

Supporting information

MS title: Colonization history of the Western Corn Rootworm (*Diabrotica virgifera virgifera*) in North America: insights from random forest ABC using microsatellite data

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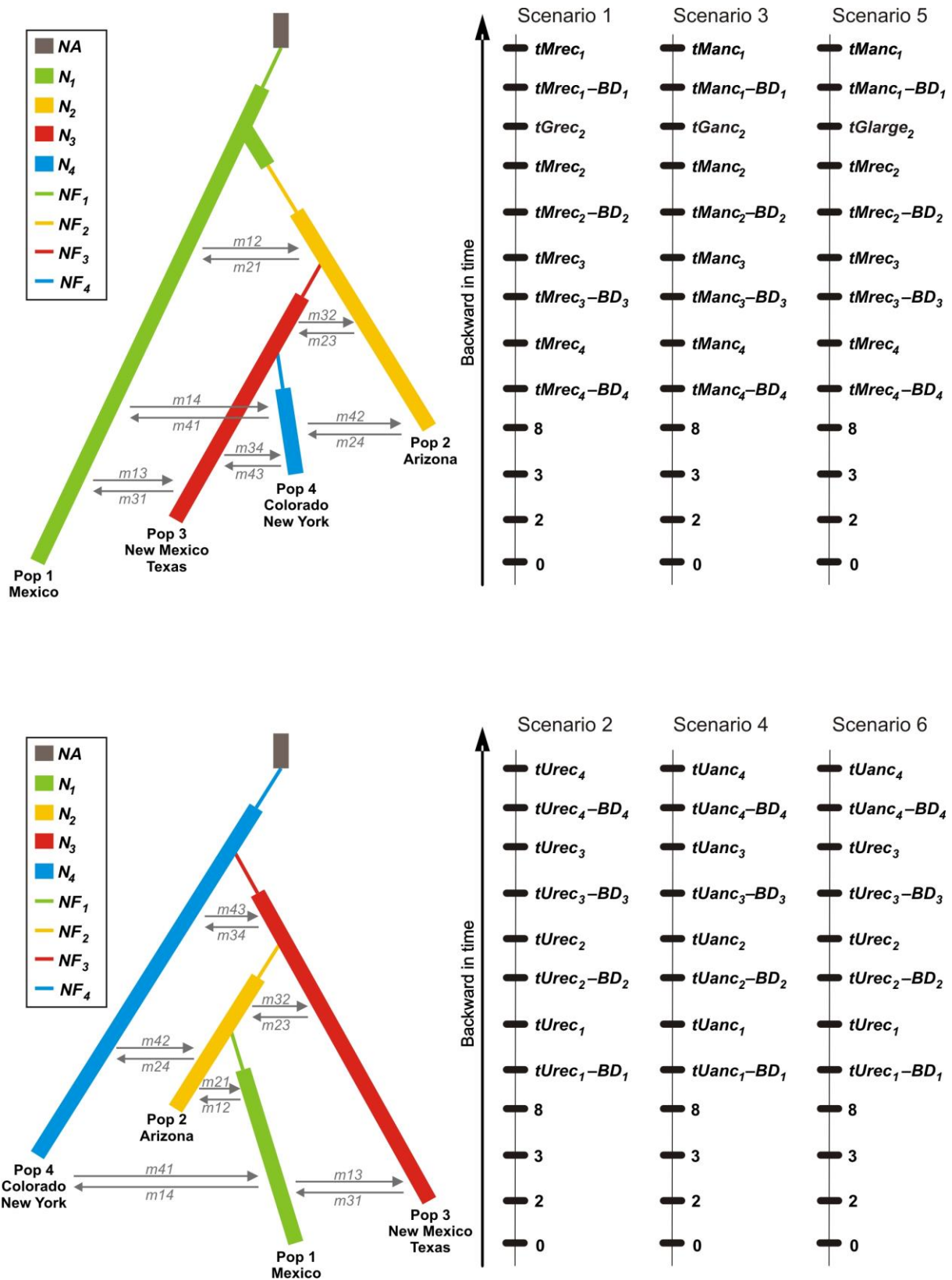


Figure S1: Graphical representation of the 6 competing scenarios considered to infer the colonization history of *Diabrotica virgifera virgifera* in North America in the ABC analyses.

Note: the four genetic units are those inferred from Bayesian clustering analyses, as presented in Figure 1. All parameters with associated prior distributions are described in Table S2. Time 0 is the sampling year 2006, and all other times are in number of generations before 2006, assuming 1 generation per year. Time is not to scale. The directions of the migration rates represent migration from one population to another backward in time.

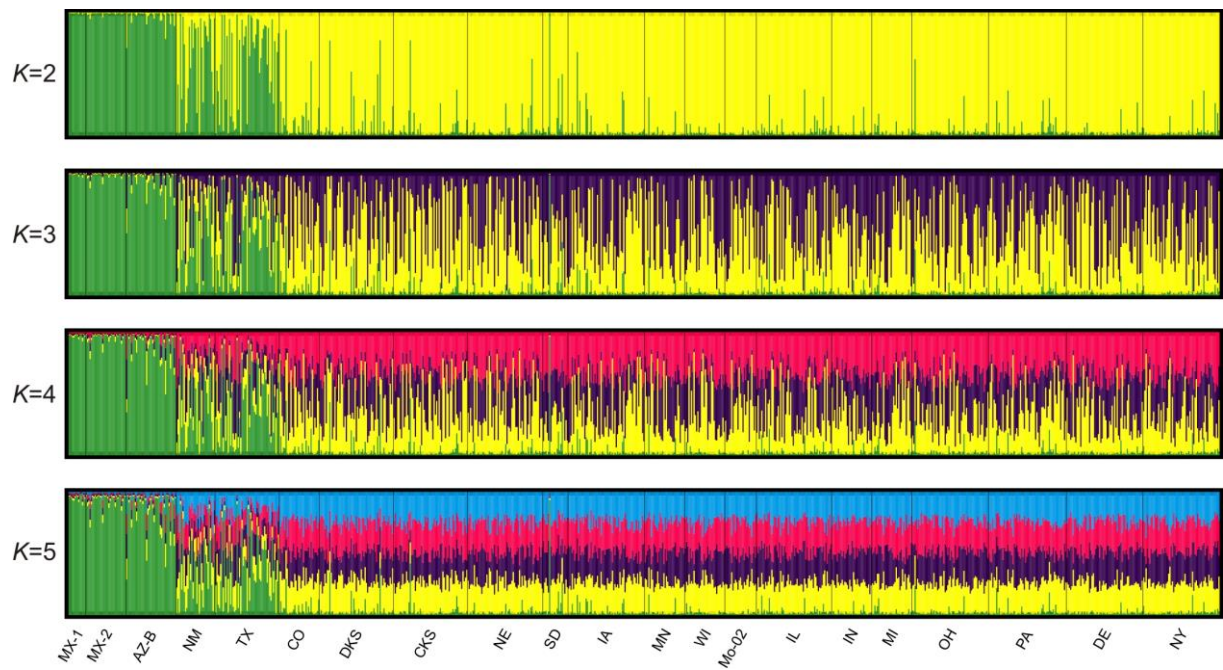


Figure S2: Genetic clustering of all site samples of *Diabrotica virgifera virgifera*. Ancestry estimation based on the Bayesian individual clustering method implemented in STRUCTURE is given for $K=2$ to $K=5$ genetic clusters. Each vertical line represents an individual and each color represents a genetic cluster. Names of site samples at the bottom of the figure are as in Figure 1 and Table S1.

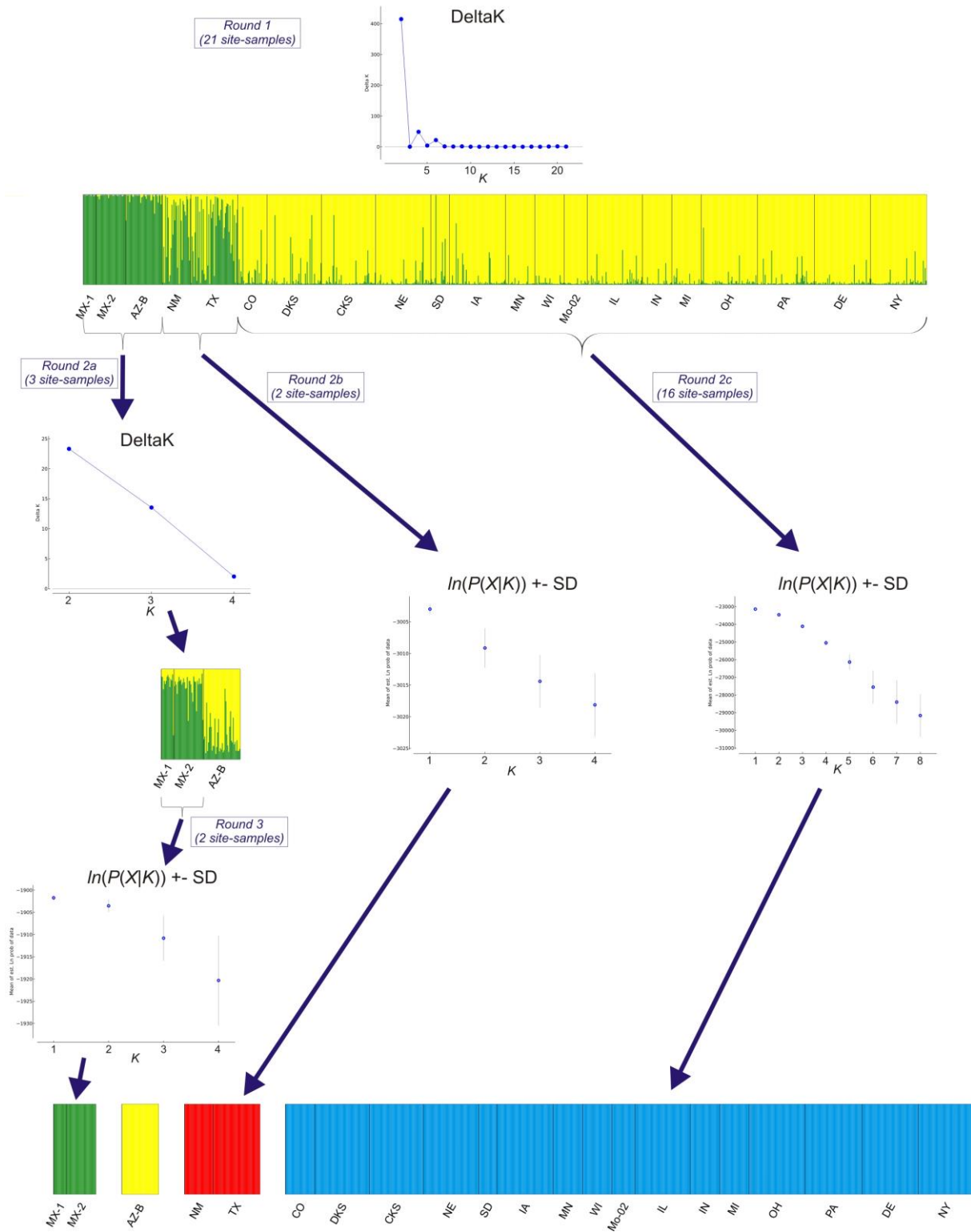


Figure S3: Q plots representing hierarchical data analyses performed with STRUCTURE to determine the number of genetic units among *Diabrotica virgifera virgifera* individuals sampled from the North American distribution of the species. Each Q plot shown for each analysis was generated using the value of K associated with either the $\ln(P(X|K))$ when it was maximum for $K=1$, or the maximum ΔK value (Evanno *et al.* 2005, *Molecular Ecology*, 14, 2611-2620) otherwise. Arrows indicate subsequent independent hierarchical analyses. Each vertical line represents an individual and each color represents a genetic cluster. Names of site samples are as in Figure 1 and Table S1. Consensus STRUCTURE plots were generated using the CLUMPAK method (Kopelman *et al.* 2015, *Molecular Ecology Resources*, 15, 1179-1191) and final plots were built with DISTRUCT (Rosenberg 2004, *Molecular Ecology Resources*, 4, 137-138).

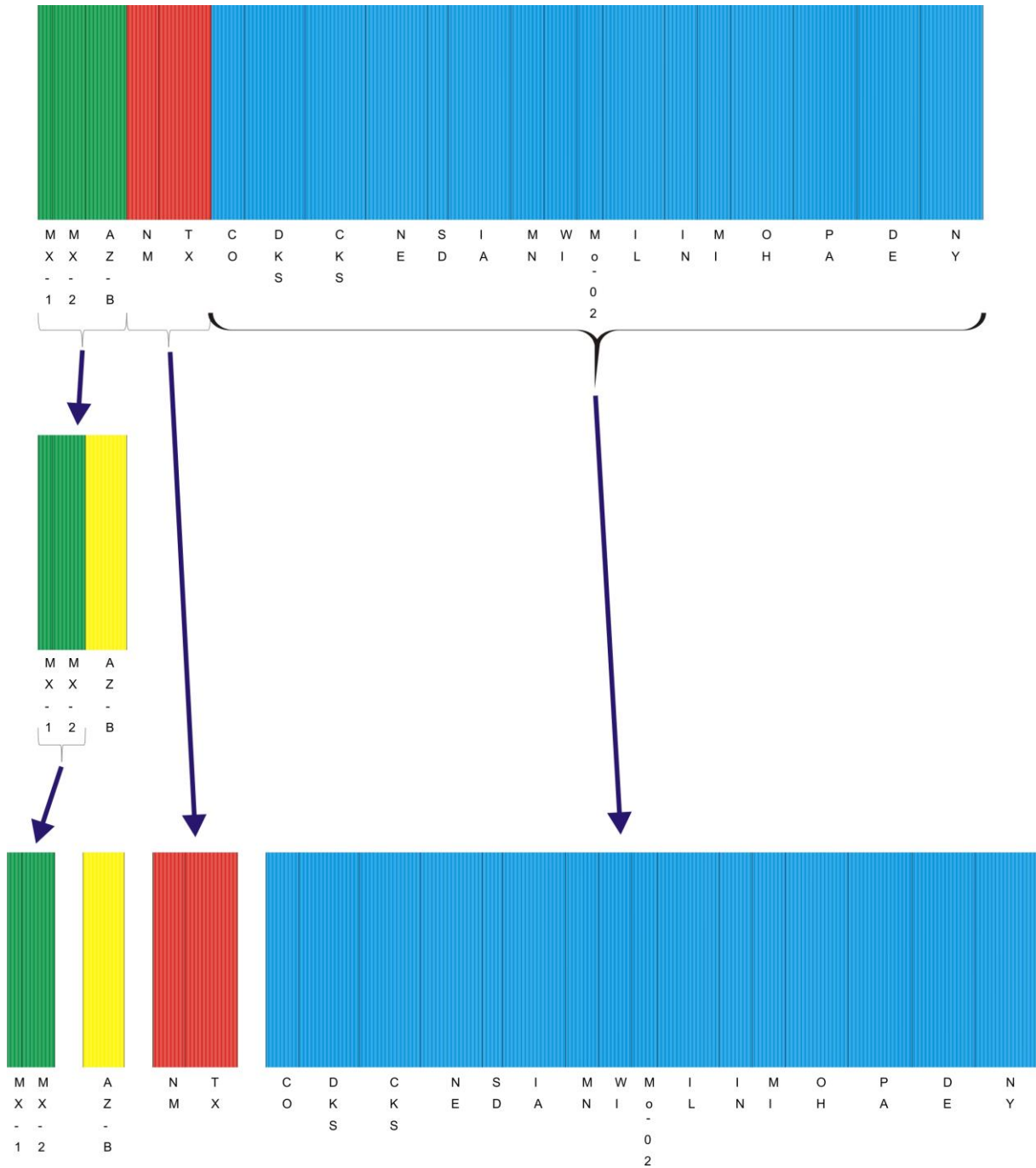


Figure S4: Q plots representing hierarchical data analyses performed with BAPS to determine the number of genetic units among *Diabrotica virgifera virgifera* individuals sampled from the North American distribution of the species. Arrows indicate subsequent independent hierarchical analyses. Each vertical line represents an individual and each color represents a genetic cluster. Names of site-samples are as in Figure 1 and Table S1.

| Site sample | Country | State | Longitude | Latitude | Sampling year | Collector | Previous publications | Sample size | NA | AR | He | F_{IS} | Loci with $r > 0.15$ |
|-------------|---------|--------------|-----------|----------|---------------|------------------|-----------------------|-------------|-------|-------|-------|----------|----------------------|
| MX-1 | Mexico | Durango | -104.417 | 24.000 | 2001 | Rosanna Giordano | B | 14 | 6.692 | 6.107 | 0.73 | 0.1093 * | DVV-ET1; Dba05 |
| MX-2 | Mexico | Durango | -104.000 | 24.468 | 2006 | Stefan Toepfer | - | 32 | 9.231 | 6.350 | 0.707 | 0.1067 * | DVV-ET1; Dba05 |
| AZ-B | USA | Arizona | -109.731 | 32.064 | 1998 | Rosanna Giordano | B | 40 | 7.846 | 5.343 | 0.665 | 0.0297 | None |
| NM | USA | New Mexico | -106.125 | 34.853 | 2004 | Uwe Stoltz | - | 31 | 7.231 | 5.187 | 0.621 | -0.0081 | None |
| TX | USA | Texas | -101.837 | 33.737 | 2004 | Greg Cronholm | A, B, C, D | 51 | 7.462 | 5.261 | 0.649 | -0.0043 | None |
| CO | USA | Colorado | -104.149 | 40.185 | 2003 | Uwe Stoltz | - | 32 | 6.231 | 4.766 | 0.603 | -0.0321 | None |
| DKS | USA | Kansas | -100.016 | 37.765 | 2003 | Lee French | A, C | 59 | 6.615 | 4.744 | 0.603 | 0.0363 | None |
| CKS | USA | Kansas | -97.657 | 39.572 | 2003 | Lee French | A | 59 | 6.462 | 4.682 | 0.607 | 0.0226 | None |
| NE | USA | Nebraska | -96.488 | 41.229 | 2003 | Lance Meinke | A | 60 | 6.615 | 4.667 | 0.595 | -0.0236 | None |
| SD | USA | South Dakota | -96.267 | 43.611 | 2005 | Uwe Stoltz | - | 20 | 5.769 | 4.745 | 0.616 | -0.0001 | None |
| IA | USA | Iowa | -93.600 | 41.732 | 2003 | Brendon Reardon | A, C, D | 61 | 6.692 | 4.667 | 0.604 | 0.0021 | None |
| MN | USA | Minnesota | -92.173 | 43.950 | 2003 | Uwe Stoltz | - | 32 | 5.538 | 4.402 | 0.591 | 0.0450 | None |
| WI | USA | Wisconsin | -90.945 | 43.870 | 2003 | Uwe Stoltz | - | 32 | 6.154 | 4.695 | 0.6 | 0.0554 | None |
| Mo-02 | USA | Illinois | -90.647 | 40.911 | 2002 | Sue Ratcliff | - | 25 | 5.615 | 4.506 | 0.572 | 0.0232 | None |
| IL | USA | Illinois | -88.243 | 40.116 | 2003 | Eli Levine | A, B, C, D | 60 | 6.385 | 4.631 | 0.624 | 0.0310 | None |
| IN | USA | Indiana | -85.833 | 39.575 | 2003 | Uwe Stoltz | - | 32 | 6.154 | 4.795 | 0.609 | -0.0337 | None |
| MI | USA | Michigan | -85.666 | 42.749 | 2003 | Uwe Stoltz | - | 32 | 5.923 | 4.493 | 0.595 | 0.0270 | None |
| OH | USA | Ohio | -81.901 | 40.447 | 2003 | Bruce Eisley | A | 61 | 6.846 | 4.687 | 0.607 | 0.0095 | None |
| PA | USA | Pennsylvania | -77.765 | 40.913 | 2003 | Dennis Calvin | A, B | 62 | 6.462 | 4.597 | 0.612 | 0.0230 | None |
| DE | USA | Delaware | -75.754 | 39.683 | 2003 | Joanne Whalen | A | 61 | 6.154 | 4.612 | 0.601 | 0.0143 | None |
| NY | USA | New York | -74.485 | 42.678 | 2003 | Ken Wise | A, C, D | 61 | 6.462 | 4.655 | 0.597 | 0.0053 | None |

Table S1: Description of *Diabrotica virgifera virgifera* samples and within-population genetic variation.

NA: mean number of alleles per locus. AR: allelic richness corrected for 10 individuals. He: mean expected heterozygosity. F_{IS} : inbreeding coefficient. Asterisks indicate significant Hardy-Weinberg tests. r : estimated proportion of null allele per locus. Publication codes: A = Kim & Sappington 2005, *Environmental Entomology*, 34, 494-503; B = Ciosi *et al.* 2008, *Molecular Ecology*, 17, 3614-3627; C = Kim *et al.* 2008, *Journal of Heredity*, 99, 112-124; D = Coates *et al.* 2009, *Journal of Heredity*, 100, 556-564. “-”: not applicable.

| Parameters | Distribution | Quantile 2.5% | Median | Mean | Quantile 97.5% |
|-----------------------------|--------------------------------------|----------------------|----------------------|----------------------|----------------------|
| $NA; N_i$ | Log-Uniform [100 – 100,000] | 119 | 3,165 | 14,450 | 84,068 |
| NF_i | Log-Uniform [2 – 100] | 2 | 14 | 25 | 90 |
| BD_i | Uniform [1 – 10] | 1 | 5 | 5.05 | 10 |
| mig_{ij} | Uniform [0 – 5×10^{-4}] | 1.3×10^{-5} | 2.5×10^{-4} | 2.5×10^{-4} | 4.9×10^{-4} |
| $tManc_i; tUanc_i; tGanc_i$ | Uniform [1,500 – 10,000] | DV | DV | DV | DV |
| $tMrec_i; tUrec_i$ | Log-Uniform [x_i – 1,500] | DV | DV | DV | DV |
| $tGrec_i$ | Uniform [x_i – 1,500] | DV | DV | DV | DV |
| $tGlarge_i$ | Uniform [x_i – 10,000] | DV | DV | DV | DV |
| mean μ | Uniform [10^{-5} – 10^{-3}] | 3.5×10^{-5} | 5.1×10^{-4} | 5.1×10^{-4} | 9.8×10^{-4} |
| mean P | Uniform [0.1 – 0.3] | 0.105 | 0.2 | 0.2 | 0.295 |

Table S2: Prior distributions of demographic, historical and genetic parameters used in ABC analyses processed to retrace the colonization history of *Diabrotica virgifera virgifera* in North America.

Notes: NA and N_i = stable effective population size (number of diploid individuals) of the ancestral unsampled population (NA) or of population i ; NF_i = effective number of founders during a bottleneck lasting BD_i generation(s) for population i ; mig_{ij} = migration rate backward in time from population i to population j ; $tManc_i$ and $tUanc_i$ = ancient foundation time of population i in the “Mexico origin” and “central-USA origin” scenarios respectively; $tMrec_i$ and $tUrec_i$ = recent foundation time of population i in the “Mexico origin” and “central-USA origin” scenarios respectively, with bounds x_i fixed from date of first observation of population i ; $tGanc_i$, $tGrec_i$ and $tGlarge_i$ = in the “Mexico origin” scenario, merging time of an unsampled native population with the sampled Mexican population, with bounds x_i fixed from date of first observation of population i . Depending on the scenarios considered, various conditions were applied to times so that coalescent times fit with each scenario’s topology. All times are expressed in number of generations, which is equivalent to years (because *Diabrotica virgifera virgifera* has 1 generation per year), and run backward in time from time 0 which corresponds to year 2006 CE. The microsatellite loci were assumed to follow a generalized stepwise mutation model (Estoup *et al.* 2002, *Molecular Ecology*, 11, 1591-1604) with two parameters: the mean mutation rate (mean μ), the mean parameter of the geometric distribution (mean P) of length in terms of the number of repeats of mutation events. All prior quantities presented were computed from 10^6 values. DV = different values were possible. See Figure S1 for a graphical representation of the evolutionary scenarios with associated historical and demographic parameters considered in the ABC analyses.

| Site sample | MX-1 | MX-2 | AZ-B | NM | TX | CO | DKS | CKS | NE | SD | IA | MN | WI | Mo-02 | IL | IN | MI | OH | PA | DE |
|-------------|----------------------|--------|--------|--------|--------|--------|-----------------------|-----------------------|-----------------------|----------------------|-----------------------|-----------------------|-----------------------|-----------------------|----------------------|-----------------------|----------------------|----------------------|-----------------------|----------------------|
| MX-2 | <u>0.0022</u> | | | | | | | | | | | | | | | | | | | |
| AZ-B | 0.0516 | 0.0326 | | | | | | | | | | | | | | | | | | |
| NM | 0.1067 | 0.0745 | 0.0567 | | | | | | | | | | | | | | | | | |
| TX | 0.0837 | 0.0588 | 0.0416 | 0.0233 | | | | | | | | | | | | | | | | |
| CO | 0.1247 | 0.1024 | 0.0803 | 0.0160 | 0.0211 | | | | | | | | | | | | | | | |
| DKS | 0.1397 | 0.1100 | 0.0893 | 0.0197 | 0.0229 | 0.0065 | | | | | | | | | | | | | | |
| CKS | 0.1397 | 0.1101 | 0.0949 | 0.0266 | 0.0246 | 0.0083 | <u>-0.0003</u> | | | | | | | | | | | | | |
| NE | 0.1412 | 0.1112 | 0.0911 | 0.0242 | 0.0250 | 0.0028 | <u>-0.0007</u> | <u>-0.0012</u> | | | | | | | | | | | | |
| SD | 0.1130 | 0.0906 | 0.0757 | 0.0198 | 0.0246 | 0.0133 | 0.0123 | <u>0.0076</u> | 0.0136 | | | | | | | | | | | |
| IA | 0.1351 | 0.1030 | 0.0898 | 0.0262 | 0.0257 | 0.0109 | <u>0.0039</u> | <u>0.0006</u> | <u>-0.0013</u> | 0.0109 | | | | | | | | | | |
| MN | 0.1397 | 0.1078 | 0.0914 | 0.0311 | 0.0314 | 0.0166 | <u>0.0051</u> | <u>0.0008</u> | <u>0.0006</u> | 0.0119 | <u>-0.0007</u> | | | | | | | | | |
| WI | 0.1383 | 0.1119 | 0.0976 | 0.0321 | 0.0267 | 0.0123 | <u>0.0058</u> | <u>-0.0028</u> | <u>-0.0010</u> | <u>0.0040</u> | <u>0.0005</u> | <u>-0.0010</u> | | | | | | | | |
| Mo-02 | 0.1601 | 0.1226 | 0.1066 | 0.0283 | 0.0328 | 0.0132 | <u>0.0023</u> | <u>-0.0033</u> | <u>0.0008</u> | <u>0.0123</u> | <u>0.0037</u> | <u>0.0054</u> | <u>-0.0006</u> | | | | | | | |
| IL | 0.1270 | 0.0978 | 0.0785 | 0.0276 | 0.0268 | 0.0169 | 0.0104 | 0.0086 | 0.0074 | 0.0069 | <u>0.0036</u> | <u>0.0005</u> | 0.0061 | <u>0.0104</u> | | | | | | |
| IN | 0.1391 | 0.1111 | 0.0976 | 0.0301 | 0.0386 | 0.0152 | <u>0.0023</u> | <u>0.0054</u> | <u>0.0027</u> | 0.0100 | <u>-0.0017</u> | <u>0.0027</u> | 0.0081 | <u>0.0064</u> | <u>0.0035</u> | | | | | |
| MI | 0.1427 | 0.1170 | 0.0929 | 0.0357 | 0.0410 | 0.0164 | 0.0114 | 0.0070 | <u>0.0011</u> | 0.0145 | <u>0.0027</u> | <u>0.0002</u> | <u>0.0073</u> | <u>0.0044</u> | <u>0.0028</u> | <u>0.0031</u> | | | | |
| OH | 0.1407 | 0.1086 | 0.0880 | 0.0266 | 0.0252 | 0.0108 | <u>0.0010</u> | <u>-0.0006</u> | <u>-0.0016</u> | 0.0135 | <u>-0.0030</u> | -0.0027 | <u>-0.0011</u> | <u>-0.0002</u> | <u>0.0015</u> | <u>-0.0035</u> | <u>0.0005</u> | | | |
| PA | 0.1329 | 0.1037 | 0.0887 | 0.0303 | 0.0234 | 0.0143 | <u>0.0049</u> | <u>0.0035</u> | <u>0.0048</u> | 0.0169 | <u>0.0004</u> | <u>0.0027</u> | <u>0.0014</u> | <u>0.0069</u> | 0.0097 | <u>0.0066</u> | 0.0125 | <u>0.0004</u> | | |
| DE | 0.1456 | 0.1141 | 0.0959 | 0.0316 | 0.0276 | 0.0180 | 0.0057 | 0.0065 | 0.0069 | 0.0182 | 0.0039 | <u>0.0029</u> | 0.0057 | <u>0.0087</u> | 0.0080 | 0.0067 | 0.0149 | <u>0.0018</u> | 0.0038 | |
| NY | 0.1410 | 0.1066 | 0.0945 | 0.0310 | 0.0242 | 0.0116 | 0.0051 | <u>-0.0003</u> | <u>-0.0006</u> | 0.0165 | <u>-0.0015</u> | <u>-0.0024</u> | <u>0.0001</u> | <u>0.0030</u> | 0.0077 | <u>0.0073</u> | 0.0070 | <u>0.0001</u> | <u>-0.0006</u> | <u>0.0029</u> |

Table S3: Pairwise estimates of F_{ST} between all *Diabrotica virgifera virgifera* site-samples. Site-sample names are as in Figure 1 and Table S1. Underline bold F_{ST} indicates non-significant pairwise differentiation, as assessed using Fisher's exact test with correction for multiple comparisons.

| Summary statistics | Observed values | Scenario 1 | Scenario 2 | Scenario 3 | Scenario 4 | Scenario 5 | Scenario 6 |
|--------------------|-----------------|------------|----------------|----------------|----------------|------------|----------------|
| NA_1 | 9.23 | 0.822 | 0.949 | 0.700 | 0.725 | 0.704 | 0.918 |
| NA_2 | 7.85 | 0.793 | 0.843 | 0.586 | 0.593 | 0.697 | 0.778 |
| NA_3 | 7.46 | 0.781 | 0.749 | 0.545 | 0.537 | 0.690 | 0.679 |
| NA_4 | 6.23 | 0.764 | 0.625 | 0.477 | 0.466 | 0.669 | 0.533 |
| NA_{tot} | 11.92 | 0.817 | 0.820 | 0.623 | 0.623 | 0.717 | 0.752 |
| He_1 | 0.71 | 0.678 | 0.907 | 0.515 | 0.528 | 0.538 | 0.849 |
| He_2 | 0.66 | 0.718 | 0.802 | 0.457 | 0.461 | 0.587 | 0.711 |
| He_3 | 0.65 | 0.765 | 0.702 | 0.438 | 0.431 | 0.644 | 0.601 |
| He_4 | 0.60 | 0.773 | 0.555 | 0.385 | 0.376 | 0.658 | 0.448 |
| He_{tot} | 0.68 | 0.711 | 0.720 | 0.384 | 0.381 | 0.566 | 0.605 |
| MGW_1 | 0.670 | 0.165 | 0.215 | 0.061 | 0.087 | 0.061 | 0.144 |
| MGW_2 | 0.688 | 0.187 | 0.212 | 0.080 | 0.086 | 0.121 | 0.133 |
| MGW_3 | 0.665 | 0.168 | 0.161 | 0.062 | 0.052 | 0.106 | 0.088 |
| MGW_4 | 0.690 | 0.221 | 0.195 | 0.106 | 0.079 | 0.171 | 0.075 |
| PA_1 | 1.77 | 0.864 | 0.997 * | 0.938 | 0.964 * | 0.805 | 0.998 * |
| PA_2 | 0.69 | 0.669 | 0.779 | 0.644 | 0.649 | 0.640 | 0.784 |
| PA_3 | 0.54 | 0.592 | 0.490 | 0.514 | 0.511 | 0.592 | 0.492 |
| PA_4 | 0.08 | 0.134 | 0.087 | 0.138 | 0.148 | 0.152 | 0.107 |
| SA | 3.85 | 0.800 | 0.818 | 0.606 | 0.608 | 0.717 | 0.742 |
| $F_{ST} 12$ | 0.034 | 0.266 | 0.273 | 0.346 | 0.345 | 0.275 | 0.263 |
| $F_{ST} 13$ | 0.059 | 0.287 | 0.267 | 0.468 | 0.469 | 0.309 | 0.276 |
| $F_{ST} 14$ | 0.101 | 0.356 | 0.358 | 0.612 | 0.609 | 0.375 | 0.378 |
| $F_{ST} 23$ | 0.036 | 0.296 | 0.300 | 0.358 | 0.358 | 0.299 | 0.303 |
| $F_{ST} 24$ | 0.080 | 0.387 | 0.405 | 0.546 | 0.546 | 0.384 | 0.424 |
| $F_{ST} 34$ | 0.014 | 0.112 | 0.130 | 0.195 | 0.191 | 0.107 | 0.135 |
| L_{12} | -19.83 | 0.377 | 0.147 | 0.546 | 0.543 | 0.512 | 0.222 |
| L_{13} | -23.10 | 0.300 | 0.109 | 0.412 | 0.406 | 0.427 | 0.167 |
| L_{14} | -26.82 | 0.236 | 0.066 | 0.286 | 0.275 | 0.360 | 0.080 |
| L_{21} | -17.40 | 0.387 | 0.281 | 0.644 | 0.639 | 0.540 | 0.379 |
| L_{23} | -18.90 | 0.302 | 0.228 | 0.579 | 0.581 | 0.431 | 0.326 |
| L_{24} | -21.21 | 0.268 | 0.193 | 0.489 | 0.494 | 0.397 | 0.264 |
| L_{31} | -19.18 | 0.284 | 0.332 | 0.574 | 0.572 | 0.420 | 0.432 |
| L_{32} | -17.94 | 0.277 | 0.327 | 0.618 | 0.622 | 0.418 | 0.430 |
| L_{34} | -16.40 | 0.332 | 0.404 | 0.673 | 0.684 | 0.469 | 0.513 |
| L_{41} | -21.83 | 0.178 | 0.352 | 0.464 | 0.468 | 0.280 | 0.454 |
| L_{42} | -19.83 | 0.199 | 0.374 | 0.540 | 0.546 | 0.318 | 0.477 |
| L_{43} | -14.64 | 0.352 | 0.537 | 0.734 | 0.740 | 0.493 | 0.625 |
| $AML_{12\ 3}$ | 0.308 | 0.449 | 0.388 | 0.278 | 0.280 | 0.419 | 0.386 |
| $AML_{13\ 2}$ | 0.539 | 0.642 | 0.489 | 0.550 | 0.555 | 0.636 | 0.498 |
| $AML_{23\ 1}$ | 0.724 | 0.652 | 0.544 | 0.698 | 0.704 | 0.661 | 0.562 |
| $AML_{12\ 4}$ | 0.275 | 0.400 | 0.326 | 0.241 | 0.244 | 0.375 | 0.322 |
| $AML_{14\ 2}$ | 0.650 | 0.667 | 0.466 | 0.648 | 0.645 | 0.660 | 0.494 |
| $AML_{24\ 1}$ | 0.853 | 0.760 | 0.634 | 0.825 | 0.829 | 0.767 | 0.665 |
| $AML_{13\ 4}$ | 0.048 | 0.084 | 0.048 * | 0.032 * | 0.032 * | 0.079 | 0.048 * |
| $AML_{14\ 3}$ | 0.311 | 0.465 | 0.284 | 0.266 | 0.268 | 0.439 | 0.298 |
| $AML_{34\ 1}$ | 0.868 | 0.768 | 0.719 | 0.821 | 0.823 | 0.769 | 0.737 |
| $AML_{23\ 4}$ | 0.105 | 0.134 | 0.096 | 0.080 | 0.079 | 0.130 | 0.097 |
| $AML_{24\ 3}$ | 0.384 | 0.388 | 0.257 | 0.326 | 0.324 | 0.391 | 0.269 |
| $AML_{34\ 2}$ | 0.762 | 0.623 | 0.576 | 0.713 | 0.709 | 0.630 | 0.601 |

Table S4: Prior checking of ABC analysis. For each summary statistic and each scenario, the proportion of simulated data (considering the total reference table) with a value below that for the observed dataset is provided. Bold with star highlights a proportion lower than 0.05 or greater than 0.95. All results (including the observed values) were obtained with the core dataset.

NA_i is the mean number of alleles per locus of population i (or for all populations considered together when $i = tot$); He_i is the mean expected heterozygosity of population i (or for all populations considered together when $i = tot$); MGW_i is the mean ratio of the number of alleles to the range of allele sizes of population i ; PA_i is the mean number of private alleles per locus of population i ; SA is the mean number of shared alleles per locus between all populations; $F_{ST} ij$ is the pairwise F_{ST} value between populations i and j ; L_{ij} is the mean individual assignment likelihood of population i being assigned to population j ; $AML_{ij\ k}$ is the maximum likelihood estimate of admixture rate of population k with parental populations i and j .

| Parameters | Prior distributions | | | | Posterior distributions | | | |
|----------------------|---------------------|---------|---------|---------|-------------------------|---------|---------|---------|
| | Q 2.5% | median | mean | Q 97.5% | Q 2.5% | median | mean | Q 97.5% |
| Raw parameters | | | | | | | | |
| N_1 | 118 | 3200 | 14675 | 84780 | 2145 | 19386 | 28289 | 85947 |
| N_2 | 119 | 3119 | 14390 | 83442 | 1170 | 7483 | 17213 | 84143 |
| N_3 | 120 | 3159 | 14340 | 84202 | 2307 | 25472 | 35466 | 91448 |
| N_4 | 119 | 3159 | 14380 | 84473 | 605 | 4243 | 14109 | 81803 |
| NA | 119 | 3124 | 14485 | 84370 | 8602 | 29917 | 34227 | 90113 |
| NF_1 | 2 | 14 | 25 | 91 | 2 | 8 | 14 | 67 |
| NF_2 | 2 | 14 | 25 | 91 | 2 | 13 | 21 | 89 |
| NF_3 | 2 | 14 | 25 | 91 | 3 | 9 | 13 | 56 |
| NF_4 | 2 | 14 | 25 | 91 | 4 | 35 | 40 | 95 |
| BD_1 | 1 | 5 | 5.09 | 10 | 1 | 6 | 5.65 | 10 |
| BD_2 | 1 | 5 | 5.05 | 10 | 1 | 5 | 5.18 | 10 |
| BD_3 | 1 | 5 | 5.05 | 10 | 1 | 7 | 6.20 | 10 |
| BD_4 | 1 | 5 | 5.05 | 10 | 1 | 4 | 4.25 | 10 |
| mig_{12} | 1.2E-05 | 2.5E-04 | 2.5E-04 | 4.9E-04 | 1.9E-05 | 2.9E-04 | 2.9E-04 | 4.9E-04 |
| mig_{13} | 1.2E-05 | 2.5E-04 | 2.5E-04 | 4.9E-04 | 9.2E-06 | 2.1E-04 | 2.2E-04 | 4.9E-04 |
| mig_{14} | 1.3E-05 | 2.5E-04 | 2.5E-04 | 4.9E-04 | 4.1E-06 | 1.4E-04 | 1.8E-04 | 4.8E-04 |
| mig_{21} | 1.2E-05 | 2.5E-04 | 2.5E-04 | 4.9E-04 | 1.8E-05 | 3.0E-04 | 2.9E-04 | 4.9E-04 |
| mig_{23} | 1.2E-05 | 2.5E-04 | 2.5E-04 | 4.9E-04 | 1.0E-05 | 2.2E-04 | 2.3E-04 | 4.8E-04 |
| mig_{24} | 1.3E-05 | 2.5E-04 | 2.5E-04 | 4.9E-04 | 8.2E-06 | 2.3E-04 | 2.3E-04 | 4.8E-04 |
| mig_{31} | 1.3E-05 | 2.5E-04 | 2.5E-04 | 4.9E-04 | 1.7E-05 | 2.4E-04 | 2.5E-04 | 4.9E-04 |
| mig_{32} | 1.2E-05 | 2.5E-04 | 2.5E-04 | 4.9E-04 | 1.7E-05 | 2.6E-04 | 2.6E-04 | 4.8E-04 |
| mig_{34} | 1.3E-05 | 2.5E-04 | 2.5E-04 | 4.9E-04 | 2.2E-05 | 3.1E-04 | 2.9E-04 | 4.9E-04 |
| mig_{41} | 1.3E-05 | 2.5E-04 | 2.5E-04 | 4.9E-04 | 4.5E-06 | 1.2E-04 | 1.5E-04 | 4.4E-04 |
| mig_{42} | 1.2E-05 | 2.5E-04 | 2.5E-04 | 4.9E-04 | 1.2E-05 | 2.2E-04 | 2.3E-04 | 4.8E-04 |
| mig_{43} | 1.3E-05 | 2.5E-04 | 2.5E-04 | 4.9E-04 | 9.8E-06 | 2.9E-04 | 2.7E-04 | 4.9E-04 |
| $tMrec_1$ | 522 | 1185 | 1134 | 1487 | 466 | 1143 | 1100 | 1482 |
| $tGrec_2$ | 335 | 847 | 851 | 1372 | 300 | 761 | 775 | 1364 |
| $tMrec_2$ | 214 | 527 | 568 | 1131 | 215 | 520 | 568 | 1212 |
| $tMrec_3$ | 161 | 322 | 369 | 835 | 157 | 259 | 285 | 566 |
| $tMrec_4$ | 141 | 196 | 231 | 520 | 140 | 168 | 189 | 352 |
| Mean μ | 3.5E-05 | 5.1E-04 | 5.1E-04 | 9.7E-04 | 1.3E-04 | 5.5E-04 | 5.6E-04 | 9.8E-04 |
| Mean P | 0.105 | 0.201 | 0.200 | 0.295 | 0.103 | 0.197 | 0.200 | 0.295 |
| Composite parameters | | | | | | | | |
| $N_{1\mu}$ | 0.02 | 1.25 | 7.42 | 53.33 | 0.78 | 8.38 | 14.25 | 56.76 |
| $N_{2\mu}$ | 0.02 | 1.21 | 7.29 | 52.31 | 0.43 | 2.99 | 7.88 | 47.88 |
| $N_{3\mu}$ | 0.02 | 1.21 | 7.27 | 52.15 | 0.60 | 10.20 | 16.46 | 71.49 |
| $N_{4\mu}$ | 0.02 | 1.22 | 7.28 | 52.80 | 0.26 | 2.02 | 6.37 | 43.28 |
| $NA\mu$ | 0.02 | 1.20 | 7.29 | 52.68 | 2.87 | 13.17 | 19.17 | 61.36 |
| $NF_{1\mu}$ | 2.7E-04 | 5.7E-03 | 1.3E-02 | 6.2E-02 | 7.2E-04 | 3.6E-03 | 7.8E-03 | 4.9E-02 |
| $NF_{2\mu}$ | 2.6E-04 | 5.7E-03 | 1.3E-02 | 6.3E-02 | 6.0E-04 | 6.4E-03 | 1.3E-02 | 6.1E-02 |
| $NF_{3\mu}$ | 2.7E-04 | 5.7E-03 | 1.3E-02 | 6.2E-02 | 8.1E-04 | 4.6E-03 | 7.8E-03 | 3.3E-02 |
| $NF_{4\mu}$ | 2.7E-04 | 5.5E-03 | 1.2E-02 | 6.1E-02 | 1.8E-03 | 1.8E-02 | 2.5E-02 | 8.2E-02 |
| $BNsev_1$ | 10 | 909 | 9319 | 83409 | 745 | 22657 | 41107 | 175233 |
| $BNsev_2$ | 10 | 911 | 9400 | 83687 | 224 | 6990 | 16985 | 125400 |
| $BNsev_3$ | 10 | 914 | 9058 | 79333 | 235 | 6625 | 17981 | 114872 |
| $BNsev_4$ | 10 | 895 | 9108 | 81213 | 91 | 3319 | 6481 | 29921 |
| M_{12} | 0.01 | 0.59 | 3.65 | 26.33 | 0.18 | 3.97 | 7.50 | 30.04 |
| M_{13} | 0.01 | 0.59 | 3.63 | 26.16 | 0.06 | 1.79 | 4.72 | 26.18 |
| M_{14} | 0.01 | 0.59 | 3.66 | 26.27 | 0.03 | 1.80 | 4.10 | 25.11 |
| M_{21} | 0.01 | 0.58 | 3.60 | 26.17 | 0.15 | 2.58 | 6.24 | 32.39 |
| M_{23} | 0.01 | 0.59 | 3.61 | 25.83 | 0.07 | 1.57 | 3.80 | 20.46 |
| M_{24} | 0.01 | 0.58 | 3.60 | 25.97 | 0.06 | 1.56 | 4.50 | 26.49 |
| M_{31} | 0.01 | 0.59 | 3.61 | 26.11 | 0.25 | 5.33 | 9.65 | 38.95 |
| M_{32} | 0.01 | 0.59 | 3.61 | 25.88 | 0.21 | 5.77 | 10.08 | 35.69 |
| M_{34} | 0.01 | 0.58 | 3.58 | 26.14 | 0.35 | 6.22 | 10.30 | 37.80 |
| M_{41} | 0.01 | 0.60 | 3.64 | 26.64 | 0.02 | 0.53 | 1.93 | 12.68 |
| M_{42} | 0.01 | 0.59 | 3.62 | 26.22 | 0.02 | 0.62 | 2.57 | 19.22 |
| M_{43} | 0.01 | 0.59 | 3.60 | 26.30 | 0.04 | 1.02 | 3.26 | 21.27 |

Table S5: Prior and posterior distributions of all parameters and several composite parameters of scenario 1. Notes about composite parameters: $NA\mu$ and $N_{i\mu}$ = effective population size (number of diploid individuals) of the ancestral unsampled population and of population i respectively, multiplied by the mean mutation rate μ ; $NF_{i\mu}$ = effective number of founders during the bottleneck of population i , multiplied by the mean mutation rate μ ; $BNsev_i$ = bottleneck severity of population i computed as $[(BD_i \times N_{parental\ population\ of\ population\ i}) / NF_i]$, with parental populations being populations A, 1, 2 and 3 for populations 1, 2, 3 and 4 respectively; M_{ij} is the effective number of migrants per generation from population i to population j backward in time, computed as $m_{ij} \times N_i$.