A Quantitative Genetic Signature of Senescence in a Short-Lived Perennial plant





Age-Dependent Increase in Additive Genetic Variance of Mean Calyx Diameter and Number of Flowers Raw estimates of additive genetic variance (VA) were calculated for each age class, as generally done in character state approaches: these are represented by the dotted line for (A) the average calyx diameter of flowers produced per day and (B) the average number of flowers produced per day, with its 95% credible interval represented by the grey area (based on the density of parameter posterior distributions). The inset in each panel depicts the same data observed over the earlier ages of growth

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The evolution of senescence (the physiological decline of organisms with age) poses an apparent paradox because it represents a failure of natural selection to increase the survival and reproductive performance of organisms. The paradox can be resolved if natural selection becomes less effective with age, because the death of post-reproductive individuals should have diminished effects on Darwinian fitness. A substantial body of empirical work is consistent with this prediction for animals, which transmit their genes to progeny via an immortal germline. However, such evidence is still lacking in plants, which lack a germline and whose reproduction is diffuse and modular across the soma. Here, we provide experimental evidence for a genetic of senescence in basis the short-lived perennial plant Silene latifolia. Our pedigree-based analysis revealed a marked increase with age in the additive genetic variance of traits closely associated with fitness. This result thus extends to plants the quantitative genetic support for the evolutionary theory of senescence.