Appendix S1. Construction of the phylogenetic tree.

We constructed a Bayesian phylogeny (Fig. S1) based on a partial sequence of the mitochondrial COI-gene using BEAST v2.4.4 (Bouckaert *et al.* 2014; see Table S1 for the origin of the COI sequences). Since the evolution of COI is subject to strong functional constraints (Pentinsaari *et al.* 2016), it offers limited information for estimating the timing and divergence of deeper nodes in the phylogenetic tree. Therefore, we provided two sources of *a priori* information. First, we set the orders, as well as the genus *Neuroterus*, as monophyletic groups within the current phylogeny (cf. Rokas *et al.* 2003; Stone *et al.* 2009). Second, we provided *a priori* information on the divergence times of the deeper nodes: Hymenoptera (283 Mya), Diptera (272 Mya) and Lepidoptera (232 Mya). A time estimate of the most recent common ancestor of all three orders (325 Mya) was used to calibrate the root of the tree. *A priori* divergence times were based on *TimeTree*, an online cross-study resource of divergence times (www.timetree.org; Hedges *et al.* 2015; Kumar *et al.* 2017). All divergence times were modeled as normal distributions with a standard deviation of 10 Mya. Branch lengths were allowed to vary under a lognormal relaxed clock model, the tree prior was set to the Yule model, and the model was run for 50 million iterations, with samples taken each 5000 iterations. The function *bModelTest* in the package BEAST was used to identify the best substitution model given the data. We used Tracer v1.6 (Rambaut *et al.* 2014) to assess whether the likelihood trace of the run had converged to a stable equilibrium and to verify that ESS values for all parameters were >200. Phylogenetic distances between the Finnish taxa, and between the Japanese taxa, were calculated using the function *cophenetic.phylo* in the R-package *ape* (Paradis, Claude & Strimmer 2004). For a single unidentified species in the Japanese dataset (*Stigmella* sp.) we lacked a representative COI-sequence; hence, the branch length for this species was set to the average of branch lengths of the other *Stigmella* species in the phylogenetic tree.

Table S1. The origin of the sequences used in the phylogenetic tree. Species are ordered alphabetically within region.

Region and species	Origin of the sequence[1]	Accession number in BOLD/GenBank
FINLAND		
Acrocercops brongniardella	BOLD	GRPAL020-10
Ancylis mitterbacheriana	BOLD	LEFIC337-10
Andricus curvator	BOLD	GBAH1733-06
Andricus inflator	BOLD	GBAH1734-06
Andricus quadrilineatus[2]	Graham Stone, pers. comm.	
Bucculatrix ulmella	BOLD	LEFID077-10
Caloptilia alchimiella	BOLD	GRPAL004-10
Coleophora flavipennella[3]	BOLD	LEFID666-10
Cynips longiventris	Graham Stone, pers. comm.	
Dyseriocrania subpurpurella	BOLD	LEFIJ674-10
Ectoedemia albifasciella	BOLD	NEPT042-10
Heliozela sericiella	BOLD	LEFID174-10
Macrodiplosis pustularis[4]	GenBank	AB859316.1
Neuroterus anthracinus	BOLD	ASGLE700-10
Neuroterus numismalis	BOLD	GBAH0989-06
Neuroterus quercusbaccarum	Graham Stone, pers. comm.	
Phyllonorycter harrisella[5]	BOLD	LEFIF331-10
Profenusa pygmaea	GenBank	JX090742.1
Stigmella roborella[6]	BOLD	LEFIF349-10
Tischeria dodonaea	BOLD	PHLAD003-11
Tischeria ekebladella	BOLD	PHLAC273-10
JAPAN		
Caloptilia sapporella	BOLD	LTOLB460-09
Phyllonorycter leucocorona	M. T. Kimura & B. Novković, pers. comm.	
Phyllonorycter persimilis	M. T. Kimura & B. Novković, pers. comm.	
Stigmella spp.[7]	M. T. Kimura & B. Novković, pers. comm.	
Tischeria decidua	BOLD	LEFIJ5476-16
Tischeria quercifolia	M. T. Kimura & B. Novković, pers. comm.	

[1] BOLD (Barcode of Life Data Systems, http://www.boldsystems.org/), GenBank (https://www.ncbi.nlm.nih.gov/genbank/)

[2] Used as a replacement of *Andricus callidoma*

[3] Representative of compound taxon *Coleophora flavipennella/kuehnella/lutipennella* scored during monitoring

[4] Synonym of *Macrodiplosis dryobia*

[5] Representative of compound taxon *Phyllonorycter harrisella/quercifoliella* scored during monitoring

[6] Representative of compound taxon *Stigmella roborella/ruficapitella/samiatella/svenssoni* scored during monitoring

[7] Representative of compound taxon *Stigmella kumatai/pulla* scored during monitoring

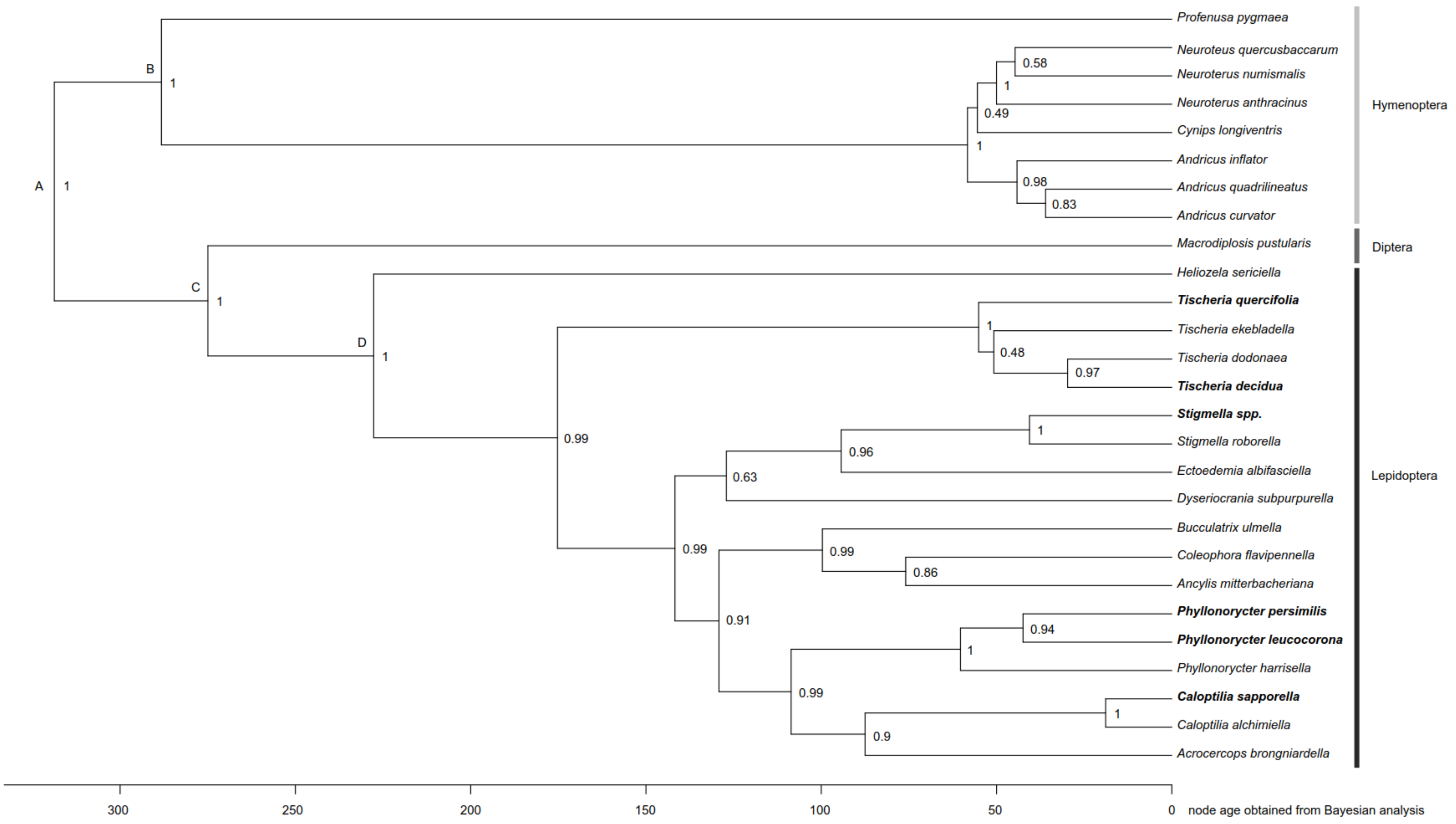

Figure S1. Phylogenetic tree of the insect herbivores in Finland and Japan, with Japanese species shown in bold. Node values indicate estimated posterior probabilities and the time line at the bottom of the tree indicates node ages from Bayesian analysis. Letters A-D indicate the nodes with divergence times provided as *a priori* information for the analysis (A = root, 325 Mya; B = Hymenoptera, 283 Mya; C = Diptera, 272 Mya; and D = Lepidoptera, 232 Mya). Details on the origin of the sequences, as well as species synonyms and representatives, are given in Table S1.

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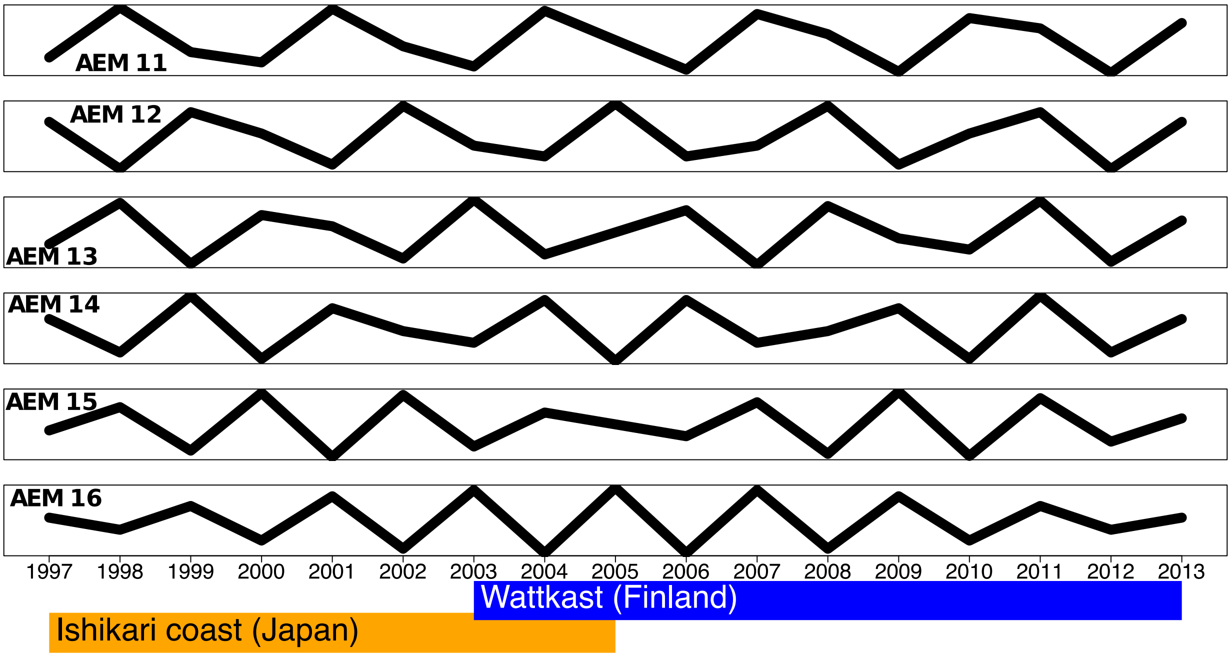

Figure S2. Illustration of the six negatively autocorrelated temporal eigenvectors (asymmetric eigenvector maps, AEMs) that were used to describe the seventeen years spanning the two independent data sets in Wattkast (Finland) and Ishikari coast (Japan). These AEMs were the ones with a negative and significant ($P < 0.05$) Moran's I. Note that the temporal eigenvectors lack a specified y-axis, since their scale is relative rather than absolute. The period of each AEM ranged from 3 years for AEM 11 to less than 2 years for AEM 16.

Appendix S2. The impact of guild and voltinism on the temporal dynamics while accounting for phylogeny.

Although there are statistical reasons why we decided to run a single model for each of the four factors that may explain the herbivore temporal dynamics (as detailed at the end of the section '*Testing for the effect of life-history, natural enemies and phylogenetic relatedness on temporal dynamics*' in the main paper), it is technically possible to carry out analyses of the impact of guild and voltinism while accounting for the effect of phylogeny. This test is relevant for the Finnish data set, where we found an imprint of phylogeny on the temporal dynamics of the herbivores. As shown in Figs S3 and S4, accounting for phylogeny did not change the estimated effect of either guild or voltinism. Note that because of the low number of samples (number of years) and the somewhat high number of parameters in models that combine the impact of guild and voltinism while accounting for the effect of phylogeny, the results presented in Figs S3 and S4 should only be considered qualitatively.

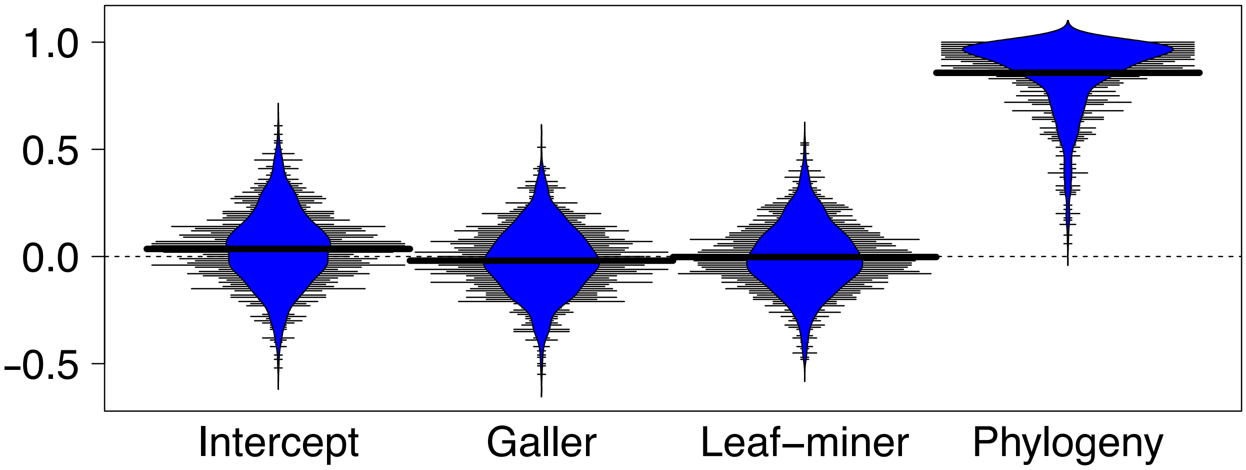

Figure S3. Violin plot describing the parameter distribution associated with the impact of feeding guild (γ in equation 2) and phylogenetic relatedness (ρ in equation 4) on the temporal dynamics of sessile insects on oak (*Quercus*) in Wattkast (Finland). The violin plots describe the smoothed distribution of the parameter of interest. The thick line describes the average of the parameter distribution and the thin segments describe the estimated model parameters rounded to the second decimal. The longer the thin segments the more frequently this parameter estimate emerged from the MCMC procedure that was used to estimate these parameters.

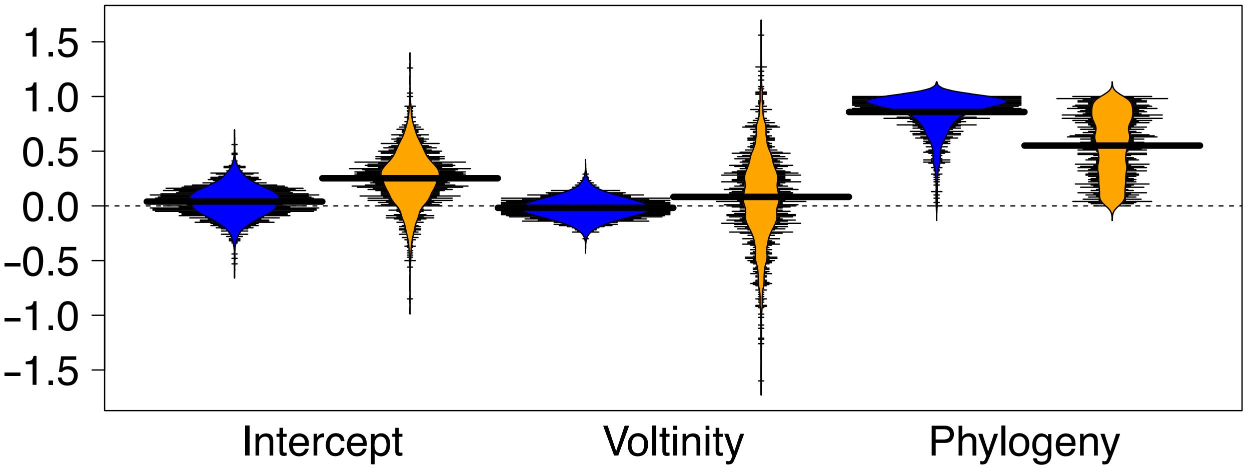

Figure S4. Violin plot describing the parameter distribution associated with the impact of voltinism (γ in equation 2) and phylogenetic relatedness (ρ in equation 4) on the temporal dynamics of sessile insects on oak (*Quercus*) in Wattkast (Finland, blue) and Ishikari (Japan, orange). The violin plots describe the smoothed distribution of the parameter of interest. The thick line describes the average of the parameter distribution and the thin segments describe the estimated model parameters rounded to the second decimal. The longer the thin segments the more frequently this parameter estimate emerged from the MCMC procedure that was used to estimate these parameters.