Figures and figure supplements

Natural selection and repeated patterns of molecular evolution following allopatric divergence

Yibo Dong et al
Figure 1. Frequency distribution of synonymous substitutions per synonymous site (Ks) of putative orthologs (POGs) from leaf transcriptomes of 20 species/variety pairs of angiosperms.
DOI: https://doi.org/10.7554/eLife.45199.003
Figure 2. Frequency distribution of nonsynonymous substitutions per non-synonymous site (Ka) of putative orthologs (POGs) of leaf transcriptomes from 20 species/variety pairs of angiosperms.
DOI: https://doi.org/10.7554/eLife.45199.004
Figure 3. Frequency distribution of Ka/Ks ratios of putative orthologs (POGs) from leaf transcriptomes of 20 species/variety pairs of angiosperms.

DOI: https://doi.org/10.7554/eLife.45199.005
Figure 4. Relative abundance of putative orthologs (POGs) with different categories of $\text{Ka/Ks}$ values. Numbers of genes in each category are provided in Supplementary file 3.

DOI: https://doi.org/10.7554/eLife.45199.006
Figure 5. Dated global phylogeny of the 20 taxon pairs and correlations of divergence time with level of divergence at synonymous sites, with abundance of genes under moderate purifying selection (Ka/Ks = 0.1 - 0.5), and with abundance of genes under strong purifying selection (ka/Ks <0.1). (a) Dated global phylogeny and divergence times of taxon pairs estimated using BEAST program and seven single-copy orthologs shared by all 40 taxa with no missing data. Number 1, 2, and 3 indicate the crown node of Magnoliidae, crown node of Monocotyledoneae, and crown node of Eudicotyledoneae, respectively. (b – d). Correlation between divergence time and (b) Ks value at peak frequency of each genus, (c) abundance of POGs with Ka/Ks values between 0.1–0.5, and (d) abundance of POGs with Ka/Ks values < 0.1. Data used for the analyses are available in Supplementary file 4.

DOI: https://doi.org/10.7554/eLife.45199.008
Figure 5—figure supplement 1. Divergence times of 20 taxon pairs estimated with 79 single copy orthologs present in 90% or more species using BEAST. DOI: https://doi.org/10.7554/eLife.45199.009
Figure 6. Positive and negative relationships between relative abundance (Y-axis) of genes with Ka/Ks values in the indicated ranges and Ks values of peak abundance (X-axis) in the 20 taxon pairs. The pattern remains when the modified Ks (see Materials and methods) is used. Data used for the analyses are available in Supplementary file 4.
DOI: https://doi.org/10.7554/eLife.45199.010
Figure 7. Relative abundance of genes with Ka/Ks > 2 annotated to Cell Component category, drawn from data in Supplementary file 5. Genes annotated to integral component of membrane (ICM) are shown in dark brown.

DOI: https://doi.org/10.7554/eLife.45199.012
Figure 7—figure supplement 1. Relative abundance of Ka/Ks > 2 genes annotated to different functions in the Biological Process category; drawn from data in Supplementary file 5.
DOI: https://doi.org/10.7554/eLife.45199.013
Figure 7—figure supplement 2. Relative abundance of $\text{Ka/Ks} > 2$ genes annotated to different functions of in the Molecular Function category, drawn from data in Supplementary file 5.
DOI: https://doi.org/10.7554/eLife.45199.014
Appendix 1—figure 1. Phylogenetic positions of orders represented by species pairs sampled in the angiosperm phylogeny. Phylogenetic tree was taken from Angiosperm phylogeny website.

DOI: https://doi.org/10.7554/eLife.45199.029
Appendix 1—figure 2. Flowchart of transcriptome sequence analyses for one species pair. The process was repeated for 20 pairs. A customized pipeline of programs was developed for running these steps.

DOI: https://doi.org/10.7554/eLife.45199.030
Appendix 1—figure 3. Plot of Ka and Ks values for each POG in 20 taxon pairs, in alphabetical order of genus names. Acorus.
DOI: https://doi.org/10.7554/eLife.45199.031
Appendix 1—figure 4. Plot of Ka and Ks values for each POG in 20 taxon pairs, in alphabetical order of genus names. Calycanthus.
DOI: https://doi.org/10.7554/eLife.45199.032
Appendix 1—figure 5. Plot of Ka and Ks values for each POG in 20 taxon pairs, in alphabetical order of genus names. *Campsis.*
DOI: https://doi.org/10.7554/eLife.45199.033
Appendix 1—figure 6. Plot of Ka and Ks values for each POG in 20 taxon pairs, in alphabetical order of genus names. Convallaria.

DOI: https://doi.org/10.7554/eLife.45199.034
Appendix 1—figure 7. Plot of Ka and Ks values for each POG in 20 taxon pairs, in alphabetical order of genus names. *Cornus*-1.
DOI: https://doi.org/10.7554/eLife.45199.035
Appendix 1—figure 8. Plot of $K_a$ and $K_s$ values for each POG in 20 taxon pairs, in alphabetical order of genus names. *Cornus*-2.

DOI: https://doi.org/10.7554/eLife.45199.036
Appendix 1—figure 9. Plot of Ka and Ks values for each POG in 20 taxon pairs, in alphabetical order of genus names. Cotinus.
DOI: https://doi.org/10.7554/eLife.45199.037
Appendix 1—figure 10. Plot of Ka and Ks values for each POG in 20 taxon pairs, in alphabetical order of genus names. Croomia.
DOI: https://doi.org/10.7554/eLife.45199.038
Appendix 1—figure 11. Plot of Ka and Ks values for each POG in 20 taxon pairs, in alphabetical order of genus names. Dysosma.
DOI: https://doi.org/10.7554/eLife.45199.039
Appendix 1—figure 12. Plot of $\text{Ka}$ and $\text{Ks}$ values for each POG in 20 taxon pairs, in alphabetical order of genus names. *Gelsemium.*

DOI: https://doi.org/10.7554/eLife.45199.040
Appendix 1—figure 13. Plot of Ka and Ks values for each POG in 20 taxon pairs, in alphabetical order of genus names. *Hamamelis*.

DOI: https://doi.org/10.7554/eLife.45199.041
Appendix 1—figure 14. Plot of $Ka$ and $Ks$ values for each POG in 20 taxon pairs, in alphabetical order of genus names. Liquidambar. DOI: https://doi.org/10.7554/eLife.45199.042
Appendix 1—figure 15. Plot of Ka and Ks values for each POG in 20 taxon pairs, in alphabetical order of genus names. *Liriodendron*. DOI: https://doi.org/10.7554/eLife.45199.043
Appendix 1—figure 16. Plot of Ka and Ks values for each POG in 20 taxon pairs, in alphabetical order of genus names. Meehania.
DOI: https://doi.org/10.7554/eLife.45199.044
Appendix 1—figure 17. Plot of Ka and Ks values for each POG in 20 taxon pairs, in alphabetical order of genus names. *Menispermum*. DOI: https://doi.org/10.7554/eLife.45199.045
Appendix 1—figure 18. Plot of Ka and Ks values for each POG in 20 taxon pairs, in alphabetical order of genus names. *Nelumbo.*
DOI: https://doi.org/10.7554/eLife.45199.046
Appendix 1—figure 19. Plot of Ka and Ks values for each POG in 20 taxon pairs, in alphabetical order of genus names. *Penthorum.*

DOI: https://doi.org/10.7554/eLife.45199.047
Appendix 1—figure 20. Plot of Ka and Ks values for each POG in 20 taxon pairs, in alphabetical order of genus names. *Phryma.*

DOI: https://doi.org/10.7554/eLife.45199.048
Appendix 1—figure 21. Plot of Ka and Ks values for each POG in 20 taxon pairs, in alphabetical order of genus names. Sassafras.
DOI: https://doi.org/10.7554/eLife.45199.049
Appendix 1—figure 22. Plot of Ka and Ks values for each POG in 20 taxon pairs, in alphabetical order of genus names. Saururus.

DOI: https://doi.org/10.7554/eLife.45199.050