

**Figure S5** Weir & Cockerham  $F_{ST}$  values (top, below the diagonal in the table) and Reynold's genetic distances (top, above the diagonal in the table) between each pair of populations. The Reynold's genetic distances were extracted from the population tree (bottom) estimated by the HAPFLK software.

|                     |     | REYNOLDS |       |       |       |       |       |       |       |
|---------------------|-----|----------|-------|-------|-------|-------|-------|-------|-------|
|                     |     | PYR      | FSS   | PTV   | ALP   | SAA   | PVC   | CRS   | ANG   |
| WEIR &<br>COCKERHAM | PYR |          | 0.092 | 0.111 | 0.091 | 0.096 | 0.091 | 0.085 | 0.198 |
|                     | FSS | 0.065    |       | 0.101 | 0.076 | 0.083 | 0.081 | 0.075 | 0.185 |
|                     | PTV | 0.089    | 0.080 |       | 0.090 | 0.100 | 0.101 | 0.094 | 0.212 |
|                     | ALP | 0.071    | 0.058 | 0.076 |       | 0.070 | 0.070 | 0.068 | 0.185 |
|                     | SAA | 0.076    | 0.064 | 0.085 | 0.059 |       | 0.077 | 0.073 | 0.181 |
|                     | PVC | 0.064    | 0.056 | 0.081 | 0.053 | 0.059 |       | 0.070 | 0.168 |
|                     | CRS | 0.062    | 0.054 | 0.077 | 0.054 | 0.059 | 0.049 |       | 0.169 |
|                     | ANG | 0.179    | 0.167 | 0.198 | 0.171 | 0.167 | 0.151 | 0.154 |       |

