**Table 2. Pairwise number of diagnostic SNP loci between the primary genetic groups identified by PCoA (Fig. 2).** Lower triangle = number of absolute fixed differences/number of fixed differences allowing 5% tolerance for shared alleles (tloc = 0.05); upper triangle = number of SNPs for each pairwise comparison. All values were highly-significant (P < 0.001) after Bonferroni correction for multiple tests except where indicated (red font and superscriptns). Also shown are the observed heterozygosity counts for each group.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Taxon | KE  (72) | KEm  (9) | KN  (15) | KS  (66) | KSxKE  (16) | KWm  (10) | KW  (16) |
| KE | - | 3628 | 3553 | 3628 | 3628 | 3623 | 3618 |
| KEm | 0ns/1 | - | 3553 | 3628 | 3628 | 3623 | 3618 |
| KN | 106/194 | 155/193 | - | 3553 | 3553 | 3548 | 3543 |
| KS | 93/344 | 60/182 | 224/455 | - | 3628 | 3623 | 3618 |
| KSxKE | 0ns/2ns | 0ns/1ns | 110/156 | 0ns/0ns | - | 3623 | 3618 |
| KWm | 141/310 | 115/181 | 291/429 | 12ns/40 | 7ns/25 | - | 3613 |
| KW | 260/414 | 225/247 | 432/525 | 38/64 | 20/39 | 14/23 | - |
| HO | 0.0218 | 0.0387 | 0.0175 | 0.0161 | 0.0919 | 0.0228 | 0.0098 |