

| C x C | 0.95 ± 0.02 | | | | | | | | |
|--------------------------|-------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|
| N _{cross} = 43 | | | | | | | | | |
| N _{total} = 115 | | | | | | | | | |
| C x M | 0.79 | | | | | | | | |
| N _{cross} = 10 | -0.68 | | | | | | | | |
| N _{total} = 22 | 1.0 | 0.96±0.02 | | | | | | | |
| M x C | 3.95 | 0.2 | | | | | | | |
| N _{cross} = 12 | 1.77 | -1.90 | | | | | | | |
| N _{total} = 25 | 0.70 | 0.62 | 0.84±0.09 | | | | | | |
| M x M | 1.71 | 2.16 | 0.43 | | | | | | |
| N _{cross} = 4 | 0.64 | 0.98 | -2.46 | | | | | | |
| N _{total} = 7 | 1.0 | 0.99 | 0.25 | 0.92±0.05 | | | | | |
| M x T | 1.86e03 | 2.35e03 | 471.87 | 1.09e03 | | | | | |
| N _{cross} = 8 | 9.02 | 8.89 | 19.86 | 17.41 | 0.01±0.01 | | | | |
| N _{total} = 14 | <0.0001 | <0.0001 | <0.0001 | <0.0001 | | | | | |
| T x M | 6.67 | 8.40 | 1.69 | 3.90 | 279.47 | 0.76 ±0.10 | | | |
| N _{cross} = 7 | 2.74 | 3.48 | 0.58 | 1.61 | 6.08 | | | | |
| N _{total} = 14 | 0.13 | 0.015 | 1.0 | 0.80 | <0.0001 | | | | |
| T x T | 2.04 | 2.57 | 0.52 | 1.19 | 1.1e-03 | 0.31 | | | |
| N _{cross} = 14 | 1.08 | 1.33 | -0.75 | 0.19 | -7.97 | -3.27 | 0.91±0.04 | | |
| N _{total} = 36 | 0.98 | 0.92 | 1.0 | 1.0 | <0.0001 | 0.03 | | | |
| T x C | 2.15 | 0.37 | 0.55 | 0.79 | 865.37 | 3.10 | 0.95 | | |
| N _{cross} = 25 | 1.31 | -1.44 | -0.72 | -0.25 | 7.58 | 3.37 | -0.21 | 0.91±0.04 | |
| N _{total} = 75 | 0.94 | 0.88 | 1.0 | 1.0 | <0.0001 | 0.022 | 1.0 | | |
| C x T | 85.65 | 107.91 | 21.68 | 50.03 | 21.76 | 12.84 | 0.02 | 39.77 | 0.20±0.07 |
| N _{cross} = 24 | 16.99 | 12.82 | 3.76 | 4.57 | 3.88 | 3.62 | -6.15 | 5.58 | |
| N _{total} = 60 | <0.0001 | <0.0001 | 0.005 | 0.0002 | 0.003 | 0.009 | <0.0001 | <0.0001 | |
| | C x C | C x M | M x C | M x M | M x T | T x M | T x T | T x C | C x T |

Table S11. Pairwise differences in seed viability (morphological seed assessment per fruit) assessed using a post-hoc Tukey method. Cross types involved *M. caespitosa* (C), *M. minor* (M), and *M. tilingii* (T), with the maternal parent in each cross listed first. N_{cross} = number of unique maternal family combinations per cross type, and N_{total} = total number of fruits scored per cross type. Values on diagonal are lsmeans +/- standard error. In each box below the diagonal, the uppermost value is the model estimate, the middle value is the z-ratio, and the bottom value is the P-value. Upper right corner: GLMM type III ANOVA of intra- and interspecific morphological seed viability with Wald χ^2 values for “Maternal Species” and “Paternal Species” (fixed effects) and “Maternal*Paternal” species interaction effect. Shades of light gray denotes a P < 0.05, medium gray denotes a P < 0.01, and dark gray denotes a P < 0.001.