Table S2 Levels of genetic variability at ten microsatellite loci in the nine populations of Pacific herring and for all populations pooled.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Locus | Sample | YS | SN | IB | NH | AS | WK | TG | SI | CW |
| *n* | 24 | 24 | 24 | 23 | 24 | 24 | 24 | 24 | 23 |
| Cpa 101 | A | 7 | 8 | 12 | 9 | 9 | 12 | 11 | 11 | 10 |
|  | *H*E | 0.835  | 0.834  | 0.850  | 0.835  | 0.881  | 0.850  | 0.837  | 0.890  | 0.857  |
|  | *H*O | 0.958  | 0.783  | 0.826  | 0.909  | 0.833  | 0.727  | 0.700  | 0.842  | 0.773  |
| Cpa 102 | A | 9 | 11 | 8 | 9 | 14 | 14 | 14 | 13 | 17 |
|  | *H*E | 0.566  | 0.785  | 0.804  | 0.839  | 0.882  | 0.850  | 0.843  | 0.907  | 0.894  |
|  | *H*O | 0.478  | 0.810  | 0.565  | 0.739  | 0.833  | 0.750  | 0.565  | 0.476  | 0.455  |
| Cpa 103 | A | 5 | 7 | 7 | 8 | 8 | 9 | 7 | 11 | 12 |
|  | *H*E | 0.653  | 0.818  | 0.759  | 0.826  | 0.753  | 0.834  | 0.768  | 0.824  | 0.897  |
|  | *H*O | 0.667  | 0.667  | 0.625  | 0.909  | 0.870  | 0.667  | 0.833  | 0.739  | 0.850  |
| Cpa 104 | A | 8 | 11 | 10 | 10 | 12 | 11 | 11 | 12 | 16 |
|  | *H*E | 0.824  | 0.840  | 0.849  | 0.865  | 0.855  | 0.840  | 0.740  | 0.832  | 0.921  |
|  | *H*O | 0.833  | 0.667  | 0.750  | 0.636  | 0.708  | 0.750  | 0.625  | 0.714  | 0.762  |
| Cpa 108 | A | 4 | 5 | 8 | 6 | 6 | 4 | 6 | 4 | 7 |
|  | *H*E | 0.160  | 0.243  | 0.469  | 0.669  | 0.634  | 0.327  | 0.504  | 0.645  | 0.733  |
|  | *H*O | 0.167  | 0.217  | 0.409  | 0.476  | 0.625  | 0.318  | 0.458  | 0.500  | 0.579  |
| Cpa 110 | A | 2 | 2 | 2 | 3 | 3 | 2 | 2 | 2 | 2 |
|  | *H*E | 0.439  | 0.503  | 0.488  | 0.532  | 0.529  | 0.510  | 0.511  | 0.496  | 0.059  |
|  | *H*O | 0.375  | 0.375  | 0.375  | 0.652  | 0.458  | 0.348  | 0.652  | 0.500  | 0.059  |
| Cpa 111 | A | 8 | 9 | 15 | 12 | 11 | 10 | 6 | 13 | 13 |
|  | *H*E | 0.723  | 0.700  | 0.908  | 0.879  | 0.860  | 0.877  | 0.477  | 0.902  | 0.895  |
|  | *H*O | 0.667  | 0.792  | 1.000  | 0.750  | 0.708  | 0.875  | 0.435  | 0.818  | 0.833  |
| Cpa 114 | A | 14 | 17 | 14 | 8 | 15 | 15 | 17 | 13 | 9 |
|  | *H*E | 0.931  | 0.933  | 0.916  | 0.848  | 0.924  | 0.919  | 0.927  | 0.872  | 0.874  |
|  | *H*O | 0.917  | 0.958  | 0.875  | 0.789  | 0.792  | 0.917  | 0.875  | 0.833  | 0.900  |
| Cha 17 | A | 11 | 16 | 9 | 16 | 12 | 12 | 14 | 17 | 14 |
|  | *H*E | 0.855  | 0.925  | 0.750  | 0.928  | 0.879  | 0.900  | 0.911  | 0.932  | 0.925  |
|  | *H*O | 1.000\*  | 1.000  | 1.000\*\*  | 1.000  | 1.000\*  | 1.000  | 1.000  | 1.000  | 1.000  |
| Cha 20 | A | 8 | 6 | 11 | 10 | 9 | 8 | 11 | 7 | 8 |
|  | *H*E | 0.733  | 0.780  | 0.890  | 0.848  | 0.762  | 0.822  | 0.909  | 0.809  | 0.870  |
|  | *H*O | 1.000\*\*  | 1.000\*\*  | 1.000  | 1.000\*  | 1.000\*\*  | 1.000\*  | 1.000  | 1.000\*\*  | 1.000\*  |
| Mean | A | 7.6 | 9.2 | 9.6 | 9.1 | 9.9 | 9.7 | 9.9 | 10.3 | 10.8 |
|  | *H*E | 0.672 | 0.736 | 0.768 | 0.807 | 0.796 | 0.773 | 0.743 | 0.811 | 0.792 |
|  | *H*O | 0.706 | 0.727 | 0.743 | 0.786 | 0.783 | 0.735 | 0.714 | 0.742 | 0.721 |

Sample size (*n*), number of allele (*A*), expected heterozygosity (*H*E) and observed heterozygosity (*H*O). Significant deviations from Hardy-Weinberg genotype ratios: \* *P*<0.05, \*\* *P*<0.01, none remain significant after sequential Bonferroni correction.