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Dear Dr. Thrall:

Please consider our paper, “Current environments and evolutionary history shape forest temporal assembly” for publication as a letter in *Ecology Letters*.

Global shifts in the timings of species life history events with climate change has led to increasing interest in how communities assemble in time. Yet progress has been slow, as species timings are highly variable across space and time, especially in systems where shifts have been greatest. Using experiments we can decompose this variability into predictable responses to environmental cues, such as temperature and daylength. But given their logistical challenges, most experiments have focused on only a few species—providing limited insights into community dynamics under future climates.


Here, we present a large-scale experiment, spanning four sites, 47 species and over 2000 individuals to test for evidence of temporal assembly. We focus on leafout of trees and shrubs for which the environmental cues—temperature and photoperiod—are well studied. Our design allows us to estimate the variability at the population, species and community-levels. To mechanistically test the relationships and variability in environmental cues and species evolutionary relationships, we paired our experimental data with a phylogenetic tree and Bayesian model.

We found species differed their timings in each site, supporting the idea that temporal assembly may structure communities. Further, we show that species timings can be robustly decomposed into stable responses to temperature and daylength, with responses surprisingly constant across populations—even those separated by 6° of latitude and 55° of longitude. But responses to cues explained little of the temporal variation across species. Differences in species timings were also explained by intrinsic differences, which themselves were related to evolutionary history. These findings suggest our understanding of one of the most well studied events—leafout—is still incomplete and that other unidentified traits or cues shape communities temporal assembly.

Our study also presents a powerful analytical approach that has broad applications across diverse species assemblages. The phylogenetic model we could be applied to other types of life history events or suites of species, allowing us to test for differences between invasive and native species in a community or across species in distinct trophic-levels or functional groups.

Both authors contributed to this work and approve this version for submission. The manuscript is 3773 words with a 150 word summary, and 3 figures and is not under consideration elsewhere. We hope you find it suitable for publication in *Ecology Letters*, and look forward to hearing from you.

Sincerely,

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Deirdre Loughnan
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