

Electronic Supplementary Material

Species with more volatile population dynamics are differentially impacted by weather

Joshua G. Harrison^{1*}, Arthur M. Shapiro³, Anne E. Espeset¹, Christopher C. Nice², Joshua P. Jahner¹, Matthew L. Forister¹

¹*Program in Ecology, Evolution, and Conservation Biology, Department of Biology, University of Nevada, Reno, NV 89557, U.S.A.*

²*Department of Biology, Texas State University, San Marcos, TX*

³*Center for Population Biology, University of California, Davis, CA 95616, U.S.A.*

*Corresponding author: joshuaharrison@unr.edu

Methods

Data were collected at ten locations in Northern California (Fig. 1 main text). Data collection began between 1972 and 1988, depending on the site (Table S1). Sites spanned an elevational gradient and included a variety of habitat types, from coastal marsh to alpine barrens. Sites were visited by A. M. S. every two weeks during “good” butterfly weather, that is during sunny days that were not too windy. Data were collected via the Pollard walk method [1] whereby a fixed path was walked during each visit and presence or absence of butterfly species noted (see <http://butterfly.ucdavis.edu/> for descriptions of path taken at each site). Presences are henceforth referred to as “day positives”. Additionally, since 1999, abundance (count) data has been collected for sites at the lowest elevations (including the North Sacramento, West Sacramento,

Rancho Cordova, Gates Canyon, and Suisun Marsh sites). The more intense data collection at the subset of sites since 1999 was inspired by extreme declines in population density that were observed for most species at low elevations [2,3]. Count data were divided by number of site visits for that year, and the coefficient of variation (CV) in this proportion across years was calculated for each resident species. CV was then averaged across sites for a given species as a way to assign an index of average population fluctuation, or volatility, to each species. Only those species observed at multiple sites and for which a total of 100 individuals or more were observed over the course of the study were included in the analysis. In total, 50 species were indexed in terms of average population fluctuation (this index henceforth referred to as “rank volatility”).

It is possible that differences in detectability between species might lead to erroneous indexing in terms of volatility. In particular, abundant species might be more subject to detection error resulting in less accurate estimates of abundance (as made from counts of individuals). It is also possible that the least abundant species would be subject to detection error and less accurate estimates of abundance. Increased error in abundance estimates (whether for the most or least common species) could, in turn, lead to inflated estimates of inter-annual population variation, which would result (for our analyses) in incorrect indexing of species in terms of volatility. To address this possibility, we calculated correlations of our rank volatility index with abundance. Abundance was calculated as the mean population size across sites and years. We found no correlation of abundance with rank volatility (Spearman’s $\rho = -0.007$, $p = 0.96$), which suggests that variation in detectability has not confounded our ranking of volatility.

Indexed species were subjected to hierarchical Bayesian analysis using the R package rjags [4] to explore the relationship between population dynamics and climate. This approach

utilizes Bayesian methodology within a hierarchical generalized linear modeling framework. In this case we modeled day positives, DP, for a given year i and site j as a binomially distributed response variable thus: $DP_{ij} \sim \text{Binomial}(p_{ij}, \text{Visits}_{ij})$ where p is the proportion of day positives out of total visits, and Visits is the number of site visits per year. We modeled this response at two hierarchies; both for individual sites and across all sites. We created separate models for each species of butterfly examined. The details of the modeling approach are defined elsewhere [5]. Briefly however, an inverse logit link function, $p_{ij} = 1/(1 + e(-\alpha_{ij}))$ was used to link the binomial response variable with a hierarchical linear model of the form:

$$\alpha_{ij} = \mu_j + \beta_{1j} \text{Covariate}_{1ij} + \beta_{2j} \text{Covariate}_{2ij} + \dots + \beta_{Kj} \text{Covariate}_{Kij}$$

The intercept term of the linear model (μ) was the species-specific mean estimate of occurrence probability across years for a given site j . K is the total number of model terms. Intercepts and beta coefficients were drawn from normal distributions with means and precisions equal to transect-wide parameters:

$$\mu_j \sim N(\mu_\mu, \tau_\mu)$$

$$\beta_{Kj} \sim N(\mu_{\beta_k}, \tau_{\beta_k})$$

Uninformative hyperpriors were used throughout and were defined as follows:

$$\mu_\mu \sim N(0, 0.00001)$$

$$\mu_{\beta_k} \sim N(0, 0.00001)$$

$$\tau_\mu \sim \text{Gamma}(0.1, 0.001)$$

$$\tau_{\beta_k} \sim \text{Gamma}(0.1, 0.001)$$

Posterior probability distributions were obtained through Markov chain Monte Carlo (MCMC) sampling using rjags. The output of this approach is estimates of posterior probability density distributions describing the uncertainty in the effect size associated with each model term

at both site- and transect-wide hierarchical levels. We used estimates of posterior probability distributions describing the transect-wide impact of model variables for the subsequent analyses described below. Terms included in the model were seasonal mean maximum and mean minimum temperatures and precipitation, year (to examine interannual population change) and two terms that were indices of the ENSO for a given year (described below). Site-specific seasonal weather was calculated using PRISM data (PRISM Climate Group). Seasonality reflected the "water year", consequently Winter encompassed December of the previous year, January, and February of the current year; Spring consisted of March, April, and May; Summer of June, July, and August; and, Autumn of September, October, and November of the previous year. For each site, precipitation, including snow, was summed for each season. ENSO indices were the top two components output from a PCA reduction of monthly values of the multivariate ENSO index (MEI) [6]. These components were obtained for each year of the study period. The MEI is itself a composite variable comprised of six metrics that together provide a measure of the strength of the ENSO for a given month. Habitat was not included as a covariate in the model. While habitat, in terms of vegetative community, does differ between sites (Table S1), we unfortunately do not have data quantifying those differences such that we could assign a continuous value describing the differences in vegetation among sites. Furthermore, characterizing each site's habitat in terms of a qualitative factor would provide no additional explanatory power to the model, as each site would necessarily be assigned a unique level. Each model was run using two search chains for 55,000 iterations, with a burn-in of 45,000 iterations. We monitored chain mixing and convergence by examining trace plots and calculating effective sample size output by each model. Effective sample size necessarily varied between species and parameters, but was always at least several hundred, and most often in the many thousands. The

final 10,000 samples generated by the Gibbs sampling algorithm were collected as representative of the posterior distribution of coefficients associated with a particular weather variable. The mean of these samples was used as a point estimate of the standardized partial regression coefficient describing the effect of a weather variable on day positives for a given species. The mean was calculated, as opposed to the median for example, because of the symmetrical distribution of samples output by the model (see Fig. S1). The percentage of these samples above or below zero was used to calculate the probability of a non-zero effect for a given variable.

Samples were also used to investigate the relationship between response to weather and average population fluctuation across indexed taxa. To accomplish this we created a 50 x 10,000 matrix for each model variable, with columns that consisted of the 10,000 samples representative of the species-specific, posterior probability distributions (PPDs) associated with the effect of the variable under examination and rows associated with the individual species. Matrices were ordered by rank volatility such that the first row contained samples associated with the most volatile species and the last row contained samples associated with the least volatile species (for a total of 50 rows). Each column of this matrix was then iteratively correlated (Pearson's product moment) with identically ordered species-specific coefficients of variation in abundance previously used to define rank volatility. Correlation coefficients generated at each iterative step were tabulated and the resulting frequency distribution of coefficients examined to determine the strength, direction, and certainty of the correlation.

To summarize, this analysis reveals for which variables a more volatile butterfly species would tend to have a more positive, or more negative, response to weather as compared with a less volatile butterfly species, while retaining the uncertainty generated at each step in the modeling process. The open-source software R (Version 3.0.1 [7]) was used for all analyses.

To account for potential phylogenetic non-independence of the data, we calculated phylogenetic independent contrasts (PIC) [8] in the *ape* package in R [7,9]. For all species in this study, a 658 base pair portion of the cytochrome oxidase I (COI) mitochondrial gene was selected from published sequences in GenBank. COI sequences were not available in GenBank for all species, so we used the criteria outlined in [10] to select replacement sequences of closely related taxa. Sequences were aligned and visually inspected in Sequencher 4.10.1.

A Bayesian phylogenetic tree was constructed in BEAST 1.8.0 [11]. A general time reversible model of evolution with invariant sites and a gamma distribution (GTR+I+G) was selected using jModeltest 2.1.5 [12]. In addition, a Yule process speciation tree prior was specified. The topology of the tree was constrained in BEAUti 1.8.0 by creating monophyletic taxon sets based on published phylogenetic trees. Butterfly family level relationships were constrained using the phylogeny of [13]. Subfamily and genus level relationships were also constrained for Hesperidae [14], Lycaenidae [15,16], Nymphalidae [17,18], and Pieridae [19]. The tree was run for 10,000,000 MCMC iterations. Upon completion, tree parameters were visually inspected in Tracer 1.6 and a final target tree was constructed in TreeAnnotator 1.8.0.

Phylogenetically-corrected (PIC) coefficient of variation data used for iterative correlation of rank volatility with samples representative of the effect of weather variables were non-normally distributed, thus precluding the use of Pearson's *r* for iterative correlation. Consequently, Spearman's rank correlation was used to iteratively correlate data generated by PIC. These correlation coefficients were compared with those generated from iterative Spearman's rank correlation on uncorrected data.

Life history information

The following life history information was tabulated for each butterfly species examined: geographic range, overwintering strategy (i.e. egg, larva, pupa, or adult), voltinism, family-level host breadth, and wingspan. Geographic range data (km²) was obtained from [10]. Host breadth and voltinism information was taken from [20]. Family-level host breadth was taken from [20]. All life history information was regionally specific. For instance, range-wide host breadth was not calculated; instead, we calculated host breadth for only that portion of California encompassing the transect. Nonparametric analyses (Kruskal-Wallis tests and Spearman's rho) were used to investigate the relationship between life history traits and rank volatility.

Results

Our analysis successfully provided insight into the relationship between climatic variation and population dynamics for each species examined (Table S2). Species-specific parameter estimates varied widely, however several trends in the impact of model variables were noted. First, for most species, increased winter and spring precipitation had a negative impact on day positives, while increased summer precipitation had the opposite effect. Second, almost every species examined was declining.

Iterative correlation of rank volatility (Pearson's r) with samples representing PPDs for each model variable showed that certain variables differentially impacted volatile species (Table S3). Climate conditions with a high certainty of differentially negatively impacting volatile species included: warmer mean minimum temperatures in the spring and autumn, warmer mean maximum temperatures in the winter, and heavier winter precipitation. Conditions that differentially positively impacted volatile species included: warmer summer mean minimum temperatures, wetter springs and autumns, and more marked ENSO events.

Iterative correlation of rank volatility and samples representative of PPDs using Spearman's rank correlation generated coefficients describing similar trends (i.e. directionality and relative impact of a given variable on fraction of day positives) in the impact of weather variables across rank volatility (Table S4). Furthermore, correlation coefficients derived from iterative correlation of data corrected using PIC also showed qualitatively similar trends in the impact of weather when compared with coefficients generated from uncorrected data (Table S4). Exceptions to this pattern of similar results between analyses conducted using corrected and uncorrected data include results for the impact of summer mean maximum temperature, spring mean maximum temperature, and MEI PC 2. Certainty of non-zero effect sizes is low for the differential impact of each of these three variables across rank volatility. When considering those variables with clear differential impact on volatile species, coefficients generated by iterative correlation using Pearson's r , Spearman's rank correlation, and Spearman's rank correlation on corrected data are all consistent in terms of directionality (Tables S3 and S4).

Correlation of life history traits and rank volatility

Neither geographic range (Spearman's rank correlation, = -0.09, $p=0.52$), family-level host breadth (Spearman's rank correlation = 0.06, $p = 0.7$), nor wingspan (Spearman's rank correlation = -0.25, $p = 0.08$) were significantly correlated with average coefficient of variation of examined butterflies (rank volatility). Rank volatility was also not significantly confounded with voltinism (Kruskal-Wallis chi-squared = 2.0, $p = 0.36$) or overwintering category (Kruskal-Wallis chi-squared = 8.6, $p = 0.13$).

REFERENCES

- (1) Pollard E. 1977. Method for assessing changes in abundance of butterflies. *Biol. Conserv.* **12**, 115–134. (doi:10.1016/0006-3207(77)90065-9)
- (2) Casner KL, Forister ML, Ram K, Shapiro AM. 2014. The utility of repeated presence data as a surrogate for counts: a case study using butterflies. *J. Insect Conserv.* **18**, 13-27. (doi:10.1007/s10841-013-9610-8)
- (3) Forister ML, Jahner JP, Casner KL, Wilson JS, Shapiro AM. 2011. The race is not to the swift: Long-term data reveal pervasive declines in California's low-elevation butterfly fauna. *Ecology.* **92**, 2222-2235. (doi:10.1890/11-0382.1)
- (4) Plummer M. 2013. rjags: Bayesian graphical models using MCMC. R package version 3-11 <http://CRAN.R-project.org/package=rjags>
- (5) Nice CC, Forister ML, Gompert Z, Fordyce JA, Shapiro AM. 2014. A hierarchical perspective on the diversity of butterfly species' responses to weather in the Sierra Nevada Mountains. *Ecology.* **95**, 2155-2168. (doi:10.1890/13-1227.1)
- (6) Wolter K, Timlin MS. 1993. Monitoring ENSO in COADS with a seasonally adjusted principal component index. In Proceedings of the 17th Climate Diagnostic, pp 52-57.
- (7) R Development Core Team. 2013 R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <http://www.R-project.org/>.
- (8) Felsenstein J. 1985 Phylogenies and the comparative method. *Am. Nat.* **125**, 1-15. (doi:10.2307/2461605)
- (9) Paradis E, Claude J, Strimmer K. 2004 APE: analyses of phylogenetics and evolution in R language. *Bioinformatics* **20**, 289-290. (doi:10.1093/bioinformatics/btg412)

- (10) Jahner JP, Bonilla MM, Badik KJ, Shapiro AM, Forister ML. 2011 Use of exotic hosts by Lepidoptera: widespread species colonize more novel hosts. *Evolution* **65**, 2719-2724. (doi:10.1111/j.1558-5646.2011.01310.x)
- (11) Drummond AJ, Rambaut A. 2007 BEAST: Bayesian evolutionary analysis by sampling trees. *BMC Evol. Biol.* **7**, 214. (doi:10.1186/1471-2148-7-214)
- (12) Darriba D, Taboada GL, Doallo R, Posada D. 2012 jModeltest 2: more models, new heuristics and parallel computing. *Nat. Methods* **9**, 772. (doi:10.1038/nmeth.2109)
- (13) Heikkilä M, Kaila L, Mutanen M, Peña C, Wahlberg N. 2012 Cretaceous origin and repeated tertiary diversification of the redefined butterflies. *Proc. R. Soc. Lond. B* **279**, 1093-1099. (doi:1098/rspb.2011.1430)
- (14) Warren AD, Ogawa JR, Brower AVZ. 2008 Phylogenetic relationships of subfamilies and circumscription of tribes in the family HesperIIDae (Lepidoptera: Hesperioidea). *Cladistics* **24**, 642-676. (doi:10.1111/j.1096-0031.2008.00218.x)
- (15) Pierce NE, Braby MF, Heath A, Lohman DJ, Mathew J, Rand DB, Travassos MA. 2002 The ecology and evolution of ant association in the Lycaenidae (Lepidoptera). *Annu. Rev. Entomol.* **47**, 733-771. (doi:10.1146/annurev.ento.47.091201.145257)
- (16) Pohl N, Sison-Mangus MP, Yee EN, Liswi SW, Briscoe AD. 2009 Impact of duplicate gene copies on phylogenetic analysis and divergence time estimates in butterflies. *BMC Evol. Biol.* **9**, 99. (doi:10.1186/1471-2148-9-99)
- (17) Wahlberg N, Weingartner E, Nylin S. 2003 Towards a better understanding of the higher systematics of Nymphalidae (Lepidoptera: Papilionoidea). *Mol. Phylogenet Evol.* **28**, 473-484. (doi:10.1016/S1055-7903(03)00052-6)

- (18) Wahlberg N, Brower AVZ, Nylin S. 2005 Phylogenetic relationships and historical biogeography of tribes and genera in the subfamily Nymphalinae (Lepidoptera: Nymphalidae). *Biol. J. Linnean Soc.* **86**, 227-251. (doi:10.1111/j.1095-8312.2005.00531.x)
- (19) Chew FS, Watt WB. 2006 The green-veined white (*Pieris napi* L.), its Pierine relatives, and the systematics dilemmas of divergent character sets (Lepidoptera, Pieridae). *Biol. J. Linnean Soc.* **88**, 413-435. (doi:10.1111/j.1095-8312.2006.00630.x)
- (20) Shapiro AM. 2007. Field guide to butterflies of the San Francisco Bay and Sacramento Valley regions. University of California Press, Berkeley and Los Angeles, California.

Table S1. Data collection start date, elevation, and general habitat type for each site.

Site	Elevation (m)	Start of data collection	Habitat type
Castle Peak	2400-2775	1977	Alpine and sub-alpine
Donner Pass	2000-2200	1973	Sub-alpine
Lang Crossing	1500-1700	1974	Mixed mesic forest, meadows, and xeric outcrops
Sierra Valley	1500	1982	Xeric woodland and scrub
Washington	800-1400	1988	Mixed mesic forest, serpentine barren
Gates Canyon	80-600	1976	Oak woodland, riparian corridor, and disturbed areas
Rancho Cordova	18-22	1975	Oak woodland
North Sacramento	8-12	1988	Riparian, disturbed areas
West Sacramento	4-10	1988	Riparian, disturbed areas
Suisun Marsh	1	1972	Coastal marsh

Supplementary Results

Table S2. Species-specific point estimates of standardized partial regression coefficients describing the effect on day positives of each weather variable as determined through hierarchical Bayesian analysis. Point estimates represent the mean of samples representative of the posterior probability distribution describing the effect of a variable on day positives. Species are arranged by average population volatility in descending order. The variable “Year” describes annual change in day positives for a species. The variables “MEI PC1” and “MEI PC2” are composite variables that act as indices for the impact of the El Niño Southern Oscillation. Those variables superscripted by † were correlated with rank volatility with a high degree of certainty.

Species	Year	Winter Min. Temp.	Winter Max Temp.†	Winter Precip.†	Spring Min. Temp.†	Spring Max Temp.	Spring Precip.†	Summer Min Temp.†	Summer Max Temp.	Summer Precip.†	Autumn Min. Temp.†	Autumn Max Temp.	Autumn Precip.	MEI PC1†	MEI PC2†
<i>Vanessa cardui</i>	0.11**	0.03	-0.17***	-0.29***	-0.13**	0.37***	0.44***	0.01	0.11**	0.25***	-0.04	-0.29***	-0.12**	0.57***	0.13***
<i>Pontia protodice</i>	-0.88***	-0.13	-0.04	-0.47***	0.09	-0.54***	-0.34***	0.38**	-0.17*	-0.05	-0.17**	0.30**	0.00	0.35***	0.18***
<i>Satyrium saepium</i>	-0.05	0.08	0.07	0.11	-0.22*	0.00	-0.12	0.06	-0.03	0.02	-0.14	0.01	0.03	0.03	-0.05
<i>Glaucopsyche lygdamus</i>	-0.19**	0.08	-0.08	-0.08	-0.02	-0.09	-0.12*	0.05	0.07	0.05	-0.05	0.01	0.04	0.03	-0.03
<i>Nymphalis californica</i>	0.02	-0.09	-0.21***	0.00	-0.15*	0.39***	0.15**	-0.01	0.11*	0.03	-0.12	-0.02	-0.07	-0.05	0.07*
<i>Satyrium sylvinus</i>	-0.33**	0.03	-0.01	0.08	-0.03	0.13	-0.01	-0.08	-0.05	-0.03	0.12	-0.04	0.00	-0.07	0.01
<i>Pyrgus scriptura</i>	-0.67*	0.18**	0.02	-0.25***	0.23**	-0.24	-0.31**	-0.12	0.17	0.11	-0.03	0.10	0.00	0.06	-0.06
<i>Junonia coenia</i>	-0.18	0.34***	-0.08*	0.02	0.10*	0.04	-0.03	-0.07*	0.03	0.09**	-0.15***	0.12**	0.09*	0.10*	0.09***
<i>Brephidium exile</i>	-0.34**	-0.13**	0.05	0.07	0.01	0.03	-0.05	0.02	0.04	0.10**	-0.08	-0.09	-0.18***	0.09**	0.00
<i>Coenonympha tullia californica</i>	-0.71**	0.05	0.13*	0.08	0.07	0.02	-0.09	0.03	-0.05	0.01	0.02	0.02	0.03	0.02	-0.05
<i>Lycaena xanthoides</i>	-0.52**	0.00	0.08	-0.07	0.08	-0.16	-0.32**	-0.07	0.17*	0.18**	-0.05	0.10	-0.04	0.13*	-0.08
<i>Lycaena helloides</i>	-0.47***	0.05	0.05	-0.02	0.10	-0.03	0.01	-0.14**	0.11**	0.03	0.17*	-0.18***	-0.10*	-0.04	0.08*
<i>Satyrium auretteorum</i>	-0.28	0.08	-0.09	0.04	0.00	0.19	0.06	0.05	-0.23	-0.04	0.15	-0.09	0.06	-0.03	0.15
<i>Euchloe ausonides</i>	-0.96***	-0.02	0.10	0.13**	0.11	0.01	0.07	-0.11	0.04	0.04	0.11	0.06	-0.02	0.00	0.11**
<i>Euphydryas chalcedona</i>	-0.33***	0.07	-0.04	0.16*	-0.27**	0.26**	0.04	-0.12	0.17**	0.03	0.15*	-0.18**	-0.11	0.03	0.02
<i>Lerodea eufala</i>	-0.70***	0.01	0.16**	-0.11*	0.18**	0.00	-0.13	0.05	0.15*	-0.07	-0.12*	0.02	0.00	-0.01	-0.11**
<i>Plebejus acmon</i>	-0.10*	0.07*	-0.01	-0.03	-0.05	0.04	-0.13***	-0.05	0.04	0.10***	-0.07*	0.01	-0.07*	0.03	0.04
<i>Poanes melane</i>	-0.17	-0.34**	0.33***	-0.10	0.52***	-0.38**	-0.28**	-0.21**	0.47**	0.04	0.14	-0.17*	-0.06	-0.04	0.05
<i>Ochlodes sylvanoides</i>	-0.16*	-0.05	-0.03	-0.06	0.12**	0.01	0.09*	-0.11**	0.15**	-0.02	0.00	-0.03	-0.03	-0.04	-0.01
<i>Everes comyntas</i>	-0.20*	-0.07	0.02	-0.09*	0.10	-0.06	-0.24***	-0.05	0.06	0.06	0.08	-0.08	0.01	0.08*	0.11**
<i>Vanessa annabella</i>	-0.92***	0.13**	0.13**	-0.10*	0.20***	-0.22***	0.05	-0.08	0.15***	0.14***	-0.03	-0.08	0.08	0.01	0.08**
<i>Phyciodes mylitta</i>	-0.25**	0.16***	0.13***	-0.19***	0.22***	-0.17**	-0.25***	-0.06	0.03	-0.03	0.09*	-0.16***	-0.05	-0.05*	0.04
<i>Erynnis propertius</i>	-0.04	-0.05	0.07	0.04	0.08	-0.02	-0.05	-0.05	0.05	0.06	-0.13	0.16*	0.03	-0.04	0.10*
<i>Battus philenor</i>	0.14	-0.09	0.10*	0.08	0.03	0.12	-0.01	-0.13**	0.07	0.00	-0.07	0.00	0.14*	-0.01	0.05
<i>Danaus plexippus</i>	-0.75***	0.09**	0.12**	-0.07*	0.10*	0.09	0.10*	0.13***	-0.12**	-0.06	0.14**	-0.07	0.02	0.00	-0.04
<i>Celastrina ladon echo</i>	-0.22	0.07	0.00	-0.02	0.06	0.04	-0.09	-0.05	0.00	-0.07	0.01	0.04	0.13**	0.03	-0.04
<i>Nymphalis antiopa</i>	-0.60***	-0.21***	0.31***	0.28***	0.21***	0.05	0.06	-0.04	0.02	0.10**	0.15**	-0.08	0.03	-0.04	0.02
<i>Polites sabuleti sabuleti</i>	-0.76**	0.23***	-0.08	-0.12*	0.06	-0.12	-0.15*	-0.11	0.09	-0.06	-0.04	0.00	-0.08	0.04	-0.09*
<i>Satyrium californica</i>	-0.07	0.16**	-0.03	-0.02	0.10	-0.09	-0.10	-0.12	0.02	-0.04	0.14	-0.17*	0.03	0.03	0.02
<i>Colias eurytheme</i>	-0.20*	0.02	0.07	-0.06	-0.02	-0.02	-0.06	-0.09*	0.04	0.10***	0.01	-0.07	0.05	0.05	0.01
<i>Chlosyne palla</i>	-0.03	0.09	-0.02	0.09	-0.12	0.22	0.06	-0.04	0.02	-0.03	-0.01	-0.01	0.03	-0.04	0.08
<i>Papilio zelicaon</i>	-0.52***	0.01	0.03	0.02	0.13*	-0.08	0.01	0.00	0.09**	0.01	0.01	0.05	0.05	-0.01	0.00
<i>Pholisora catullus</i>	-1.17***	0.03	0.03	-0.07	0.38***	-0.29**	-0.14*	-0.17**	0.21**	0.11**	0.18**	0.02	-0.04	0.03	-0.06

<i>Limenitis lorquini</i>	-0.16	-0.09*	0.21***	0.19***	0.20**	-0.12	-0.10*	-0.05	0.01	-0.01	0.19**	-0.07	0.12**	-0.10***	0.09***
<i>Anthocharis sara sara</i>	-0.51**	0.15	-0.13	-0.11	0.12	-0.16	-0.18*	0.07	0.02	0.03	-0.02	0.14	-0.02	-0.06	0.03
<i>Erynnis tristis</i>	-0.30***	-0.12*	0.20***	0.06	0.02	0.03	-0.10	-0.05	0.08	0.01	0.00	0.06	0.11*	-0.08	0.06
<i>Atalopedes campestris</i>	0.03	0.08*	0.02	-0.09*	0.13**	-0.02	-0.09	-0.13**	0.21***	0.07*	-0.11*	-0.05	-0.05	0.11***	0.04
<i>Incisalia augustinus</i>															
<i>iroides</i>	-0.05	0.00	0.08	0.00	-0.08	0.21	-0.04	-0.16*	0.14	0.02	0.07	-0.07	-0.06	-0.01	0.08
<i>Vanessa virginiensis</i>	-0.26*	0.25***	0.11**	0.00	0.10	-0.25***	-0.15***	-0.29***	0.21	0.12**	-0.02	0.03	0.05	0.00	0.02
<i>Papilio eurymedon</i>	-0.05	0.12	-0.02	0.04	0.02	0.06	0.00	-0.09	-0.03	-0.02	0.01	0.08	0.05	-0.04	0.02
<i>Papilio multicaudatus</i>	-0.14	0.05	0.13	0.07	0.16	-0.02	-0.09	-0.31**	0.07	0.02	0.30	-0.33**	-0.07	0.12	0.00
<i>Strymon melinus</i>	-0.20***	0.05	-0.03	-0.08*	0.12**	-0.03	-0.09*	-0.11**	0.12***	0.05	0.01	0.00	-0.08*	0.04	0.07*
<i>Hylephila phyleus</i>	-0.16	0.00	0.02	-0.09*	0.06	0.03	-0.01	-0.10**	0.13**	0.05	-0.05	0.02	-0.05	-0.01	0.03
<i>Papilio rutulus</i>	0.09	0.04	0.08**	0.03	-0.04	0.08	-0.03	-0.12**	-0.01	-0.01	-0.06	0.08	0.08*	-0.05*	0.10***
<i>Vanessa atalanta</i>	-0.32**	0.09*	-0.03	0.03	0.18**	-0.03	0.06	-0.11*	0.17***	0.07*	0.12**	-0.07	-0.03	0.06*	0.04
<i>Pieris napi</i>	-0.16*	0.13	-0.08	-0.04	0.06	-0.07	-0.09	-0.09	0.03	0.10	0.09	-0.06	-0.06	0.01	0.09
<i>Adelpha bredowii</i>															
<i>californica</i>	-0.23*	0.05	-0.02	0.08	0.13*	0.03	-0.02	-0.08	0.02	-0.08	0.09	-0.10	-0.08	-0.04	0.00
<i>Pieris rapae</i>	-0.27***	0.02	0.07	0.00	0.05	-0.07	-0.10*	-0.08*	0.06	0.10***	0.05	-0.07	0.05	0.05*	0.01
<i>Pyrgus communis</i>	-0.11	0.05	0.01	-0.07	0.06	0.09	-0.05	-0.08*	0.03	0.07**	-0.03	0.00	-0.04	-0.05*	0.06*
<i>Ochlodes agricola</i>	0.04	0.16	0.09	-0.03	0.06	-0.19	-0.18	-0.34**	0.07	0.10	0.14	-0.17	-0.07	0.02	0.00

Superscripts used to denote percentage of samples above or below zero thus quantifying probability of a non-zero effect for a given variable. Probability that effects differ from zero indicated as follow:
 ≥ 90% probability of a non-zero effect is denoted by *, ≥ 95% probababilty by **, and ≥ 99% probabiilty by ***

Table S3. Means of the distributions of correlation coefficients generated by iterative correlation (Pearson's r) of rank volatility with samples representative of species-specific posterior probability distributions describing the effect of a given model variable. This shows if a given variable differentially impacts more volatile species as compared with less volatile species. The percentage of samples above or below zero is provided to quantify the certainty of a non-zero correlation.

Variable	Mean	% of samples > 0	% of samples < 0
Winter maximum temperature	-0.23	0.6	99.4
Winter minimum temperature	-0.10	10.2	89.8
Winter precipitation	-0.37	0.0	100.0
Spring maximum temperature	0.10	90.7	9.3
Spring minimum temperature	-0.19	0.6	99.4
Spring precipitation	0.24	99.9	0.1
Summer maximum temperature	-0.09	14.8	85.2
Summer minimum temperature	0.36	100.0	0.0
Summer precipitation	0.18	96.0	4.0
Autumn maximum temperature	-0.02	43.6	56.4
Autumn minimum temperature	-0.21	1.0	99.0
Autumn precipitation	-0.10	15.1	84.9
MEI principle component #1	0.66	100.0	0.0
MEI principle component #2	0.17	96.9	3.1
Year	-0.04	20.1	79.6

Table S4. Means of the distributions of correlation coefficients generated by iterative correlation (Spearman's rank correlation) of rank volatility with samples representative of species-specific posterior probability distributions describing the effect of a given model variable. This shows if a given variable differentially impacts more volatile species as compared with less volatile species. The percentage of samples above or below zero is provided to quantify the certainty of a non-zero correlation. Numbers contained in parentheses describe the output of the same analysis when using data corrected for phylogenetic autocorrelation.

Variable	Mean	% of samples > 0	% of samples < 0
Winter maximum temperature	-0.11 (-0.17)	16.2 (10.0)	83.8 (90.0)
Winter minimum temperature	-0.12 (-0.02)	12.2 (42.9)	87.8 (57.0)
Winter precipitation	-0.10 (-0.20)	13.4 (4.9)	86.6 (95.1)
Spring maximum temperature	0.06 (-0.05)	74.2 (34.3)	25.8 (65.7)
Spring minimum temperature	-0.14 (-0.03)	8.5 (40.4)	91.3 (59.5)
Spring precipitation	0.02 (0.05)	56.7 (65.0)	43.3 (35.0)
Summer maximum temperature	-0.07 (0.04)	24.9 (62.6)	75.1 (37.4)
Summer minimum temperature	0.33 (0.22)	100.0 (95.1)	0.0 (4.9)
Summer precipitation	0.02 (0.11)	57.1 (79.1)	42.9 (20.8)
Autumn maximum temperature	0.06 (0.15)	72.4 (86.1)	27.7 (13.9)
Autumn minimum temperature	-0.21 (-0.23)	1.8 (3.9)	98.2 (96.1)
Autumn precipitation	-0.04 (-0.07)	36.4 (33.3)	63.6 (66.7)
MEI principle component #1	0.18 (0.28)	96.0 (98.6)	4.0 (1.4)
MEI principle component #2	0.00 (-0.04)	49.6 (37.7)	50.4 (62.2)
Year	-0.19 (-0.15)	1.0 (7.4)	98.7 (92.6)

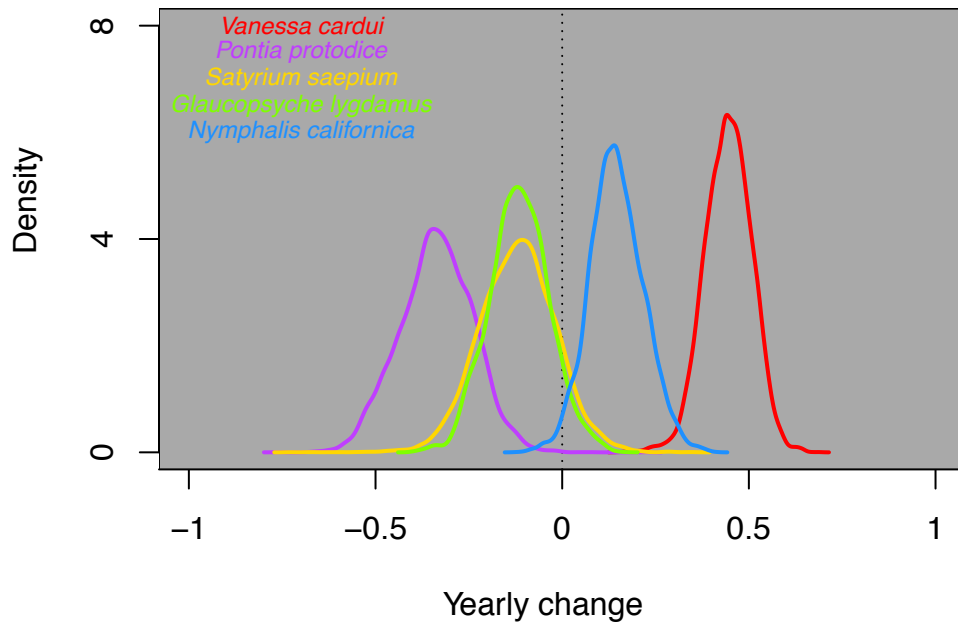


Fig. S1 Estimates of posterior probability distributions describing the impact of year on day positives for the five most volatile species examined. Estimates of posterior probability distributions for other species and for other model terms also described similarly symmetrical distributions.