Distribution
How did the authors reach their conclusions in Figure 2.C, where they claim a migration from West Palearctic (D) to East Palearctic (B) to SE Asia (A)? This doesn't seem to corroborate with the phylogeny unless there was either poor sampling or extinction in East Palearctic. Would another possible explanation be dispersion from N. Africa to India before India's collision with SE Asia?

It seems like this phylogeny needs dates. Otherwise, how reasonable are the hypotheses about migration across the Bering and N Atlantic land bridges?

What is the estimated age of Heracleum? In their S-DIVA results, the authors mention regions of Asia that groups originated in, but does this agree with estimated age of the group and geologic history?

On the other hand, I think It would have been interesting comparing the results of BBMCMC with S-DIVA analysis (not using uncertainty). I am not sure about doing conclusions about biogeographic issues within clades with polytomies (e.g. clades starting at node 2 or node 1). A more resolved hypothesis could change dramatically the scenario.

Evolution
It would be interesting to investigate what factors are driving the speciation of Heracleum in Asia. Considering that most species are wind-dispersed, I wonder what benefits (if any) the small changes in fruit structure give the plants. It is also possible that there are reproductive barriers between taxa relating to flower structure.

Sampling
In such a diverse and poorly understood group such as Heracleum, I too am concerned that many of the species included in this study are represented by only a single accession. While I understand this is a poorly known group, surely there are collections that could have yielded morphological and/or genetic data stored in the worlds larger Herbaria.

Do the results presented hear mirror those of other recently diversified groups such as Aquilegia, or other groups which are bulky and hard to press in a typical herbarium press, like the palms? Is bulkiness really a valid excuss for poor representation?

Taxonomic issues and interpretation of data
They agree with put H xiaojinense as a synonym of Angelica apaensis, base on ITS sequences (and morphology). However, cpDNA does not support this hypothesis. On the other hand, H. canescens is nested in H. candicans in both DNA set, but they do not propose it as a synonym. What do you think about those decisions?

The authors conclude that the discordance between ITS and cpDNA may be due to lineage sorting and not hybridization. Do you agree with their conclusions based on the

results that they presented? How would you address hybridization and lineage sorting in their situation?