**Supplementary Informations**

Bulletin of Entomological Research

**A simple molecular identification method of the *Thrips tabaci* (Thysanoptera: Thripidae) cryptic species complex**

Péter Farkas1, Zsuzsanna György2, Annamária Tóth3, Annamária Sojnóczki1, József Fail1\*

1Department of Entomology, Faculty of Horticultural Science, Szent István University, Budapest, Hungary

2Department of Genetics and Plant Breeding, Faculty of Horticultural Science, Szent István University, Budapest, Hungary

3Department of Plant Pathology, Faculty of Horticultural Science, Szent István University, Budapest, Hungary

\* Corresponding author

E-mail: fail.jozsef@kertk.szie.hu

**Supplementray Figure 1.** Phylogenetic tree of *T. tabaci* based on 328bp of the mtCOI gene based on the MP analysis using MEGA6 software.

**Supplementray Figure 2.** Phylogenetic tree of *T. tabaci* based on 328bp of the mtCOI gene based on the HKY+G model using JModelTest 2.1.10. and BEAST 2.4.8. Software.

**Supplementray Figure 1.**

Phylogenetic tree of *T. tabaci* based on 328bp of the mtCOI gene*.* The tree is generated by the Maximum Parsimony (MP) method using MEGA6 (Tamura *et al.,* 2013)*.* Bootstrap values (percentage of 1000 replicates) are shown above the branches. Accession numbers shows the sequences data of *T. tabaci* obtained from DNA databases. *Thrips palmi* (AF378690) and *Thrips angusticeps* (AF378679) served as outgroups.



**Supplementray Figure 2.** Phylogenetic tree of *T. tabaci* based on 328bp of the mtCOI gene*.* The HKY+G model (Hasegawa *et al*., 1985) was selected by JModelTest 2.1.10. (Darriba *et al*., 2012) and phylogenetic tree was generated using BEAST 2.4.8. software ([Bouckaert](http://www.ploscompbiol.org/article/info%3Adoi/10.1371/journal.pcbi.1003537) *et al.,* 2014). *Thrips palmi* (AF378690) and *Thrips angusticeps* (AF378679) served as outgroups.



**References:**

1. [Bouckaert, R., Heled, J., Kühnert, D., Vaughan, T., Wu, C-H., Xie, D., Suchard, M.A., Rambaut, A. & Drummond, A. J. (2014) BEAST 2: A Software Platform for Bayesian Evolutionary Analysis. PLoS Computational Biology 10(4). e1003537. doi:10.1371/journal.pcbi.1003537](http://www.ploscompbiol.org/article/info%3Adoi/10.1371/journal.pcbi.1003537)
2. Darriba, D., Taboada, G.L., Doallo, R. & Posada, D. (2012) JModelTest2: more models, new heuristics and high-performance computing. Nature Methods 9(8), 772. doi: [10.1038/nmeth.2109](https://dx.doi.org/10.1038/nmeth.2109)

# Hasegawa, M., Kishino, H. & Yano, T. (1985). Dating the human-ape split by a molecular clock of mitochondrial DNA. Journal of Molecular Evolution22, 160-174.

1. Tamura, K., Stecher, G., Peterson, D., Filipski, A. & Kumar, S. (2013) MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution,30, 2725-2729. <https://doi.org/10.1093/molbev/mst197>