

Table S1. Primers and internal primer pairs (newly designed) used for cpDNA sequencing.

| Primer      | Sequence (5' – 3')             | Reference          |
|-------------|--------------------------------|--------------------|
| rpl20       | TTTGTTCTACGTCTCCGAGC           | Hamilton 1999      |
| 5'-rps12    | GTCGAGGAACATGTACTAGG           | Hamilton 1999      |
| rpl20-int1F | AGT GAA GAG GAA AAG GTG GA     |                    |
| rpl20-int1R | GGA GCC CCT TAC TTC ATT TA     |                    |
| rpl20-int2F | AAA CGG ACT AAG AGG GTC AG     |                    |
| rpl20-int2R | TAA CAA AAC GGA TTC TTC CA     |                    |
| rpl16-F71   | TTG CTA TGC TTA GTG TGT GAC TC | Jordan et al 1996  |
| rpl16-R1516 | CCCTTCATTCTTCCTCTATGTTG        | Jordan et al. 1996 |
| rpl16-int1F | CGG GCG AAT ATT TAC TCT TT     |                    |
| rpl16-int1R | AAA TGG AAG GGT GAG AGA AA     |                    |
| rpl16-int2F | ATT CAT AGG TTC CGT CGT TC     |                    |
| rpl16-int2R | TCT GGA TAC AAA AAC CCA GT     |                    |
| rpl16-int3F | TTG ATG CTT CTT TTT CAT TTC A  |                    |
| rpl16-int3R | TCC ATT GTA GAA TTC AAA CCT    |                    |

Table S2. The 95% confidence interval of the pairwise  $F_{ST}$  between populations, corrected using the ENA method. The upper and lower diagonal shows the upper and lower limit of the confidence interval, respectively.

|     | MO1   | MO2   | MY1   | MY2   | TH1   | TH2   | MA1   | MA2   | SIN   | IN1   | IN2   | MA3   | TH3   | VIE   | MA4   | PH1   | PH2   | JPN   | PA1   | PA2   | MIC   | AU1   | AU2   | NC1   | NC2   |
|-----|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| MO1 |       | 0.076 | 0.422 | 0.455 | 0.424 | 0.392 | 0.602 | 0.425 | 0.440 | 0.215 | 0.386 | 0.567 | 0.461 | 0.463 | 0.566 | 0.307 | 0.413 | 0.451 | 0.338 | 0.410 | 0.372 | 0.509 | 0.599 | 0.675 | 0.690 |
| MO2 | 0.402 |       | 0.621 | 0.538 | 0.469 | 0.458 | 0.729 | 0.454 | 0.459 | 0.270 | 0.411 | 0.654 | 0.584 | 0.512 | 0.568 | 0.345 | 0.529 | 0.496 | 0.382 | 0.384 | 0.390 | 0.532 | 0.645 | 0.734 | 0.754 |
| MY1 | 0.874 | 0.927 |       | 0.202 | 0.192 | 0.156 | 0.410 | 0.426 | 0.517 | 0.417 | 0.465 | 0.632 | 0.558 | 0.562 | 0.590 | 0.373 | 0.472 | 0.533 | 0.434 | 0.475 | 0.468 | 0.576 | 0.610 | 0.693 | 0.713 |
| MY2 | 0.743 | 0.766 | 0.497 |       | 0.113 | 0.080 | 0.196 | 0.271 | 0.378 | 0.383 | 0.309 | 0.454 | 0.384 | 0.400 | 0.494 | 0.285 | 0.368 | 0.436 | 0.315 | 0.354 | 0.376 | 0.460 | 0.465 | 0.553 | 0.568 |
| TH1 | 0.754 | 0.775 | 0.507 | 0.303 |       | 0.033 | 0.193 | 0.218 | 0.292 | 0.338 | 0.258 | 0.414 | 0.364 | 0.394 | 0.430 | 0.209 | 0.295 | 0.369 | 0.270 | 0.283 | 0.295 | 0.397 | 0.453 | 0.531 | 0.529 |
| TH2 | 0.761 | 0.794 | 0.461 | 0.197 | 0.172 |       | 0.168 | 0.228 | 0.328 | 0.363 | 0.296 | 0.359 | 0.339 | 0.343 | 0.464 | 0.245 | 0.330 | 0.412 | 0.304 | 0.326 | 0.336 | 0.443 | 0.492 | 0.531 | 0.547 |
| MA1 | 0.891 | 0.950 | 0.817 | 0.642 | 0.540 | 0.555 |       | 0.332 | 0.402 | 0.459 | 0.390 | 0.605 | 0.550 | 0.587 | 0.582 | 0.357 | 0.468 | 0.516 | 0.370 | 0.420 | 0.432 | 0.520 | 0.565 | 0.643 | 0.669 |
| MA2 | 0.692 | 0.699 | 0.629 | 0.527 | 0.482 | 0.514 | 0.569 |       | 0.035 | 0.294 | 0.154 | 0.261 | 0.186 | 0.189 | 0.261 | 0.186 | 0.309 | 0.325 | 0.191 | 0.205 | 0.195 | 0.386 | 0.477 | 0.474 | 0.523 |
| SIN | 0.746 | 0.771 | 0.733 | 0.628 | 0.588 | 0.620 | 0.634 | 0.137 |       | 0.269 | 0.136 | 0.290 | 0.206 | 0.303 | 0.303 | 0.115 | 0.276 | 0.339 | 0.200 | 0.189 | 0.156 | 0.404 | 0.506 | 0.547 | 0.590 |
| IN1 | 0.431 | 0.507 | 0.708 | 0.630 | 0.624 | 0.616 | 0.715 | 0.492 | 0.500 |       | 0.162 | 0.415 | 0.311 | 0.291 | 0.395 | 0.132 | 0.185 | 0.324 | 0.235 | 0.309 | 0.183 | 0.419 | 0.509 | 0.569 | 0.587 |
| IN2 | 0.586 | 0.579 | 0.607 | 0.519 | 0.481 | 0.515 | 0.649 | 0.339 | 0.399 | 0.337 |       | 0.295 | 0.232 | 0.230 | 0.300 | 0.125 | 0.180 | 0.258 | 0.150 | 0.175 | 0.210 | 0.339 | 0.446 | 0.500 | 0.534 |
| MA3 | 0.870 | 0.943 | 0.870 | 0.740 | 0.771 | 0.733 | 0.942 | 0.580 | 0.673 | 0.731 | 0.464 |       | 0.044 | 0.178 | 0.491 | 0.375 | 0.509 | 0.447 | 0.406 | 0.388 | 0.407 | 0.513 | 0.646 | 0.683 | 0.702 |
| TH3 | 0.805 | 0.864 | 0.780 | 0.681 | 0.672 | 0.627 | 0.860 | 0.478 | 0.589 | 0.677 | 0.382 | 0.341 |       | 0.213 | 0.402 | 0.260 | 0.331 | 0.412 | 0.326 | 0.337 | 0.326 | 0.489 | 0.598 | 0.655 | 0.669 |
| VIE | 0.766 | 0.825 | 0.793 | 0.675 | 0.694 | 0.660 | 0.818 | 0.472 | 0.532 | 0.669 | 0.451 | 0.626 | 0.497 |       | 0.358 | 0.351 | 0.482 | 0.456 | 0.356 | 0.342 | 0.375 | 0.534 | 0.630 | 0.649 | 0.666 |
| MA4 | 0.823 | 0.880 | 0.852 | 0.733 | 0.744 | 0.719 | 0.879 | 0.591 | 0.621 | 0.730 | 0.643 | 0.881 | 0.794 | 0.783 |       | 0.274 | 0.380 | 0.480 | 0.392 | 0.346 | 0.382 | 0.506 | 0.600 | 0.647 | 0.662 |
| PH1 | 0.521 | 0.560 | 0.576 | 0.445 | 0.452 | 0.503 | 0.588 | 0.376 | 0.414 | 0.307 | 0.327 | 0.602 | 0.523 | 0.544 | 0.535 |       | 0.129 | 0.268 | 0.204 | 0.199 | 0.192 | 0.346 | 0.442 | 0.475 | 0.515 |
| PH2 | 0.734 | 0.788 | 0.724 | 0.607 | 0.567 | 0.603 | 0.668 | 0.472 | 0.488 | 0.482 | 0.388 | 0.748 | 0.685 | 0.707 | 0.738 | 0.357 |       | 0.407 | 0.241 | 0.258 | 0.233 | 0.385 | 0.538 | 0.598 | 0.621 |
| JPN | 0.675 | 0.750 | 0.729 | 0.635 | 0.612 | 0.657 | 0.798 | 0.589 | 0.638 | 0.605 | 0.566 | 0.760 | 0.714 | 0.700 | 0.776 | 0.438 | 0.568 |       | 0.318 | 0.365 | 0.376 | 0.363 | 0.418 | 0.535 | 0.562 |
| PA1 | 0.598 | 0.576 | 0.595 | 0.529 | 0.483 | 0.549 | 0.532 | 0.362 | 0.370 | 0.389 | 0.330 | 0.622 | 0.534 | 0.562 | 0.568 | 0.361 | 0.412 | 0.534 |       | 0.116 | 0.142 | 0.329 | 0.423 | 0.482 | 0.507 |
| PA2 | 0.590 | 0.570 | 0.646 | 0.548 | 0.517 | 0.584 | 0.605 | 0.448 | 0.458 | 0.477 | 0.372 | 0.655 | 0.553 | 0.594 | 0.613 | 0.401 | 0.450 | 0.582 | 0.228 |       | 0.185 | 0.324 | 0.445 | 0.459 | 0.474 |
| MIC | 0.691 | 0.695 | 0.651 | 0.593 | 0.556 | 0.599 | 0.614 | 0.442 | 0.452 | 0.473 | 0.404 | 0.681 | 0.595 | 0.606 | 0.614 | 0.414 | 0.483 | 0.631 | 0.301 | 0.420 |       | 0.327 | 0.450 | 0.495 | 0.523 |
| AU1 | 0.791 | 0.827 | 0.843 | 0.756 | 0.740 | 0.774 | 0.827 | 0.685 | 0.718 | 0.684 | 0.613 | 0.849 | 0.794 | 0.808 | 0.810 | 0.609 | 0.654 | 0.690 | 0.587 | 0.599 | 0.675 |       | 0.306 | 0.426 | 0.442 |
| AU2 | 0.870 | 0.922 | 0.895 | 0.815 | 0.803 | 0.816 | 0.924 | 0.761 | 0.808 | 0.782 | 0.763 | 0.942 | 0.899 | 0.873 | 0.906 | 0.706 | 0.799 | 0.827 | 0.672 | 0.687 | 0.761 | 0.789 |       | 0.457 | 0.484 |
| NC1 | 0.925 | 0.985 | 0.952 | 0.873 | 0.859 | 0.863 | 0.979 | 0.770 | 0.828 | 0.823 | 0.782 | 0.985 | 0.942 | 0.914 | 0.933 | 0.733 | 0.844 | 0.852 | 0.698 | 0.711 | 0.775 | 0.852 | 0.943 |       | 0.063 |
| NC2 | 0.922 | 0.980 | 0.950 | 0.868 | 0.850 | 0.859 | 0.979 | 0.781 | 0.832 | 0.825 | 0.783 | 0.982 | 0.939 | 0.912 | 0.929 | 0.742 | 0.840 | 0.853 | 0.695 | 0.705 | 0.773 | 0.849 | 0.942 | 0.987 |       |



Table S4. Estimated null allele frequency for all population-locus combinations. Frequencies above 0.1 are shaded. Population codes are defined in Table 1.

[illegible]

Table S5. Genetic diversity parameters of the eleven microsatellite loci employed in this study.

| <b>Locus</b> | <b>N</b> | <b>A<sub>R</sub></b> | <b>H<sub>O</sub></b> | <b>H<sub>E</sub></b> |
|--------------|----------|----------------------|----------------------|----------------------|
| SA102        | 13       | 7.659                | 0.279 ± 0.055        | 0.339 ± 0.049        |
| SA115        | 8        | 3.834                | 0.256 ± 0.055        | 0.261 ± 0.050        |
| SA110        | 14       | 8.106                | 0.465 ± 0.043        | 0.552 ± 0.035        |
| SA117        | 11       | 5.546                | 0.173 ± 0.037        | 0.228 ± 0.045        |
| SA123        | 6        | 5.083                | 0.181 ± 0.043        | 0.207 ± 0.046        |
| SA112        | 8        | 3.583                | 0.150 ± 0.045        | 0.187 ± 0.047        |
| SA103        | 21       | 6.733                | 0.324 ± 0.051        | 0.380 ± 0.056        |
| SA108        | 12       | 6.821                | 0.213 ± 0.044        | 0.252 ± 0.045        |
| SA106        | 15       | 7.327                | 0.255 ± 0.052        | 0.328 ± 0.057        |
| SA105        | 20       | 6.434                | 0.214 ± 0.057        | 0.264 ± 0.061        |
| SA113        | 19       | 8.64                 | 0.469 ± 0.046        | 0.599 ± 0.045        |

N, total number of alleles; A<sub>R</sub>, allelic richness rarefied to a minimum of 10 diploid individuals; H<sub>O</sub>, observed heterozygosity; H<sub>E</sub>, expected heterozygosity

Table S6. Pairwise  $F'_{ST}$  between population pairs.

|            | MO1   | MO2   | MY1   | MY2   | TH1   | TH2   | MA1   | MA2   | SIN   | IN1   | IN2   | MA3   | TH3   | VIE   | MA4   | PH1   | PH2   | JPN   | PA1   | PA2   | MIC   | AU1   | AU2   | NC1   |
|------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| <b>MO1</b> |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| <b>MO2</b> | 0.385 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| <b>MY1</b> | 0.857 | 0.929 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| <b>MY2</b> | 0.864 | 0.898 | 0.509 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| <b>TH1</b> | 0.874 | 0.887 | 0.513 | 0.330 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| <b>TH2</b> | 0.843 | 0.864 | 0.447 | 0.221 | 0.127 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| <b>MA1</b> | 0.954 | 0.975 | 0.770 | 0.604 | 0.526 | 0.495 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| <b>MA2</b> | 0.886 | 0.893 | 0.834 | 0.716 | 0.706 | 0.662 | 0.757 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| <b>SIN</b> | 0.891 | 0.902 | 0.909 | 0.836 | 0.822 | 0.796 | 0.823 | 0.157 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| <b>IN1</b> | 0.501 | 0.597 | 0.852 | 0.872 | 0.864 | 0.831 | 0.913 | 0.762 | 0.704 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| <b>IN2</b> | 0.777 | 0.783 | 0.859 | 0.791 | 0.763 | 0.746 | 0.895 | 0.513 | 0.518 | 0.524 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| <b>MA3</b> | 0.902 | 0.943 | 0.913 | 0.834 | 0.834 | 0.768 | 0.939 | 0.647 | 0.691 | 0.829 | 0.596 |       |       |       |       |       |       |       |       |       |       |       |       |       |
| <b>TH3</b> | 0.852 | 0.907 | 0.856 | 0.792 | 0.788 | 0.727 | 0.917 | 0.540 | 0.593 | 0.772 | 0.540 | 0.315 |       |       |       |       |       |       |       |       |       |       |       |       |
| <b>VIE</b> | 0.852 | 0.893 | 0.903 | 0.829 | 0.847 | 0.770 | 0.925 | 0.587 | 0.682 | 0.786 | 0.605 | 0.602 | 0.569 |       |       |       |       |       |       |       |       |       |       |       |
| <b>MA4</b> | 0.921 | 0.924 | 0.925 | 0.895 | 0.892 | 0.859 | 0.945 | 0.707 | 0.720 | 0.869 | 0.792 | 0.866 | 0.808 | 0.827 |       |       |       |       |       |       |       |       |       |       |
| <b>PH1</b> | 0.715 | 0.769 | 0.788 | 0.728 | 0.732 | 0.718 | 0.869 | 0.645 | 0.572 | 0.489 | 0.553 | 0.785 | 0.709 | 0.786 | 0.715 |       |       |       |       |       |       |       |       |       |
| <b>PH2</b> | 0.859 | 0.911 | 0.848 | 0.840 | 0.792 | 0.770 | 0.866 | 0.765 | 0.698 | 0.633 | 0.616 | 0.858 | 0.779 | 0.894 | 0.850 | 0.531 |       |       |       |       |       |       |       |       |
| <b>JPN</b> | 0.845 | 0.879 | 0.921 | 0.880 | 0.853 | 0.875 | 0.988 | 0.851 | 0.873 | 0.833 | 0.778 | 0.859 | 0.850 | 0.880 | 0.925 | 0.724 | 0.869 |       |       |       |       |       |       |       |
| <b>PA1</b> | 0.835 | 0.833 | 0.900 | 0.868 | 0.859 | 0.850 | 0.874 | 0.647 | 0.618 | 0.712 | 0.606 | 0.864 | 0.801 | 0.843 | 0.873 | 0.753 | 0.772 | 0.902 |       |       |       |       |       |       |
| <b>PA2</b> | 0.845 | 0.807 | 0.931 | 0.884 | 0.859 | 0.866 | 0.923 | 0.699 | 0.659 | 0.840 | 0.625 | 0.835 | 0.778 | 0.823 | 0.830 | 0.731 | 0.779 | 0.928 | 0.427 |       |       |       |       |       |
| <b>MIC</b> | 0.866 | 0.870 | 0.904 | 0.900 | 0.860 | 0.855 | 0.911 | 0.706 | 0.636 | 0.690 | 0.695 | 0.864 | 0.804 | 0.838 | 0.836 | 0.730 | 0.730 | 0.955 | 0.532 | 0.668 |       |       |       |       |
| <b>AU1</b> | 0.942 | 0.943 | 0.988 | 0.977 | 0.967 | 0.970 | 0.991 | 0.963 | 0.958 | 0.948 | 0.914 | 0.948 | 0.955 | 0.978 | 0.981 | 0.952 | 0.898 | 0.889 | 0.928 | 0.894 | 0.926 |       |       |       |
| <b>AU2</b> | 0.966 | 0.973 | 0.955 | 0.940 | 0.947 | 0.949 | 0.968 | 0.975 | 0.986 | 0.980 | 0.976 | 0.992 | 0.992 | 0.993 | 0.991 | 0.977 | 0.984 | 0.926 | 0.970 | 0.953 | 0.973 | 0.814 |       |       |
| <b>NC1</b> | 0.981 | 0.988 | 0.981 | 0.973 | 0.954 | 0.943 | 0.974 | 0.929 | 0.959 | 0.981 | 0.956 | 0.983 | 0.980 | 0.982 | 0.978 | 0.944 | 0.957 | 0.943 | 0.967 | 0.927 | 0.956 | 0.895 | 0.899 |       |
| <b>NC2</b> | 0.981 | 0.989 | 0.982 | 0.972 | 0.941 | 0.942 | 0.975 | 0.962 | 0.985 | 0.987 | 0.975 | 0.987 | 0.982 | 0.983 | 0.979 | 0.971 | 0.961 | 0.965 | 0.976 | 0.926 | 0.966 | 0.894 | 0.906 | 0.577 |

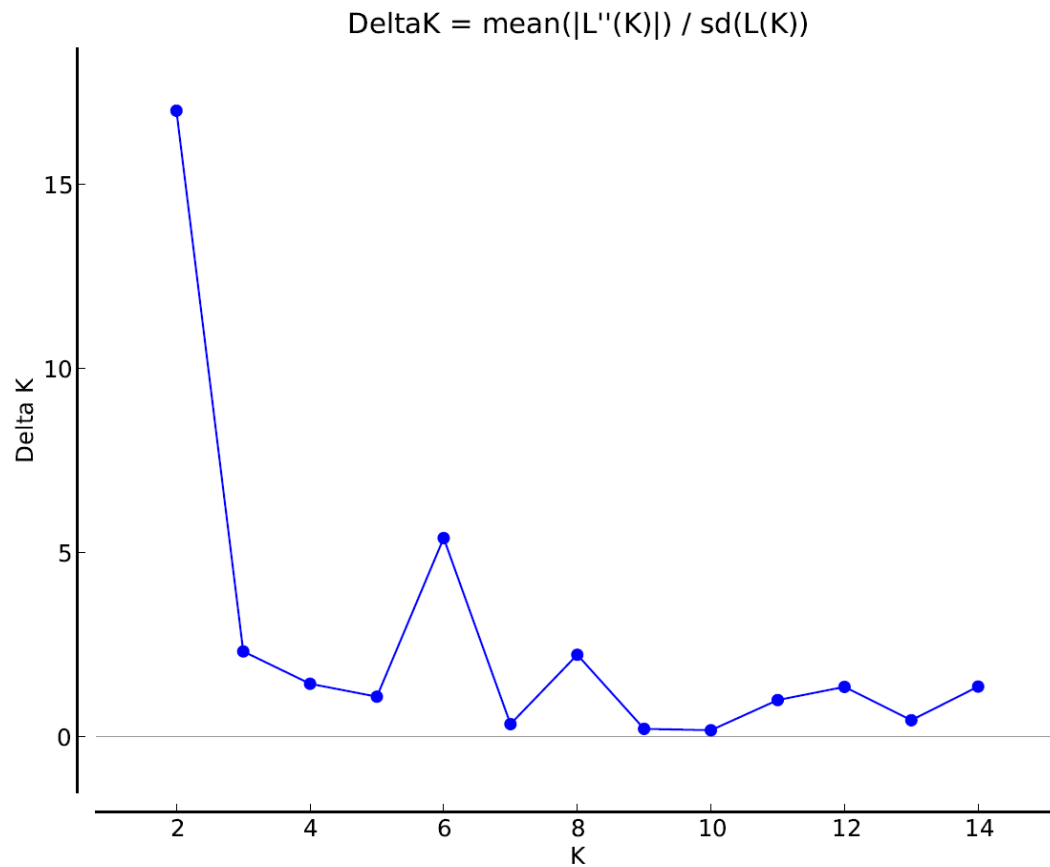


Figure S1. Graph showing K value against  $\Delta K$  according to STRUCTURE HARVESTER, indicating that the most likely number of clusters in the total population was two.