**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 allele  size(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 |  |  |