**Table 1**: Heritable genetic variation among families and populations

*Model: Trait ~ (1 | Population/Family) + Block*

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **Genetic variation within/among ALL** **populations** | | | | | |
| Population level | | | Family level | | |
| χ² | *p* | PVE | χ² | *p* | PVE |
| ***Growth traits*** | | | | | | |
| Height, before flowering |  |  |  |  |  |  |
| Height, after flowering |  |  |  |  |  |  |
| LDMC |  |  |  |  |  |  |
| Mortality\* |  |  |  |  |  |  |
| Ramets, before flowering\* |  |  |  |  |  |  |
| Ramets, after flowering\* |  |  |  |  |  |  |
| Relative growth rate |  |  |  |  |  |  |
| SLA |  |  |  |  |  |  |
| ***Herbivore community*** | | | | | | |
| *Danaus plexippus* abundance\* |  |  |  |  |  |  |
| *Labidomera clivicollis* abundance\* |  |  |  |  |  |  |
| *Liriomyza asclepiadis* abundance\* |  |  |  |  |  |  |
| ***Defense traits*** | | | | | | |
| Herbivory, before flowering: Binary\* |  |  |  |  |  |  |
| Herbivory, before flowering: Quantitative |  |  |  |  |  |  |
| Herbivory, after flowering: Binary\* |  |  |  |  |  |  |
| Herbivory, after flowering: Quantitative |  |  |  |  |  |  |
| Latex exudation |  |  |  |  |  |  |
| Weevil damage: Binary\* |  |  |  |  |  |  |
| Weevil damage: Quantitative |  |  |  |  |  |  |
| ***Reproductive traits*** | | | | | | |
| Date of first flower\* |  |  |  |  |  |  |
| Date of first follicle\* |  |  |  |  |  |  |
| Flower size |  |  |  |  |  |  |
| Flowering duration\* |  |  |  |  |  |  |
| Flowering success\* |  |  |  |  |  |  |
| Follicles\* |  |  |  |  |  |  |
| Inflorescences\* |  |  |  |  |  |  |
| Mean flowers per inflorescence\* |  |  |  |  |  |  |

*PVE = percent variance explained*

\*Variables were analyzed with generalized linear mixed models. PVE was calculated as: random effect variance/(random effect variance + residual variance) with the *get\_variance()* function from the *insight* R package. Remaining variables were analyzed with general linear mixed models and PVE was calculated as: random effect variance/(random effect variance + residual variance) with the *VarCorr()* function from the *lme4* R package.