

Figure S1: Additional population genomic analyses. Related to Figure 1.

PCAs including (A,B) and excluding tetraploids (D-F) for all PCs that explained a significant proportion of variation. Species relationships do not qualitatively differ from Figure 1. (C) Neighbor-Joining DensiTree for members of the *M. guttatus* species complex using *M. dentilobus* as the outgroup. Each neighbor-joining tree is calculated from a 500 SNP window, with a step size of 100SNPs, then all trees are layered over the backbone of the whole-genome neighbor-joining tree, depicted in Figure 1. Color coded names are the same as Figure 1. Species corresponding to colored points are denoted in legend.

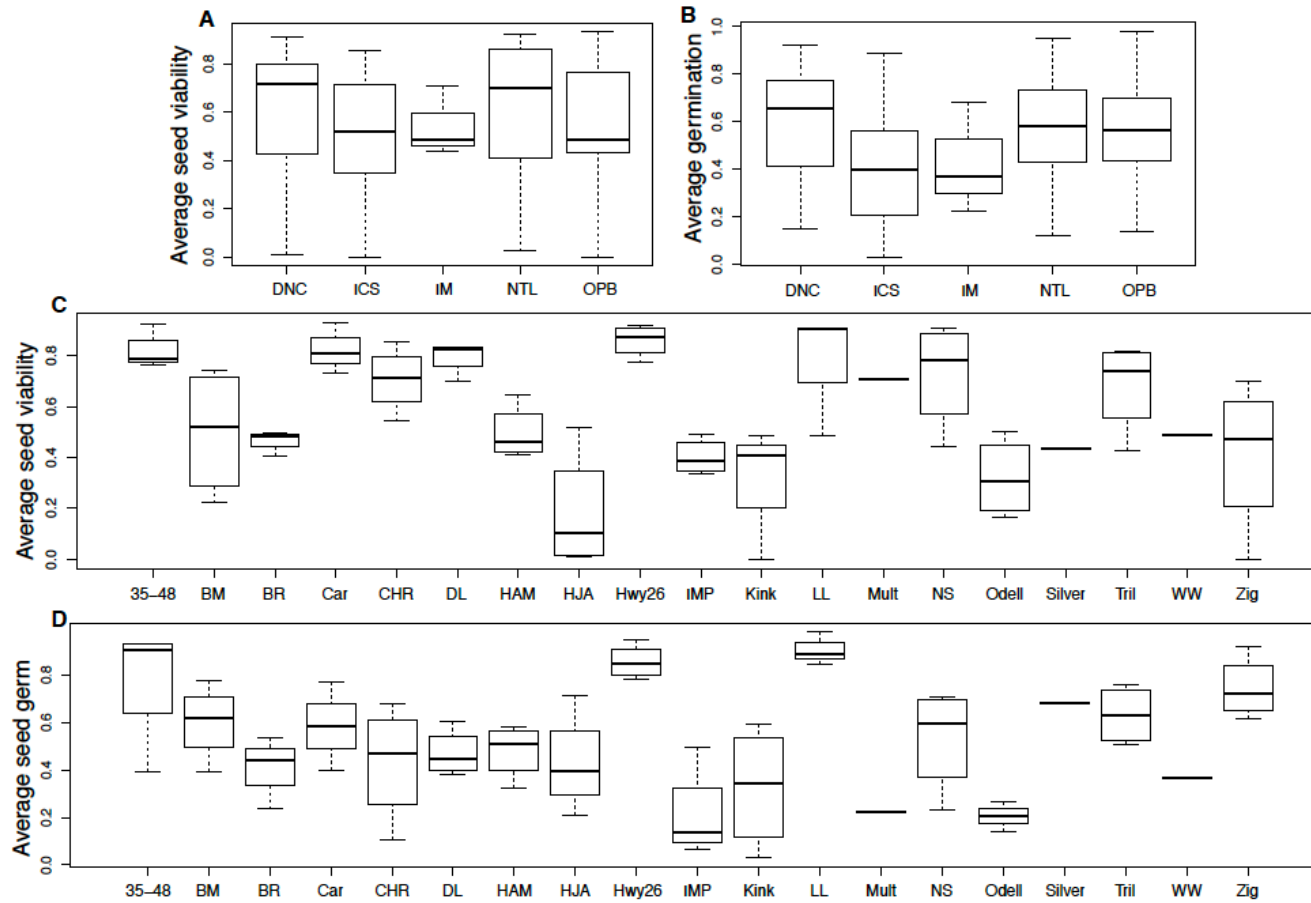


Figure S2: Population averages for hybrid seed viability averaged across 5 populations of *M. guttatus* (A,B) and 19 *M. decorus* populations (C,D). Related to Figure 2.

Viability is measured by morphology (A,C) and germination rate (B,D).

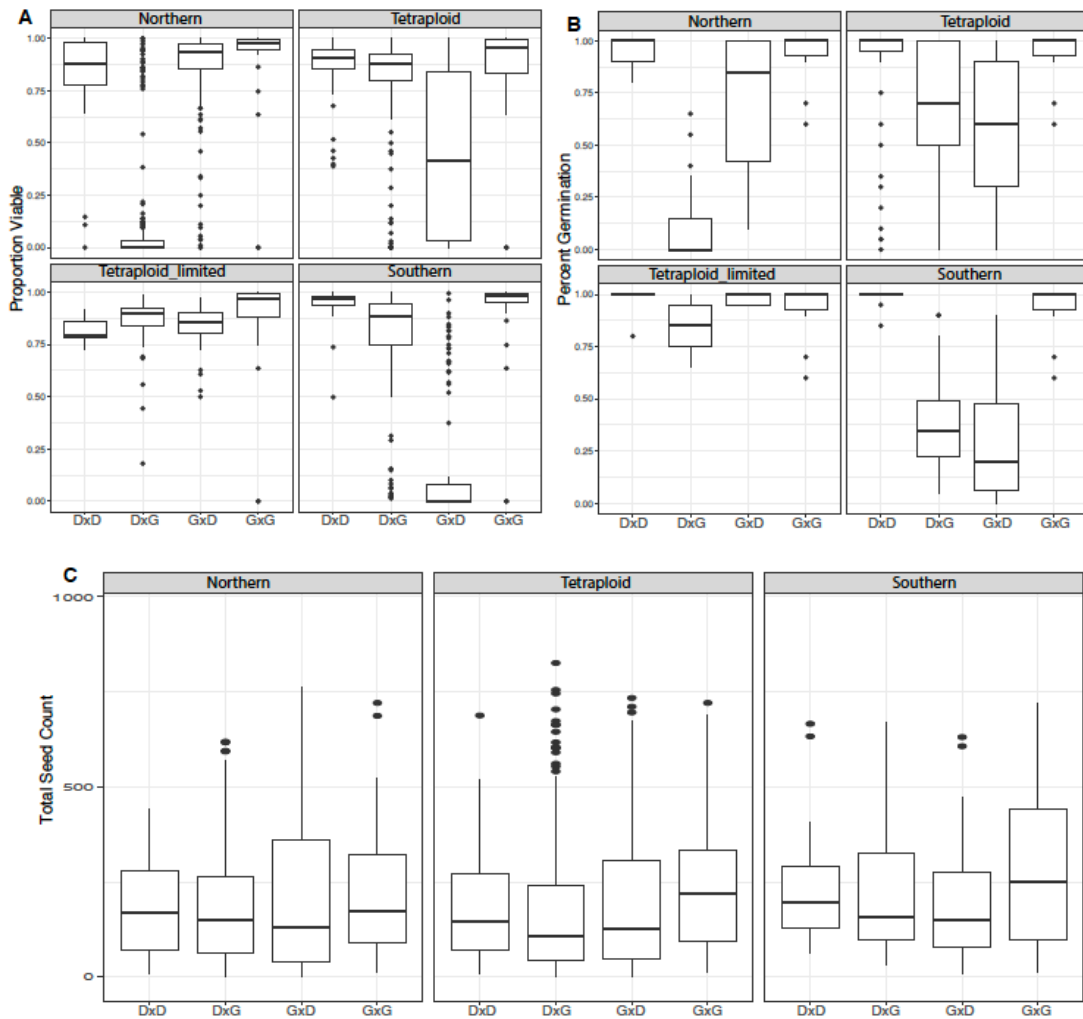


Figure S3: Hybrid seed inviability and total seed count between *M. decorus* and *M. guttatus* averaged by genetic clade of *M. decorus*. Related to Figure 2.

(A) morphologically determined inviable seeds and (B) germination proclivity (C) total seed count. Maternal parent in the cross is listed first. Panels refer to each genetic clade of *M. decorus*.

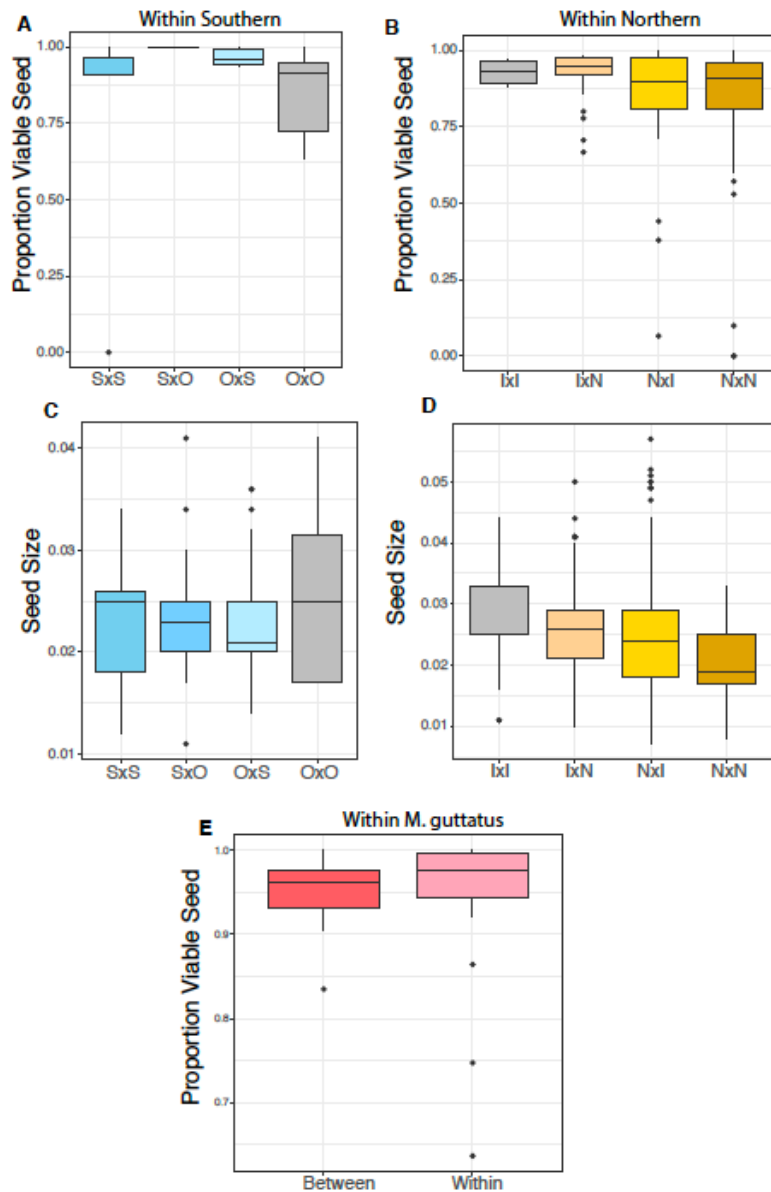


Figure S4: Within clade control crosses. Related to Figure 4.

Average proportion of viable seeds (A,B) and seed sizes (C,D) for crosses within southern (A,C) and northern (B,D) clades of *M. decorus*. And (E) the average proportion viable seeds for crosses within and between populations of *M. guttatus*. S= southern populations, O= focal population *Odell Creek*, N= northern populations, I= focal population *IMP*.

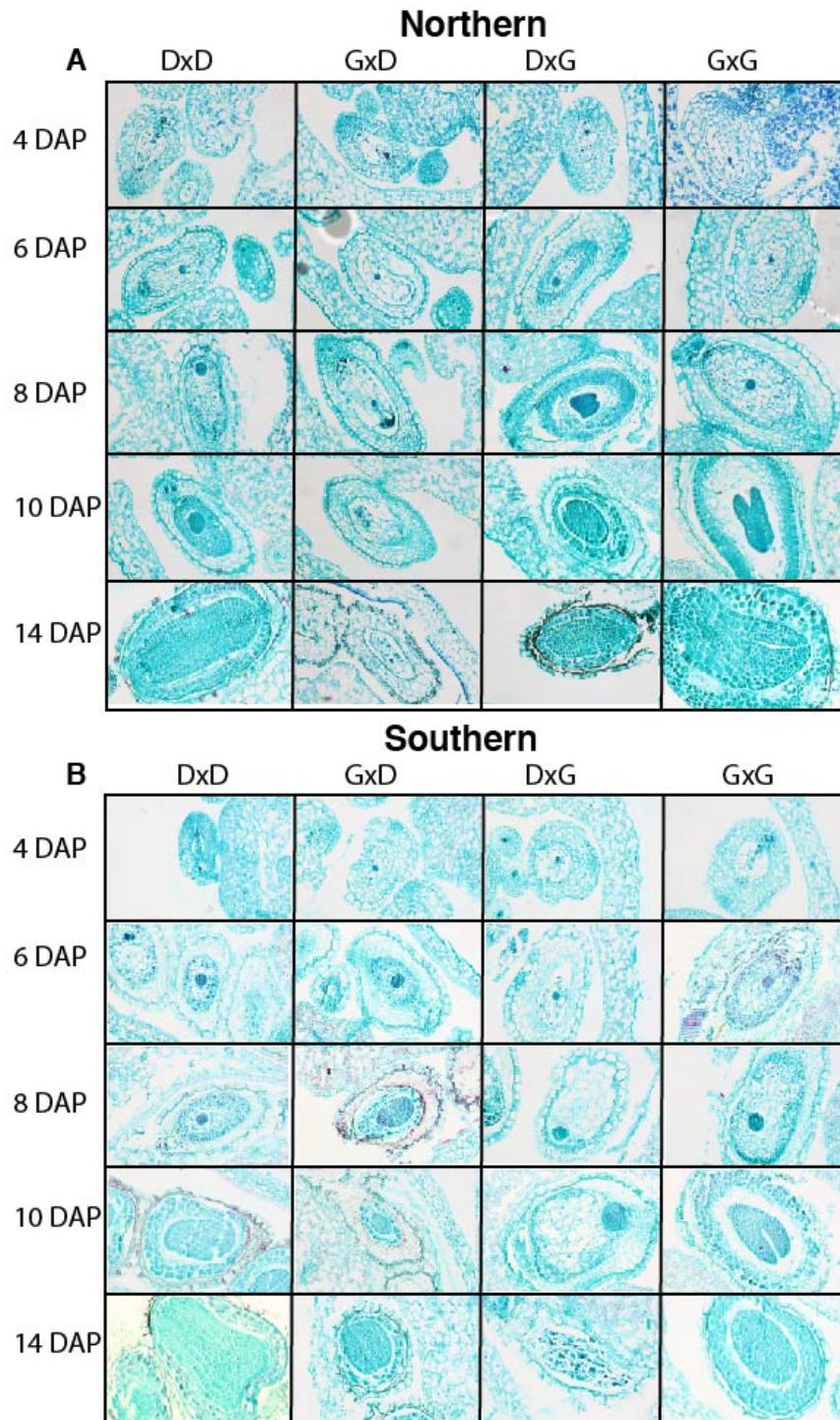


Figure S5: Reciprocal hybrids between *M. guttatus* and *M. decorus* show significant parent-of-origin effects on endosperm growth. Related to Figure 3.

Developing seeds between *M. guttatus* and (A) Northern *M. decorus* and (B) Southern *M. decorus* at 4, 6, 8, 10, and 14 Days After Pollination (DAP). For all crosses maternal parent is listed first.

| Sample | Species | Lat | Long | LH | MD | %MID | SRA |
|------------|---------------------------------|-----------|---------|----|--------|--------|------------|
| A25 | <i>M. tilingii</i> | -118.5767 | 42.6364 | P | 3.97 | 0.398 | SRX6914883 |
| AHQT | <i>M. guttatus</i> | -110.813 | 44.431 | A | 18.7 | 0.158 | SRX142379 |
| ALK4 | <i>M. guttatus</i> | -157.36 | 57.2 | P | 3.391 | 0.282 | SRX6914884 |
| BOG10 | <i>M. guttatus</i> | -118.8058 | 41.9236 | P | 10.45 | 0.178 | SRX030570 |
| BR | <i>M. decorus</i> (northern) | -122.104 | 44.371 | P | 17.99 | 0.1452 | SRX6914892 |
| CACG6 | <i>M. guttatus</i> | -121.3667 | 45.7107 | A | 37.24 | 0.192 | SRX525044 |
| CACN9 | <i>M. nasutus</i> | -121.3667 | 45.7107 | A | 27.35 | 0.324 | SRX525048 |
| CG | <i>M. guttatus</i> | | | P | 4.178 | 0.321 | SRX6914893 |
| CSS4 | <i>M. guttatus</i> | -122.4152 | 38.8611 | A | 12.12 | 0.265 | SRX6435296 |
| DL | <i>M. decorus</i> (southern) | -122.1334 | 43.1575 | P | 20.06 | 0.199 | SRX6914895 |
| DPRN104 | <i>M. nasutus</i> | -120.344 | 37.828 | A | 25.42 | 0.150 | SRX525050 |
| HACK | <i>M. decorus</i> (northern) | -122.0338 | 45.6070 | P | 21.08 | 0.151 | SRX6914894 |
| HJA | <i>M. decorus</i> (northern) | -122.1762 | 44.2332 | P | 18.97 | 0.211 | SRX6914896 |
| HWY15 | <i>M. decorus</i> (northern) | -122.1 | 44.2 | P | 19.78 | 0.191 | SRX6914897 |
| IM767 | <i>M. guttatus</i> | -122.5087 | 45.5757 | A | 8.318 | 0.230 | SRX487581 |
| IMPIA | <i>M. decorus</i> (northern) | -122.5087 | 45.5757 | P | 3.827 | 0.219 | SRX2211949 |
| IMPO | <i>M. decorus</i> (northern) | -122.5087 | 45.5757 | P | 51.49 | 0.176 | SRX6914898 |
| INV | <i>M. guttatus</i> | -122.87 | 38.08 | U | 8.99 | 0.188 | SRX6914899 |
| KINK | <i>M. decorus</i> (northern) | -121.9962 | 44.3032 | P | 15.97 | 0.242 | SRX6914885 |
| KOOT | <i>M. nasutus</i> | -115.983 | 48.104 | A | 34.51 | 0.198 | SRX525049 |
| LL | <i>M. decorus</i> (northern) | -122.0542 | 44.1739 | P | 21.64 | 0.248 | SRX6914886 |
| LMC24 | <i>M. guttatus</i> | -123.0839 | 38.8639 | A | 7.866 | 0.183 | SRX030680 |
| LVR | <i>M. tilingii</i> | -119.2257 | 37.9508 | P | 37.51 | 0.183 | SRX1532174 |
| MAR | <i>M. guttatus</i> | -123.2944 | 43.4786 | A | 10.07 | 0.285 | SRX030542 |
| MED84 | <i>M. guttatus</i> | -120.3136 | 37.8166 | P | 26.42 | 0.340 | SRX552649 |
| MEX | <i>M. guttatus</i> | -111.0945 | 29.1013 | U | 5.528 | 0.202 | SRX6914887 |
| NHN26 | <i>M. nasutus</i> | -124.16 | 49.273 | A | 26.309 | 0.130 | SRX525051 |
| ODELL | <i>M. decorus</i> (southern) | -121.9627 | 43.5479 | P | 21.51 | 0.205 | SRX6914889 |
| ODELL-gutt | <i>M. guttatus</i> | -121.9627 | 43.5479 | P | 13.58 | 0.153 | SRX6914888 |

| | | | | | | | |
|-------|--------------------|------------|---------|---|-------|-------|------------|
| REM8 | <i>M. guttatus</i> | -122.4114 | 38.8604 | A | 7.354 | 0.181 | SRX030546 |
| SCH | <i>M. guttatus</i> | -107.03526 | 39.0184 | P | 26.28 | 0.150 | SRX371892 |
| SF5 | <i>M. nasutus</i> | -121.0225 | 45.2644 | A | 9.18 | 0.241 | SRX116529 |
| SLP19 | <i>M. guttatus</i> | -120.46186 | 37.8482 | A | 23.82 | 0.196 | SRX142377 |
| SOL | <i>M. guttatus</i> | -119.1751 | 41.3789 | U | 5.791 | 0.265 | SRX6914890 |
| SWB | <i>M. guttatus</i> | -123.6904 | 39.0359 | P | 9.684 | 0.211 | SRX030679 |
| TSG3 | <i>M. guttatus</i> | -131.9157 | 53.4188 | P | 4.288 | 0.257 | SRX2019854 |
| YJS6 | <i>M. guttatus</i> | -114.5845 | 44.9512 | P | 8.233 | 0.204 | SRX030545 |
| YV06 | <i>M. guttatus</i> | -119.7464 | 37.723 | U | 16.38 | 0.170 | SRX6914891 |

Table S1: Whole-genome resequencing sample summary. Related to STAR Methods.

Lat= Latitude, Long= Longitude, LH= life history (A=Annual, P=Perennial, U=unknown). MD= Mean depth for variable sites, and % MID= % Missing data, as calculated by VCFtools. SRA samples can be found under BioProject PRJNA574603.

| Pop | Pop code | Lat | Long | OCS | FIS | Ploidy | clade | MSV | MSG | PSV | PSG | MSS | PSS | SVS | SGS | SSS | RI V | RI G |
|------------------------|----------|-------|---------|-----|-----|--------|-------|------------|--------|------------|-------|------------|------------|------------|-----------|-----------|------------|-----------|
| Big Meadow Campground | BM | 44.49 | -121.98 | X | X | 4x | 4x | 0.640 | 0.6225 | 0.3595 | 0.582 | 0.0310 | 0.0554 | 0.462 | 0.0019 | -0.273 | 0.450 | 0.4047 |
| Browder Ridge Quarry | BR | 44.37 | -122.10 | X | X | 2x | North | 0.004 | 0.0266 | 0.9181 | 0.78 | 0.0287 | 0.0396 | 0.990 | 0.9501 | -0.070 | 0.493 | 0.4508 |
| CAR | CAR | 47.03 | -122.03 | X | X | 4x | 4x | 0.821 | 0.4733 | 0.8268 | 0.695 | 0.0851 | 0.1344 | 0.003 | 0.1609 | -0.224 | 0.094 | 0.0186 |
| CHR | CHR | 46.78 | -121.77 | X | X | 4x | 4x | 0.831 | 0.4325 | 0.5794 | 0.432 | 0.0897 | 0.1062 | 0.224 | 0.0082 | -0.083 | 0.224 | 0.1601 |
| Diamond Lake | DL | 43.15 | -122.13 | X | X | 2x | South | 0.831 | 0.3775 | 0.7571 | 0.562 | 0.0137 | 0.0247 | 0.048 | 0.2284 | -0.282 | 0.127 | 0.0543 |
| Hackleme n's Creek | HACK | 44.40 | -122.07 | | X | 2x | North | | | | | | | | | | | |
| HAM | HAM | 47.56 | -123.03 | X | X | 4x | 4x | 0.833 | 0.83 | 0.1566 | 0.132 | 0.1096 | 0.1388 | 0.720 | 0.7554 | -0.117 | 0.455 | 0.4105 |
| HJA | HJA | 44.23 | -122.17 | X | X | 2x | North | 0.047 | 0.1725 | 0.3173 | 0.682 | 0.0884 | 0.0422 | 0.085 | -0.663 | 0.309 | 0.799 | 0.7827 |
| Hwy 26 near Gov't Camp | Hwy26 | 45.29 | -121.73 | X | X | 4x | 4x | 0.845 | 0.8225 | 0.8720 | 0.887 | 0.0882 | 0.1467 | 0.018 | 0.0386 | -0.249 | 0.056 | 0.0221 |
| HWY15 | Hwy15 | 44.39 | -122.14 | | X | 2x | North | | | | | | | | | | | |
| IMP | IMP | 44.39 | -122.14 | X | X | 2x | North | 0.0005 | 0.01 | 0.8009 | 0.405 | 0.0542 | 0.0328 | 0.998 | 0.9640 | 0.222 | 0.559 | 0.5229 |
| Junction of 35 + 48 | 35-48 | 45.30 | -121.66 | X | X | 4x | 4x | 0.840 | 0.6675 | 0.7900 | 0.9 | 0.113 | 0.1161 | 0.032 | 0.2410 | -0.013 | 0.104 | 0.0296 |
| Kink Creek | KINK | 44.30 | -121.99 | X | X | 2x | North | 0.0004 | 0.0725 | 0.6501 | 0.77 | 0.0924 | 0.0380 | 0.748 | 0.3656 | 0.363 | 0.642 | 0.6127 |
| Lumberlost campground | LL | 44.17 | -122.05 | X | X | 2x | North | 0.6946 | 0.8566 | 0.8392 | 0.953 | 0.0568 | 0.0642 | 0.137 | 0.0551 | 0.106 | 0.157 | 0.0870 |
| Multnomah Falls | Mult | 45.57 | -122.11 | X | | 4x | 4x | 0.8595 | 0.2875 | 0.5509 | 0.162 | | | 0.218 | 0.2777 | | 0.225 | 0.1605 |
| N. Santiam River | NS | 44.52 | -121.99 | X | X | 4x | 4x | 0.91038916 | 0.435 | 0.54980183 | 0.63 | 0.02869011 | 0.05211796 | 0.33163112 | 0.1531141 | 0.2709871 | 0.19769726 | 0.1308387 |

| | | | | | | | | | | | | | | | | | | |
|------------------------|-------|-------|---------|---|---|----|-------|-----------|--------|----------|--------|--------|--------|-------|--------|--------|-------|--------|
| Odell Creek | Odell | 43.54 | -121.96 | X | X | 2x | South | 0.5504898 | 0.34 | 0.089684 | 0.067 | 0.0282 | 0.0653 | 0.814 | 0.6420 | -0.299 | 0.648 | 0.6189 |
| Silver Falls | Silf | 44.87 | -122.65 | X | | 4x | 4x | 0.8517864 | 1 | 0.021223 | 0.3625 | | | 0.951 | 0.4678 | | 0.520 | 0.4803 |
| Trillium Lake Il_Marsh | Trill | 45.26 | -121.74 | X | X | 4x | 4x | 0.8805005 | 0.8275 | 0.483639 | 0.432 | 0.1047 | 0.1113 | 0.370 | 0.3040 | -0.030 | 0.250 | 0.1880 |
| Wildwood Rec. Area | WW | 45.34 | -121.99 | X | | 4x | 4x | 0.9086650 | 0.05 | 0.062957 | 0.687 | | | 0.870 | 0.8644 | | 0.466 | 0.421 |
| ZigZag river | Zig | 45.31 | -121.88 | X | X | 4x | 4x | 0.6436899 | 0.85 | 0.179246 | 0.637 | 0.1404 | 0.1836 | 0.452 | 0.1464 | -0.133 | 0.547 | 0.5101 |

Table S2: Population Collections of *M. decorus*. Related to STAR Methods.

Pop= Population full name, Pop code = abbreviation for population name, Lat= latitude, Long= longitude, Under the OCS and FIS headings an X indicates that the population was used in either the Original Crossing Survey (OCS) or Focal Individual Survey (FIS). Average seed viability (SV; as denoted by morphology), average germination (SG), and F1 seed size (SS) are reported as a function of whether individuals from each population served as the maternal or paternal parent (M or P respectively; i.e. MSV= maternal seed viability). Average asymmetry between reciprocal F1s are also given for seed viability (SVS; based on morphology), germination (SGS), and size (SSS). Average reproductive isolation ('RI') is also given for seed viability (RI_V; based on morphology) and germination rate (RI_G).

| | <i>M. guttatus</i> | <i>M. tilingii</i> | <i>M. nasutus</i> | Northern <i>M. decorus</i> | Southern <i>M. decorus</i> |
|----------------------------|--------------------|--------------------|-------------------|----------------------------|----------------------------|
| <i>M. guttatus</i> | 0.05100774 | 0.0801329 | 0.17211806 | 0.17555226 | 0.02138452 |
| <i>M. tilingii</i> | 0.06450129 | 0.02583097 | 0.61174323 | 0.40709871 | 0.28061806 |
| <i>M. nasutus</i> | 0.05836323 | 0.06621548 | 0.00923355 | 0.62232452 | 0.42164968 |
| Northern <i>M. decorus</i> | 0.05699806 | 0.06247355 | 0.06397935 | 0.01890065 | 0.08914903 |
| Southern <i>M. decorus</i> | 0.05795935 | 0.06479419 | 0.06481871 | 0.04233677 | 0.05140645 |

Table S3: Average diversity, divergence, and differentiation of species of the *M. guttatus* species complex at 4-fold degenerate sites. Related to Figure 5.

Pi within species is highlighted in blue and appears on the diagonal, and average dxy between species is highlighted in green and appears below the diagonal, while Fst between species is highlighted in yellow and appears above the diagonal.