Supplementary material

Appendix 1 – Additional methods information

SDM details

We applied a three-fold cross-validation with a 20/80% data split and sampled pseudo-absences five times for each of the three model runs (= 15 models for each model algorithm). In each single model the presences and pseudo-absences were equally weighted (Barbet-Massin et al. 2012).

The GLMs included quadratic terms but no interactions. The GAMs were fitted without interaction and a smoothing factor of four. The GBMs used out-of-bag estimates of model improvement with the main parameters set as follows: n.trees = 3000, interaction depth = 4, shrinkage = 0.001, bag fraction = 0.5. The RFs were fitted with 500 classification trees, a minimum node size of five and a maximum number of 100 terminal nodes.

Relative importance was derived from a randomization procedure using Pearson correlation between the fitted values of the model and the fitted values of the model where one of the predictor variable was shuffled. The variable importance score is then calculated by subtracting the Pearson correlation coefficient from one. This procedure was repeated three times with each of the modelling methods and separately for all predictors.

Site selection for transplant experiment

For the transplant experiment, we selected a smaller area of ca. 16 x 16 km in the centre of the SDM area at the species’ northern range margin, with steep microclimatic gradients and various forest types. We narrowed down the potential sites by excluding forest patches younger than 30 years, sites which were potentially very wet (TWI > 18), sites with peaty and rocky soils, sites that were not owned by our project partner Sveaskog (main forest owner in the area) and sites where no thinning or clearcutting was planned. All site features were used at a 50 m resolution. From the remaining sites, we did a stratified random selection of 60 sites ensuring an orthogonal design that covered
gradients in microclimate, light and soil conditions. We used the following variables: forest age (Sveaskog forest inventory data), proportion of conifers (Sveaskog forest inventory data), maximum temperature (from national grid, Meineri & Hylander 2017) and canopy cover (modelled from canopy cover pictures, forest age, forest biomass and their interaction). All environmental raster grids were classified to low (< 10%), medium (10 - 90%) and high (> 90%), except forest age, which was classified only into low (30-70 years) and high (70 years). For logistic reasons we only selected sites with a minimum of 25 m and a maximum of 250 m distance to a paved or unpaved road. Sites were then randomly sampled from the available combinations of all four site variables. This procedure yielded high variation in habitat suitability according to the SDM, and we also added 6 sites with very high suitability (>70%), to be able to compare the results of the transplant experiment with the results of the distribution model for a wider range of values. Final establishment of sites in the field was made after on in-situ evaluation of suitability (e.g. no fresh clear-cut). Across the 60 sites selected for the transplant, experiment canopy cover ranged from 22 to 77 %, soil moisture from 11 to 60 %, Growing Degree Days from 139 to 221 and Freezing Degree Days from -100 to -25. Predicted habitat suitability across the transplant sites ranged from 6 to 86 % where 100 % is the most suitable. During the experiment, two sites were destroyed, leaving 58 sites for the analysis.

Transplantation details

Each adult was planted separately, whereas 2-3 juveniles or 15 seeds were planted together. Plantings were approximately 50 cm apart from each other, and the holes used for adults and juveniles were 25 cm deep and 5 - 8 dm³ in volume. Seeds were sown at the soil surface and covered with a thin layer of soil. Adult plants were protected from large herbivores with chicken wire cages.

The number of fruits per plant and the number of seeds in each fruit was counted for up to five fruits. If the plant had more than five fruits, the total number of seeds was estimated as the total number of fruits multiplied by the average number of seeds per fruit.
Calculation of Growing Degree Days and Freezing Degree Days

The Growing Degree Day index corresponds to the sum of daily mean temperatures (Tmean) above a given threshold (here 5°C) following

$$\text{GDD} = \sum_i T_{\text{mean},i} \quad \text{with} \quad T_{\text{mean},i} = 0.5 \times (T_{\text{min},i} + T_{\text{max},i})$$

and

$$T_{\text{mean},i} = 0 \quad \text{if} \quad T_{\text{mean},i} < 5^\circ C$$

The Freezing Degree Days index was calculated as the sum of daily minimum temperatures below 0°C following

$$\text{FDD} = \sum_i T_{\text{min},i} \quad \text{with} \quad T_{\text{min},i} = 0 \quad \text{if} \quad T_{\text{min},i} > 0^\circ C$$

Both GDD and FDD were estimated for the period 1st April – 31st May when most of the shoot growth takes place.

Parametrization of the IPM

We built an IPM for *L. vernus* based on standardized and log-transformed size as a state variable and the vital rate models identified by statistical models. We checked for obvious hump-shaped responses to environmental variables in bi-plots, but as we did not find any we included only linear terms in the vital rate models. The integral projection model included functions of survival, growth, reproduction and size distribution of the recruits. Growth was modelled as a normal distribution, with the mean given by the linear regression and the standard deviation given by the variance around the regression line. Size limits were set to $1.1 \times$ maximum observed size ($= 2.52$) and $0.9 \times$ minimum observed size ($= -1.74$). The probability of attaining a size outside the range was included in the probability of attaining the respective extreme size. Growth multiplied by survival formed the state transition kernel. The fecundity kernel (recruitment) consisted of the product of probability of flowering, number of seeds per flowering individual, recruitment rate and size distribution of recruits. The size distribution of recruits was assumed to be normal and with mean and variance estimated from all seedlings at all sites that had germinated in field in 2017. The discretized IPM kernel (IPM matrix) had the dimensions of $100 \times 100$. 
References


Fig. A 1. Distribution of soil variables for 58 sites. Vertical line indicates measured values for the standard garden soil used for half of the transplants at each site. P-values are from one-sample t-tests comparing the garden soil with the site soils (n=58, two-sided t-test). The garden soil was expected to provide the better growing conditions compared to the original site soil due to higher organic content, pH and nutrient richness.
Fig. A 2. Example of a transplant site.

Fig. A 3. Temperature sensor installation in field. Left: White tube hosts the logger at 1 m height, in the background and on the right picture: the logger at 5 cm height in a plastic cup.
Fig. A 4. Model evaluation for the species distribution model. Boxplots summarize scores over three model runs and five sets of pseudo-absences for each of the four model algorithms.
Fig. A.5. Predicted habitat suitability map produced by an ensemble species distribution model for *Lathyrus vernus*. Values range from 0% (not suitable) to 100% (suitable).
Fig. A 6. Effect of the environment on each single vital rate shown as standardized model coefficients of the models for survival, growth, number of seeds and probability of recruitment. Model coefficients for probability of flowering were not shown, since the optimal model included only size as a predictor. A vertical line at 0 (linear regressions) or 1 (binomial regressions) separates negative from positive effects.
Fig. A 7. Vital rates as functions of size (log-transformed and standardized size).
Fig. A 8. Relationship between light (canopy openness) with full foliage in summer (light.summer) and without foliage in spring (light.spring), Growing Degree Days in spring (GDD.spring) and in the growing season (GDD.growingseason) and Freezing Degree Days in spring (FDD.spring) for the 60 transplant sites. Numbers are spearman rank correlation coefficients. The variables “light.summer”, “GDD.spring” and “FDD.spring” were used in the demographic model.
Fig. A 9. Relationship between mapped variables used in the SDM and locally measured site variables: pH, proportion of conifers (%), Growing Degree Days (GDD), soil moisture and light. Mind that some variables have different units: In the SDM, GDD was calculated for the entire year, whereas on-site measured GDD is based on April and May only (core growing season); soil moisture for the SDM was expressed as the topographic wetness index, TWI, whereas on-site soil moisture was measured in volume percent. In the SDM, light is a function of solar radiation in spring and summer [MW h⁻¹ m⁻²], whereas on site it is measured in canopy openness [%].
Table A 1. Standardized model coefficients with standard error from the population vital rate models (only fixed effects shown). Significance codes: p < 0.001 ‘***’, p < 0.01 ‘**’, p < 0.05 ‘*’, p < 0.1 ‘’. GDD = growing degree days (base 5), FDD = freezing degree days (base 0), biomass_16_log = log-transformed size in 2016, (biomass_16_log)^2 = the quadratic term for size in 2016, biomass_17_log = size in 2017.

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<th>model</th>
<th>survival</th>
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<td>(Intercept)</td>
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<td>(biomass_16_log)^2</td>
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