**Table S1**. Characterization of 25 cpSSR marker in the *Glycyrrhiza* species

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Primer name | Forward/  Reverse | Repeated  motif | Excepted  size | Product  Size | *NA* | *NE* | *I* | *h* | *uh* |
| GL-cpSSR-01 | CGCGTCTTCTAAAATACGAGAAA/  TGCATGAACGTAATGCTCATAAT | (TA)5 | 287 | 285 - 291 | 4 | 2.125 | 0.956 | 0.529 | 0.550 |
| GL-cpSSR-02 | AAACGTTTCATTTTTGTGCCTTA/  ACTAAACTCGGCCCAATCTTTTA | (AT)5ACT(AT)5 | 238 | 220 - 242 | 7 | 4.829 | 1.694 | 0.793 | 0.825 |
| GL-cpSSR-03 | AAACGTTTCATTTTTGTGCCTTA/  ACTAAACTCGGCCCAATCTTTTA | (TA)6 | 238 | 220 - 240 | 6 | 2.690 | 1.291 | 0.628 | 0.652 |
| GL-cpSSR-04 | ACTACTTCAACCATTTCCGAACA/  GTCATAAGACAATTCCGGATTCA | (TA)5 | 242 | 230 - 236 | Monomorphic | | | | |
| GL-cpSSR-05 | TTGTTTCATTGCTTCATTTTTCA/  GGTGCTCTGACCAATTGAACTAC | (AT)5 | 243 | 235 - 247 | 5 | 2.772 | 1.218 | 0.639 | 0.664 |
| GL-cpSSR-06 | GTTGGTCCAGAATCAAAGAGAGA/  AATGGCGAGCAAAATAAAACATA | (AT)6 | 231 | 229 - 247 | 2 | 1.624 | 0.572 | 0.384 | 0.399 |
| GL-cpSSR-07 | ATTTGAACTGGGGAAAAAGGAT/  CGAAATTTTTGCTTTTGTGATTG | (AT)5 | 247 | 241 - 247 | 3 | 1.699 | 0.727 | 0.412 | 0.427 |
| GL-cpSSR-08 | ACTTGGGATTCAAGTATCCACCT/  CCATCTTGCAAATAAGGCATATC | (AT)5 | 249 | 247 | Monomorphic | | | | |
| GL-cpSSR-09 | ACCATTCGAGGTATTTCTGTGAA/  TAGGACTCCGACCATAACACAAT | (AT)5 | 256 | 256 | Monomorphic | | | | |
| GL-cpSSR-10 | TTCATCCCTTTAAATGCAGTCAT/  CTTTTTGTCATTTATCCCCACAC | (AAT)4 | 236 | 217 - 232 | 2 | 1.800 | 0.367 | 0.444 | 0.462 |
| GL-cpSSR-11 | TGGGATTATTTACAAGCGGTATT/  TGAGGGGGTGGATAATCCTT | (TAA)4 | 229 | 226 - 292 | 4 | 2.042 | 0.958 | 0.510 | 0.530 |
| GL-cpSSR-12 | CGAATTTTCATTTTTATTGTGTTTT/  TCGGATCTTATTTGATCCATTTTT | (AT)5 | 300 | 285 - 291 | 5 | 3.000 | 1.265 | 0.667 | 0.692 |
| GL-cpSSR-14 | ATAAAATGGATCGCTTGTGTGTC/  CTATCCCCCAATCCCATTTATTA | (TA)5 | 250 | 252 - 321 | 5 | 2.344 | 1.097 | 0.573 | 0.595 |
| GL-cpSSR-16 | GAATCACTAGGGGGTTAGGAGTC/  TGAGCAGAAAGGATTTCTCAAAA | (AT)6 | 236 | 234 - 238 | 3 | 1.807 | 0.733 | 0.447 | 0.465 |
| GL-cpSSR-17 | ATTGATTCCTTTTCCAACCAAAT/  TCGTAGGAACAAAAAGAAGCAGA | (TA)5 | 255 | 255 - 269 | 3 | 2.651 | 1.030 | 0.623 | 0.647 |
| GL-cpSSR-18 | AATCTTAGGTATTCGCAGGTTCC/  GCATCCATATTAAAAATTCATCCA | (AT)5 | 239 | 233 - 237 | 3 | 1.874 | 0.753 | 0.466 | 0.484 |
| GL-cpSSR-19 | TCTTGGAATAATTTGTTGGTTGC/  GTAGCAGCAAATGCTAGTCACAA | (TA)5 | 214 | 211 - 217 | 2 | 1.257 | 0.358 | 0.204 | 0.212 |
| GL-cpSSR-20 | TCTTGTTCATTCGCAACAAAATA/  TTCCTCTGTTAGAGGTGTTCCAG | (GA)5 | 251 | 248 | Monomorphic | | | | |
| GL-cpSSR-21 | CATGCAGTACCAGACACGAAATA/  ATGCTTTTCTTGCGTATTCTTGA | (AT)5 | 244 | 243 | Monomorphic | | | | |
| GL-cpSSR-22 | GCCAGGATGATAAAAAGCTTAAC/  CACTGGATCTGTTTCCCAGAGTA | (AG)5 | 250 | 249 - 255 | 3 | 1.874 | 0.753 | 0.466 | 0.484 |
| GL-cpSSR-23 | CGATTGAAAATTCGATAATCTGC/  GCGTGTGCGCATTTATTTTAT | (AT)6 | 251 | 220 - 314 | 7 | 3.663 | 1.516 | 0.727 | 0.755 |
| GL-cpSSR-24 | TGTTATCTGTTTGTTATGCGAAGA/  TTGATTCATTTTTCGATCTAATGG | (AT)5 | 244 | 219 - 306 | 7 | 3.857 | 1.540 | 0.741 | 0.769 |
| GL-cpSSR-25 | GATCGAAAAATGAATCAACAAAA/  TGACACTAATTTTGAATTTTGGAA | (TTAAT)2(TAA)4 | 255 | 253 - 298 | 6 | 2.594 | 1.236 | 0.615 | 0.638 |
| GL-cpSSR-26 | TGTGAGAACCCCTTGAATCATTA/  TTGGATATGTTATTTGGGGATCA | (ATATA)2(AT)6 | 238 | 240 - 319 | 3 | 1.163 | 0.315 | 0.140 | 0.145 |
| GL-cpSSR-28 | AAACGAATGTTCTTAGTTTTGGTG/  AAAGTAAAAATGGGCCAATAACG | (TAA)4 | 227 | 166 - 238 | 8 | 3.556 | 1.584 | 0.719 | 0.746 |

*NA*, No. of Different Alleles; *NE*, No. of Effective Alleles; *I*, Shannon's Information Index; *h*, Diversity; *uh*, Unbiased Diversity