|  |  |  |  |
| --- | --- | --- | --- |
| Locality | Sample Size | Latitude | Longitude |
| Herring Bay, MD (MD1) | 25 | 38.754362 | -76.550857 |
| Kent Island, MD (MD2) | 38 | 38.936302 | -76.363836 |
| Patuxent River, MD (MD3) | 63 | 38.444332 | -76.607811 |
| Buzzard’s Island, Patuxent River, MD (MD4) | 60 | 38.489969 | -76.652694 |
| Sandy Island Cove, Nanticoke River, MD (MD5) | 55 | 38.260110 | -75.947966 |
| Back Cove, Smith Island, MD (MD6) | 17 | 38.021666 | -75.998875 |
| Janes Island, MD (MD7) | 56 | 38.007513 | -75.849861 |
| Marshy Creek, Kent Island, MD (MD8) | 64 | 38.954972 | -76.227814 |
| Northeast Cove, Bloodsworth Island, MD (MD9) | 43 | 38.167177 | -76.062002 |
| Tylerton, Smith Island, MD (MD10) | 64 | 37.964927 | -76.020185 |
| St. Jerome’s Creek, MD (MD11) | 16 | 38.134924 | -76.347049 |
| Mobjack Bay, VA (VA1) | 45 | 37.325137 | -76.350877 |
| Wachapreague, VA (VA2) | 38 | 37.602862 | -75.686380 |
| Metompkin Island, VA (VA3) | 20 | 37.752026 | -75.546442 |
| Cedar Island, VA (VA4) | 13 | 37.633496 | -75.612748 |

Appendix S1. Sampling localities and their abbreviations. Sampling took place from 2003-2005.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus | Repeat Motif | Fragment Size (bp) | Genbank Accession # |
| A18 | (GT)14 | 109 - 123 | AF337648 |
| B08 | (TAC)10 | 215 - 242 | AF517228 |
| B67 | (TAC)13 | 144 - 153 | AF517232 |
| B91 | (TAC)6 | 125 - 137 | AF517234 |
| D21 | (ATCT)15 | 150 - 158 | AF517236 |
| D55 | (ATCT)10 | 170 - 218 | AF517240 |
| D62 | (ATCT)11 | 128 - 172 | AF517241 |
| D87 | (ATCT)22 | 223 - 287 | AF517244 |
| D90 | (ATCT)9 | 109 - 145 | AF517247 |
| D93 | (ATCT)18 | 148 - 184 | AF517248 |
| D114 | (ATCT)13 | 86 - 130 | AF517251 |
| D121 | (ATCT)8 | 129 - 181 | AF517252 |

Appendix S2. Summary of loci amplified for subsequent analyses.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| MD1 |  |  |  |  |
| Locus | Ho | He | AR | NA |
| B91 | 0.44737 | 0.50351 | 2.000 | 2 |
| B08 | 0.97368 | 0.85333 | 5.954 | 7 |
| D93 | 0.75758\* | 0.67739 | 2.735 | 3 |
| A18 | 0.92105 | 0.76140 | 4.840 | 5 |
| D87 | 0.81579 | 0.85825 | 7.652 | 9 |
| B67 | 0.39474 | 0.44737 | 2.000 | 2 |
| D90 | 0.86842 | 0.85263 | 7.799 | 9 |
| D55 | 0.92105 | 0.86000 | 8.352 | 10 |
| D114 | 0.71053 | 0.64807 | 6.936 | 8 |
| D121 | 0.94737\*\*\* | 0.87789∆ | 9.590 | 12 |
| D62 | 0.78947 | 0.84035 | 8.384 | 10 |
| Avg | 0.77700 | 0.74365 | 6.022 | 7.0 |
| \* 0.05 \*\* 0.01 \*\*\*0.001 | | | | |

Appendix S3. Observed heterozygosity (Ho), expected heterozygosity (He), allelic richness (AR), and number of alleles (NA) by locus for population MD1. Significant deviations from Hardy-Weinberg equilibrium are denoted with asterisks. Triangles indicate loci deviating from Hardy-Weinberg equilibrium after Bonferroni correction.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| MD2 |  |  |  |  |
| Locus | Ho | He | AR | NA |
| B91 | 0.40625 | 0.45485 | 2.000 | 2 |
| B08 | 0.76562 | 0.84990 | 6.742 | 7 |
| D93 | 0.51562 | 0.57591 | 5.365 | 7 |
| A18 | 0.73438 | 0.76784 | 4.895 | 5 |
| D87 | 0.81250 | 0.83095 | 7.548 | 9 |
| B67 | 0.39062 | 0.38570 | 2.000 | 2 |
| D90 | 0.93750\* | 0.85753 | 7.958 | 9 |
| D55 | 0.89062 | 0.88595 | 8.094 | 10 |
| D114 | 0.85938 | 0.77227 | 4.736 | 5 |
| D121 | 0.85938 | 0.88189 | 8.381 | 11 |
| D62 | 0.82540 | 0.83327 | 6.815 | 9 |
| Avg | 0.72702 | 0.66025 | 5.867 | 6.9 |
| \* 0.05 \*\* 0.01 \*\*\*0.001 | | | | |

Appendix S3. Observed heterozygosity (Ho), expected heterozygosity (He), allelic richness (AR), and number of alleles (NA) by locus for population MD2. Significant deviations from Hardy-Weinberg equilibrium are denoted with asterisks.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| MD8 |  |  |  |  |
| Locus | Ho | He | AR | NA |
| B91 | 0.58730 | 0.49943 | 2.187 | 3 |
| B08 | 0.82540 | 0.83175 | 7.061 | 8 |
| D93 | 0.36842 | 0.37246 | 3.680 | 6 |
| A18 | 0.66667 | 0.68063 | 5.425 | 7 |
| D87 | 0.90476 | 0.86133 | 8.221 | 12 |
| B67 | 0.33333 | 0.38971 | 2.000 | 2 |
| D90 | 0.87302 | 0.81600 | 7.535 | 10 |
| D55 | 0.82540 | 0.83975 | 9.273 | 11 |
| D114 | 0.88889 | 0.82997 | 7.226 | 11 |
| D121 | 0.88889 | 0.87721 | 8.925 | 12 |
| D62 | 0.79365\* | 0.79695 | 6.452 | 8 |
| Avg | 0.72324 | 0.70865 | 6.180 | 8.2 |
| \* 0.05 \*\* 0.01 \*\*\*0.001 | | | | |

Appendix S3. Observed heterozygosity (Ho), expected heterozygosity (He), allelic richness (AR), and number of alleles (NA) by locus for population MD8. Significant deviations from Hardy-Weinberg equilibrium are denoted with asterisks.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| MD3 |  |  |  |  |
| Locus | Ho | He | AR | NA |
| B91 | 0.46667 | 0.48403 | 2.000 | 2 |
| B08 | 0.80000 | 0.85630 | 7.077 | 8 |
| D93 | 0.52542 | 0.42981 | 2.377 | 3 |
| A18 | 0.70000 | 0.75378 | 5.585 | 8 |
| D87 | 0.78333 | 0.79496 | 8.302 | 14 |
| B67 | 0.41667 | 0.45364 | 2.000 | 2 |
| D90 | 0.81667 | 0.81190 | 7.092 | 9 |
| D55 | 0.83333 | 0.86765 | 7.216 | 10 |
| D114 | 0.84746 | 0.83138 | 7.571 | 10 |
| D121 | 0.90000 | 0.87955 | 9.099 | 12 |
| D62 | 0.71667 | 0.79174 | 6.409 | 8 |
| Avg | 0.70966 | 0.72316 | 5.884 | 7.8 |
| \* 0.05 \*\* 0.01 \*\*\*0.001 | | | | |

Appendix S3. Observed heterozygosity (Ho), expected heterozygosity (He), allelic richness (AR), and number of alleles (NA) by locus for population MD3. No loci were found to be out of HWE.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| MD4 |  |  |  |  |
| Locus | Ho | He | AR | NA |
| B91 | 0.50000 | 0.57308 | 2.000 | 2 |
| B08 | 0.80000 | 0.79744 | 7.454 | 8 |
| D93 | 0.65000 | 0.53462 | 2.752 | 3 |
| A18 | 0.85000 | 0.77179 | 5.841 | 7 |
| D87 | 1.00000 | 0.90769 | 7.398 | 12 |
| B67 | 0.05263 | 0.05263 | 2.000 | 2 |
| D90 | 0.84211 | 0.83926 | 6.581 | 8 |
| D55 | 0.75000 | 0.83462 | 8.355 | 11 |
| D114 | 0.60000 | 0.56026 | 7.565 | 9 |
| D121 | 1.00000 | 0.90128 | 8.732 | 11 |
| D62 | 0.90000 | 0.79487 | 6.433 | 9 |
| Avg | 0.72224 | 0.68796 | 5.919 | 7.5 |
| \* 0.05 \*\* 0.01 \*\*\*0.001 | | | | |

Appendix S3. Observed heterozygosity (Ho), expected heterozygosity (He), allelic richness (AR), and number of alleles (NA) by locus for population MD4. No loci were found to be out of HWE.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| MD5 |  |  |  |  |
| Locus | Ho | He | AR | NA |
| B91 | 0.46154 | 0.51692 | 2.218 | 3 |
| B08 | 0.84615 | 0.81231 | 7.289 | 9 |
| D93 | 0.50000 | 0.49275 | 3.481 | 6 |
| A18 | 0.92308 | 0.76615 | 4.766 | 5 |
| D87 | 0.84615 | 0.86462 | 8.345 | 11 |
| B67 | 0.23077 | 0.40923 | 2.000 | 2 |
| D90 | 0.92308 | 0.74769 | 7.523 | 9 |
| D55 | 0.92308 | 0.87385 | 8.488 | 11 |
| D114 | 0.69231 | 0.68308 | 6.386 | 8 |
| D121 | 1.00000 | 0.92000 | 9.461 | 13 |
| D62 | 0.69231 | 0.80000 | 7.702 | 10 |
| Avg | 0.73077 | 0.71696 | 6.151 | 7.9 |
| \* 0.05 \*\* 0.01 \*\*\*0.001 | | | | |

Appendix S3. Observed heterozygosity (Ho), expected heterozygosity (He), allelic richness (AR), and number of alleles (NA) by locus for population MD4. No loci were found to be out of HWE.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| MD9 |  |  |  |  |
| Locus | Ho | He | AR | NA |
| B91 | 0.42105 | 0.51895 | 2.279 | 3 |
| B08 | 0.89474 | 0.82877 | 7.132 | 8 |
| D93 | 0.50000 | 0.50491 | 4.301 | 6 |
| A18 | 0.78947 | 0.71789 | 5.055 | 6 |
| D87 | 0.81579 | 0.86772 | 7.089 | 8 |
| B67 | 0.55263 | 0.46421 | 2.000 | 2 |
| D90 | 0.84211 | 0.80211 | 8.182 | 10 |
| D55 | 0.81579 | 0.86456 | 8.513 | 11 |
| D114 | 0.78947 | 0.73474 | 7.134 | 9 |
| D121 | 0.94737 | 0.90035 | 9.869 | 13 |
| D62 | 0.76316 | 0.77158 | 7.802 | 11 |
| Avg | 0.73923 | 0.72507 | 6.305 | 7.9 |
| \* 0.05 \*\* 0.01 \*\*\*0.001 | | | | |

Appendix S3. Observed heterozygosity (Ho), expected heterozygosity (He), allelic richness (AR), and number of alleles (NA) by locus for population MD9. No loci were found to be out of HWE.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| MD6 |  |  |  |  |
| Locus | Ho | He | AR | NA |
| B91 | 0.44000 | 0.50694 | 2.000 | 2 |
| B08 | 0.80000 | 0.82857 | 7.536 | 8 |
| D93 | 0.40000 | 0.46694 | 2.980 | 3 |
| A18 | 0.48000 | 0.66449 | 3.979 | 4 |
| D87 | 0.84000 | 0.84082 | 8.146 | 9 |
| B67 | 0.40000 | 0.37224 | 2.000 | 2 |
| D90 | 0.80000 | 0.81714 | 7.096 | 8 |
| D55 | 0.84000 | 0.85469 | 10.046 | 11 |
| D114 | 0.80000 | 0.74939 | 4.625 | 5 |
| D121 | 0.92000 | 0.88816 | 10.598 | 12 |
| D62 | 0.88000 | 0.86857 | 7.633 | 8 |
| Avg | 0.69091 | 0.71436 | 6.058 | 6.5 |
| \* 0.05 \*\* 0.01 \*\*\*0.001 | | | | |

Appendix S3. Observed heterozygosity (Ho), expected heterozygosity (He), allelic richness (AR), and number of alleles (NA) by locus for population MD6. No loci were found to be out of HWE.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| MD7 |  |  |  |  |
| Locus | Ho | He | AR | NA |
| B91 | 0.54545 | 0.49158 | 2.000 | 2 |
| B08 | 0.83636\* | 0.84570 | 7.577 | 9 |
| D93 | 0.55556 | 0.55746 | 3.467 | 6 |
| A18 | 0.85455 | 0.74395 | 5.425 | 7 |
| D87 | 0.80000 | 0.86305 | 8.731 | 13 |
| B67 | 0.41818 | 0.46188 | 2.214 | 3 |
| D90 | 0.78182 | 0.83253 | 8.184 | 11 |
| D55 | 0.89091 | 0.85455 | 8.421 | 10 |
| D114 | 0.69091 | 0.73862 | 6.851 | 9 |
| D121 | 0.85185 | 0.88629 | 9.497 | 12 |
| D62 | 0.88462 | 0.84037 | 7.158 | 9 |
| Avg | 0.73729 | 0.73782 | 6.320 | 8.3 |
| \* 0.05 \*\* 0.01 \*\*\*0.001 | | | | |

Appendix S3. Observed heterozygosity (Ho), expected heterozygosity (He), allelic richness (AR), and number of alleles (NA) by locus for population MD7. Significant deviations from Hardy-Weinberg equilibrium are denoted with asterisks.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| MD10 |  |  |  |  |
| Locus | Ho | He | AR | NA |
| B91 | 0.47059 | 0.42781 | 2.000 | 2 |
| B08 | 0.82353 | 0.86096 | 7.437 | 8 |
| D93 | 0.41176 | 0.55793 | 3.095 | 5 |
| A18 | 0.70588 | 0.65419 | 5.374 | 8 |
| D87 | 0.70588 | 0.79857 | 8.972 | 12 |
| B67 | 0.47059 | 0.49911 | 2.000 | 2 |
| D90 | 0.94118 | 0.82531 | 7.349 | 9 |
| D55 | 0.88235 | 0.89483 | 9.174 | 12 |
| D114 | 0.58824 | 0.63815 | 7.154 | 10 |
| D121 | 0.88235 | 0.90553 | 9.109 | 13 |
| D62 | 0.87500 | 0.86492 | 7.315 | 11 |
| Avg | 0.70521 | 0.72066 | 6.271 | 8.4 |
| \* 0.05 \*\* 0.01 \*\*\*0.001 | | | | |

Appendix S3. Observed heterozygosity (Ho), expected heterozygosity (He), allelic richness (AR), and number of alleles (NA) by locus for population MD10. No loci were found to be out of HWE..

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| MD11 |  |  |  |  |
| Locus | Ho | He | AR | NA |
| B91 | 0.48214 | 0.50306 | 2.000 | 2 |
| B08 | 0.89286 | 0.85698 | 6.928 | 7 |
| D93 | 0.53571 | 0.49373 | 3.000 | 3 |
| A18 | 0.75000 | 0.73198 | 5.690 | 6 |
| D87 | 0.92857 | 0.87130 | 8.635 | 10 |
| B67 | 0.39286 | 0.46959 | 2.000 | 2 |
| D90 | 0.83929 | 0.84749 | 6.883 | 7 |
| D55 | 0.87500 | 0.87950 | 9.377 | 10 |
| D114 | 0.83636 | 0.75430 | 6.853 | 7 |
| D121 | 0.87500 | 0.89318 | 9.168 | 10 |
| D62 | 0.81818 | 0.82969 | 6.440 | 7 |
| Avg | 0.74782 | 0.73916 | 6.089 | 6.5 |
| \* 0.05 \*\* 0.01 \*\*\*0.001 | | | | |

Appendix S3. Observed heterozygosity (Ho), expected heterozygosity (He), allelic richness (AR), and number of alleles (NA) by locus for population MD11. No loci were found to be out of HWE.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| VA1 |  |  |  |  |
| Locus | Ho | He | AR | NA |
| B91 | 0.48837 | 0.51737 | 2.000 | 2 |
| B08 | 0.74419 | 0.84213 | 6.733 | 7 |
| D93 | 0.51163 | 0.59590 | 3.647 | 5 |
| A18 | 0.58140\* | 0.71546 | 3.972 | 4 |
| D87 | 0.81395 | 0.79754 | 7.339 | 9 |
| B67 | 0.53488 | 0.41724 | 2.000 | 2 |
| D90 | 0.83721 | 0.85855 | 7.220 | 9 |
| D55 | 0.86047 | 0.85445 | 8.484 | 11 |
| D114 | 0.62791 | 0.72011 | 7.499 | 10 |
| D121 | 0.88372 | 0.89877 | 8.172 | 11 |
| D62 | 0.74419 | 0.84761 | 7.106 | 9 |
| Avg | 0.69345 | 0.73319 | 5.834 | 7.2 |
| \* 0.05 \*\* 0.01 \*\*\*0.001 | | | | |

Appendix S3. Observed heterozygosity (Ho), expected heterozygosity (He), allelic richness (AR), and number of alleles (NA) by locus for population VA1. Significant deviations from Hardy-Weinberg equilibrium are denoted with asterisks.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| VA3 |  |  |  |  |
| Locus | Ho | He | AR | NA |
| B91 | 0.44444 | 0.88343 | 2.943 | 3 |
| B08 | 0.81250 | 0.82862 | 6.417 | 7 |
| D93 | 0.51562 | 0.53851 | 2.600 | 3 |
| A18 | 0.67188 | 0.71026 | 5.487 | 6 |
| D87 | 0.88889 | 0.88190 | 9.929 | 11 |
| B67 | 0.43750 | 0.42077 | 1.632 | 2 |
| D90 | 0.85246 | 0.83403 | 7.227 | 8 |
| D55 | 0.79365\* | 0.47543 | 7.613 | 9 |
| D114 | 0.81250 | 0.75320 | 5.266 | 6 |
| D121 | 0.85714 | 0.87594 | 10.439 | 13 |
| D62 | 0.80952 | 0.83327 | 5.798 | 7 |
| Avg | 0.71783 | 0.70349 | 5.941 | 6.8 |
| \* 0.05 \*\* 0.01 \*\*\*0.001 | | | | |

Appendix S3. Observed heterozygosity (Ho), expected heterozygosity (He), allelic richness (AR), and number of alleles (NA) by locus for population VA3. Significant deviations from Hardy-Weinberg equilibrium are denoted with asterisks.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| VA4 |  |  |  |  |
| Locus | Ho | He | AR | NA |
| B91 | 0.62500 | 0.51613 | 2.000 | 2 |
| B08 | 0.93750 | 0.86492 | 6.920 | 7 |
| D93 | 0.56250 | 0.58266 | 5.000 | 5 |
| A18 | 0.81250 | 0.74798 | 4.994 | 7 |
| D87 | 0.75000 | 0.78024 | 8.689 | 9 |
| B67 | 0.50000 | 0.51613 | 2.000 | 2 |
| D90 | 1.00000 | 0.85282 | 9.603 | 10 |
| D55 | 1.00000 | 0.90524 | 9.757 | 10 |
| D114 | 0.81250 | 0.80242 | 6.763 | 7 |
| D121 | 0.87500 | 0.89113 | 10.757 | 11 |
| D62 | 0.81250 | 0.79234 | 5.920 | 6 |
| Avg | 0.78977 | 0.75018 | 6.582 | 6.7 |
| \* 0.05 \*\* 0.01 \*\*\*0.001 | | | | |

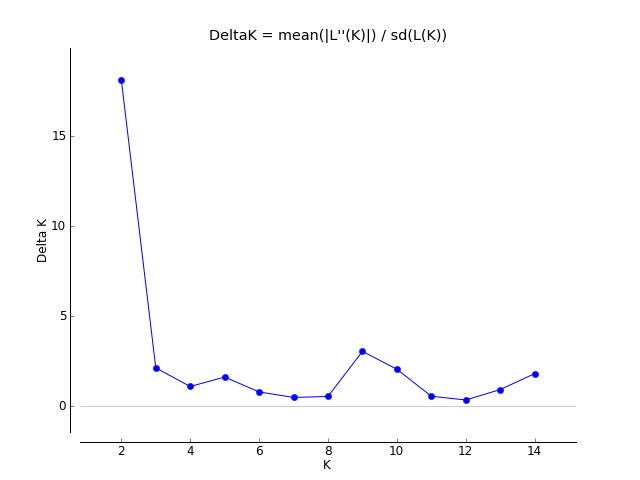
Appendix S3. Observed heterozygosity (Ho), expected heterozygosity (He), allelic richness (AR), and number of alleles (NA) by locus for population VA4. No loci were found to be out of HWE.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| VA2 |  |  |  |  |
| Locus | Ho | He | AR | NA |
| B91 | 0.55556 | 0.50162 | 2.000 | 3 |
| B08 | 0.88889 | 0.84694 | 6.920 | 7 |
| D93 | 0.48889 | 0.56829 | 5.000 | 4 |
| A18 | 0.71111 | 0.69613 | 4.994 | 5 |
| D87 | 0.84444 | 0.83620 | 8.689 | 9 |
| B67 | 0.48889 | 0.48539 | 2.000 | 2 |
| D90 | 0.84444 | 0.84270 | 9.603 | 10 |
| D55 | 0.73333 | 0.87640 | 9.757 | 10 |
| D114 | 0.80000 | 0.78427 | 6.763 | 7 |
| D121 | 0.75556\*\*\* | 0.86142 | 10.757 | 11 |
| D62 | 0.82222 | 0.82722 | 5.920 | 6 |
| Avg | 0.72121 | 0.73878 | 6.024 | 7.3 |
| \* 0.05 \*\* 0.01 \*\*\*0.001 | | | | |

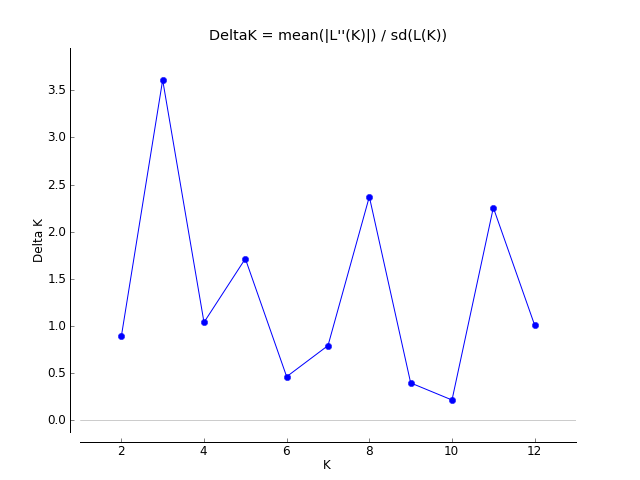
Appendix S3. Observed heterozygosity (Ho), expected heterozygosity (He), allelic richness (AR), and number of alleles (NA) by locus for population VA2. Significant deviations from Hardy-Weinberg equilibrium are denoted with asterisks.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus Pair | *P-*value | Locus Pair | *P*-value |
| B91 x B08 | 0.660 | D93 x D87 | 0.097 |
| B91 x D93 | 0.670 | D93 x B67 | 0.350 |
| B91 x A18 | 0.272 | D93 x D90 | 0.295 |
| B91 x D87 | 0.755 | D93 x D55 | 0.634 |
| B91 x B67 | 1.00 | D93 x D114 | 0.518 |
| B91 x D90 | 0.290 | D93 x D121 | 0.299 |
| B91 x D55 | 0.100 | D93 x D62 | 0.801 |
| B91 x D114 | 0.078 | A18 x D87 | 0.359 |
| B91 x D121 | 0.884 | A18 x B67 | 0.625 |
| B91 x D62 | 0.455 | A18 x D90 | 0.526 |
| B08 x D93 | 0.069 | A18 x D55 | 0.964 |
| B08 x A18 | 0.002 | A18 x D114 | 0.315 |
| B08 x D87 | 0.191 | A18 x D121 | 0.954 |
| B08 x D67 | 0.837 | A18 x D62 | 0.375 |
| B08 x D90 | 0.305 | D87 x B67 | 0.900 |
| B08 x D55 | 0.670 | D87 x D90 | 0.681 |
| B08 x D114 | 0.264 | D87 x D55 | 0.368 |
| B08 x D121 | 0.065 | D87 x D114 | 0.069 |
| B08 x D62 | 0.468 | D87 x D121 | 0.378 |
| B08 x A18 | 0.042 | D87 x D62 | 0.737 |
| B67 x D90 | 0.048 | D90 x D62 | 0.393 |
| B67 x D55 | 0.308 | D55 x D114 | 0.121 |
| B67 x D114 | 0.666 | D55 x D121 | 0.110 |
| B67 x D121 | 0.949 | D55 x D62 | 0.978 |
| B67 x D62 | 0.637 | D114 x D121 | 0.149 |
| D90 x D55 | 0.290 | D114 x D62 | 0.590 |
| D90 x D114 | 0.081 | D121 x D62 | 0.531 |
| D90 x D121 | 0.028 |  | |

Appendix S4. Pairwise tests of linkage disequilibrium for all loci, based on 1000 permutations and an adjusted *P*-value of 0.00090.



Appendix S5. ∆K plot under the Evanno method for the initial run of STRUCTURE finding the Patuxent River as a genotypic cluster



Appendix S5. ∆K plot under the Evanno method for the second run of STRUCTURE finding KI, ICB, and CoB as populations.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Variation Source | d.f. | Sum of Squares | Percent of Genetic Variation Explained | *P*-value |
| **Sampling Locality** |  |  |  |  |
| Among Populations | 14 | 22699.4 | 0.88 | < 0.0001 |
| Within Populations | 1219 | 1146833.2 | 99.12 | < 0.0001 |
| Total | 1233 | 1169532.6 | 100 |  |
|  |  |  |  |  |
| **Bay Landscape** |  |  |  |  |
| Among Groups | 2 | 8407.6 | 0.88 | 0.0154 |
| Among Populations | 12 | 14291.8 | 0.34 | 0.0808 |
| Within Populations | 1219 | 1146833.2 | 98.78 | < 0.0001 |
| Total |  | 1169532.6 | 100 |  |
|  |  |  |  |  |
| **STRUCTURE Cluster** |  |  |  |  |
| Among Groups | 3 | 11321.4 | 0.96 | 0.0031 |
| Among Populations | 11 | 11378 | 0.13 | 0.3147 |
| Within Populations | 1219 | 1146833.2 | 98.91 | 0.0002 |
| Total |  | 1169532.6 | 100 |  |

Appendix S6. AMOVA results indicating terrapin populations in Chesapeake Bay are weakly structured. Genetic data were partitioned by sampling locality, bay landscape (samples taken within tributary systems, Chesapeake Bay proper, and outside the bay), and by STRUCTURE cluster.

|  |  |  |  |
| --- | --- | --- | --- |
| Population | TPM | SMM | Mode-shift |
| Kent Island | 0.18 | 0.35 | L-shaped |
| Patuxent River | 0.12 | 0.42 | L-shaped |
| Coastal Bay | 0.45 | 0.71 | L-shaped |
| Inner CB | 0.48 | 0.90 | L-shaped |
| Combined | 0.65 | 0.94 | L-shaped |

Appendix S7. *P*-values for bottleneck detection under each model in BOTTLENECK. Parameters for the TPM include 95% step-wise mutations and a 12% variance on multi-step mutations. “L-shaped” distributions under a mode-shift test indicate a failure to detect a bottleneck. All results are based on 50,000 permutations. The bottom row represents the entire pooled dataset