**APPENDIX 2. Characteristics of 32 SSR markers developed for *G. straminea*.**

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| Locus  | Primer sequences (5'-3')  | Repeat motif | Expected allele |
| size(bp) |
| Un106 | F: GGCTCTACCGAATAACATCA AA  | (AC)8 | 269 |
| 　 | R: GACATGGAAACAGTTGAAGACA  |  |  |
| Un150 | F: CATTTCATCT ACAGTGCAAG | (GCT)4 | 195 |
| 　 | R: CTACAAACTG TATGCTGCAA G  |  |  |
| Un322 | F: TGGGGTGCTCGTTATCTTCTTC  | (TCT)6 | 180 |
| 　 | R: GGATGGAGCTTGATGTTGATGAG  |  |  |
| Un084 | F: GATGGCTTCT GTGGAGCAAGTAGT  | (AGG)6 | 270 |
| 　 | R: ATTGTCTCGACCTGCTTTGATGC  |  |  |
| Un1264 | F: TCCTTGATGCCATTCTTGTT  | (AGG)5 | 150 |
| 　 | R: TCTTCTCTCTAAATTAACCCCA |  |  |
| Un1398 | F: TGGGGGTGTGTGGCTCTCATCTT | (GGA)6 | 182 |
| 　 | R: CAGCTGGCCTACTTGAGAGCATTGA |  |  |
| Un1742 | F: TCAGATACAATGAAGTGTCA AAGAA  | (TA)10 | 298 |
| 　 | R: TATTTTGCAGAGTATCAGTGGCTAA  |  |  |
| Un1838 | F: GCCATCTGAC TGTACTTGCTAGCTG  | (AC)9 | 208 |
| 　 | R: TGCCGTTAGG TGTTAGACCA AGGT  |  |  |
| Un1989 | F: CAGAGATGTTATTATTGCCTCGTTG  | (TC)9 | 252 |
| 　 | R: CAACTGAAAA TGGAAATGTG AAGAC  |  |  |
| Un222 | F: TCTTTGAGGGTCTCGAGCAG  | (AT)6 | 175 |
| 　 | R: ATCAAGCTCGTGCACTGTTC  |  |  |
| Un229 | F: GGCTCAGGAGACCTCCGATG  | (CAA)7 | 240 |
| 　 | R: CATGGGGGCTACTATGACTTCA  |  |  |
| Un23581 | F: CACGGCTGTCAACACCTA  | (GAA)6 | 260 |
| 　 | R: ACTGAATCCATGTCTCCAAT  |  |  |
| Un26358 | F: TTGCACCTGCTGCTAAAATG | (ATG)7 | 355 |
| 　 | R: TGCTATCCCCAAACAGACAC |  |  |
| Un2638 | F: CTGTCTGGGA AAGAAATTAA ACTC  | (AG)10 | 100 |
| 　 | R: CACCATAACATTAATCAAATTCACA  |  |  |
| Un26568 | F: CTCGGTATCCAGCGATCAGA  | (CAG)6 | 180 |
| 　 | R: CACCTTTGTCCACTCCAGCA  |  |  |
| Un26825 | F: ATGGTAAGGGCGGCAGTGAG | (GGT)5 | 198 |
| 　 | R: AAACCCCAACCCCAACAAAC |  |  |
| Un27084 | F: CTTTGGAGGTTTCTTTGTC  | (CAT)6 | 200 |
| 　 | R: GTAATAGGTAGGTGGAGGTG  |  |  |
| Un27221 | F: TTCTACTGCCAACCAATCAA  | (CCG)6 | 210 |
| 　 | R: CAACAGCAGTATATGCAAATG  |  |
| Un27382 | F: ATCTTTTCGTGGAGTCGTTA  | (GGT)5 | 200 |
| 　 | R: AACCCTAATTCTAATTGCTT  |  |  |
| Un28099 | F: TCCAAACCAGTGAACCAATC | (CCA)6 | 210 |
| 　 | R: CTATTCTGCA AGTGCTCCAA |  |  |

 Continues

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| Locus  | Primer sequences (5'-3')  | Repeat motif | Expected allelesize(bp) |
| Un28224 | F: CGAACCCACGACAGCAACAA  | (TA)10 | 205 |
| 　 | R: GCTAGCTCGGGATCGACGGA  |  |  |
| Un2853 | F: GACAGGCGGCCTAAGACAGA  | (TAT)7 | 230 |
| 　 | R: CAAGATGGCAAGCAGGAAAC |  |  |
| Un28758 | F: AGAATCTGCT TCATCATCGC  | (TGG)7 | 210 |
| 　 | R: CCAACTACTGGTGCCTTTCAT  |  |  |
| Un29002 | F: AGAGGGTTTCGTGGAATAGG | (TGC)6 | 215 |
| 　 | R: AGATTCGCTACGTCGATAAA |  |  |
| Un29024 | F: CCCATTGTCAAATGTTTCCT  | (TGG)6 | 212 |
| 　 | R: CACATCCAACACCACCACA |  |  |
| Un29324 | F: TGGATGATTGCGGGGCTGAC | (TGC)5 | 188 |
| 　 | R: CTATGCCGAACCCTCCGCCT  |  |  |
| Un2939 | F: TTCTGCTAAATTAGTTGGTA | (AT)8 | 160 |
| 　 | R: AATCTGTTCTAGGCTCATC  |  |  |
| Un29540 | F: TCACAAACCAAAACCGAACC  | (TC)10 | 150 |
| 　 | R: CCGGCAACAA GACGACATAA |  |  |
| Un30991 | F: GTGTGTGCCGGTGGAAATTA AAACT  | (TG)11 | 110 |
| 　 | R: AATGCCCAAACCCTCCTCTTCGTCT  |  |  |
| Un35051 | F: AAATAGGGAGATGCAAACGG | (AAT)6 | 210 |
| 　 | R: AAATGTCTGCGGCTGGTAAT |  |  |
| Un3735 | F: GCAGGAATGGTGGTAGACAA  | (ATT)6 | 120 |
| 　 | R: ACCAGAAGATAACAAACCCA AG  |  | 　 |
| Un39037 | F: AAGGATCCAAGTGCGTGTAC | (AT)8 | 148 |
| 　 | R: AACCAGACGGTCAGAATCAC |  | 　 |