

Appendix S1: Public data sources for fruiting phenology

1. National Phenology Network (NPN; United States): Geographic scope is all of the U.S., although some areas are more represented than others. Phenology data goes back to 2011. First few years of data are sparse and mostly flowering/leaf-out; data collection within the past five years much more widespread, particularly for fruiting data. Many species represented, particularly in the past five years. Data collected by both researchers and trained citizen scientists. <https://www.usanpn.org/home>
2. Budburst (United States): Geographic scope is all of the U.S., although certain locations are more represented than others. Phenology data goes back to 2007. Certain species (such as trout lilies) are targeted for observations more than others. Data collected by citizen scientists. <https://budburst.org>
3. NECTAR (North and Central America, Europe, 1 Australian location): Extensive collection of Long-Term Ecological Research (LTER) and other individual site data sources in concert with a paper by Wolkovich et al. (2012). Geographic scope includes both temperate and tropical locations. Data spans different time periods depending on source, but some go back to 1990's or 1980's. Some data sources in the collection do not include fruiting data. Data collected by researchers.

Wolkovich, E.M., Cook, B.I., Allen, J.M., Crimmins, T.M., Betancourt, J.L., Travers, S.E., Pau, S., Regetz, J., Davies, T.J., Kraft, N.J.B., Ault, T.R., Bolmgren, K., Mazer, S.J., McCabe, G.J., McGill, B.J., Parmesan, C., Salamin, N., Schwartz,

M.D., and Cleland, E.E. (2012). Warming experiments underpredict plant phenological responses to climate change. *Nature*, 485, 494-497.

4. Pan European Phenology (PEP; Europe): Geographic scope is all of Europe, although western European nations generally have more records. Phenology data goes back to the 1800's, for some species in some locations. Many species are represented, particularly for flowering phenophases, but fewer species are represented for fruiting phenophases. Data collected by researchers. <http://www.pep725.eu>

5. Spain Sierra Nevada (Spain): Geographic scope is high elevation areas within the Sierra Nevada Mountains, Spain. Phenology comprised of two time periods: 1988-1990 and 2009-2013. Over 70 species represented. Data collected by researchers.

Pérez-Luque, A.J., Sánchez-Rojas, C.P., Zamora, R., Pérez-Pérez, R., Bonet, F.J. (2015). Dataset of phenology of Mediterranean high-mountain meadows flora (Sierra Nevada, Spain). *PhytoKeys*, 27, 89-107.

6. New Zealand Plant Conservation Network (New Zealand): Geographic scope is across New Zealand and all associated islands. Although the dataset goes back to the late 1700's, few fruiting records occur before 2010. Many species, but only about half of them have fruiting data. <https://www.nzpcn.org.nz>

7. Environmental Data Initiative (EDI) Data Portal (based in the United States and supported by the U.S. National Science Foundation (NSF), data from many locations):

Collection of environmental data generally, although phenological data is specifically collected. However, browsable categories include “bud burst,” “flowering,” “recruitment,” and “seedling establishment” but not “fruiting” or “seed set.” Data collected by researchers at LTER sites, as well as Long Term Research in Environmental Biology (LTREB) and Organization of Biological Field Stations (OBFS) sites, along with data collected as part of research associated with the Macro-system Biology (MSB) programs at NSF. <https://environmentaldatainitiative.org>

We expect that some additional field stations and other research locales as well as individual researchers are in possession of additional sources of fruiting phenology data, including historical records. However, because these datasets have not yet been collected in a public database, they are not readily available to any researcher who wishes to explore questions related to fruiting phenology over wide geographic areas or, if available, time scales of multiple decades.

Appendix S2: Case Study: Fruiting phenology shifts and life stage linkage in European species

How is fruiting phenology shifting and what does this shift tell us about the linkage between flowering and fruiting life history stages?

Methods

We assembled a dataset from the Pan European Phenological Database (PEP725; Templ et al. 2018; see description of PEP725 in Appendix S2). We selected only angiosperms observed annually from 1980-2015, with records occurring consistently over that time period in one location. Within this 35-year period, each decade was warmer than the previous one (Lorenz et al. 2019). We selected all broad-leaved woody plants that were identified to species, excluding non-native species, for analysis. Based on this data selection criteria, there were only 14 species with sufficient fruiting phenology data over 35 years in PEP725 for analysis.

The only fruiting stage recorded, and therefore the one we used, for most of the species was “first ripe fruits,” a phenological stage recorded at the level of the individual plant. Most of these species had observations from multiple countries. We used only data from those countries for which there were observations for the entire time period. For most species this resulted in the final dataset coming from a single country, although for *Aesculus hippocastanum* and *Sambucus nigra* we used data from 4 countries, and for *Ribes rubrum* and *Sorbus aucuparia* we used data from 2 countries. Using a multi-year dataset allowed us to take a cross-year average of fruiting times (“first ripe fruits”) and distinguishing a longer-term signal of change from normal year-to-year variation.

In our Bayesian, multi-species analysis of this data, we allowed the slope - the rate of phenological change in fruiting over decades - to vary by species by specifying that species-specific slope parameters arise from a common distribution with mean, μ , and variance

parameter, tau (O’Hara and Sillanpaa 2009). Given that we have very little information about fruiting time responses to climate change, we gave mu an uninformative prior. We ran a posterior predictive check for the normality of the response variable (first fruiting day). All analyses were performed in R (R Core Team 2016) using JAGS (Plummer 2003) via the R package R2jags (Su and Yajima 2009). We ran the multi-species analysis with three chains for 30,000 iterations. We checked for convergence by ensuring the scale reduction factors approached one for all parameters (Gelman and Rubin 1992).

Results

All but three of the 14 species showed a significance advance in fruiting (date of first ripe fruits; Fig. 1). Fruiting for animal-dispersed species advanced an average of 2.1-9.1 days^{-10yr} overall, with the exception of one species, the common hazel (*Corylus avellana*), in which there was no change (Fig. 1). We found no significant advance or delay for the two wind-dispersed species (Fig. 1). Due to the limited sample size within each group of dispersal type used in this analysis, we do not yet have the capacity to make inferences about how different dispersal modes are responding to environmental cues, selection pressures, or physiological limitations.

What are the relative changes between flowering and fruiting life history stages?

Methods

We selected from our 14 species used for the fruiting phenology analysis only those species for which was recorded both flowering and fruiting (“first ripe fruits”) for >100 individuals. This allowed us to track FTFI by individual. Some, but not all, of our individuals were tracked over the entire 35-year period.

As with our fruiting phenology analysis, we used a Bayesian, multi-species framework, but with the change in FTF interval by decade as the slope within the regression. We included a random effect for species arising from a common distribution across all 6 species. This all-species average serves the purpose of pulling each species closer towards the cross-species mean, which gives us more confidence in the individual species averages (O’Hara and Sillanpaa 2009). We ran a posterior predictive check for the normality of the response variable (FTFI). All analyses were performed in R (R Core Team 2016) using JAGS (Plummer 2003) via the R package R2jags (Su and Yajima 2009). We ran the multi-species analysis with three chains for 30,000 iterations. We checked for convergence by ensuring the scale reduction factors approached one for all parameters (Gelman and Rubin 1992).

Results

The FTFI for *Aesculus hippocastanum* increased between 1980 and 2015 by 1.7-2.3 days^{-10yr}. The FTFI did not significantly change for *Sorbus aucuparia*, *Vaccinium myrtillus*, and *Sambucus nigra*. The FTFI for *Ribes rubrum* and *Ribes grossularia* decreased (0.6-1.2 and 0.7-1.3 days^{-10yr}, respectively).

Appendix S1 References

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