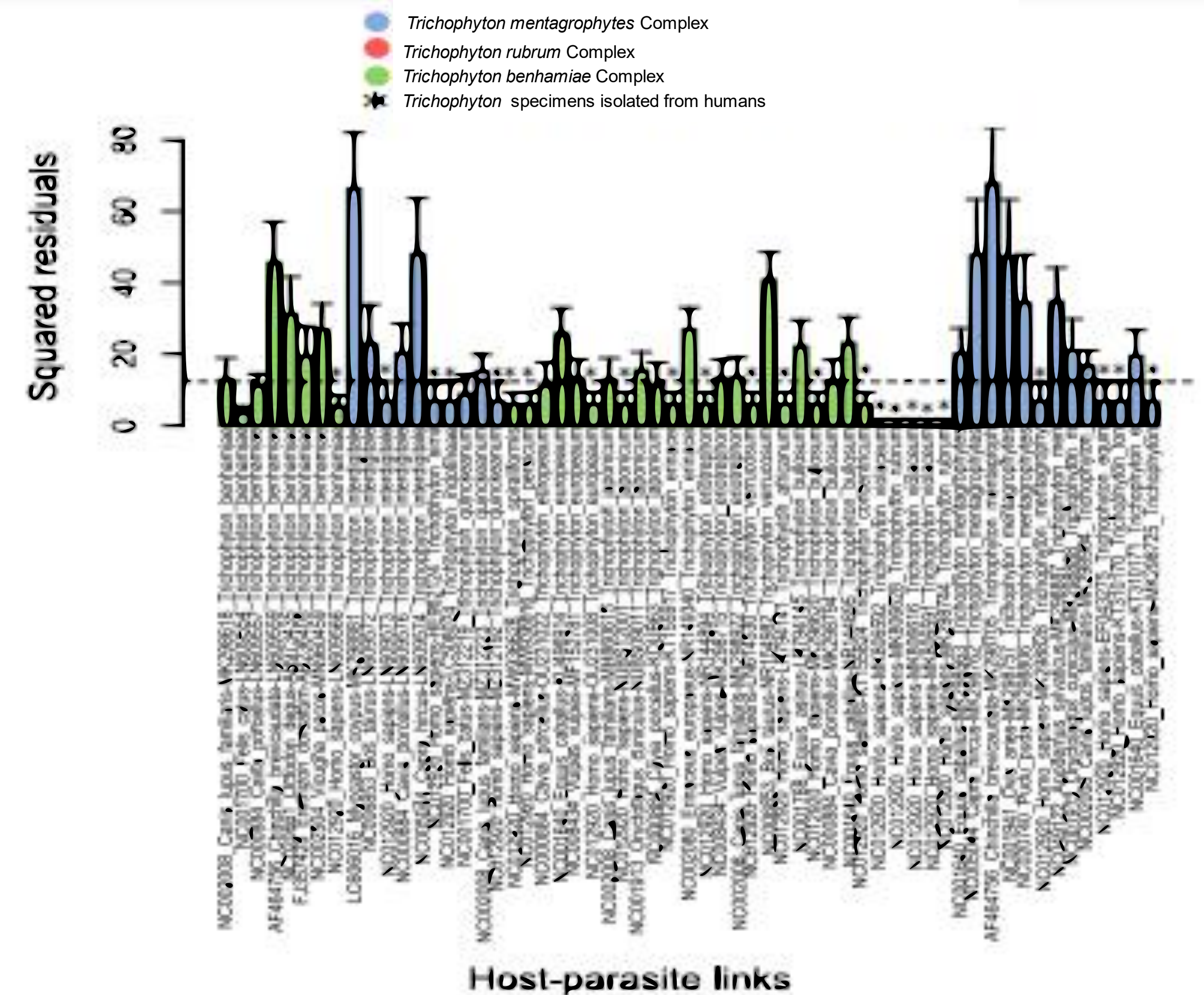


Fig. 2. Procrustes Coevolution Analysis between *Trichophyton* and its various hosts. Contribution of each fungus-host relationship to the overall phylogenetic congruence. Error bars encompass a 95% confidence level.

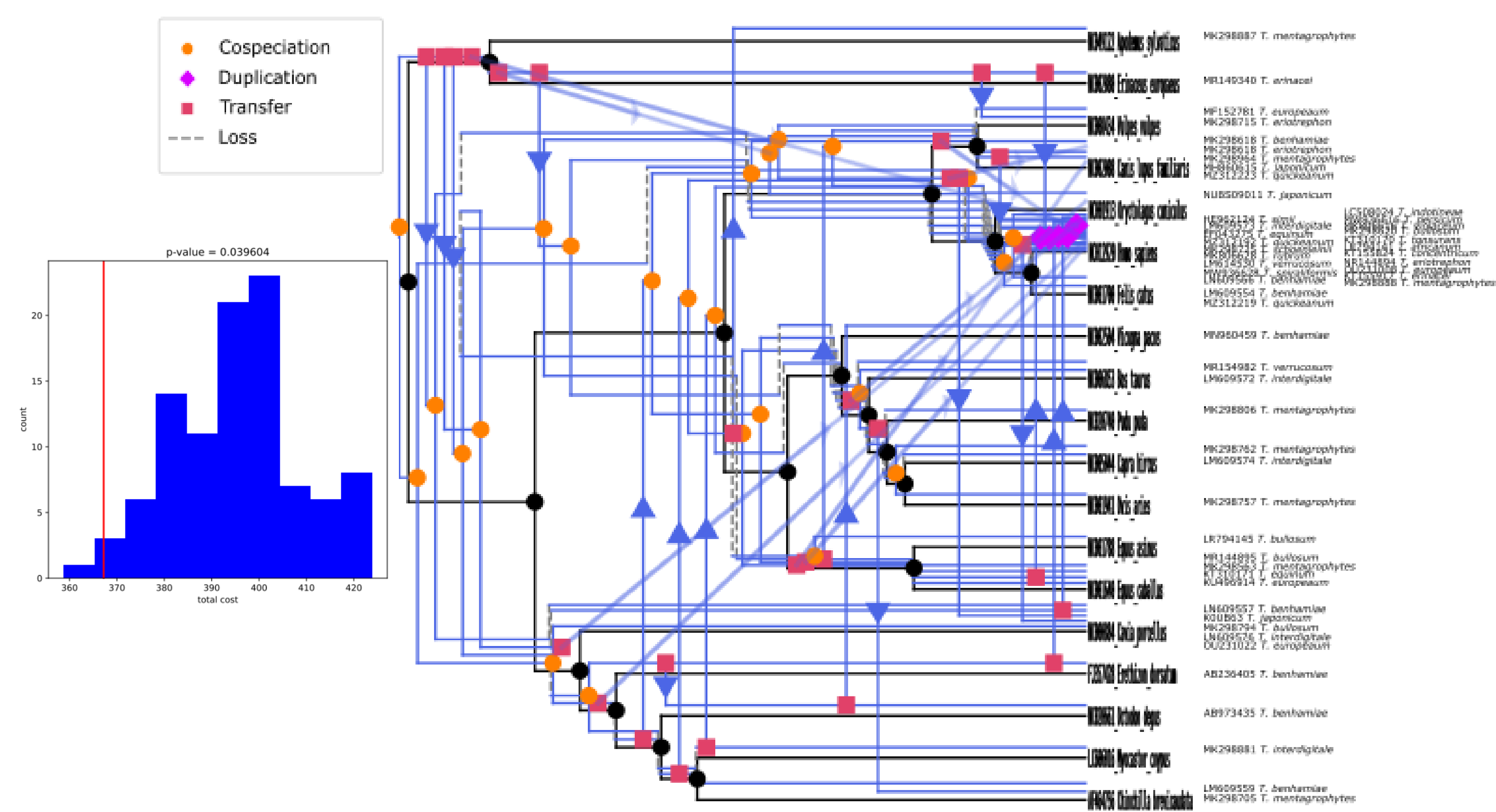


Fig 3. Possible cophylogenetic reconstruction of *Trichophyton* spp. and their hosts returned by eMPress.

## Conclusions

The outcomes of this study reveal a robust co-speciational relationship between *Trichophyton* genus and humans, suggesting a shift of the prevalent conception of the infection as a zoonosis. Instead, the evidence suggest the appropriateness of categorizing it as a zoonanthroponosis. This also hints that the hosts are not exerting enough selective pressure on the fungi, allowing the expansion of the host range. This plausibly accounts for the manifest epidemic nature and divergent characteristics exhibited by these fungal entities within the recent years (4).

## Acknowledgements



## References

1. Microbial Genomics 2021; 7(11): 000707.
2. PLoS One 2018; 13(3): e0193408.
3. Molecular Phylogenetics and Evolution 2021; 165: 107297.
4. Mycopathologia 2021; 186(1) 315-326.

