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# Appendix B from L. T. Burghardt et al., "Modeling the Influenc of Genetic and Environmental Variation on the Expression of Plant Life Cycles across Landscapes"

(Am. Nat., vol. 185, no. 2, p. 212)

## Additional Figures

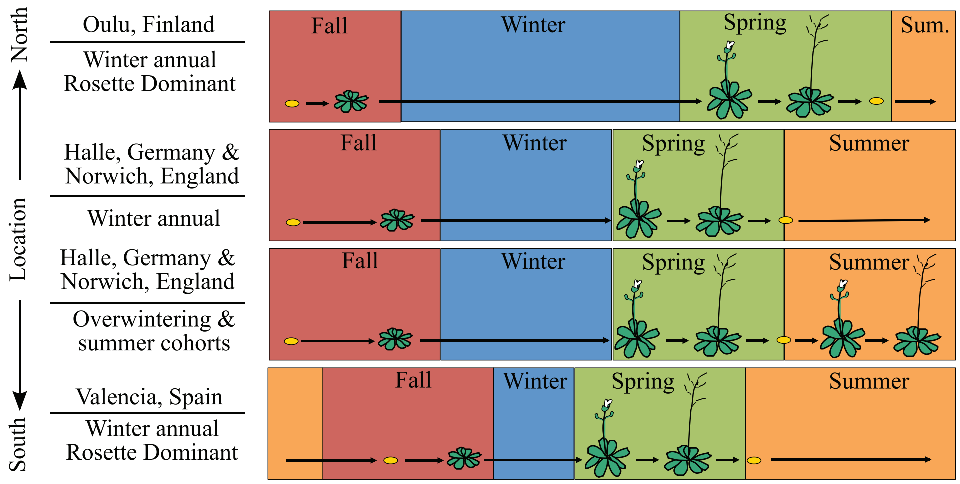


**Figure B1:** Illustrations of observed life cycles from four locations in Europe. Colored blocks indicate different seasons (red = fall, blue = winter, green = spring, and orange = summer), and the width of blocks indicates changes across latitude (i.e., summer is longer in Spain than Finland). Note that these life cycles are constructed based only on knowledge of aboveground life-stage expression, and they depict the dominant life cycle inferred for each location.

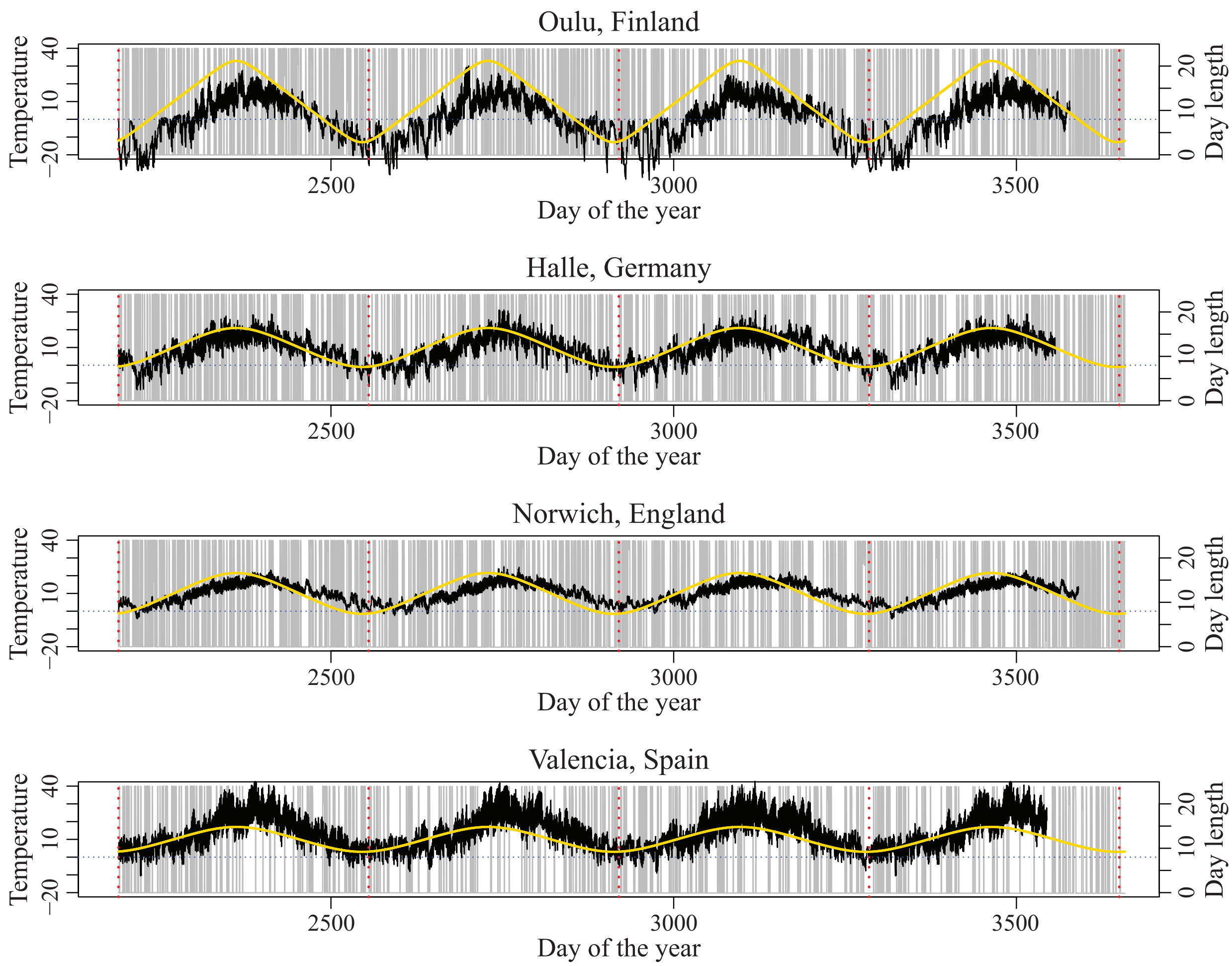


**Figure B2:** Example of 4 years of environmental inputs for each site. Yellow lines indicate day length, black lines indicate hourly temperatures, and gray lines show precipitation events.

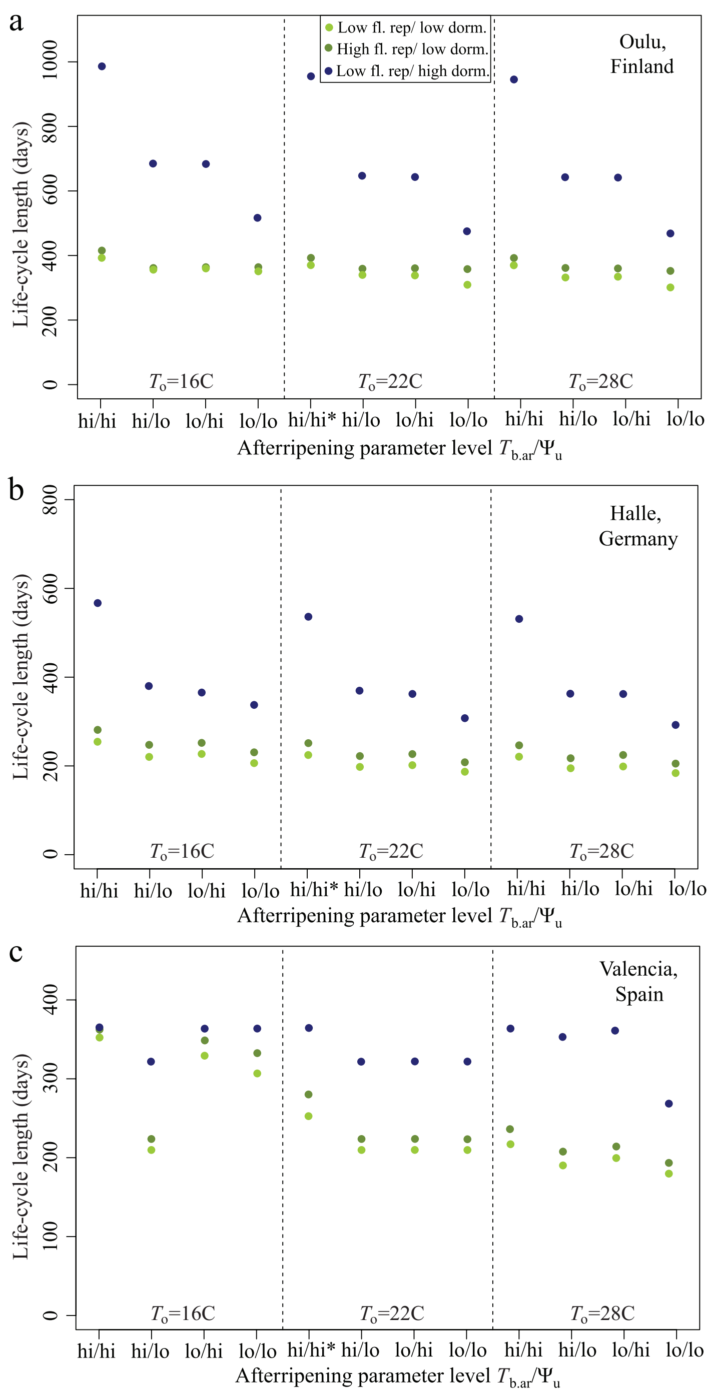


**Figure B3:** Effects of variation in germination parameters on life-cycle length in Oulu, Finland (*a*), Halle, Germany (*b*), and Valencia, Spain (*c*), for three dormancy/flora repression genotypes. Variable parameters were $T_o$ (temperature optimum for germination: 16°, 22°, and 28°C), $T_{b.ar}$ (base temperature for afterripening: high = 3, low = −3), and $\Psi_u$ (upper limit of moisture or maximal afterripening: high = −50, low = −200). Asterisks denote the default parameter combination used in all simulations presented in the main text. Lowering the afterripening parameters increased afterripening rate, which reduced the magnitude of the dormancy effect (visible when comparing the blue circles across high/low combinations). However, except in Valencia with $T_o$ = 16, flora repression had a much smaller effect on life-cycle length than did dormancy (difference between light green and dark green circles vs. difference between light green and blue circles).

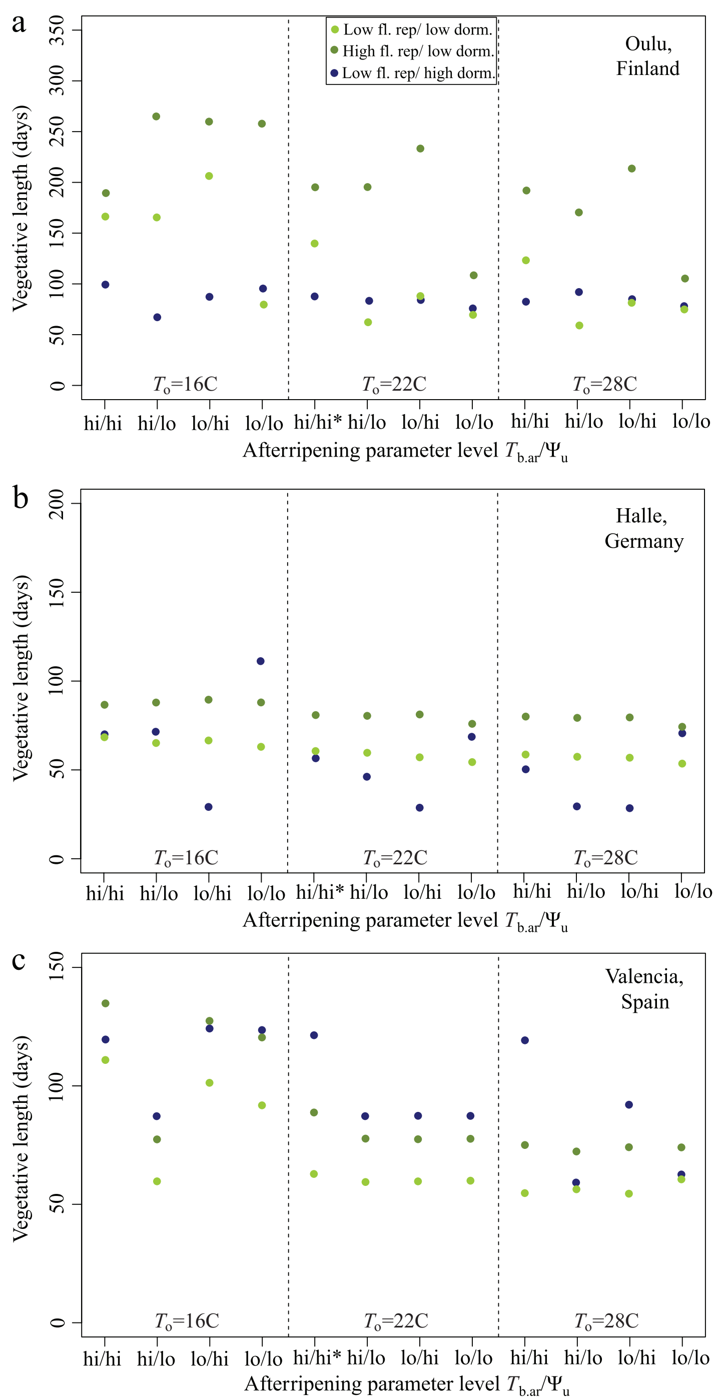


**Figure B4:** Effects of variation in germination parameters on the length of the vegetative stage in Oulu, Finland (*a*), Halle, Germany (*b*), and Valencia, Spain (*c*). Variable parameters were $T_o$ (temperature optimum for germination: 16°, 22°, and 28°C), $T_{b.ar}$ (base temperature for afterripening: high = 3, low = −3), and $\Psi_u$ (upper limit of moisture or maximal afterripening: high = −50, low = −200). Asterisks denote the default parameter combination used in all simulations in the article. Floral repression level consistently increased the vegetative-stage length in all parameter combinations (difference between light green and dark green circles). The magnitude of the difference did change across parameters, particularly in Oulu due to fluctuatin proportions of winter annuals. The effect of primary dormancy level on vegetative-stage length varied (difference between light green and blue circles). This is perhaps to be expected because many of the germination parameters varied also reduced dormancy levels.

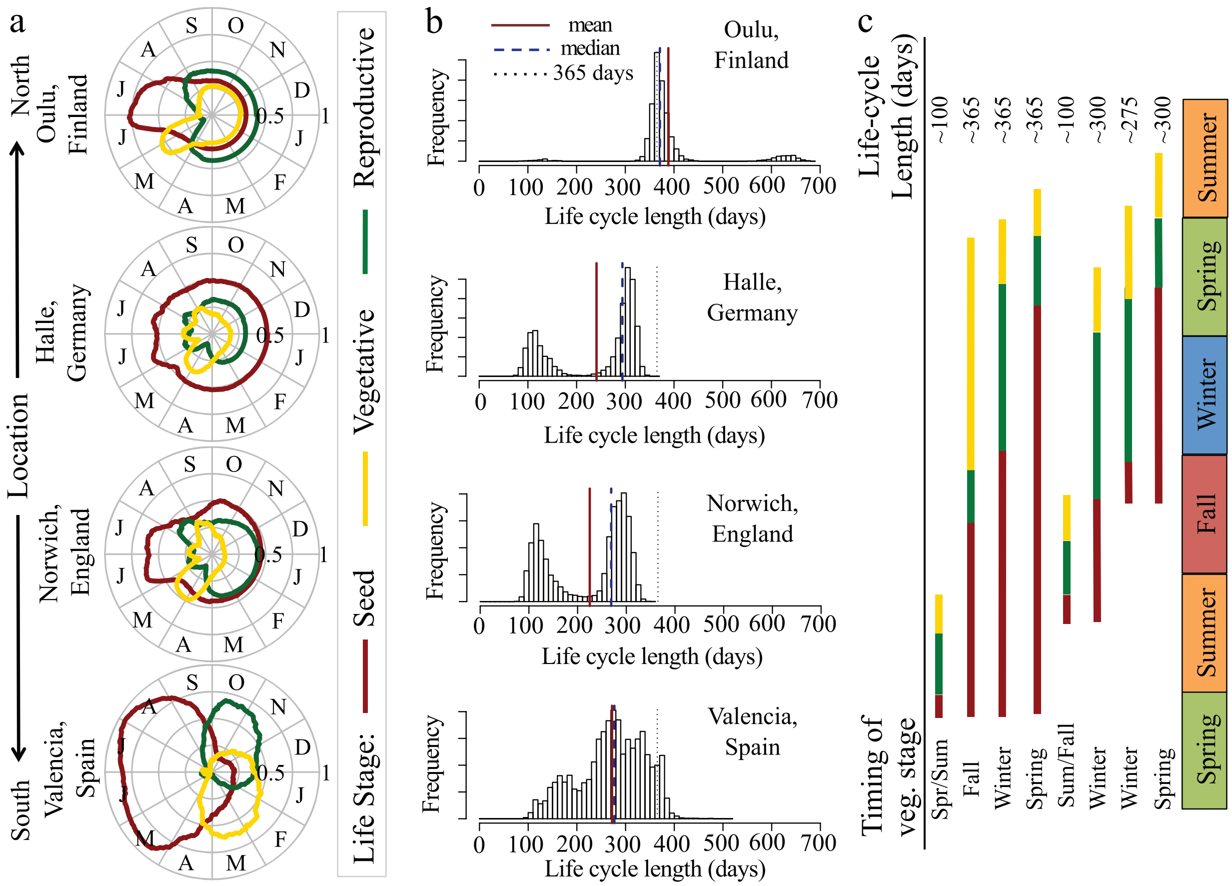


**Figure B5:** Color version of figur 3 in the main text.

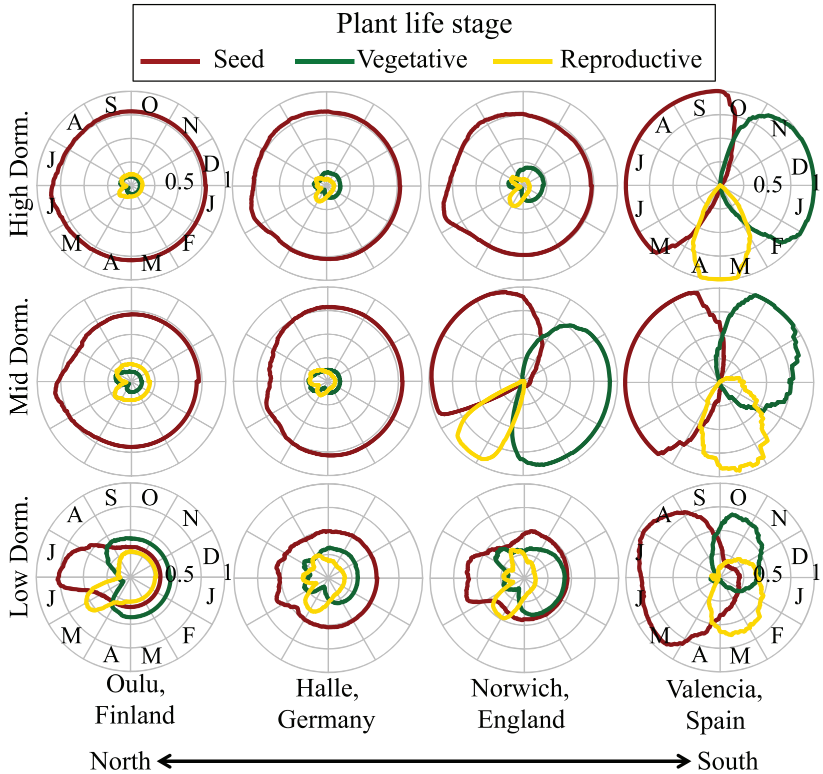


**Figure B6:** Effect on life-stage phenology of altering dormancy level in a low–flora repression background. Moving from right to left changes location, and moving from top to bottom varies dormancy level. For each graph, distance from the center of the circle indicates the proportion of individuals in a given life stage, January 1 occurs at 3 o'clock, and the year moves clockwise. All graphs are identically scaled so that the outermost diameter represents 100% of individuals. Model results were averaged over the last 45 years of a 60-year simulation.

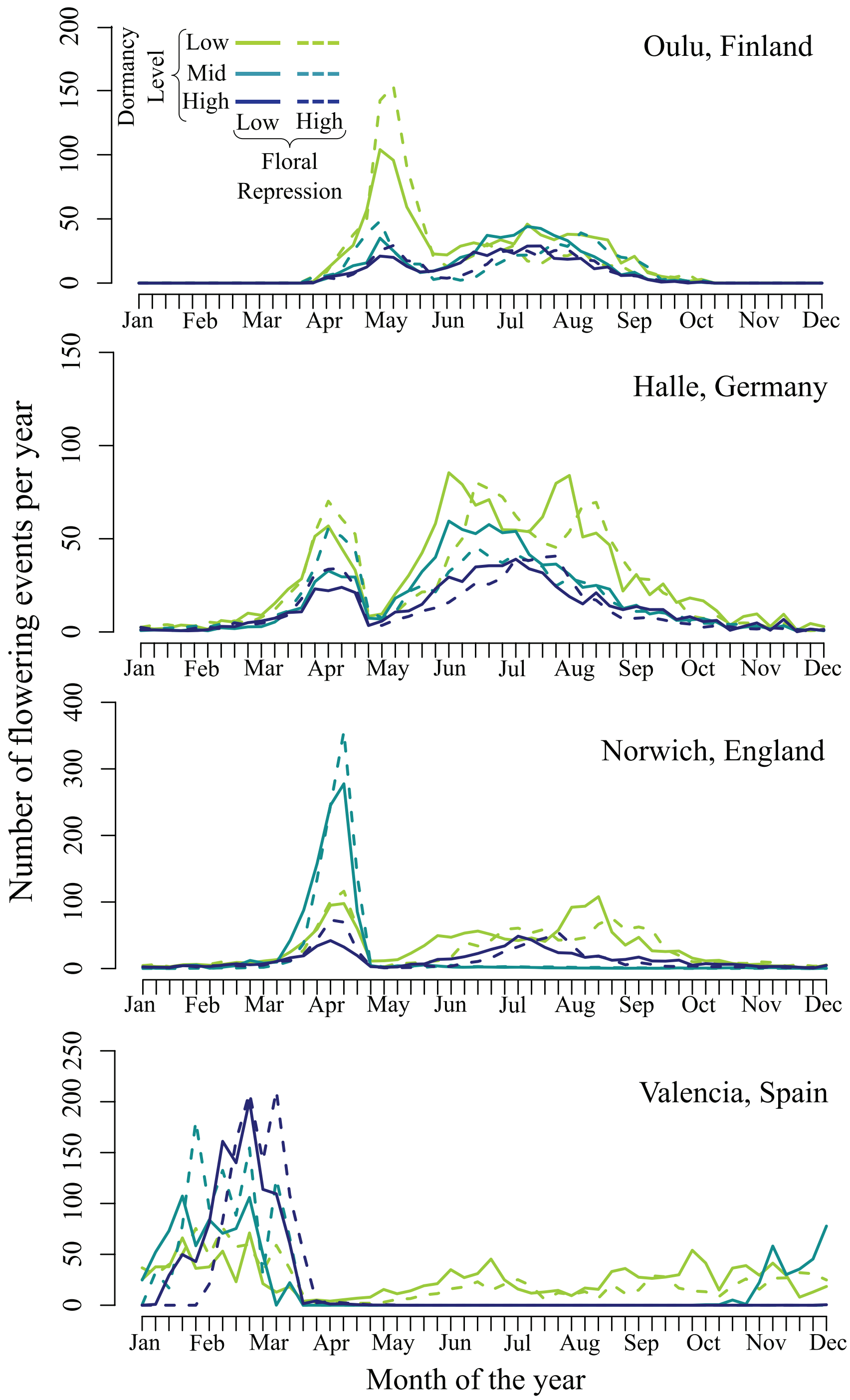


**Figure B7:** Predicted frequency distribution of flowerin times in a population for each genotype in each of the four locations studied. Model results were averaged over the last 45 years of a 60-year simulation.

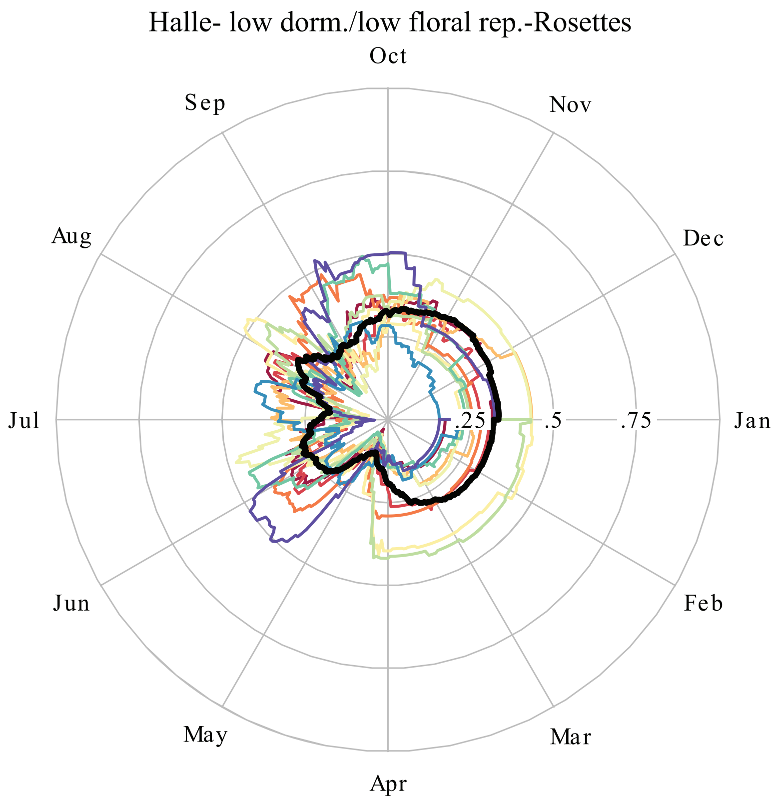


**Figure B8:** Proportion of individuals in the rosette stage over the year for a low-dormancy and low–flora repression genotype in Halle, Germany. Individual lines represent 10 distinct, consecutive years color coded in rainbow order (dark red = year 1). The black line indicates the average proportion over the course of the last 45 years of a 60-year simulation. A different environmental replicate is used from the circle graphs in figure 3 and 5 in the main text. Some years, the summer cohort happens in early summer; in other years, it happens in late summer. The timing of fall germination also varies yearly.

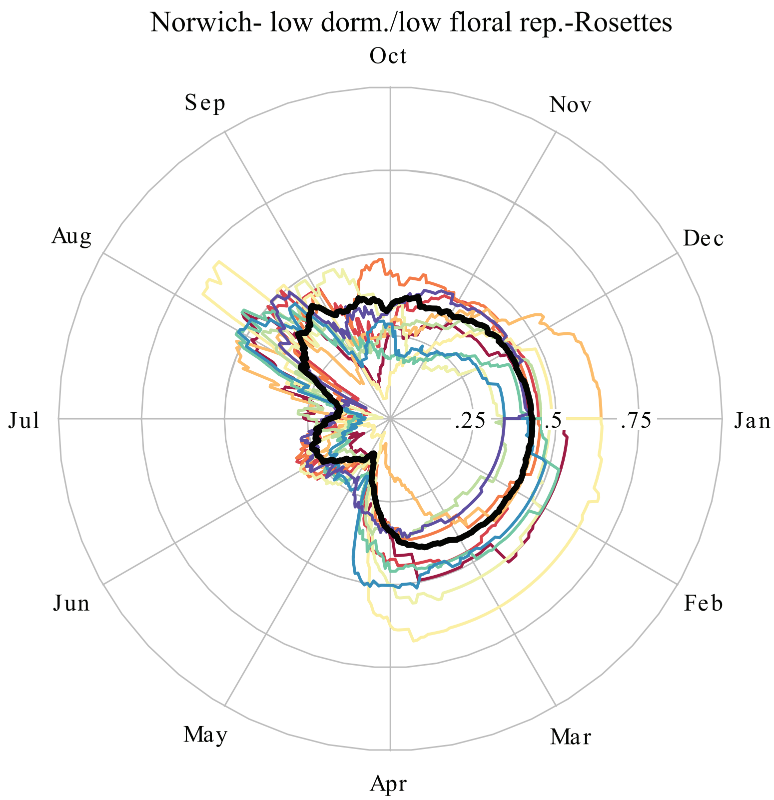


**Figure B9:** Proportion of individuals in the rosette stage over the year for a low-dormancy and low–flora repression genotype in Norwich, England. Individual lines represent 10 distinct, consecutive years color coded in rainbow order (dark red = year 1). The black line indicates the average proportion over the course of the last 45 years of a 60-year simulation. A different environmental replicate is used from the circle graphs in figure 3 and 5 in the main text. Late-summer cohorts are more frequent than early ones. The timing of fall germination also varies yearly.

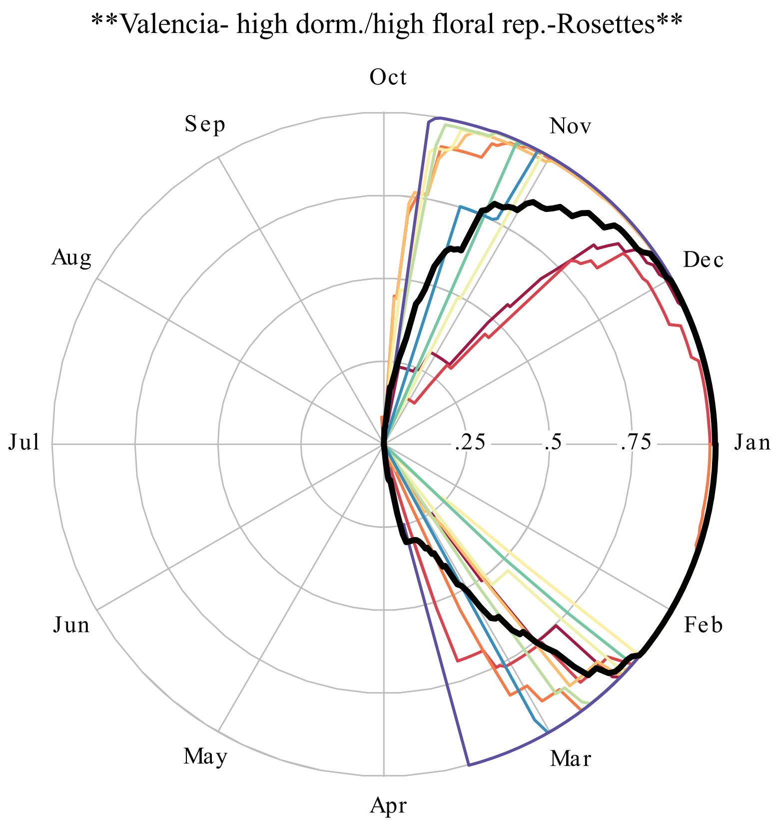


**Figure B10:** Proportion of individuals in the rosette stage over the year for a high-dormancy and high–flora  repression genotype predicted to occur in Valencia, Spain. Individual lines represent 10 distinct, consecutive years color coded in rainbow order (dark red = year 1). The black line indicates the average proportion over the course of the last 45 years of a 60-year simulation. A different environmental replicate is used from the circle graphs in figur s 3 and 5 in the main text.

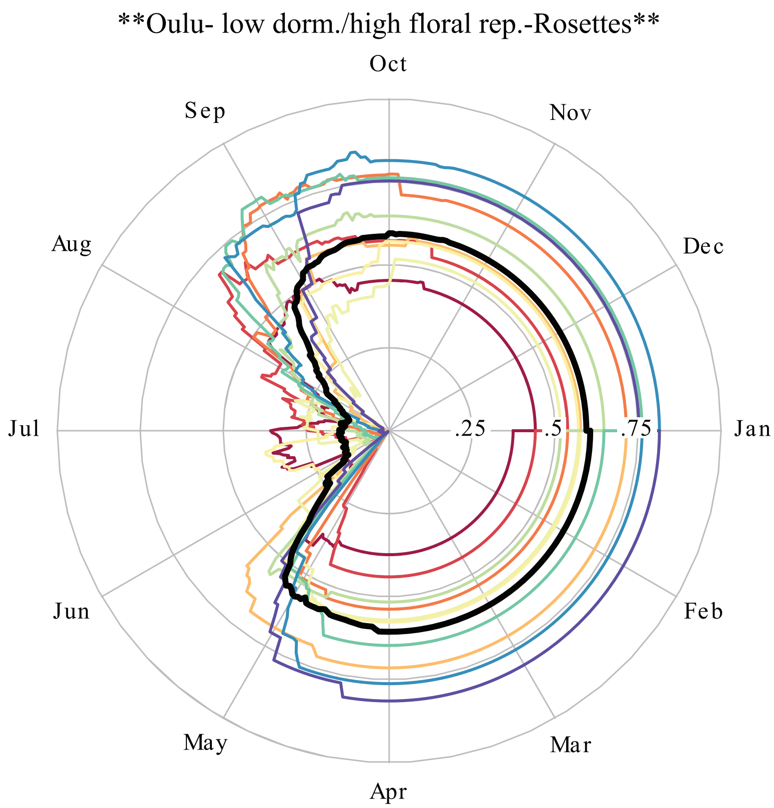


**Figure B11:** Proportion of individuals in the rosette stage over the year for a low-dormancy and high–flora repression genotype predicted to occur in Oulu, Finland. Individual lines represent 10 distinct, consecutive years color coded in rainbow order (dark red = year 1). The black line indicates the average proportion over the course of the last 45 years of a 60-year simulation. A different environmental replicate is used from the circle graphs in figur s 3 and 5 in the main text.

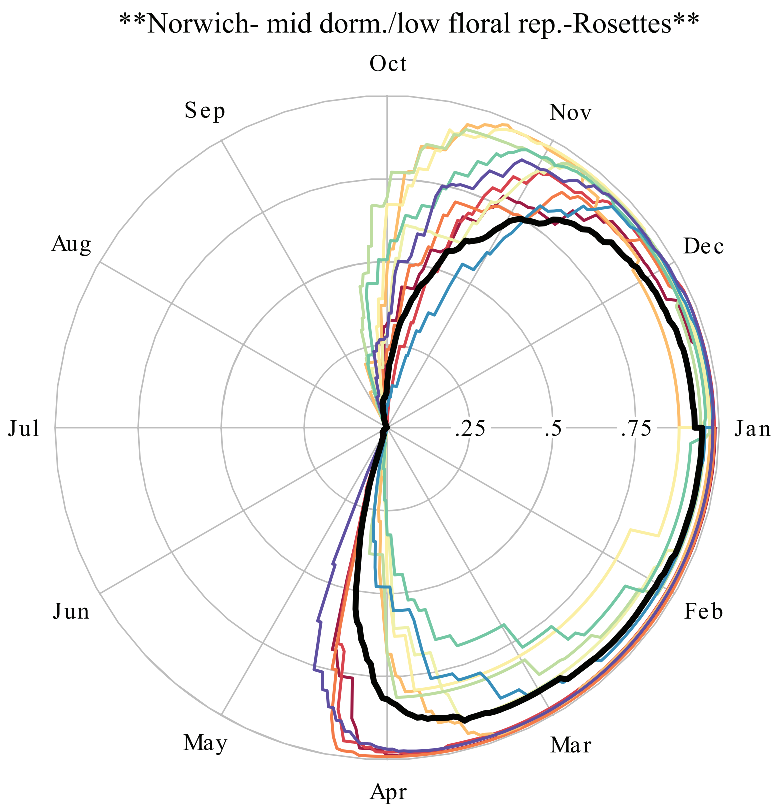


**Figure B12:** Proportion of individuals in the rosette stage over the year for a mid-dormancy and low–flora repression genotype predicted to occur in Norwich, England. Individual lines represent 10 distinct, consecutive years color coded in rainbow order (dark red = year 1). The black line indicates the average proportion over the course of the last 45 years of a 60-year simulation. A different environmental replicate is used from the circle graphs in figur s 3 and 5 in the main text.

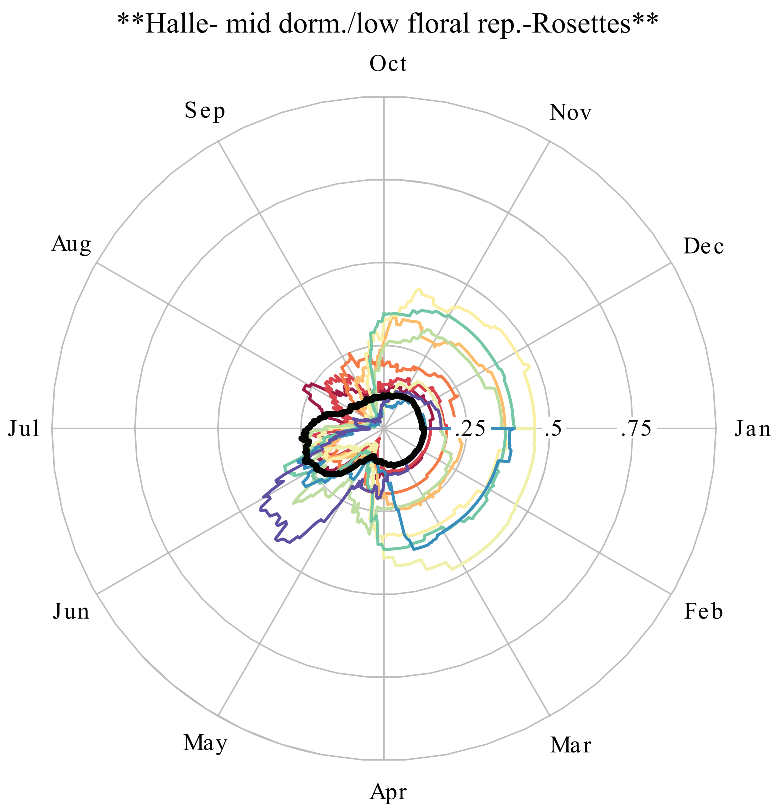


**Figure B13:** Proportion of individuals in the rosette stage over the year for a mid-dormancy and low–flora repression genotype predicted to occur in Halle, Germany. Individual lines represent 10 distinct, consecutive years color coded in rainbow order (dark red = year 1). The black line indicates the average proportion over the course of the last 45 years of a 60-year simulation. A different environmental replicate is used from the circle graphs in figure 3 and 5 in the main text. The graph demonstrates life-cycle expression drifting across years due to dormancy/environment mismatch.

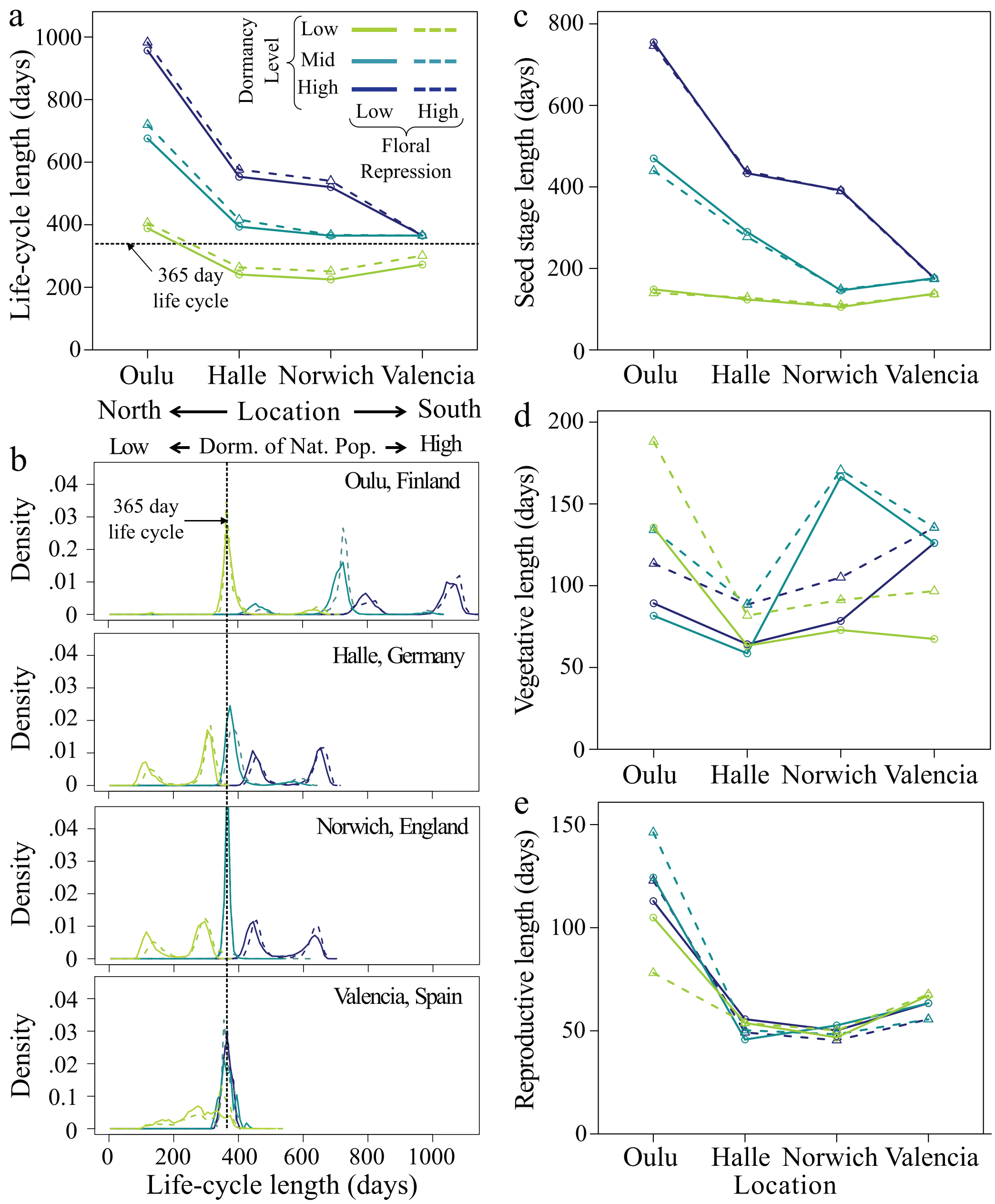


**Figure B14:** Color version of figur 4 in the main text.

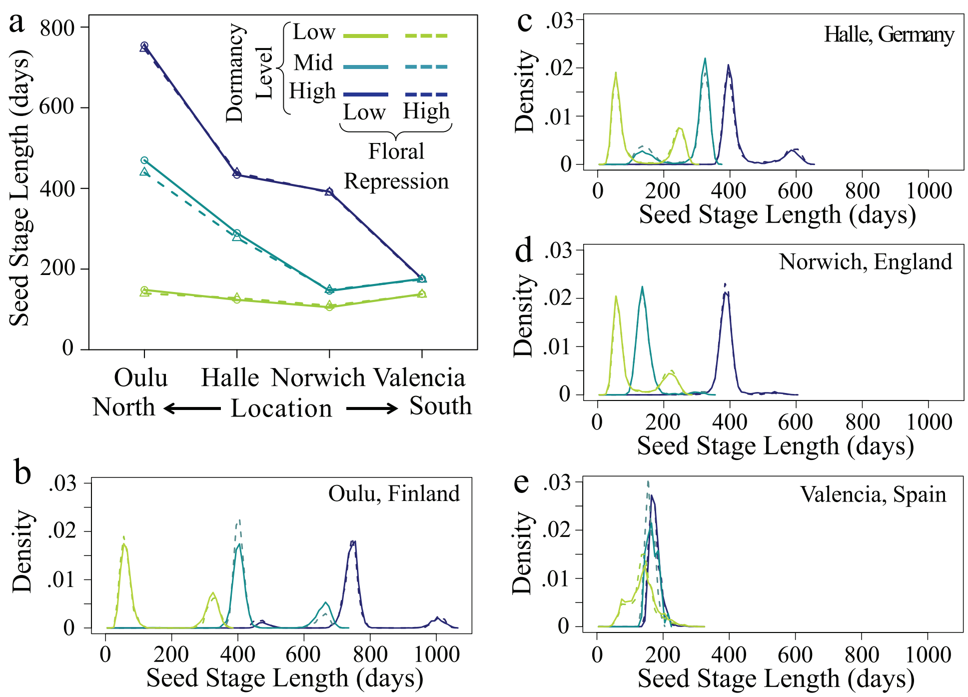


**Figure B15:** *a*, Reaction norm of different genotypes in response to the four sites for the average time spent as a seed. *b–e*, Density distribution of the duration of the seed stage interval for each genotype in each location. Model results were averaged over the last 45 years of a 60-year simulation.

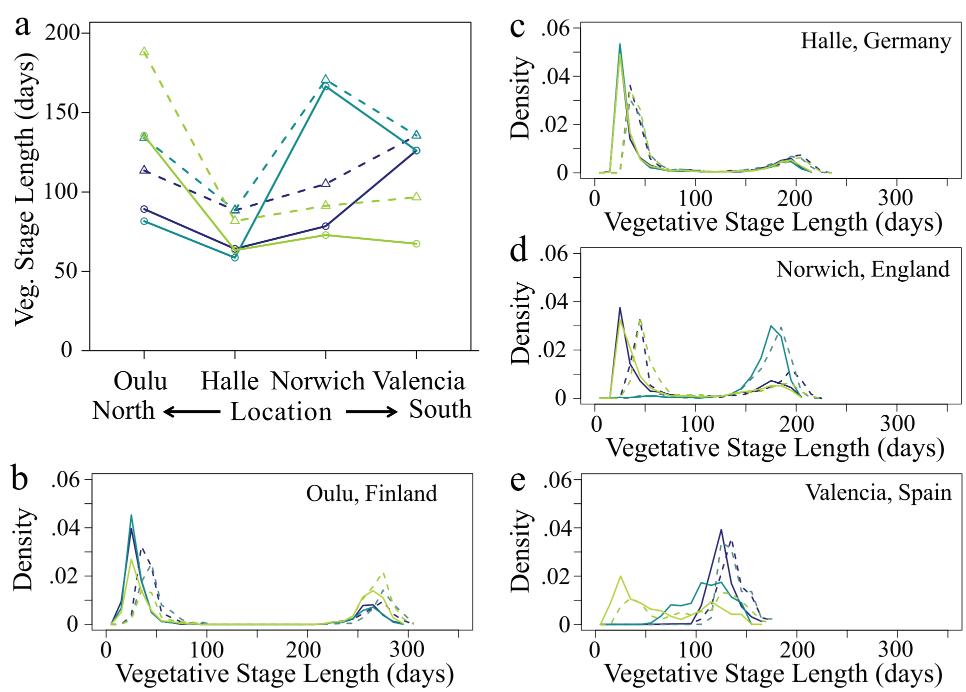


**Figure B16:** *a*, Reaction norm of different genotypes in response to the four sites for the average time spent as a vegetative rosette. *b–e*, Density distribution of the duration of the seed stage interval for each genotype in each location. Model results were averaged over the last 45 years of a 60-year simulation. Color coding is the same as in figur B15.

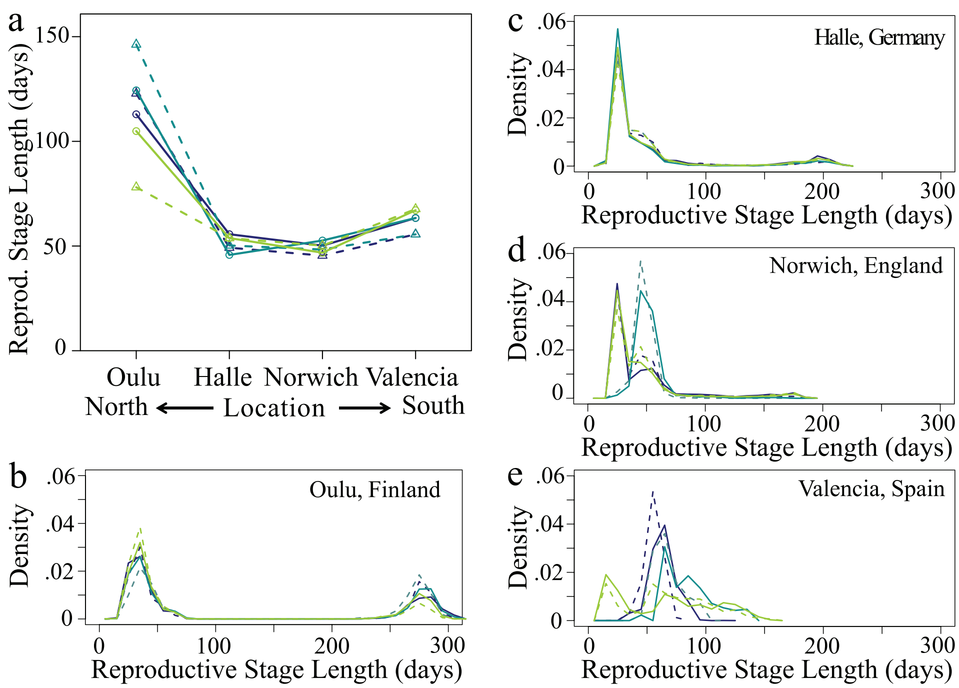


**Figure B17:** *a*, Reaction norm of different genotypes in response to the four sites for the average time spent as a reproductive plant. *b*–*e*, Density distribution of the duration of the seed stage interval for each genotype in each location. Model results were averaged over the last 45 years of a 60-year simulation. Color coding is the same as in figur B15.

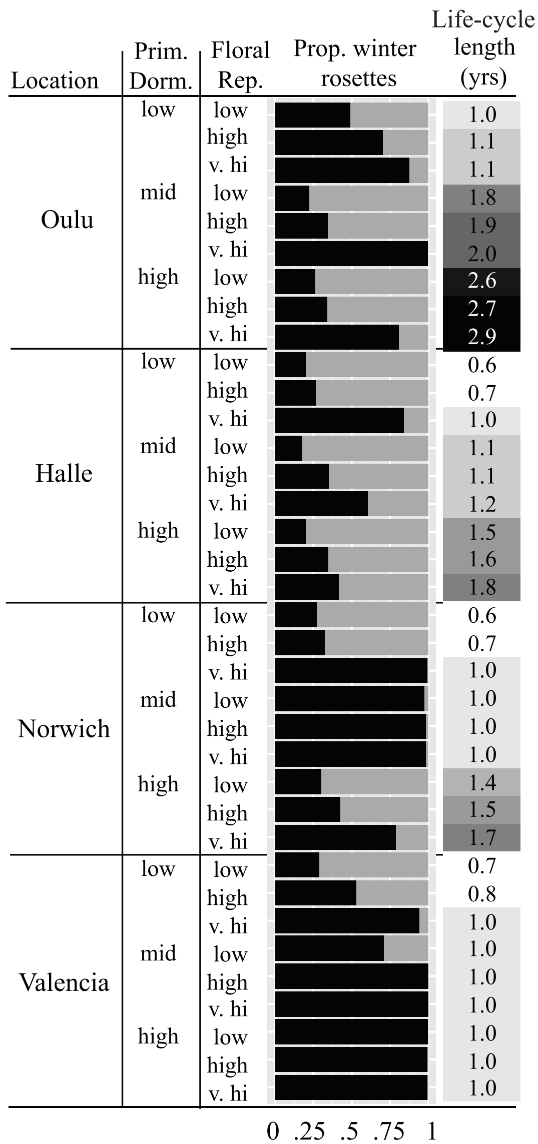


**Figure B18:** Summary of life-cycle phenology (proportion of life cycles with winter rosettes) and life-cycle length (in years) for each combination of parameters in each of the four locations in the study. Floral repression ($F_i$): low = 0.598, high = 0.737, and very high = 0.88. Primary dormancy ($\Psi_{mean}$): low = 0, mid = 1.25, and very high = 2.5. Model results were averaged over the last 45 years of a 60-year simulation.

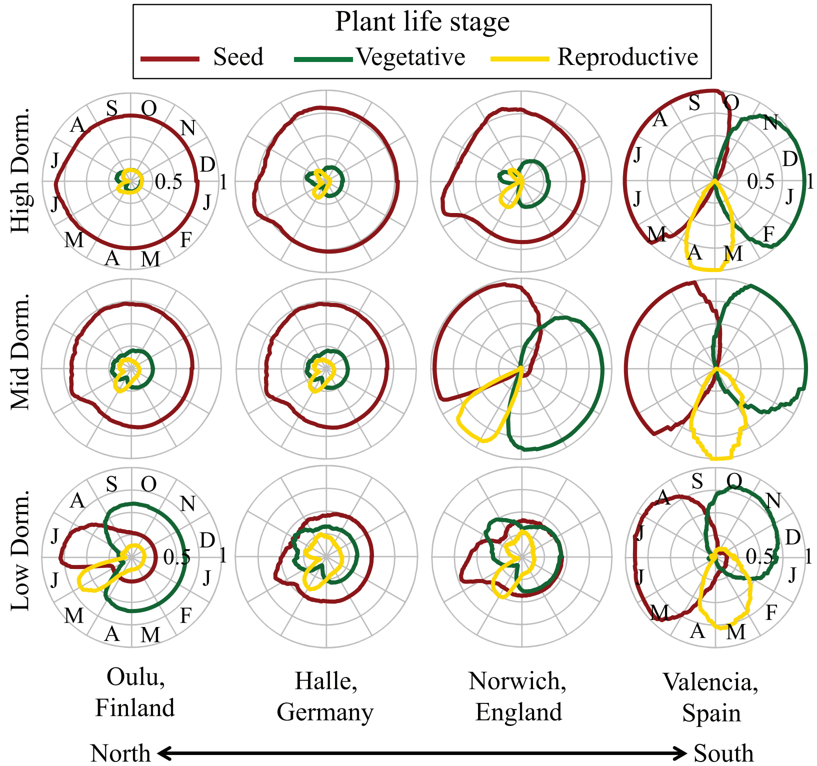


**Figure B19:** Color version of figur 5 in the main text.