**S1 Table. Microsatellite loci characterization.** Repeat motifs, primer sequences, PCR annealing temperatures (TA), numbers of alleles (NA), allele size ranges in base pairs (bp), observed (*H*O) and expected (*H*E) heterozygosities, probability of heterozygote deficits (*P*), probabilities that two random individuals in the population could present identical allelic composition (I), and the probability that the loci would not exclude a pair of candidate unrelated parents (PP) for eight microsatellite loci used for paternity tests in *S. pileata*/*bouvreuil*.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| ***Locus*** | ***Motif*** | **Primer sequences (5’ – 3’)** | **TA (°C)** | **NA** | **Allele range (bp)** | ***H*E** | ***H*O** | ***P\**** | ***I*** | ***PP*** |
| Sma5 | (AAT)16 | F: GTCCTTGCATGTGACAGTGG | 64.7 | 10 | 331-370 | 0.23 | 0.11 | 0.006 | 0.236 | 0.499 |
| R: CAGTCAGTGTGCCATGAACC |
| Sma11 | (AC)15 | F: TGAAATTGAACCATCCAGTGCC | 64.7 | 20 | 217-261 | 0.25 | 0.25 | 0.438 | 0.451 | 0.157 |
| R: ACCATAGTTCCATTGCTTCCAG |
| Sma21 | (AT)12 | F: GAGCAGGTACAAGGACTC | 64.5 | 5 | 255-287 | 0.15 | 0.12 | 0.056 | 0.016 | 0.056 |
| R: GATCTCCACTTCCTCCAGC |
| Sma22 | (AG)13 | F: GCATCTTCTGTACTGAGAGC | 63.3 | 6 | 402-418 | 0.18 | 0.15 | 0.056 | 0.220 | 0.464 |
| R: AACCTCAACAGACACGGAAC |
| Sma25 | (AC)14 | F: CTGTAGAAGAACTGCCAG | 61.4 | 18 | 216-278 | 0.24 | 0.24 | 0.307 | 0.129 | 0.312 |
| R: ACACTCTCACACAGCTTTGC |
| Sma29 | (AC)14 | F: CAAACAGGGCAAAGGGTGAC | 64.5 | 7 | 171-195 | 0.15 | 0.17 | 0.825 | 0.088 | 0.252 |
| R: TCAGCCTCGAGTTAACAC |
| Sma31 | (AC)14 | F: AGAAGTAGTCCCTCTAGC | 61.4 | 8 | 161-181 | 0.18 | 0.18 | 0.431 | 0.010 | 0.037 |
| R: TTGTCTGACTGGCTTGTAG |
| Sma32 | (AC)12 | F: GCCAGCTGAAATCCATAGGC | 64.5 | 8 | 355-371 | 0.21 | 0.22 | 0.769 | 0.035 | 0.117 |
| R: CTCTCCTGTGCTCCTTCCAG |

\* Corrected *P* values after Bonferroni correction is 0.006.