#1

1. Citation: Chase, M. W., D. E. Soltis, R. G. Olmstead, D. Morgan, D. H. Les, B. D. Mishler, M. R. Duvall, R. A. Price, H. G. Hills, Y.-L. Qiu, K. A. Kron, J. H. Rettig, E. Conti, J. D. Palmer, J. R. Manhart, K. J. Sytsma, H. J. Michaels, W. J. Kress, K. G. Karol, W. D. Clark, M. Hedren, B. S. Gaut, R. K. Jansen, K.-J. Kim, C. F. Wimpee, J. F. Smith, G. R. Furnier, S. H. Strauss, Q.-Y. Xiang, G. M. Plunkett, P. S. Soltis, S. M. Swensen, S. E. Williams, P. A. Gadek, C. J. Quinn, L. E. Eguiarte, E. Golenberg, G. H. Learn, Jr., S. W. Graham, S. C. H. Barrett, S. Dayanandan, and V. A. Albert. 1993. Phylogenetics of seed plants: an analysis of nucleotide sequences from the plastid gene rbcL. Annals of the Missouri Botanical Garden 80: 528-580.

2. Supermatrix vs supertree?: Matrix-based paper (single gene rbcL)

3. method: MP, ML, Bayesian: MP

4. BS values given?: only partly (like to Hamamelidae)

5. Comments: no GB numbers/TreeBase or Dryad data

#2

1. Citation: Savolainen, V., M. W. Chase, C. M. Morton, D. E. Soltis, C. Bayer, M. F. Fay, A. De Bruijn, S. Sullivan, and Y.-L. Qiu. 2000. Phylogenetics of flowering plants based upon a combined analysis of plastid atpB and rbcL gene sequences. Systematic Biology 49: 306-362.

2. Supermatrix vs supertree?: Supermatrix

3. method: MP, ML, Bayesian: MP

4. BS values given?: Yes

5. Comment: Data set and tree are present in Dryad, but no information about this published in the paper. Savolainen et al. mentioned that data submitted here: <http://www.keil.ukans.edu/delta>

But this link does not work.

#3

1. Citation: Soltis, D. E., P. S. Soltis, M. W. Chase, M. E. Mort, D. C. Albach, M. Zanis, V. Savolainen, W. J. Hahn, S. B. Hoot, M. F. Fay, M. Axtell, S. M. Swensen, L. M. Prince, W. J. Kress, K. C. Nixon, and J. S. Farris. 2000. Angiosperm phylogeny inferred from 18S rDNA, rbcL, and atpB sequences. Botanical Journal of the Linnean Society 133: 381-461.

2. Citation: Supermatrix vs supertree?: Supermatrix

3. method: MP, ML, Bayesian: MP

4. BS values given?: Yes

5. Comments: GB Numbers are given, no TreeBase/Dryad data

#4

1. Citation: Soltis, P. S., D. E. Soltis, M. J. Zanis, and S. Kim. 2000. Basal lineages of angiosperms: Relationships and implications for floral evolution. International Journal of Plant Science161 (Supplement): S97-S107

2. Supermatrix vs supertree?: Supermatrix

3. method: MP, ML, Bayesian: MP, ML

4. BS values given?: Yes

5. Comments: no supporting data are available (even GB numbers), but clear references to the sources of the data are given (D. Soltis et al., 2000 for example).

#5

1. Citation: Qiu, Y.-L., J.-Y. Lee, F. Bernasconi-Quadroni, D. E. Soltis, P. S. Soltis, M. Zanis, E. Zimmer, Z. Chen, V. Savolainen, and M. Chase. 2000. Phylogeny of basal angiosperms: analyses of five genes from three genomes. International Journal of Plant Sciences 161 (Supplement): S3-S27

2. Supermatrix vs supertree?: Supermatrix

3. method: MP, ML, Bayesian: MP

4. BS values given?: Yes

5. Comments: GB Numbers are given. No data in a TreBase/Dryad.

#6

1. Citation: Burleigh, G. G., and S. Mathews. 2004. Phylogenetic signal in nucleotide data from seed plants: implications for resolving the seed plant tree of life. American. Journal of Botany. 91: 1599-1613

2. Supermatrix vs supertree?: Supermatrix

3. method: MP, ML, Bayesian: MP, ML

4. BS values given?: Yes

5. Comments: No GB numbers provided, only link to GB (We sampled data from GenBank http://www.ncbi.nlm.nih.gov) in a way that maximized both the taxonomic sampling among gymnosperms and the number of loci sampled). Authors mentioned the Supplemental Data of the Article, but no Supplements are available from the site.

#7

1. Citation: Burleigh JG, Bansal MS, Eulenstein O, Hartmann S, Wehe A, Vision TJ.Genome-scale phylogenetics: inferring the plant tree of life from 18,896 gene trees. Syst Biol. 2011 Mar;60(2):117-25.

2. Supermatrix vs supertree: Supertree

3. method: MP, ML, Bayesian: MP, ML

4. BS values given? Yes

5. Comments if appropriate- Complicated analysis incl. NJ approach. No trees are available in Supporting Data:

<http://sysbio.oxfordjournals.org/content/60/2/117/suppl/DC1>

as well as in a /TreeBase/Dryad

The Dryad however contain the full data set of the alignments (!) used in the paper (Burleigh et al, 2011, p. 118).

#8

1. citation: Soltis, D. E. [et al. 2011], Smith, S. A., Cellinese, N., Wurdack, K. J., Tank, D. C., Brockington, S. F., Refulio-Rodriguez, N. F., Walker, J. B., Moore, M. J., Carlsward, B. S., Bell, C. D., Latvis, M., Crawley, S., Black, C., Diouf, D., Xi, Z., Rushworth, C. A., Gitzendanner, M. A., Sytsma, K. J., Qiu, Y. L., Hilu, K. W., Davis, C. C., Sanderson, M. J., Beaman, R. S., Olmstead, R. G., Judd, W. S., Donoghue, M. J., & Soltis, P. S. 2011. Angisoperm phylogeny: 17 genes, 640 taxa. American J. Bot. 98: 704-730.

2. Supermatrix vs supertree: Supermatrix

3. method: MP, ML, Bayesian: MP, ML

4. BS values given? Yes

5. Comment: Focused mostly on ML. Multiple trees submitted in a TreeBase – not easy to find the most important one.

#9

1. citation: Hilu, K. [et al. 2003], Borsch, T., Muller, K., Soltis, D. E., Soltis, P. S., Savolainen, V., Chase, M. W., Powell, M. P., Alice, L. A., Evans, R., Sauquet, H., Neinhuis, C., Slotta, T. A. B., Rohwer, J. G., Campbell, C. S., & Chatrou, L. W. 2003. Angiosperm phylogeny based on matK sequence information. American J. Bot. 90: 1758-1766.

2. Supermatrix vs supertree?: Matrix-based paper

3. method: MP, ML, Bayesian: MP, Bayesian

4. BS values given?: Yes

5. Comments if appropriate--Nothing in a TreeBase/Dryad. Files in this Data Supplement: Appendix 1 - Taxa sampled, vouchers, GenBank accession numbers, and references. Appendix 2 - Taxa and primers used for the amplification of matK. Only GB Numbers provided therefore!

#10

1. citation: Zanis/Dryad, M. J. [et al. 2002], Soltis, D. E., Soltis, P. S., Mathews, S., & Donoghue, M. J. 2002. The root of the angiosperms revisited. Proc. National Acad. Sci. U.S.A. 99: 6848-6853.

2. Supermatrix vs supertree?: Supermatrix

3. method: MP, ML, Bayesian: all

4. BS values given?: Yes

5. Comments if appropriate-- Nothing in a TreeBase/Dryad "A table of exemplars, genes, and voucher and GenBank information is available from M.J.Z."

#11

1. citation: Duarte, J. M. [et al. 2008], Wall, P. K., Zahn, L. M., Soltis, P. S., Leebens-Mack, J., Carlson, J. E., Ma, H., & dePamphilis, C. W. 2008. Utility of Amborella trichopoda and Nuphar advena expressed sequence tags for comparative sequence analysis. Taxon 57: 1110-1122.

2. Supermatrix vs supertree?

3. method: MP, ML, Bayesian: MP, ML

4. BS values given? Yes

5. Comments if appropriate--Nothing in a TreeBase/ Dryad. Only link to Cornell ETS database provided.

#12

1. citation: Jansen, R. K. [et al. 2007], Cai, Z., Raubeson, L. A., Daniell, H., dePamphilis, C. W., Leebens-Mack, J., Müller, K. F., Guisinger-Bellian, M., Haberle, R. C., Hansen, A. K., Chumley, T. W., Lee, S.-B., Peery, R., McNeal, J. R., Kuehl, J. V., & Boore, J. L. 2007. Analysis of 81 genes from 64 chloroplast genomes resolves relationships in angiosperms and identifies genome-scale evolutionary patterns. Proc. National Acad. Sci. U.S.A. 104: 19369-19374.

2. Supermatrix vs supertree?: Supermatrix

3. method: MP, ML, Bayesian: all

4. BS values given?: yes

5. Comments if appropriate--Nothing in a TreeBase/Dryad. Despite of the huge Supplement, only GB Numbers eventually provided.

#13

1. citation: Qiu, Y.-L. [et al. 2005], Dombrovska, O., Lee, J., Li, L., Whitlock, B. A., Bernasconi-Quadroni, F., Rest, J. S., Davis, C. C., Borsch, T., Hilu, K. W., Renner, S. S., Soltis, D. E., Soltis, P. S., Zanis, M. J., Cannone, J. J., Gutell, R. R., Powell, M., Savolainen, V., Chatrou, L. W., & Chase, M. W. 2005. Phylogenetic analysis of basal angiosperms based on nine plastid mitochondrial and nuclear genes. Internat. J. Plant Sci. 166: 815-842.

2. Supermatrix vs supertree?: Supermatrix

3. method: MP, ML, Bayesian: all

4. BS values given?: yes

5. Comments if appropriate--Nothing in a TreeBase/Dryad, no Suppelment available

#14

1. citation: Qiu, Y.-L. [et al. 2006a], Li, L., Wang, B., Chen, Z., Knoop, V., Groth-Malonek, M., Dombrovska, O., Lee, J., Kent, L., Rest, J. S., Estabrook, G. F., Hendry, T. A., Taylor, D. W., Testa, C. M., Ambros, M., Crandall-Stotler, B., Duff, R. J., Stech, M., Frey, W., Quandt, D., & Davis, C. C. 2006a. The deepest divergences in land plants inferred from phylogenomic evidence. Proc. National Acad. Sci. U.S.A. 103: 15511-15516.

2. Supermatrix vs supertree?: Supermatrix

3. method: MP, ML, Bayesian: all

4. BS values given?: yes

5. Comments if appropriate--Big Supporting files in a TreeBase, but multiple trees provided, not easy to took the “most important one”.

#15

1. citation: Qiu, Y.-L. [et al. 2010], Li, L., Wang, B., Xue, J.-Y., Hendry, T. A., Li, R.-Q., Brown, J. W., Liu, Y., Hudson, G. T., & Chen, Z.-D. 2010. Angiosperm phylogeny inferred from sequences of four mitochondrial genes. J. Syst. Evol. 48: 391-425.

2. Supermatrix vs supertree?: Supermatrix

3. method: MP, ML, Bayesian: ML

4. BS values given?: Yes

5. Comments if appropriate--Nothoing in a TreeBase/Dryad, GB numbers in a paper

#16

1. citation: Leebens-Mack, J. [et al. 2005], Raubeson, L. A., Cui, L., Kuehl, J. V., Fourcade, M. H., Chumley, T. W., Boore, J. L., Jansen, R. K., & dePamphilis, C. W. 2005. Identifying the basal angiosperm node in chloroplast genome phylogenies: Sampling one's way out of the Felsenstein zone. Mol. Biol. Evol. 22: 1948-1963.

2. Supermatrix vs supertree?: Supermatix

3. method: MP, ML, Bayesian: MP, ML

4. BS values given?: Yes

5. Comments if appropriate--Nothing in a TreeBase/Dryad. Paper Supplement published in ppt format! GB numbers provided however

#17

1. citation: Moore, M. J. [et al. 2007], Bell, C. D., Soltis, P. S., & Soltis, D. E. 2007. Using plastid genome-scale data to resolve enigmatic relationships among basal angiosperms. Proc. National Acad. Sci. U.S.A. 104: 19363-19368

2. Supermatrix vs supertree?: Supermatrix

3. method: MP, ML, Bayesian: all

4. BS values given? Yes

5. Comments if appropriate- Only huge Matrix (over 900 pages!) in provided in pdf, no trees, only pictures, tests etc. I HAVE NO IDEA WHY MIKE PUT THE PDF, NOT STANDARD NEXUS FILE (in text). I was not able to make both actions: copy/paste from the pdf or to convert the pdf to text-file in Adobe Package (converted with asterisks etc)

#18

1. citation: Mathews, S., & Donoghue, M. J. 1999. The root of angiosperm phylogeny inferred from duplicate phytochrome genes. Science 286: 947-949.

2. Supermatrix vs supertree?: Matrix-based paper

3. method: MP, ML, Bayesian: MP

4. BS values given?: Yes

5. Comments if appropriate--TreeBase S588. BUT 1. Some topologies from submission are not in a paper! 2. Multiple trees submitted, not easy to specify the “most important” one.

#19

1. citation: Moore, M. J. [et al. 2010], Soltis, P. S., Bell, C. D., Burleigh, J. G., & Soltis, D. E. 2010. Phylogenetic analysis of 83 plastid genomes further resolves the early diversification of eudicots. Proc. National Acad. Sci. U.S.A. 107: 4623-4628.

2. Supermatrix vs supertree?

3. method: MP, ML, Bayesian: ML

4. BS values given?: Yes

5. Comments if appropriate--Nothing in a Treebase. All Support Files in a doc/pdf

#20

1. citation: Savolainen, V. [et al. 2000b], Fay, M. F., Albach, D. C., Backlund, A., van der Bank, M., Cameron, K. M., Johnson, S. A., Lledó, M. D., Pintaud, J.-C., Powell, M., Sheahan, M. C., Soltis, D. E., Soltis, P. S., Weston, P., Whitten, W. M., Wurdack, K. J., & Chase, M. W. 2000b. Phylogeny of the eudicots: A nearly complete familial analysis based on rbcL gene sequences.Kew Bull. 55: 257-309.

2. Supermatrix vs supertree? Matrix based approach

3. method: MP, ML, Bayesian: MP

4. BS values given?: Yes

5. Comments if appropriate: Nothing in a TreeBase, GB Numbers given in ms.

#21

1. citation: Morton C. M. 2011. Newly Sequenced Nuclear Gene (*Xdh*) for Inferring Angiosperm Phylogeny. Annals of the Missouri Botanical Garden, 98(1):63-89.

2. Supermatrix vs supertree?

3. method: MP, ML, Bayesian: MP, ML

4. BS values given? Yes.

5. Comments if appropriate--Only GenBank Numbers are given, nothin available from bith TreeBase/Dryad