

## Questions generated by Bell et al. 2010 paper

- **General questions of what chronograms indicate**

Is the molecular data measuring lineage splitting events or is it indicating the divergence of the DNA sequences/"genes" and not the actual lineage splitting?

- **Data set questions**

A data set from 1999 was used, why not use a more recent, perhaps better, one?

The tree they generated from this data set differs markedly from APGIII (e.g. position of monocots, *Amborella*, Chloranthaceae). Can you constrain a tree in BEAST, and would the age results be different?

The authors said that they did partitioned analysis (i. e. for each individual gene), but they seemed to combine those analyses and estimated one age for each node.

- **PL/BEAST software general questions**

Why do the authors describe the use of NPRS as a weakness of a previous paper, then go on to use NPRS to generate a starting tree?

Is Beast the best or only program for this project?

Can the estimations of molecular clocks and the way the BEAST software is used be explained more thoroughly, as I have not had experience with these methods?

It would be helpful to know more background on the major differences between the lognormal and exponential distribution from the Ho and Philips' (2009) paper. Bell et al. (2010) briefly went over them (p1297) and later justified their selection of the exponential distribution with an estimated age of 141-154 Ma.

For the ages estimation method used in this paper setting the priors is a critical point. However, is not clear for me what is the meaning of setting the priors to lognormal or exponential distribution for the fossils distributions.

The fossil calibration points used were not the quite fixed, often well known, geologic times but rather "fossil constraints are modeled as distributions that cover a broader range of possible ages"?, page1300. Why not use the rather fixed well known fossil ages?

- **Fossil questions**

Just one of the most basal families is represented by a fossil. Would the inclusion of an expanded phylogeny of the basal families be able to move the calculated origin frame of the group back or forwards?, or would it also narrow the estimate frame?

How drastically, and in what way, would the results have changed had the authors been able to include fossils from basal divergences while also including more taxonomic sampling from the tips. As their results are similar to previous studies, I doubt this would have drastically changed the paper.

The oldest fossil used was 108.8 Mya. Why not use older angiosperm fossils like *Archaeofractaceae* 124.6 Mya (Sun et al, Science 2003), the Rannunculales fossil, "*Leefructus mirus*", 124 Mya (Sun, Dilcher et al, Nature 2011) or the various mesofossils and Eudicot pollens of Friss > 120 Mya? Would this improve the calibration points?

- **Age questions**

On p 1301, the authors note the limitations to their age estimates. Do you think they adequately addressed these issues?

The authors say that their calculated dates for most of the angiosperm groups are younger than previous molecular estimates, is the usage of a methodology that allows lineage-specific rate heterogeneity the major source of difference or could it be the usage of several calibration points vs just one in the article of Wikstrom et al. (2001)?

The age of the chosen fossil constraints can bias age estimates of nodes. While young fossils tend to shift dates forward, older fossils tend to shift dates back in time, so how could this bias be overcome?

Is 140-180 Mya really a narrow range( page 1299)?

The authors acknowledge that increasing the number of fossil constraints could reduce the error bars around each node, and that additional taxonomic sampling to capture the basal divergences of each clade could improve the accuracy of the estimates. What would be the impact of increasing the amount of molecular data in this analysis, as only three regions were used? How much data is enough for an analysis like this?

- **Radiation questions**

It would also be interesting to learn if the layers of rapid radiation discussed in the Discussion tend to occur soon after a groups appearance, or later on, or if this rapid radiation occurs at different times for different groups.