

Biogeography and Chromosome Number Evolution of Linaceae

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Introduction

Linaceae is a diverse family of flowering plants, distributed throughout the temperate and tropical regions of the world. It contains 13 genera and approximately 260 species including 3 genera and 16 species native to California. Using a fossil calibrated phylogeny, we examined the historical biogeography and chromosome evolution of Linaceae and tested previously published biogeographic and ancestral chromosome number hypotheses.

Materials and Methods

- We acquired information about the biogeographic origins of the different species from the Global Biodiversity Information Facility and Tropicos, and chromosome numbers from the Chromosome Counts Database
- We used multiple maximum likelihood models of geographic range evolution that represented different biogeographic scenarios in the R package BioGeoBears.
- Linum pollen fossil observations were used to cross-validate our biogeographic range evolution results (Cavagnetto, 1996).
- We used Bayesian models of anagenetic and cladogenetic chromosome number evolution to estimate both the mode of chromosome evolution and ancestral chromosome numbers in the software RevBayes.

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References

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Results

Figure 1: Maximum a posteriori estimates of ancestral chromosome numbers for Linaceae inferred using the ChromoSSE model.

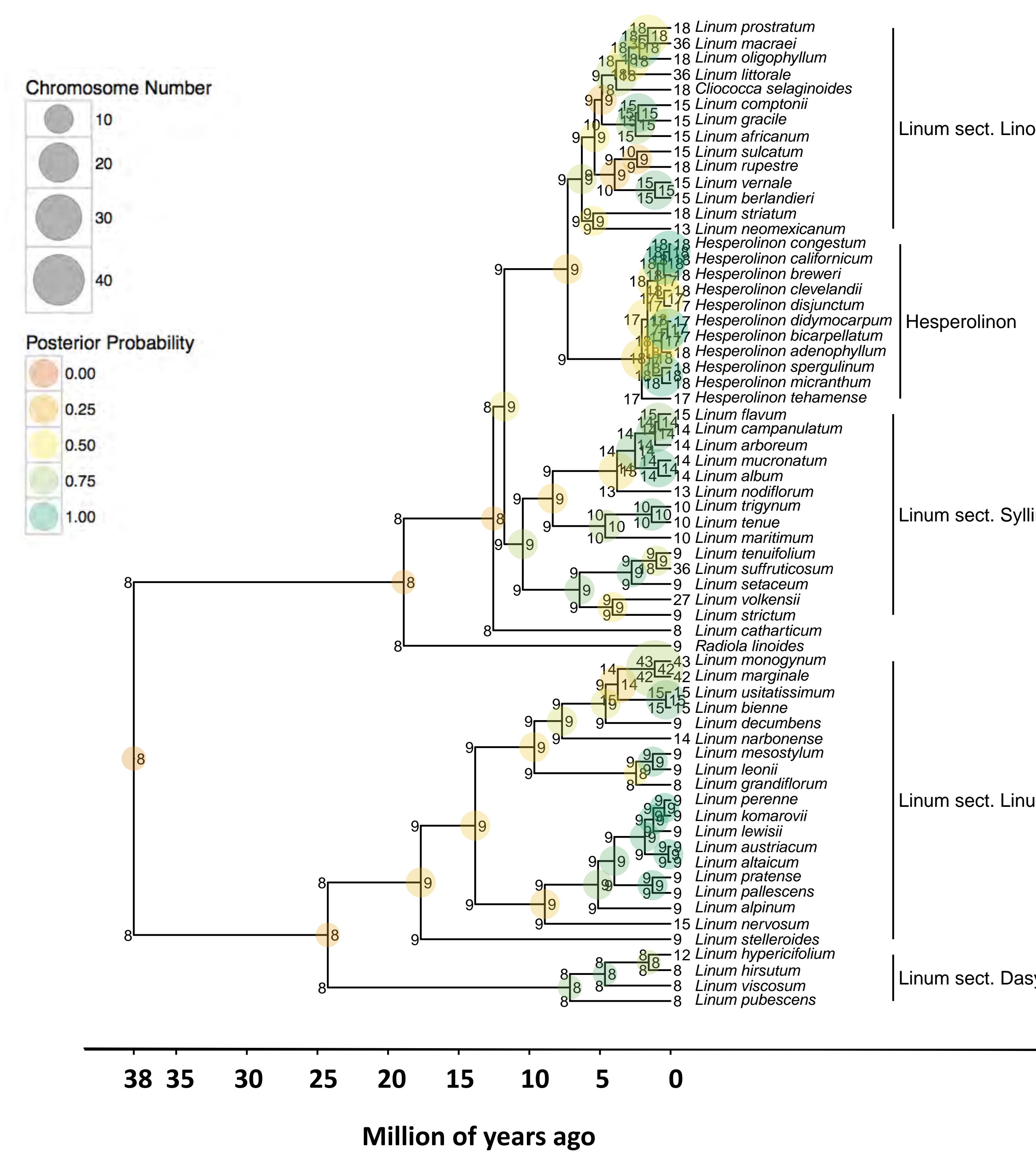
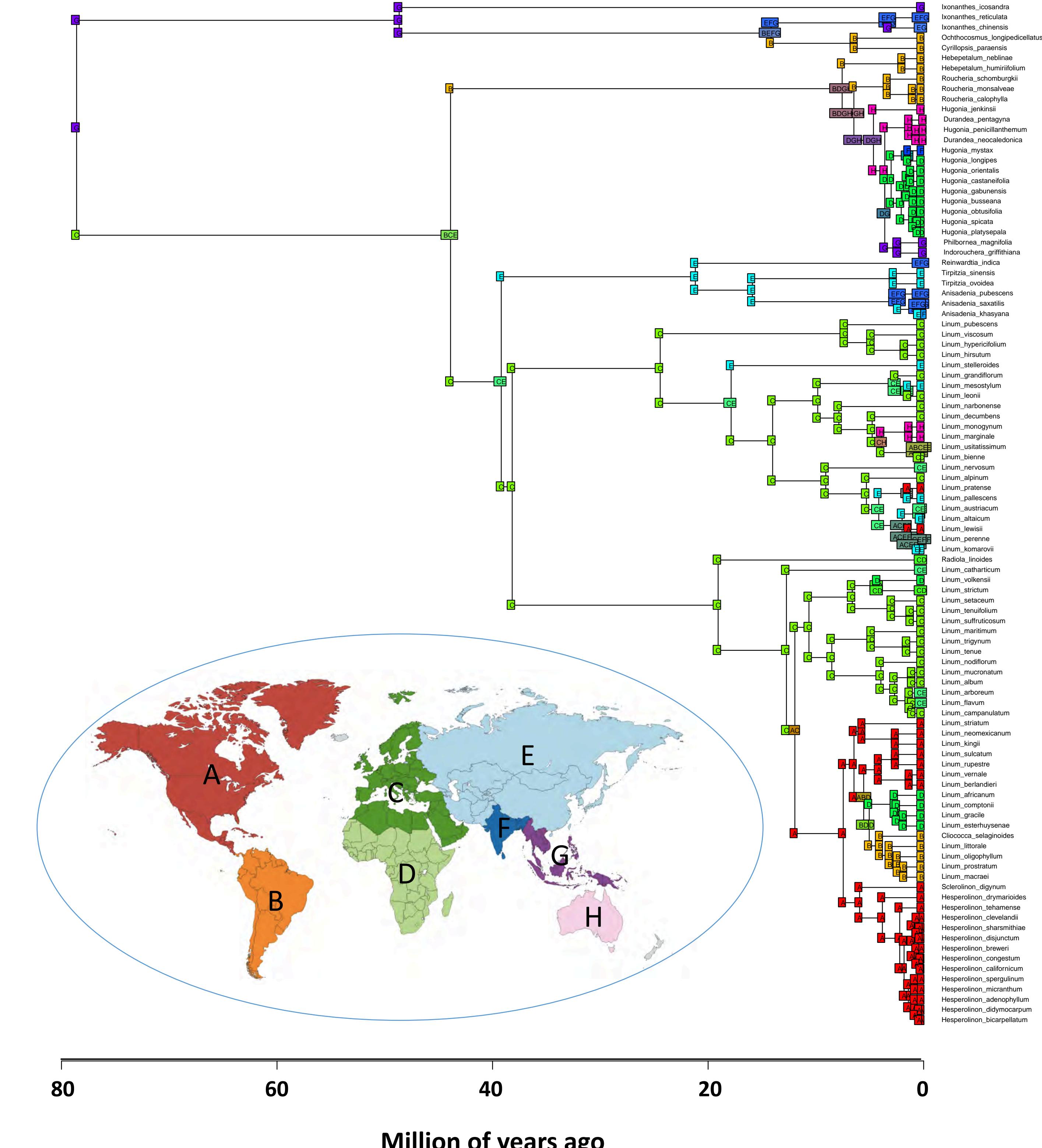


Figure 2: Maximum likelihood estimate of biogeographic range evolution for Linaceae inferred using the Dispersal-Extinction-Cladogenesis (DEC+J) model.



Discussion and Conclusion

Biogeography Findings:

The Likelihood Ratio Test and Akaike information criterion indicate vicariance and long distance dispersal. We found support for a dispersal origin of Hugonoidaeae in South America approximately 45 million years ago and a North America founder speciation event for *Linum sect. Linopsis* from Europe about 35-40 million years ago. We found evidence that all yellow-flowered flax in North America results from a single colonization from Europe or the Mediterranean region approximately 11.8 million years ago. The ancestor of the blue-flowered flax originated from Europe or the Mediterranean region approximately 24 million years ago.

Chromosome Number Evolution:

The estimated ancestral chromosome numbers for *Linum sect. Linopsis* is $n=9$, *Linum sect. Linum* is $n=9$, and *Linum sect. Dasylinum* is $n=8$, supporting previously proposed hypotheses of ancestral chromosome numbers (McDill, 2009). The ancestral chromosome number for all of *Linum sensu lato* is 8. Though repeated polyploidization events are reconstructed, particularly in *Linum sect. Linopsis*, all polyploidization events occurred relatively recently (<5 Ma). 21% of all speciation events in Linoideae are associated with dysploid chromosome gains, while only 7% of all speciation events are associated with polyploidy. These results suggest that cladogenetic dysploidization played a greater role than cladogenetic polyploidization during the diversification of Linaceae.