

Leaf Color Change Date in Harvard Forest

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Introduction

Starting in 1991, Researcher John O’Keefe and his team collected various phenological statistics for a number of species of trees in the Prospect Hill Tract Harvard Forest in Petersham, MA. He has continued to record the statistics and compile them in an online data archive in order to provide researchers with data to investigate if certain trends are correlated with certain species. In this data archive, one particular data set has statistics regarding the mean day of the year in which each tree of various given species has 50% of their leaves change color for autumn. We will be investigating how this day (listed in Julian days within the data set) is correlated with species type and investigate the annual trends for each species throughout the last 30 years.

Current literature agrees that there is likely a trend of later fall coloring within deciduous species due to longer growing seasons as a result of climate change. However, it is unknown if differences between species or this climactic variation describe more change in fall leaf phenology. Because of climate change, we expect warmer temperatures to last longer into the year. Regardless, our initial hypothesis is that species will still be an important defining factor because the varying species have different physiological traits. This impacts the leaf color-changing process, which we predict will have a net result of later Julian days for the 50% quota to be reached by each species. Leaf color change affects nutrient cycling, so understanding the relationship between climate change and leaves changing color in different species is crucial for predicting if the long-term effects of climate change or different species are the dominant factor when leaves change. If climate change is the only defining factor, we would see a time-dependent differentiating change from year to year. In contrast, if species were another defining factor, we would see an asymmetric time-dependent differentiating change that isn’t as dependent on the year-to-year as it would be on each species.

Hypotheses

Null: There is no species effect on leaf color change date. Climactic variation over the years will explain most variation

HA1: The leaf color change date would be different for each species, but not change from year to year.

HA2: The leaf color change date would be later as years progress, with each species’ leaf color change date being different as well.

Methods

Data Acquisition/ O’Keefe and his team’s data was collected through weekly observations of percent leaf coloration and percent leaf fall started in September each year. Researchers observed when 50% of the leaves of trees of different species had changed color and started to fall, and recorded those dates. They recorded this data for 33 unique types of species from 1991 to the present day, with the most recent data coming from 2022.

Analysis/ From our desired data set, we filtered down to the 14 species that had recorded mean Julian dates for 50% of the leaves changing colors for every year from 1991 until present. To assess the variation in date of leaf color change in each species per year, we first created a scatter plot of the Julian date vs. year and had each species of tree which were represented by the different colors. We added trend lines for each species to better make a preliminary visualization the overall trend for each species. We also made a graph of residuals, and confirmed the data fit the assumptions of linear models (linear, independence, equal variance and normally distributed residuals).

```

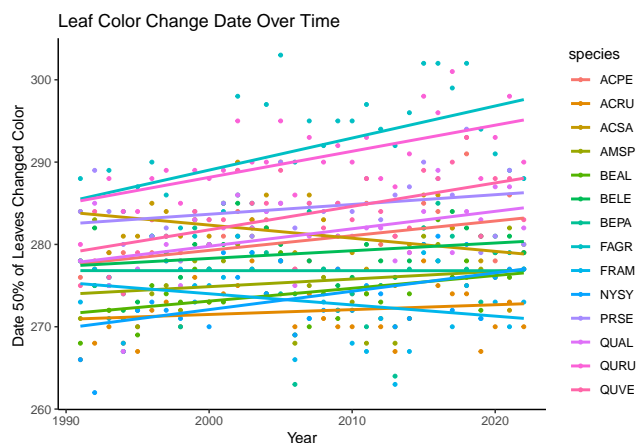
pheno <- read.csv(file="hf003-08-fall-mean-spp.csv") #read in the data
pheno_trimmed <- pheno %>% #pipe in data
  #filter in species present for every year from 1991 to present
  filter(species=="ACRU"|species=="ACSA"|species=="ACPE"|species=="AMSP"|
    species=="BEAL"|species=="BELE"|species=="BEPA"|species=="FAGR"|
    species=="FRAM"|species=="NYSY"|species=="PRSE"|species=="QUAL"|
    species=="QURU"|species=="QUVE")

pheno_trimmed %>%
  ggplot(aes(x = year, y = lc_doy)) + #set year as x axis and julian day of change as the y
  geom_point(aes(color=species, fill=species), size=1) +
  ggtitle("Leaf Color Change Date Over Time")+ #add title
  #adding in trend lines by species
  geom_smooth(aes(group=species,color=species), method = "lm", formula = y ~ x, se = F)+
  xlab("Year") + #label x axis
  ylab("Date 50% of Leaves Changed Color ") + #label y axis
  theme_classic() #changing background

```

```
## Warning: Removed 2 rows containing non-finite values (`stat_smooth()`).
```

```
## Warning: Removed 2 rows containing missing values (`geom_point()`).
```



To get an idea whether climatic variation, species effects, or an interaction between the two had important effects on trends in leaf color change date, we decided to run an ANCOVA with the data based upon a linear model. Explanatory variables (groups) would include year (a continuous variable to act as a proxy for climatic variation interannually), species, and the interaction between the two. Due to autocorrelation of climatic trends as well as strong influence of one year's leaf color change data to the next, we selected ANCOVA over ANOVA intentionally, with year as a covariate with leaf change date. The F and p values of the ANCOVA will be informative of whether there are important differences between years and species (or the interaction between the two). Pairwise comparisons were run post-hoc using a Tukey Test to look at specific comparisons between species. The results of that can be seen in the supplementary information.

```

options(contrasts = c("contr.sum", "contr.ply")) #options for later post hoc comparison
model_1 <- lm(lc_doy ~ year * species, data=pheno_trimmed) #build linear model
#summary(model_1) #this prints out long, so see the supplementary info
#resid_panel(model_1, plot="all") #check on residuals, see SI
Anova(model_1, type = 3) #run an ANCOVA

```

```
## Anova Table (Type III tests)
```

```
##
```

```
## Response: lc_doy
```

```
##           Sum Sq Df F value    Pr(>F)
## (Intercept)      2.9  1  0.1725    0.6781
## year           643.6  1 37.8977 1.750e-09 ***
## species        842.7 13  3.8169 7.958e-06 ***
## year:species    861.6 13  3.9027 5.367e-06 ***
## Residuals      7098.7 418
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

pwc <- pheno_trimmed %>% tukey_hsd(lc_doy ~ species) #pair wise comparisons
#pwc #look at the PWC of species, also see SI
```

Results

Extremely low p-values for comparisons between different species, different years, and the interaction between the two show year, species, and the year-species interaction show that all of these factors have an important effect on variation in leaf change date ($p < .0001$ for all). However, the F-value for year that is 10 times larger ($F=37.9$) than that for species ($F=3.8$) and the year:species interaction ($F=3.9$) show that year is the dominating contributor to the trend in leaf color change date shift (which itself has $R^2=.69$ and $p < .0001$). Pairwise comparisons reveal varying levels of similarity between species in how much and in what direction then influence the date shift trend.

Conclusion

Based on the analysis, we can conclude leaf turn date is more climate dependent than species-dependent, but species-dependent is still significant. We also see the interaction between species and year is significant, which means different species aren't responding in the same way to climate changes as years go on. This is not what we hypothesized, but makes intuitive sense, as different tree species respond differently to changing climate. Further testing will help clarify what effect species differences affect the leaf drop date, and help us understand which species are more or less affected by climate change from year to year. One of the further tests we can do is compare different genera and different species within genera to see if the leaf change date is more dependent on species or genus.

Contribution Statement

We extend our appreciation to everyone who made this project possible, specifically Mr. O'Keefe and his team at Harvard that collected the data that we were able to use as well as Dr. McLachlan and his team of TAs (specifically Gretchen and Eva) that helped to advise and educate us on biostatistics. This project would not have been possible without your work as well, so we thank you for making this opportunity for our group!

Citations

O'Keefe J. 2023. Phenology of Woody Species at Harvard Forest since 1990. Harvard Forest Data Archive: HF003 (v.35). Environmental Data Initiative: <https://doi.org/10.6073/pasta/eb0dd36c6ec62a918340b6bda38be832>.

Supplementary Information

Linear Model Results and Coefficients

```
summary(model_1)

##
## Call:
## lm(formula = lc_doy ~ year * species, data = pheno_trimmed)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -13.8127  -2.6427   0.1924   2.6173  12.0243
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)      17.68169    42.57334    0.415 0.678119
## year              0.13061     0.02122    6.156 1.75e-09 ***
## species1        -95.44268   152.62876   -0.625 0.532099
## species2         135.77451   152.62876    0.890 0.374207
## species3         583.58224   152.62876    3.824 0.000152 ***
## species4          72.06813   152.62876    0.472 0.637045
## species5        -55.41739   152.62876   -0.363 0.716724
## species6          73.29907   152.62876    0.480 0.631305
## species7         259.86633   152.62876    1.703 0.089386 .
## species8        -507.42989   158.62931   -3.199 0.001485 **
## species9          528.32143   152.62876    3.461 0.000593 ***
## species10       -192.45020   152.62876   -1.261 0.208047
## species11         28.44716   152.62876    0.186 0.852236
## species12       -162.02406   152.62876   -1.062 0.289050
## species13       -363.03852   158.62931   -2.289 0.022601 *
## year:species1     0.04791    0.07607    0.630 0.529169
## year:species2    -0.07159    0.07607   -0.941 0.347136
## year:species3    -0.29007    0.07607   -3.813 0.000158 ***
## year:species4    -0.03805    0.07607   -0.500 0.617146
## year:species5     0.02481    0.07607    0.326 0.744437
## year:species6    -0.03695    0.07607   -0.486 0.627352
## year:species7    -0.13098    0.07607   -1.722 0.085826 .
## year:species8     0.25878    0.07904    3.274 0.001149 **
## year:species9    -0.26661    0.07607   -3.505 0.000506 ***
## year:species10    0.09281    0.07607    1.220 0.223100
## year:species11   -0.01184    0.07607   -0.156 0.876338
## year:species12    0.08145    0.07607    1.071 0.284901
## year:species13    0.18614    0.07904    2.355 0.018983 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.121 on 418 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.7089, Adjusted R-squared:  0.6901
## F-statistic: 37.71 on 27 and 418 DF, p-value: < 2.2e-16
```

Pairwise Comparisons

```
print(pwc, n=100)
```

```
## # A tibble: 91 x 9
##   term      group1 group2 null.value estimate conf.low conf.high p.adj
##   * <chr>   <chr> <chr>      <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
## 1 species ACPE  ACRU         0    -8.56    -12.3     -4.80     0
## 2 species ACPE  ACSA         0     0.875    -2.88     4.63     1 e+ 0
## 3 species ACPE  AMSP         0    -4.97    -8.73    -1.21    8.68e- 4
## 4 species ACPE  BEAL         0    -6.31   -10.1    -2.55    2.40e- 6
## 5 species ACPE  BELE         0    -1.53    -5.29     2.23    9.84e- 1
## 6 species ACPE  BEPA         0    -3.63    -7.38     0.133   7.14e- 2
## 7 species ACPE  FAGR         0    11.3     7.52    15.1     0
## 8 species ACPE  FRAM         0    -7.31   -11.1    -3.55    1.37e- 8
## 9 species ACPE  NYSY         0    -6.91   -10.7    -3.15    1.20e- 7
## 10 species ACPE PRSE         0     4.00     0.242    7.76    2.49e- 2
## 11 species ACPE QUAL         0     0.719    -3.04     4.48     1 e+ 0
## 12 species ACPE QURU         0     9.92     6.13    13.7     0
```

## 13 species ACPE QUVE	0	3.19	-0.570	6.95	1.99e- 1
## 14 species ACRU ACSA	0	9.44	5.68	13.2	0
## 15 species ACRU AMSP	0	3.59	-0.164	7.35	7.74e- 2
## 16 species ACRU BEAL	0	2.25	-1.51	6.01	7.55e- 1
## 17 species ACRU BELE	0	7.03	3.27	10.8	6.22e- 8
## 18 species ACRU BEPA	0	4.94	1.18	8.70	9.8 e- 4
## 19 species ACRU FAGR	0	19.9	16.1	23.7	0
## 20 species ACRU FRAM	0	1.25	-2.51	5.01	9.98e- 1
## 21 species ACRU NYSY	0	1.66	-2.10	5.41	9.7 e- 1
## 22 species ACRU PRSE	0	12.6	8.80	16.3	0
## 23 species ACRU QUAL	0	9.28	5.52	13.0	0
## 24 species ACRU QURU	0	18.5	14.7	22.3	0
## 25 species ACRU QUVE	0	11.7	7.99	15.5	0
## 26 species ACSA AMSP	0	-5.84	-9.60	-2.09	2.17e- 5
## 27 species ACSA BEAL	0	-7.19	-10.9	-3.43	2.70e- 8
## 28 species ACSA BELE	0	-2.41	-6.16	1.35	6.59e- 1
## 29 species ACSA BEPA	0	-4.5	-8.26	-0.742	4.89e- 3
## 30 species ACSA FAGR	0	10.4	6.64	14.2	0
## 31 species ACSA FRAM	0	-8.19	-11.9	-4.43	6.60e-11
## 32 species ACSA NYSY	0	-7.78	-11.5	-4.02	9.63e-10
## 33 species ACSA PRSE	0	3.13	-0.633	6.88	2.26e- 1
## 34 species ACSA QUAL	0	-0.156	-3.91	3.60	1 e+ 0
## 35 species ACSA QURU	0	9.04	5.25	12.8	0
## 36 species ACSA QUVE	0	2.31	-1.45	6.07	7.18e- 1
## 37 species AMSP BEAL	0	-1.34	-5.10	2.41	9.95e- 1
## 38 species AMSP BELE	0	3.44	-0.320	7.20	1.14e- 1
## 39 species AMSP BEPA	0	1.34	-2.41	5.10	9.95e- 1
## 40 species AMSP FAGR	0	16.3	12.5	20.1	0
## 41 species AMSP FRAM	0	-2.34	-6.10	1.41	6.98e- 1
## 42 species AMSP NYSY	0	-1.94	-5.70	1.82	9.01e- 1
## 43 species AMSP PRSE	0	8.97	5.21	12.7	0
## 44 species AMSP QUAL	0	5.69	1.93	9.45	4.36e- 5
## 45 species AMSP QURU	0	14.9	11.1	18.7	0
## 46 species AMSP QUVE	0	8.16	4.40	11.9	8.48e-11
## 47 species BEAL BELE	0	4.78	1.02	8.54	1.77e- 3
## 48 species BEAL BEPA	0	2.69	-1.07	6.45	4.73e- 1
## 49 species BEAL FAGR	0	17.6	13.8	21.4	0
## 50 species BEAL FRAM	0	-1	-4.76	2.76	1 e+ 0
## 51 species BEAL NYSY	0	-0.594	-4.35	3.16	1 e+ 0
## 52 species BEAL PRSE	0	10.3	6.55	14.1	0
## 53 species BEAL QUAL	0	7.03	3.27	10.8	6.22e- 8
## 54 species BEAL QURU	0	16.2	12.4	20.0	0
## 55 species BEAL QUVE	0	9.5	5.74	13.3	0
## 56 species BELE BEPA	0	-2.09	-5.85	1.66	8.37e- 1
## 57 species BELE FAGR	0	12.8	9.05	16.6	0
## 58 species BELE FRAM	0	-5.78	-9.54	-2.02	2.87e- 5
## 59 species BELE NYSY	0	-5.37	-9.13	-1.62	1.68e- 4
## 60 species BELE PRSE	0	5.53	1.77	9.29	8.64e- 5
## 61 species BELE QUAL	0	2.25	-1.51	6.01	7.55e- 1
## 62 species BELE QURU	0	11.4	7.66	15.2	0
## 63 species BELE QUVE	0	4.72	0.961	8.48	2.23e- 3
## 64 species BEPA FAGR	0	14.9	11.1	18.7	0
## 65 species BEPA FRAM	0	-3.69	-7.45	0.0704	6.05e- 2
## 66 species BEPA NYSY	0	-3.28	-7.04	0.477	1.63e- 1

```
## 67 species BEPA PRSE      0  7.63    3.87   11.4   2.38e- 9
## 68 species BEPA QUAL      0  4.34    0.586   8.10   8.34e- 3
## 69 species BEPA QURU      0 13.5     9.75   17.3    0
## 70 species BEPA QUVE      0  6.81    3.05   10.6   1.96e- 7
## 71 species FAGR FRAM      0 -18.6   -22.4  -14.8    0
## 72 species FAGR NYSY      0 -18.2   -22.0  -14.4    0
## 73 species FAGR PRSE      0  -7.30  -11.1   -3.52   1.96e- 8
## 74 species FAGR QUAL      0 -10.6   -14.4   -6.80    0
## 75 species FAGR QURU      0  -1.39   -5.21    2.43   9.95e- 1
## 76 species FAGR QUVE      0  -8.12  -11.9   -4.33   1.79e-10
## 77 species FRAM NYSY      0  0.406  -3.35    4.16    1 e+ 0
## 78 species FRAM PRSE      0 11.3     7.55   15.1    0
## 79 species FRAM QUAL      0  8.03    4.27   11.8   2.06e-10
## 80 species FRAM QURU      0 17.2    13.4   21.0    0
## 81 species FRAM QUVE      0 10.5     6.74   14.3    0
## 82 species NYSY PRSE      0 10.9     7.15   14.7    0
## 83 species NYSY QUAL      0  7.62    3.87   11.4   2.38e- 9
## 84 species NYSY QURU      0 16.8    13.0   20.6    0
## 85 species NYSY QUVE      0 10.1     6.34   13.9    0
## 86 species PRSE QUAL      0  -3.28   -7.04    0.477   1.63e- 1
## 87 species PRSE QURU      0  5.92    2.13    9.71   1.92e- 5
## 88 species PRSE QUVE      0  -0.813  -4.57    2.95    1 e+ 0
## 89 species QUAL QURU      0  9.20    5.41   13.0    0
## 90 species QUAL QUVE      0  2.47   -1.29    6.23   6.18e- 1
## 91 species QURU QUVE      0  -6.73  -10.5   -2.94   3.94e- 7
## # i 1 more variable: p.adj.signif <chr>
```

Residuals

```
resid_panel(model_1,plot="all")
```

