Table S1. Collection information and sequencing depth for samples used in RAD-seq SNP discovery.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Species** | **Sample#** | **Collection information** | **No. reads** | **Mean coverage** |
| *O. bruceata* | 497 | USA; New Jersey; Middletown; Coll: R. Fine | 893,323 | 239.8 |
|  | 634 | USA; Wisconsin; Oconto Falls; Coll: L. Williams | 1,158,658 | 291.4 |
|  | 636 | USA; Wisconsin; Oconto Falls.; Coll: L. Williams | 1,027,796 | 270.6 |
|  | 11-385.03 | CANADA; New Brunswick; Dalhousie; Coll G. Boettner | 1,830,530 | 387.5 |
|  | 11-392.01 | USA; New York; Westchester; Coll: J.C. Kircher | 1,296,739 | 270.2 |
|  | 11-392.03 | USA; New York; Westchester; Coll: J.C. Kircher | 1,363,872 | 319.3 |
|  | 11-393.01 | USA; New Jersey; Bordentown; Coll: M. O’Conor | 1,387,290 | 303.4 |
|  | 11-394.02 | USA; Pennsylvania; Harborcreek; Coll: J. Fuller | 1,338,816 | 233.8 |
|  | 11-394.03 | USA; Pennsylvania; Harborcreek; Coll: J. Fuller | 1,632,419 | 264.7 |
|  | 11-394.04 | USA; Pennsylvania; Harborcreek; Coll: J. Fuller | 1,232,185 | 248.7 |
|  | 11-395.01 | USA; New Jersey; Scotch Plains; Coll. M. O’Conor | 1,123,437 | 267.4 |
|  | 11-395.02 | USA; New Jersey; Scotch Plains; Coll. M. O’Conor | 914,982 | 226.6 |
|  | 11-397.01 | USA; New York; Saratoga Springs; Coll.: K. Schlosser | 1,105,068 | 225.5 |
|  | 11-397.03 | USA; New York; Saratoga Springs; Coll.: K. Schlosser | 1,021,736 | 237.4 |
|  | 11-398.01 | USA; Minnesota; Rochester; Coll: E. Hayes | 897,589 | 223.4 |
|  | 11-398.02 | USA; Minnesota; Rochester; Coll: E. Hayes | 823,182 | 184.6 |
|  | 11-398.03 | USA; Minnesota; Rochester; Coll: E. Hayes | 496,885 | 121.7 |
|  | 11-398.04 | USA; Minnesota; Rochester; Coll: E. Hayes | 708,271 | 152.0 |
|  | 11-400.02 | USA; Connecticut; Greenwich; Coll: G. Boettner | 1,068,391 | 236.4 |
|  | 547 | USA; Oregon; Salem; Coll: R. Kimmick | 410,381 | 67.2 |
|  | 11-389.04 | USA; Washington; Federal Way; C. Phillips | 1,028,806 | 181.3 |
|  | 11-390.03 | USA; Washington; Tenino; Coll: E. Lagasa | 1,816,813 | 448.6 |
|  | 11-396.03 | USA; Maine; Westfield; Coll: G. Boettner | 1,076,387 | 261.8 |
| *O. brumata* | 7981 | USA; Massachusetts; Acton; Coll: G. Boettner | 3,521,446 | 422.2 |
|  | 1948 | GERMANY; Hesse; Coll: Berg | 3,264,821 | 241.8 |
|  | 11-374.03 | SLOVAKIA; Banská Štiavnica; Coll: M. Turcáni | 3,196,456 | 281.2 |
|  | 11-375.01 | CZECH REPUBLIC; Prague; Coll: M. Turcáni | 3,646,304 | 336.8 |
|  | 11-376.03 | SPAIN; Lugo; Coll: M. Lombardero | 2,207,336 | 203.2 |
|  | 11-377.06 | SWITZERLAND; Delemont; Coll: M. Kenis | 4,942,589 | 372.4 |
|  | 11-379.13 | SCOTLAND; Aberdeenshire; Coll: Adam Vanbergen | 3,258,431 | 246.9 |
|  | 11-379.15 | SCOTLAND; Aberdeenshire; Coll: Adam Vanbergen | 3,894,348 | 378.6 |
|  | 11-380.05 | ENGLAND; Surrey; Coll: C. Tilbury | 4,756,502 | 403.8 |
|  | 11-381.03 | SERBIA; Negotin; Coll: M. Glavendekić | 2,226,245 | 126.5 |
|  | 11-381.05 | SERBIA; Negotin; Coll: M. Glavendekić | 1,613,448 | 65.3 |
|  | 11-382.03 | GERMANY; Baten-Württenberg; Coll: M. Kenis | 3,332,184 | 278.5 |
|  | 11-386.01 | FRANCE; Orléans; Coll: R. Mazet; | 3,157,591 | 273.1 |
|  | 11-386.04 | FRANCE; Orléans; Coll: R. Mazet; | 3,511,334 | 295.4 |
|  | 11-413.03 | SWEDEN; Uppsala; Coll: H. Bylund | 2,544,524 | 191.0 |
|  | 11-413.04 | SWEDEN; Uppsala; Coll: H. Bylund | 2,833,428 | 180.8 |
|  | 11-414.03 | SWEDEN; Uppsala; Coll: H. Bylund | 2,676,277 | 256.6 |
|  | 1935 | CANADA; Nova Scotia; Annapolis; Coll: G. Boettner | 3,883,218 | 429.5 |
|  | 11-411.03 | CANADA; British Columbia;Victoria ; Coll: G. Boettner | 983,087 | 125.5 |
|  | 11-412.032 | CANADA; British Columbia; Victoria; Coll: G. Boettner | N/A | N/A |
| *O. brumata* x *bruceata* | 7631,2 | USA; Massachusetts; Littleton; Coll: G. Boettner | N/A | N/A |
|  | 20491 | USA; New Hampshire; Hampton; Coll: G. Boettner | 2,175,356 | 227.9 |
|  | 23481 | USA; Massachusetts; Lincoln; Coll: G. Boettner | 2,788,082 | 311.5 |
| *O. fagata* | 11-378.01 | SWITZERLAND; Jura; Coll: M.J.W. Cock | 1,388,809 | 265.7 |
|  | 11-378.02 | SWITZERLAND; Jura; Coll: M.J.W. Cock | 1396947 | 288.9 |

1 *a priori* putative hybrids based on G6PD alleles (Elkinton et al. 2010)

2 not included in analyses because of sequencing failure

Table S2. Primer sequences (5’ to 3’) for the 46 microsatellite loci that were tested in winter moth. The 24 loci that amplified consistently and were in Hardy-Weinberg equilibrium are identified with an asterisk (\*). Loci that also amplified in Bruce spanworm are identified with a cross (†).

|  |  |  |
| --- | --- | --- |
| Locus Name | Forward primer | Reverse primer |
| WM00070 | AGAGGGTTAGACGGACTGAC | TCTGGATACCCACGACACAG |
| WM00485 | CCTCGTAAACAAACCGCGTC | CAGTGAATGTAGCCGGCTCA |
| WM00672\* | TTGCTTTGTTTAAGTCTCTAGCAA | TCTAGCTGTCTTCGTGAGGAAC |
| WM00863† | GCCGGGATCACATCTGTCAA | CGTTTCGAGTGGCGTTTGAG |
| WM00952\*† | CGTCCAGATCGTAATCGCCA | CTTTCACCAGGGACTTCGGG |
| WM01184 | ATGCACTCACAAGCACTGGA | GTATTGCAGACGGGCGTTTC |
| WM01585\* | TCAAGTTTCGTCAAGATTAGTTGAA | CGAAGCTCCGTACGACAACT |
| WM01619\*† | AACTGCACATGAAACACGCA | ACGTTACACTGATTCCAAGTCG |
| WM01762\* | TGGTATCACCGTTTCTCTGCC | TCCGAAGTGAAATGCTAAAGTTCC |
| WM01835 | GATGGACCGACGTCAGGAAG | ACCGTTAGGATCTTTGTCCTTCC |
| WM02191\* | AGTCTGTTTAGCGTGAAATGGT | CGCTCCTGTGCAAGTTAGCA |
| WM02232† | TCCTTGCCAATAACGTGTGAC | CTAACTCGGCACCTCACTGG |
| WM02339\*† | GCTCCGACAACTTGACCTGA | GCGTGACGATACAAGCAACA |
| WM02392 | TGAGCTGTAAGGGTTGGACC | CGCAAGCTCTAGCACCCTAG |
| WM02534 | GGCAGAAACCAGTCCTGTCA | TGAATGCGGCGATTAAGTTTCA |
| WM02544 | ACGTAGCCCAAATACTGCGA | GTGGCGCTAACATAAACCGG |
| WM02565\* | ATTTACGGGAACTCTCAACGAC | TCGCATTCCCTGAATCTAGAGC |
| WM02953 | GGTTTGTACGGAACCTGTGC | CTGAGAAGAGGCTGACCCTG |
| WM03270\* | AGGCATTCTACGGGAGGTCA | CGAAGCAATGCTAATGCTCGT |
| WM03280\* | TCTCTTCCGATCGAATTTCGCA | ATCGCACAGAACCGTTTGGA |
| WM03296 | CCTGTAAGGTACCCACTGCA | ACACATTCGTCCAAGTTTACTTAGAG |
| WM03463 | AATCTCTAACGCACGAGAATGG | GGAACGGTGTGCTGATCAAA |
| WM03475\*† | ACATTGAGTCATGCGGTCGT | TTCTGGTCGTTTCCATCGCA |
| WM03667 | GACTCGCTCGCATCTCAAGT | ACACCAGTAGCAGTCTAAGCG |
| WM05159\* | TGGACAACGGAAATCCTCTACA | CCCACTTGATCGTGTACTTTCA |
| WM07650\*† | CCCTCCTTAGCTTTCTCACAACT | TGTTAGCACCATTGATATTGGTTCA |
| WM12042\* | CCAGGGTTCCAGCTATCTGC | GGAGCGTGGGAGACTTGAAA |
| WM12853\*† | GGCGCTTGGCTCTCATATTG | CCTGGACGCGCACTATGTAG |
| WM13672 | ACCGAACTGGCTGAAGAAGG | TAATCCGTCGAGCCGTTTCA |
| WM16696\* | CACCCAGGATACGATGGCAT | TCGACGTGTGGGTTTCTCAA |
| WM17017 | CTCCTTCAATAGGCGTTCTGC | GTCTGCAGGCAATTCTTAGACG |
| WM17094 | TGGTTGTACTAACTCGGCACC | GGGTCGTTGAGGCTTATTGA |
| WM18760\* | ACGTCTGACCCTTGTGTCTG | GGCACCAACTCAGATAAGAGGT |
| WM22363† | CGACGCTGAGGACTTTGACT | GATGACTCGTTCCACGGTGA |
| WM24011\* | CCCGATTTAAATGTCTCGCGA | AGGTAATTTCATGTTTGCTCGTGA |
| WM24441 | TGTGGGAGGCTTCATCCAAC | TCCACCGACTTCTTGCTACC |
| WM24979\* | CTAGGCATTCGTAGGCGCAA | AGCCTAACGACCACTATGTGA |
| WM28247\*† | CATGGTCACTTGCGGTGGTA | ATGTAAGCCGCAGTTACATCT |
| WM29309\*† | CCGTCTATGATCTGTGCTGCT | AGACCAGAGCGTTTCCTTGG |
| WM30125† | CGATGGACCAAAGACATTATAGAGG | TATCATAATCTACGAGGGATCAGATGA |
| WM31399\* | GTTCACACCGCTGATAAGCA | TTCTGTGGCCTGTTGGATTT |
| WM32817 | CGGGCGTTCCACTAGCAATA | GCACACTGAAGATGATAGGCC |
| WM32864 | ACTGGGTTATGGCTTGACGG | TGTAGTTGCTTGTTGACATTAAGGT |
| WM32985\*† | TGAACCACCGGCTTTATAAAGGA | TACGAGAATCCAGCCCTCCA |
| WM33617 | CCTGTAGTGAATGGCTCGACC | ACTCCTCTACTTTCCATCGTTGG |
| WM34463\*† | CGTGAATTGGGCTTCAGAATTG | TGTCACCATTTGCTTTAATCACCC |

Table S3. Frequencies of null alleles estimated using MICRO-CHECKER (van Oosterhout *et al.,* 2004). Numbers in bold indicate loci and populations that were identified as likely to have null alleles.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Winter moth | | Bruce spanworm | |
| Locus | Reinhardshagen | Marcillac | Harborcreek | Oconto |
| WM00070 | **0.2390** | **0.2286** |  |  |
| WM00485 | **0.1745** | **0.1994** |  |  |
| WM00672 | 0.0695 | **0.1070** |  |  |
| WM00863 | 0.1009 | **0.1691** | -0.5025 | -0.1847 |
| WM00952 | -0.0392 | 0.0794 | **0.1943** | **0.2398** |
| WM01184 | 0.0326 | 0.0197 |  |  |
| WM01585 | -0.0673 | 0.0126 |  |  |
| WM01619 | -0.0307 | 0.0130 | -0.0624 | -0.0855 |
| WM01762 | **0.1741** | **0.1958** |  |  |
| WM01835 | **0.1371** | **0.2355** |  |  |
| WM02191 | **0.2429** | **0.1125** |  |  |
| WM02232 | -0.5173 | 0.0206 | -0.1810 | -0.2701 |
| WM02339 | 0.0210 | -0.0290 | 0.1194 | **0.1646** |
| WM02392 | 0.0596 | 0.0802 |  |  |
| WM02534 | **0.2092** | **0.1840** |  |  |
| WM02544 | 0.0976 | -0.1576 |  |  |
| WM02565 | **0.1709** | -0.0109 |  |  |
| WM02953 | -0.0802 | -0.1409 |  |  |
| WM03270 | 0.0048 | 0.0688 |  |  |
| WM03280 | 0.0379 | 0.0331 |  |  |
| WM03296 | **0.2109** | 0.0518 |  |  |
| WM03463 | 0.0536 | 0.0430 |  |  |
| WM03475 | 0.0534 | 0.0227 | 0.0995 | 0.1008 |
| WM03667 | 0.0551 | **0.1891** |  |  |
| WM05159 | 0.0466 | 0.0131 |  |  |
| WM07650 | 0.0483 | 0.0376 | **0.1494** | -0.0934 |
| WM12042 | -0.0338 | 0.0348 |  |  |
| WM12853 | -0.0085 | -0.0183 | 0.0108 | 0.0236 |
| WM13672 | **0.1368** | 0.1184 |  |  |
| WM16696 | **0.2070** | 0.1337 |  |  |
| WM17017 | **0.3955** | **0.4527** |  |  |
| WM17094 | **0.2199** | -0.1153 |  |  |
| WM18760 | 0.0566 | -0.0006 |  |  |
| WM22363 | -0.1313 | -0.0937 | 0.0471 | 0.0290 |
| WM24011 | -0.0137 | -0.0156 |  |  |
| WM24441 | -0.1313 | 0.0848 |  |  |
| WM24979 | -0.0047 | 0.0431 |  |  |
| WM28247 | -0.0253 | -0.0192 | -0.1835 | -0.2235 |
| WM29309 | -0.0696 | -0.0360 | -0.2600 | -0.1728 |
| WM30125 | 0.1005 | 0.0285 | -0.0533 | 0.1359 |
| WM31399 | -0.0247 | 0.0487 |  |  |
| WM32817 | 0.0207 | 0.0654 |  |  |
| WM32864 | -0.1502 | 0.0549 |  |  |
| WM32985 | 0.0480 | 0.1507 | 0.1410 | 0.1405 |
| WM33617 | -0.1524 | -0.0636 |  |  |
| WM34463 | 0.0399 | **0.0903** | 0.0668 | 0.0914 |

Table S4. Combinations of winter moth and Bruce spanworm microsatellite loci suitable for PCR multiplexing. The first two combinations include loci that amplify in both species and the remaining combinations amplify only in winter moth.

|  |  |  |
| --- | --- | --- |
| **Combination** | **Locus** | **Dye** |
| WM\_BSw1 | WM01619 | 6-FAM |
|  | WM03475 | 6-FAM |
|  | WM02339 | NED |
|  | WM00952 | PET |
|  | WM34463 | VIC |
| WM\_BSw2 | WM29309 | 6-FAM |
|  | WM07650 | PET |
|  | WM32985 | 6-FAM |
|  | WM12853 | NED |
|  | WM28247 | VIC |
| WM1 | WM01762 | 6-FAM |
| WM2 | WM31399 | 6-FAM |
|  | WM00672 | 6-FAM |
|  | WM16696 | 6-FAM |
|  | WM24011 | NED |
|  | WM03280 | NED |
| WM3 | WM01585 | 6-FAM |
|  | WM05159 | 6-FAM |
|  | WM24979 | NED |
|  | WM12042 | NED |
|  | WM03270 | VIC |
| WM4 | WM02191 | NED |
|  | WM18760 | PET |
|  | WM02565 | VIC |

Table S5. Sample information and individual results for NewHybrids (Anderson & Thompson, 2002), Structure (Pritchard *et al.,* 2000), and COI mitochondrial haplotype analyses. For NewHybrids results, the species or hybrid class with the highest probability is indicated, followed by the probability of assignment to each class. For Structure results, the probability of assignment to each species is shown. For COI mitochondrial haplotype analysis, the matching maternal lineage is indicated.

|  |  | NewHybrids | | | | | | |  | Structure | |  | COI |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample # | Locality | Hybrid class  assignment1 | Winter moth | Bruce spanworm | F1 | F2 | Winter moth Backcross | Bruce spanworm backcross |  | Winter moth | Bruce spanworm |  | Maternal lineage1 |
| 763 | MA: Littleton | BSw | 0.000 | 1.000 | 0.000 | 0.000 | 0.000 | 0.000 |  | 0.103 | 0.897 |  | BSw |
| 774 | MA: Littleton | BSw | 0.000 | 0.998 | 0.000 | 0.001 | 0.000 | 0.001 |  | 0.155 | 0.845 |  | BSw |
| 796 | MA: Acton | WM | 0.832 | 0.000 | 0.000 | 0.000 | 0.168 | 0.000 |  | 0.984 | 0.016 |  | WM |
| 798 | MA: Acton | WM | 0.789 | 0.000 | 0.000 | 0.002 | 0.209 | 0.000 |  | 0.879 | 0.121 |  | WM |
| 800 | MA: Acton | WMback | 0.000 | 0.000 | 0.000 | 0.051 | 0.948 | 0.000 |  | 0.708 | 0.292 |  | WM |
| 801 | MA: Acton | WM | 0.631 | 0.000 | 0.000 | 0.004 | 0.365 | 0.000 |  | 0.929 | 0.071 |  | WM |
| 826 | MA: Acton | WMback | 0.000 | 0.000 | 0.000 | 0.032 | 0.968 | 0.000 |  | 0.712 | 0.288 |  | BSw |
| 842 | MA: Acton | F1 | 0.000 | 0.000 | 0.891 | 0.049 | 0.059 | 0.001 |  | 0.507 | 0.493 |  | BSw |
| 920 | RI: West Greenwich | WMback | 0.000 | 0.000 | 0.004 | 0.219 | 0.776 | 0.000 |  | 0.686 | 0.314 |  | WM |
| 930 | RI: West Greenwich | F1 | 0.000 | 0.000 | 0.835 | 0.054 | 0.111 | 0.000 |  | 0.559 | 0.441 |  | BSw |
| 985 | MA: Littleton | WMback | 0.000 | 0.000 | 0.004 | 0.067 | 0.929 | 0.000 |  | 0.677 | 0.323 |  | WM |
| 1008 | MA: Littleton | F1 | 0.000 | 0.000 | 0.972 | 0.004 | 0.024 | 0.000 |  | 0.569 | 0.431 |  | WM |
| 1015 | MA: Acton | F1 | 0.000 | 0.000 | 0.981 | 0.002 | 0.017 | 0.000 |  | 0.554 | 0.446 |  | WM |
| 1018 | MA: Acton | F1 | 0.000 | 0.000 | 0.701 | 0.037 | 0.261 | 0.000 |  | 0.646 | 0.354 |  | WM |
| 1023 | MA: Acton | F2 | 0.000 | 0.000 | 0.000 | 0.776 | 0.224 | 0.000 |  | 0.656 | 0.344 |  | BSw |
| 1708 | MA: Littleton | F2 | 0.000 | 0.000 | 0.021 | 0.947 | 0.026 | 0.006 |  | 0.541 | 0.459 |  | BSw |
| 1716 | MA: Acton | WMback | 0.000 | 0.000 | 0.007 | 0.052 | 0.940 | 0.000 |  | 0.677 | 0.323 |  | WM |
| 1957 | NH: Milford | F1 | 0.000 | 0.000 | 0.928 | 0.007 | 0.065 | 0.000 |  | 0.595 | 0.405 |  | WM |
| 1966 | NH: Londonderry | F1 | 0.000 | 0.000 | 0.610 | 0.026 | 0.364 | 0.000 |  | 0.626 | 0.374 |  | BSw |
| 1970 | NH: Londonderry | F1 | 0.000 | 0.000 | 0.645 | 0.203 | 0.150 | 0.001 |  | 0.514 | 0.486 |  | WM |
| 1979 | NH: Atkinson | F1 | 0.000 | 0.000 | 0.931 | 0.021 | 0.047 | 0.000 |  | 0.499 | 0.501 |  | WM |
| 1982 | NH: Kingston | WMback | 0.000 | 0.000 | 0.442 | 0.048 | 0.510 | 0.000 |  | 0.615 | 0.385 |  | WM |
| 2045 | NY: Oyster Bay | BSw | 0.000 | 1.000 | 0.000 | 0.000 | 0.000 | 0.000 |  | 0.017 | 0.983 |  | BSw |
| 2047 | NH: Hampton | F1 | 0.000 | 0.000 | 0.608 | 0.069 | 0.323 | 0.000 |  | 0.601 | 0.399 |  | WM |
| 2049 | NH: Hampton | WMback | 0.000 | 0.000 | 0.051 | 0.224 | 0.725 | 0.000 |  | 0.596 | 0.404 |  | WM |
| 2145 | MA: Concord | WMback | 0.000 | 0.000 | 0.361 | 0.024 | 0.614 | 0.000 |  | 0.699 | 0.301 |  | BSw |
| 2174 | MA: Acton | WMback | 0.000 | 0.000 | 0.046 | 0.040 | 0.914 | 0.000 |  | 0.683 | 0.317 |  | WM |
| 2175 | MA: Acton | WMback | 0.000 | 0.000 | 0.085 | 0.097 | 0.818 | 0.000 |  | 0.634 | 0.366 |  | WM |
| 2176 | MA: Acton | F1 | 0.000 | 0.000 | 0.931 | 0.007 | 0.063 | 0.000 |  | 0.607 | 0.393 |  | WM |
| 2179 | MA: Littleton | F1 | 0.000 | 0.000 | 0.992 | 0.004 | 0.004 | 0.000 |  | 0.478 | 0.522 |  | WM |
| 2189 | MA: Littleton | F1 | 0.000 | 0.000 | 0.635 | 0.039 | 0.326 | 0.000 |  | 0.629 | 0.371 |  | WM |
| 2197 | MA: Harvard | F1 | 0.000 | 0.000 | 0.940 | 0.010 | 0.049 | 0.000 |  | 0.535 | 0.465 |  | BSw |
| 2200 | MA: Harvard | F1 | 0.000 | 0.000 | 0.742 | 0.053 | 0.205 | 0.000 |  | 0.582 | 0.418 |  | BSw |
| 2202 | MA: Harvard | WMback | 0.000 | 0.000 | 0.265 | 0.126 | 0.610 | 0.000 |  | 0.632 | 0.368 |  | BSw |
| 2209 | MA: Harvard | F2 | 0.000 | 0.000 | 0.235 | 0.727 | 0.032 | 0.006 |  | 0.474 | 0.526 |  | WM |
| 2280 | MA: Acton | WMback | 0.000 | 0.000 | 0.000 | 0.048 | 0.952 | 0.000 |  | 0.666 | 0.334 |  | BSw |
| 2304 | MA: LIttleton | F1 | 0.000 | 0.000 | 0.870 | 0.013 | 0.118 | 0.000 |  | 0.568 | 0.432 |  | WM |
| 2306 | MA: LIttleton | WMback | 0.000 | 0.000 | 0.054 | 0.049 | 0.897 | 0.000 |  | 0.693 | 0.307 |  | BSw |
| 2321 | MA: LIttleton | F1 | 0.000 | 0.000 | 0.848 | 0.018 | 0.134 | 0.000 |  | 0.596 | 0.404 |  | BSw |
| 2348 | MA: Lincoln | WMback | 0.000 | 0.000 | 0.001 | 0.057 | 0.942 | 0.000 |  | 0.659 | 0.341 |  | BSw |
| 2349 | MA: Lincoln | F1 | 0.000 | 0.000 | 0.840 | 0.016 | 0.144 | 0.000 |  | 0.608 | 0.392 |  | WM |
| 2387 | RI: Jamestown | F1 | 0.000 | 0.000 | 0.496 | 0.050 | 0.453 | 0.000 |  | 0.651 | 0.349 |  | WM |
| 2396 | RI: Kingston | WMback | 0.000 | 0.000 | 0.146 | 0.111 | 0.743 | 0.000 |  | 0.635 | 0.365 |  | WM |
| 2398 | RI: Kingston | WMback | 0.000 | 0.000 | 0.175 | 0.153 | 0.673 | 0.000 |  | 0.575 | 0.425 |  | WM |
| 2454 | MA: Westminster | F1 | 0.000 | 0.000 | 0.710 | 0.020 | 0.270 | 0.000 |  | 0.631 | 0.369 |  | WM |
| 2466 | MA: Fitchburg | WMback | 0.000 | 0.000 | 0.125 | 0.097 | 0.778 | 0.000 |  | 0.612 | 0.388 |  | WM |
| 2523 | MA: Harvard | F1 | 0.000 | 0.000 | 0.932 | 0.008 | 0.061 | 0.000 |  | 0.599 | 0.401 |  | WM |
| 2594 | MA: Concord | WMback | 0.000 | 0.000 | 0.020 | 0.063 | 0.917 | 0.000 |  | 0.675 | 0.325 |  | BSw |
| 2626 | MA: Concord | F1 | 0.000 | 0.000 | 0.694 | 0.017 | 0.289 | 0.000 |  | 0.635 | 0.365 |  | WM |
| 2975 | MA: Fitchburg | F1 | 0.000 | 0.000 | 0.952 | 0.011 | 0.037 | 0.000 |  | 0.508 | 0.492 |  | WM |
| 3034 | CT: Hamden | BSw | 0.000 | 1.000 | 0.000 | 0.000 | 0.000 | 0.000 |  | 0.065 | 0.935 |  | BSw |
| 3039 | CT: Norwalk | BSw | 0.000 | 1.000 | 0.000 | 0.000 | 0.000 | 0.000 |  | 0.083 | 0.917 |  | BSw |
| 3040 | CT: Norwalk | BSw | 0.000 | 1.000 | 0.000 | 0.000 | 0.000 | 0.000 |  | 0.034 | 0.966 |  | BSw |
| 3165 | MA: Athol | F1 | 0.000 | 0.000 | 0.910 | 0.034 | 0.055 | 0.001 |  | 0.483 | 0.517 |  | WM |

1 BSw: Bruce spanworm, WM: winter moth, F1: F1 hybrid, F2: F2 hybrid, BSwBack: Bruce spanworm backcross, WMBack: winter moth backcross

**References**

**Anderson, E.C. & Thompson,** **E.A.** (2002) A model-based method for identifying species hybrids using multilocus genetic data. *Genetics* **160**, 1217-1229.

**Pritchard, J.K., Stephens, M., & Donnelly, P.** (2000) Inference of population structure using multilocus genotype data. *Genetics* **155**, 945-959.

**van Oosterhout, C., Hutchinson, W.F., Wills, D.P.M., & Shipley, P.** (2004) MICRO-CHECKER: software for identifying and correcting genotyping errors in microsatellite data. *Molecular Ecology Notes* **4**, 535-538.