

BREEDING AND GENETICS

Identification of 700 New Microsatellite Loci from Cotton (*G. hirsutum* L.)

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ABSTRACT

Microsatellite markers, also known as SSRs, comprise a keystone technology for genetic linkage analysis, QTL mapping, marker-assisted breeding, and genome analysis. In order to contribute to a growing body of molecular marker resources for cotton research and improvement, 700 primer pairs were developed to amplify new microsatellite markers, designated Gh for *Gossypium hirsutum*. These primers were designed using microsatellite sequences that were isolated from genomic DNA of *G. hirsutum* cv. Tamcot Sphinx by a biotinylated-oligonucleotide capture method. A total of 4,512 clones from (GA)_n, (AGA)_n, and (CA)_n microsatellite-enriched libraries were sequenced. From these, 1,059 primer pairs were developed. Of the first 700 primer-pairs to be characterized, 602 primer pairs (86%) produced one or more distinct PCR amplification products within the expected size range in at least one of the test cotton genotypes, *G. hirsutum* acc. TM-1 and *G. barbadense* acc. 3-79. Further, 201 primer pairs (28.7%) yielded size polymorphisms between TM-1 and 3-79 that were easily resolved using high-resolution agarose electrophoresis. A subset of 165 polymorphic markers was fully genotyped on a TM-1 x 3-79 interspecific recombinant inbred (RI) population of 191 individuals. In this analysis, segregation distortion was low (10.3% of loci) and functional redundancy of marker loci was low (1.2% of loci). Data from these markers are being incorporated in an integrated SSR map from the TM-1 x 3-79 recombinant inbred

population. Updates regarding sequence, primer, polymorphism, and linkage information from the remainder of the Gh microsatellite collection will be uploaded directly to CottonDB and CMD databases.

Microsatellites, also known as simple sequence repeats (SSRs) and simple sequence length polymorphisms (SSLPs), are DNA-based molecular markers widely used in genome mapping and a variety of biological and biotechnological applications (Goldstein and Schlotterer, 1999). Expansion and contraction of SSR repeats leads to high levels of interspecific and intraspecific polymorphism. Of the several types of molecular markers available for genetic linkage analysis, microsatellite markers have the inherent advantages of being codominant, reproducible, economical, and highly portable between experimental populations. The use of SSRs or microsatellites to create molecular linkage maps in plants was first used by Akkaya et al. (1992) and has become the backbone technology for molecular-genetic linkage maps for a variety of model plants used in research (Bell and Ecker, 1994), as well as in economically important crop species, including rice (Chen et al., 1997), corn (Sharпова et al., 2002), wheat (Röder et al., 1998), and soybean (Cregan et al., 1999; Song et al., 2004). The use of molecular markers in plant breeding applications is becoming widespread (Collard et al., 2005; Varshney et al., 2005). Cotton, however, lags behind other economically important species in the application of genomics and molecular markers in crop genetic improvement. To address this deficit, there has been a coordinated multi-laboratory and multinational effort to develop and deploy a large number of publicly-available microsatellite markers for cotton, and to incorporate these markers into a dense linkage map for use in genome characterization and molecular breeding.

These efforts have included the independent development of several sets of microsatellite markers. These collections of markers are described and referenced by Blenda et al. (2006). The coordination of these efforts has been greatly facilitated by

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the International Cotton Genome Initiative (ICGI, Brubaker et al. 2000) and the Genetics and Breeding Initiative supported by Cotton Incorporated; however, the need for additional microsatellite markers remains substantial. With a linkage map for tetraploid cotton on the order of 5,000 cM (Lacape et al., 2003; Nguyen et al., 2004; Rong et al., 2004), more than 500 polymorphic markers are required to obtain an average marker density of ± 10 cM, which is optimal for QTL mapping. With interspecific (e.g. *G. hirsutum* x *G. barbadense*) crosses, the rate of microsatellite polymorphism ranges from $\pm 20\%$ in SSRs derived from expressed sequenced tags (ESTs) and bacterial artificial chromosome (BAC) end sequences (Park et al., 2005; Frelichowski et al., 2006), to ± 50 from SSR captures from genomic DNA (Reddy et al., 2001; Nguyen et al., 2004). The development of an SSR map from an interspecific cross requires testing from a pool of 1,000 to 2,500 markers. For intraspecific crosses within *G. hirsutum*, polymorphism rates for SSRs are on the order of $\pm 11\%$ (Reddy et al., 2001; Frelichowski et al., 2006) requiring a pool of some 4,500 markers to achieve 10 cM density. Further, many markers may not be usable in any particular application for technical reasons. For example, Lacape et al. (2007) were unable to use 136 out of 320 markers (42.5%) from the publicly available collection because of technical obstacles, such as poor amplification and ambiguities in allele assignment. Finally, marker densities higher than 10 cM will be desirable for integrating physical and genetic maps, linkage disequilibrium (LD) mapping, fine mapping of Mendelian loci, advanced marker-assisted breeding, and map-based cloning.

In an effort to contribute to the primary pool of publicly available cotton microsatellite markers, a set of new markers designated 'Gh' for *Gossypium hirsutum*, the genome of their origin, was developed. Emerging cotton SSR marker collections have shown little redundancy (Reddy et al., 2001) implying the potential for the development of a very large number of microsatellite markers that would comprise a comprehensive and saturated molecular marker map. The goal of this research was to build a universally accessible set of molecular-genetic markers that could be exploited using widely available agarose gel electrophoresis technologies. This manuscript reports on the development and initial characterization of 700 new microsatellite primer pairs. A biotinylated-oligonucleotide capture method

was employed to isolate CA and GA dinucleotide repeats, as well as AGA trinucleotide repeats. Although AT dinucleotide repeats are very abundant in both the rice and Arabidopsis genomes (Lawson and Zhang, 2006) and are likely to be abundant in cotton, the high-stringency capture method used in this manuscript is not amenable to their isolation because of the low melting temperature of AT microsatellite repeats.

MATERIALS AND METHODS

Microsatellite-containing clone libraries were generated from genomic DNA of *G. hirsutum* cv. Tamcot Sphinx (El Zik and Thaxton, 1996). Reference genotypes *G. barbadense* acc. 3-79 and *G. hirsutum* acc. TM-1 have been described (Kohel et al., 1970; Kohel et al., 2001), as have recombinant inbred lines (RILs) from a TM-1 x 3-79 interspecific cross (Kohel and Yu, 2004).

Two new microsatellite-enriched libraries were generated using the biotinylated oligonucleotide capture method (Reddy et al., 2001) with the following minor modifications. The capture oligonucleotides employed were $b(\text{CA})_{20}$, $b(\text{GA})_{20}$, $b(\text{AGA})_{15}$, where "b" denotes a 5' biotin modification. The two final washes of biotinylated-DNA duplex bound to streptavidin-coated paramagnetic beads were carried out in 3X SSC at 60 °C to provide a high level of stringency to maximize the efficiency of microsatellite capture. Captured fragments were cloned into the plasmid vector pCR4-TOPO using a Topo-TA cloning kit (Invitrogen; Carlsbad, CA). Clones were unidirectionally sequenced using the M13(-21) forward primer. Sequence quality was determined by phred (Ewing et al., 1998; Ewing and Green, 1998). Quality scores were $Q_{10} = 713$ and $Q_{20} = 582$. Sequences were trimmed based on quality (phred cut-off of 10) and to remove vector and adaptor-primer AP11 (employed in the capture). BLAST (Altschul et al., 1990) was used to identify redundant sequences within the collection and to identify those sequences that are redundant with other publicly available microsatellite marker loci in GenBank (non-redundant nucleotide collection) (<http://www.ncbi.nlm.nih.gov/Genbank/GenbankOverview.html>), the CottonDB database (<http://cottondb.tamu.edu>), and the Cotton Microsatellite Database (CMD) (<http://www.cottonssr.org>) described by Blenda et al. (2006).

Using sequences from non-redundant clones, PCR primers flanking each microsatellite motif were designed to achieve a salt (50mM Na²⁺)-adjusted melting temperature (T_m) of 62-64 °C, and to produce theoretical minimum amplicons (i.e. hypothetical amplicons with a single repeat unit) in the 60-120bp size range. Primers were evaluated using publicly available web-based applications (Sigma-Genosys; Woodlands, TX) for internal structure and potential for homodimer and heterodimer formation. Thirty-five cycles of standard PCR were used to amplify products, using a primer annealing temperature of 55 °C. Samples were electrophoresed in 20cm long horizontal gel system (Owl Separation Systems; Portsmouth, NH) with 0.5X TBE (45mM tris-borate, 1 mM EDTA, pH 8) running buffer and 3-3.5% hi-resolution agarose (e.g. Metaphor agarose, Cambrex or SFR agarose; Amresco; Solon, OH). Gels were stained with ethidium bromide and photographed under UV light. PCR product sizes were estimated by comparison to DNA size standard ladders (E and K Scientific; Santa Clara, CA).

RESULTS AND DISCUSSION

From a total of 4,512 clones derived from two independent (GA)_n, (AGA)_n, and (CA)_n microsatellite-enriched libraries, 4,224 templates were unidirectionally sequenced, yielding 3,629 sequences that passed sequence quality, empty vector, and contamination tests. From these clones, primer-pairs for 1,059 SSR loci (designated Gh, for *Gossypium hirsutum*) were designed. This manuscript reports the primer sequences and the initial characterization of the first 700 of these primer pairs, designated Gh1 to Gh700 (Table 1A - Supplement). Clone sequences from which these primers were designed have been deposited into GenBank and assigned the accession numbers DQ907948 through DQ908629. The mean primer length was 24.5 bp. The mean G+C content of the primers was 43.2% and the mean salt-adjusted (50mM Na²⁺) T_m of the primers was 62.8 °C. The mean expected amplicon size, based on sequence from *G. hirsutum* Tamcot Sphinx, was 137.5 bp.

Primer pairs were tested using template genomic DNA from *G. hirsutum* TM-1, *G. barbadense* 3-79, and from an F₁ hybrid genotype from a TM1 x 3-79 interspecific cross. Overall, 86% of all primer pairs produced one or more distinct PCR amplifi-

cation products within the expected amplicon size range (based on cloned sequences from Tamcot Sphinx) in at least one of the parental genotypes, with approximately 67% of all primer pairs producing a single amplification product. In 201 of the first 700 Gh primer pairs screened (28.7%), size polymorphism was observed in amplification products between TM-1 and 3-79 using a standard agarose gel system with a high resolution agarose. This rate of interspecific polymorphism was lower than the rates of 45.4% and 56% observed for previous SSR captures from genomic DNA (Reddy et al., 2001; Nguyen et al., 2004, respectively). Efficiency of polymorphism detection is highly dependent on the assay system. Since the analysis was performed using simple agarose gel analysis, this was considered the minimum estimate for the rate of polymorphism between these two template genotypes. It should be noted that 65 Gh primer pairs that yielded products initially classified as “monomorphic” on agarose gels were rescreened using a 12% Spreadex (Elchrom Scientific AG; Dugelli, Switzerland) polyacrylamide slab gel system (data not shown). In this higher resolution gel system, 24 products (37.5%) displayed small but discernible size polymorphisms, so the actual rate of interspecific polymorphism in this collection will likely approach 50% when a high-resolution detection system, such as capillary electrophoresis, is employed in the analysis. Since the goal was the development of a large collection of markers that could be genotyped using the simple, facile agarose gel platform, subsequent characterization focused on those markers with the most easily scored size polymorphisms.

A set of 161 of the first 700 Gh primer sets that showed clear and interpretable patterns of polymorphism between TM-1 and 3-79 (primer pairs are underlined in Table 1A) was selected for further analyses (Table 1), including mapping in an interspecific RIL population. In this set of primer pairs, PCR yielded an average of 1.29 amplification products per tetraploid genomic template. Six of the 161 primer pairs (3.7%) amplified the products of two polymorphic loci, while the remainder amplified a single polymorphic locus. The total number of polymorphic loci uncovered by this primer set is 167. In those six primer sets that amplified two loci, allelism relationships among the amplification products were established on the basis of segregation in an RIL population.

Table 1. Approximate sizes of amplification products from polymorphic Gh markers

Locus ^a	Type ^b	Size (bp) ^c		Shared bands
		TM1 allele	3-79 allele	
Gh002	Cod	75	65	—
Gh012	Cod	108	120	—
Gh022	Cod	85	95	—
Gh027	Cod	70	80	—
Gh032	Cod	90	80	—
Gh034	Cod	130	120	—
Gh037	Cod	95	90	—
Gh039	Cod	125	120	—
Gh048	Cod	90	98	—
Gh051	Cod	155	165	—
Gh052	Cod	133	120	—
Gh055	Cod	175	170	—
Gh056	Cod	125	115	—
Gh058	Cod	175	100	—
Gh067	Cod	170	180	—
Gh071	Cod	155	170	—
Gh073	Cod	125	130	105
Gh074	Cod	170	180	—
Gh075	Cod	150	120	—
Gh077	Dom	—	175	125
Gh082	Cod	175	155	—
Gh083	Cod	133	125	—
Gh092	Dom	160	—	150
Gh096	Cod	170	215	—
Gh098	Cod	130	145	—
Gh100	Dom	—	150	175
Gh107	Cod	380	280	—
Gh109	Cod	90	80	—
Gh110	Cod	200	175	—
Gh111	Cod	280	250	—
Gh112	Cod	130	140	—
Gh117	Cod	260	240	200, 250
Gh118	Cod	148	135	—
Gh119	Cod	150	165	—
Gh124	Cod	180	200	—
Gh128	Dom	—	90	—
Gh129	Cod	120	140	—
Gh132	Dom	165	—	155
Gh133	Cod	152	145	—
Gh142	Cod	235	225	176, 240
Gh146	Dom	185	—	190
Gh153	Cod	195	185	—
Gh166	Cod	210	205	190, 225
Gh167	Cod	130	243	—
Gh171	Cod	205	215	—
Gh182	Cod	150	165	—
Gh185	Cod	85	90	—
Gh188	Cod	200	175	—
Gh198	Cod	190	180	—
Gh199	Dom	—	120	75
Gh200	Cod	144	114	—
Gh209	Cod	215	220	200, 230
Gh210	Cod	145	100	120, 90
Gh211	Cod	185	105	110
Gh215	Dom	195	—	185
Gh216	Cod	98	115	90
Gh220	Cod	88	98	—
Gh224	Cod	120	100	—

Table 1. continued

Locus ^a	Type ^b	Size (bp) ^c		Shared bands
		TM1 allele	3-79 allele	
Gh229	Cod	122	126	120
Gh236	Dom	125	—	115, 150
Gh237	Cod	100	140	—
Gh243a	Cod	130	125	—
Gh243b	Cod	90	100	—
Gh246	Cod	121	140	—
Gh247a	Cod	140	132	—
Gh247b	Cod	126	122	—
Gh252a	Cod	113	116	—
Gh252b	Cod	110	105	—
Gh260	Cod	98	106	100
Gh262	Dom	150	—	200
Gh272	Cod	123	135	—
Gh273	Cod	99	96	—
Gh277	Cod	104	126	116
Gh283	Cod	115	130	—
GH285	Dom	100	—	—
Gh288	Cod	180	165	—
Gh295	Cod	95	75	—
Gh300	Cod	120	112	—
Gh301	Dom	95	—	75
Gh302	Cod	261	290	—
Gh310a	Cod	144	166	—
Gh310b	Cod	124	146	—
Gh312	Cod	110	102	100
Gh316	Dom	—	165	190
Gh325	Cod	140	155	110
Gh329	Cod	265	280	—
Gh330	Cod	105	115	—
Gh336	Cod	98	86	—
Gh345	Cod	115	103	—
Gh350a	Cod	150	75	—
Gh350b	Cod	77	50	—
Gh354	Cod	170	130	—
Gh369	Cod	154	133	—
Gh371	Cod	85	83	—
Gh379	Cod	140	166	—
Gh380	Cod	103, 120	108	—
Gh381	Cod	123	111, 136	—
Gh390	Cod	209	143	—
Gh416	Cod	126, 161	129	—
Gh422	Cod	116	126	—
GH424	Dom	95, 105	—	100
Gh428	Cod	195	170	—
GH433	Dom	175	—	105
Gh434	Cod	168	150	145
Gh441	Cod	146	130	—
Gh443	Cod	150	120	—
Gh447	Cod	98	102	94
Gh449	Cod	126	110	—
Gh458	Cod	81	75	—
Gh459	Cod	170	200	—
Gh462	Cod	170	152	149
GH463	Dom	150	—	140
Gh465	Cod	150	175	—
Gh466	Cod	150	75	—
GH470	Dom	130	—	105
Gh471	Cod	100	105	75

Table 1. continued

Locus ^x	Type ^y	Size (bp) ^z		Shared bands
		TM1 allele	3-79 allele	
Gh478	Cod	90	100	—
Gh484	Cod	125	130	—
Gh486	Cod	120	125	—
Gh495	Cod	80	72	85
Gh498	Cod	128	140	130
Gh499	Cod	148	144	—
Gh501	Cod	195	205	190
Gh506	Cod	134	160	—
Gh508	Cod	139	131	129
Gh511	Dom	155	—	150
Gh513	Cod	166	175	166
Gh515	Cod	130	120	125
Gh523	Cod	160	150	146
Gh525	Dom	95	—	75
Gh526	Cod	125	200	—
Gh527	Dom	200	—	205
Gh532	Cod	150	175	—
Gh537	Cod	200	190	—
Gh539	Cod	100	106	—
Gh542	Cod	105	80	—
Gh548	Cod	120	140	—
GH551	Dom	—	165	160
Gh561	Cod	80	70	—
GH564	Dom	—	195	200
Gh565	Cod	114	126	—
Gh567	Cod	89	93	87
Gh568	Dom	—	130	125
Gh573	Cod	142	138	100,120
Gh584	Cod	140	120	—
Gh591	Dom	—	130	125
Gh592	Cod	120	124	—
Gh594	Cod	177	102	—
Gh597	Cod	134	138	—
Gh603	Cod	154	158	—
Gh629	Cod	128	132	126
Gh634	Cod	193	145	—
Gh641	Cod	90	94	—
Gh645	Cod	80	76	—
Gh646	Dom	—	118	100
Gh649a	Cod	128	132	—
Gh649b	Cod	126	122	—
Gh660	Cod	95	91	—
Gh662	Cod	80	82	95
Gh669	Cod	102	104	—
Gh678a	Cod	122,124	104	—
Gh678b	Cod	102	100	—
Gh681a	Cod	165	180	—
Gh681b	Cod	150	135	—
Gh684	Cod	102	90	—
Gh691	Cod	125	105	85
Gh697	Cod	100	95	90

^x Multiple polymorphic loci that are amplified by a given primer pair are appended with an 'a' or 'b' (e.g. loci Gh243a and Gh243b are amplified by primer set GH243).

^y Cod indicates codominant markers, and Dom indicates dominant markers.

^z Estimated using 3% agarose gel electrophoresis.

Amplification product sizes were estimated from agarose gels on the basis of comparisons to DNA standard size ladders (Table 1). Fifty-four of the primer pairs (33.5%) yielded amplification products that were scored as ‘monomorphic’, or shared in common between TM-1 and 3-79, in addition to the polymorphic products. Many of these shared bands were minor amplification products. Of the 167 polymorphic loci, 25 were scorable as dominant markers, yielding polymorphic products in only one of the two parental genotypes. One commonly employed explanation for such dominant markers is that there has been divergence in the primer binding sites, such that efficient amplification is only achieved in one of the parental alleles. In this study, 15 of the dominant amplification products were produced by the template of *G. hirsutum* TM-1, a reasonable outcome since the primers were designed using cloned sequence of *G. hirsutum* Tamcot Sphinx. In ten of the markers, *G. barbadense* 3-79 produced the dominant polymorphic band. An alternate explanation for these ‘dominant’ markers is suggested by the fact that 23 of 25 markers that were scored as dominant also displayed additional shared amplification products (possibly arising from homeologous loci). Specific

amplification from a single microsatellite locus was observed in only one of 15 dominant TM-1 loci, and only one of ten 3-79 loci. Loci might be scored as dominant polymorphisms, if one of the two alleles is in fact obscured by co-migration with an allele derived from an independent locus. Considered together, these findings suggest that the vast majority of the markers that were scored as ‘dominant’ are in fact co-dominant markers in which one of the alleles is obscured by the amplification product of another locus.

Primer pairs for 165 of the polymorphic Gh loci, including 149 codominant loci and 16 dominant loci, were used to genotype 191 individuals in a TM1 x 3-79 RIL population (Kohel and Yu, 2004). Overall, 51.3% of the alleles scored were TM1, 44.4% were 3-79, and 4.3% were either unscorable or heterozygous. All markers genotyped in the RIL population were tested for segregation distortion. Seventeen of 149 codominant markers and 1 of 16 of the dominant markers had a chi square value (95% significance level) indicating deviation from an equal genomic contribution by each parent (Table 2). Among markers that showed segregation distortion, 54% of the alleles were scored as TM-1, and 40 % were 3-79. Similar

Table 2. Loci showing significant (95%) allele segregation distortion in the TM1 x 3-79 interspecific RIL population

Type ^w	Locus ^x	Number of heterozygous genotypes			Chi ² test ^y	Direction ^z
		TM1	3-79	Het.		
Cod	Gh032	101	56	4	12.9	TM1
Cod	Gh082	96	53	17	12.4	TM1
Cod	Gh083	49	108	17	22.1	3-79
Cod	Gh110	96	58	8	9.37	TM1
Cod	Gh146	97	53	0	12.9	TM1
Cod	Gh237	104	63	11	10	TM1
Cod	Gh277	92	51	13	11.7	TM1
Cod	Gh350a	109	63	3	12.3	TM1
Cod	Gh466	110	57	6	16.8	TM1
Cod	Gh478	107	54	5	17.4	TM1
Cod	Gh513	89	53	40	9.12	Heterozygotes
Cod	Gh542	107	51	1	19.8	TM1
Cod	Gh548	108	63	6	11.8	TM1
Cod	Gh573	108	56	5	16.4	TM1
Cod	Gh649a	65	108	2	10.6	3-79
Cod	Gh649b	111	60	4	15.2	TM1
Cod	Gh662b	53	123	3	27.8	3-79
Dom	Gh568	64	109	0	11.7	3-79

^w Cod indicates codominant markers, and Dom indicates dominant markers.

^x Multiple polymorphic loci that are amplified by a given primer pair are appended with an ‘a’ or ‘b’ (e.g. loci Gh243a and Gh243b are amplified by primer set GH243).

^y Chi-squared values for simple inheritance (1:1 ratio).

^z Direction of segregation distortion.

levels of distortion and unequal parental contribution have been seen in previous molecular mapping using interspecific crosses of *Gossypium* (Lacape et al., 2003). One marker, Gh513, showed strong distortion in favor of heterozygous genotypes (22%) suggesting very strong selection in favor of heterozygous genotypes in the region of this locus during development of the RIL population. The overall low level of observed segregation distortion (10.3%) indicates that the overwhelming majority of the markers in this collection will be useful and informative in linkage and QTL mapping in interspecific RIL populations. Further, most of the markers that showed distortion were effectively incorporated into linkage maps using Joinmap (ver. 3.0, Kyazma, Wageningen, Netherlands) (Van Ooijen and Voorrips, 2001).

To identify markers that provided redundant linkage information, markers showing complete cosegregation in the RIL population were screened using Joinmap ver. 3.0. No pairs of markers showed complete cosegregation; however, the genotypic data of two pairs of Gh markers (Gh111/Gh112, and Gh098/Gh539) were in each case different by only two individuals out of the entire population, demonstrating very tight linkage. Although numbered consecutively, Gh111 and Gh112 were designed from different clone sequences.

Linkage information from the Gh markers will be included in a separate publication (unpublished data). In an effort to integrate several cotton genome mapping projects, a comprehensive microsatellite-based map is being developed using the TM-1 x 3-79 RIL population and 1,062 codominant and 75 dominant SSRs from more than ten independent marker collections, including publicly available markers (accessible through the CMD website). A set of 165 polymorphic Gh markers was incorporated into this map, comprising $\pm 15\%$ of the total mapping data. Additional markers from the Gh collection are currently being characterized. After these analyses are complete, sequence, primer, polymorphism, and linkage information from these additional Gh markers will be uploaded directly to CottonDB and CMD databases.

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DISCLAIMER

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REFERENCES

- Akkaya, M.S., A.A. Bhagwat, and P.B. Cregan. 1992. Length polymorphisms of simple sequence repeat DNA in soybean genetics. *Genetics* 132:1131-1139.
- Altschul, S.F., W. Gish, W. Miller, E.W. Myers, and D. J. Lipman. 1990. Basic local alignment search tool. *J. Mol. Biol.* 215:403-410.
- Bell, C. J. and J.R. Ecker. 1994. Assignment of 30 microsatellite loci to the linkage map of *Arabidopsis*. *Genomics* 19:137-144.
- Blenda, A., J. Scheffler, B. Scheffler, et al. [25 authors]. 2006. CMD: a cotton microsatellite database resource for *Gossypium* genomics. *BMC Genomics* 7:132.
- Brubaker, C., R. Cantrell, M. Giband, B. Lyon, and T. Wilkins. 2000 Letter to Journal of Cotton Science community from the Steering Committee of the International Cotton Genome Initiative (ICGI)[Online]. *J. Cotton Sci.* 4:149-151. Available at <http://www.cotton.org/journal/2000-04/2/149.cfm>
- Chen, X., S. Temnykh, Y. Xu, Y.G. Cho, and S. R. McCouch. 1997. Development of a microsatellite framework map providing genome-wide coverage in rice (*Oryza sativa* L.). *Theor. Appl. Genet.* 95:553-567.
- Collard, B.C.Y., M.Z.Z. Jahufer, J.B. Brouwer, and E.C.K. Pang. 2005. An introduction to markers, quantitative trait loci (QTL) mapping and marker-assisted selection for crop improvement: the basic concepts. *Euphytica* 142:169-196.
- Cregan, P. B., T. Jarvik, A.L. Bush, R.C. Shoemaker, K.G. Lark, A.L. Kahler, N. Kaya, T.T. VanToai, D.G. Lohnes, J. Chung, and J.E. Specht. 1999. An integrated genetic linkage map of the soybean genome. *Crop Sci.* 39:1464-1490.
- El-Zik, K.M. and P.M. Thaxton. 1996. Registration of 'Tamacot Sphinx' cotton. *Crop Sci.* 36: 1074.

- Ewing, B., L. Hillier, M.C. Wendl, and P. Green. 1998. Base-calling of automated sequencer traces using phred. I. Accuracy assessment. *Genome Res.* 8:175-185.
- Ewing, B., and P. Green. 1998. Base-calling of automated sequencer traces using phred. II. Error probabilities. *Genome Res.* 8:186-194.
- Frellichowski, J.E., M. Palmer, D. Main, J.P. Tomkins, R.G. Cantrell, D. Stelly, J. Yu, R.J. Kohel, and M. Ulloa. 2006. Genetic mapping of microsatellites derived from BAC-end sequences of *Gossypium hirsutum* Acala 'Maxxa'. *Mol. Genet. Genom.* 275:479-491.
- Goldstein, D. B., and C. Schlotterer 1999. *Microsatellites: evolution and applications*. Oxford University Press, USA.
- Kohel, R. J., T.R. Richmond, and C. F. Lewis. 1970. Texas Marker-1. A description of a genetic standard for *Gossypium hirsutum* L. *Crop Sci.* 10:670-671.
- Kohel, R. J., J. Yu, Y. Park, and G.R. Lazo. 2001. Molecular mapping and characterization of traits controlling fiber quality in cotton. *Euphytica* 121:163-172.
- Kohel, R.J., and J.Z. Yu. 2004. Permanent recombinant inbred mapping population for cotton genome research. p. 44. *In Proc. Int. Cotton Genome Initiative Workshop*, Hyderabad, India, 10-13 Oct. 2004. Available online at <http://icgi.tamu.edu/meeting/2004/Abstracts.pdf>. (verified 4 Nov. 2007).
- Lacape, J-M., T-B. Nguyen, S. Thibivilliers, B. Bojinov, B. Courtois, R.G. Cantrell, B. Burr, and B. Hau. 2003. A combined RFLP-SSR-AFLP map of tetraploid cotton based on a *Gossypium hirsutum* x *Gossypium barbadense* backcross population. *Genome* 46:612-626.
- Lacape, M., D. Dessauw, M. Rajab, J.L. Noyer, and B. Hau. 2007. Microsatellite diversity in tetraploid *Gossypium* germplasm: assembling a highly informative genotyping set of cotton SSRs. *Mol. Breed.* 19:45-58.
- Lawson, M. L., and L. Zhang. 2006. Distinct patterns of SSR distribution in the *Arabidopsis thaliana* and rice genomes. *Genome Biol.* 7: R14.
- Nguyen, T.B., M. Giband, P. Brottier, A.M. Risterucci, and M. Lacape. 2004. Wide coverage of the tetraploid cotton genome using newly developed microsatellite markers. *Theor. Appl. Genet.* 109:167-175.
- Park, Y. H., M.S. Alabady, M. Ulloa, B. Sickler, T.A. Wilkins, J. Yu, D.M. Stelly, R.J. Kohel, O.M. El-Shihy, and R. G. Cantrell. 2005. Genetic mapping of new cotton fiber loci using EST-derived microsatellites in an interspecific recombinant inbred line (RIL) cotton population. *Mol. Gen. Genome* 274: 428-441.
- Reddy O. U. K., A.E. Pepper, I. Abdurakhmonov, S. Saha, J. Jenkins, T. Brooks, Y. Bolek, and K. M. El-Zik. 2001. New dinucleotide and trinucleotide microsatellite marker resources for cotton genome research. *J. Cotton Res.* 5:103-113.
- Röder, M. S., V. Korzun, K. Wendehake, J. Plaschke, M.-H. Tixier, P. Leroy, and M.W. Ganal. 1998. A microsatellite map of wheat. *Genetics.* 149:2007-2023.
- Rong, J., C. Abbey, J.E. Bowers, et al. [24 authors]. 2004. A 3347-locus genetic recombination map of sequence-tagged sites reveals features of genome organization, transmission and evolution of cotton (*Gossypium*). *Genetics.* 166: 89-417.
- Sharopova, N., M.D. McMullen, L. Schultz, et Al. [26 authors]. 2002. Development and mapping of SSR markers for maize. *Plant Mol. Biol.* 48:463-481.
- Song, Q. J., L.F. Marek, R.C. Shoemaker, K.G. Lark, V.C. Concibido, X. Delannay, J.E. Specht, and P.B. Cregan. 2004. A new integrated genetic linkage map of the soybean. *Theor. Appl. Genet.* 109:122-128.
- Van Ooijen, J.W., and R.E. Voorrips. 2001. Joinmap 3.0 software for the calculation of genetic linkage maps. Plant Research International, Wageningen, the Netherlands.
- Varshney, R. K., A. Graner, and M.E. Sorrells. 2005. Genomics-assisted breeding for crop improvement. *Trends Plant Sci.* 10:621-30.

Table 1A. Primers for 700 Gh microsatellites with GenBank accession numbers for the clone sequences from which primers were designed

Primers ^a	Acc. #		Forward (F) and reverse (R) primers	T _m ^b	SSR motif ^c
Gh1	DQ907948	F	GCATGCTATCAATTGGGTTTGCATG	64	CATG(3)
		R	TTGGATTCCGTTAGCTTCTTGAGC	64	
Gh2	DQ907949	F	GAATTGAAGCAAACCTCATAATTACC	62	CTT(12)
		R	CTACCCTCATCTCATTCCAAAAAAC	63	
Gh3	DQ907950	F	CTCAACCTCCACATGGC	58	CAA(3)
		R	GCTGCTCACAAGAGGGATG	60	
Gh4	DQ907951	F	GAACCTGAGCGAGAACAACAG	61	GAA(4)
		R	CATGTTTCTGATTTCTCTGCC	60	
Gh5	DQ907952	F	CCGTAATTCCTGTGTAGACAATAAAAG	64	GAA(6)
		R	CTAGGTCCTATTAGCATCACTTTC	65	
Gh6	DQ907953	F	GTTTTTATGTGCCGAATGTGAGTTG	63	A(10)
		R	GGTTGACCATGATACACATAGTGAGCTC	68	
Gh7	DQ907954	F	CGAGAAGATGAGATTGGAGGAG	62	AG(18)
		R	CAAAGGTTTTGTGTGCTCG	58	
Gh8	DQ907955	F	CAACAAAACCCTTTTGAGTAAACG	59	AGA(3)
		R	CTCCTTCTCTAAATCATCAATTATTTAG	63	
Gh9	DQ907956	F	GGGCGGAGAATAGTCTTTAGGAC	65	CT(11)
		R	CAAATTATATCTATGTTTTAACATATCGGGG	64	
Gh10	DQ907957	F	CGACCCCTCTCCTTCTC	61	T(9)
		R	GGGGGAGAGGAAAGAGAGAG	63	
Gh11	DQ907958	F	CCTACCTTACTTCAGCCTGGAG	65	T(9)
		R	GCTACTGGATTGGGAAAGGC	60	
Gh12	DQ907959	F	GGTAAAGTAAGTTCATGAGGTTTATTTG	63	GT(15)
		R	CCAATATTACTCCAAGCAATC	59	
Gh13	DQ907960	F	CCCGGGCTTAAGTTTC	58	AAAG(3)
		R	GGGTCTTGGTTTTATCCCAAATC	61	
Gh14	DQ907961	F	GCTACTGGATTGGGAAAGGC	60	A(9)
		R	CCTACCTTACTTCAGCCTGGAG	65	
Gh15	DQ907962	F	GCTATTCTGCTTATTGTTATCCTGCTG	66	T(15)
		R	CCATACCATTACCCCAATCTG	62	
Gh16	DQ907963	F	GGAAACCACCCATTCTTTTG	58	A(11)
		R	CTACTTTCGGTGCCACC	58	
Gh17	DQ907964	F	GCATTACTCATGAATTAATAAGG	61	GTT(3)
		R	CCTATCTCCATTTTCATCAAAG	59	
Gh18	DQ907965	F	CCAAAAAGGAGAGTTGAAGGG	60	A(8)
		R	CTTCTGGTTTCTGTTTGATCC	60	
Gh19	DQ907966	F	CTATCCAGCAATGATAAGGCTAGG	64	A(8)
		R	CAAGTCCTACTCTTTGGAAAAATTCTG	64	
Gh20	DQ907967	F	GCTTGAAATAAATGAAAGTGAAAAAGG	62	AG(6)
		R	CAAAATTGTTACACACTGCCTTTTCTC	64	
Gh21	DQ907967	F	GGCAGTGTGTAACAATTTTGTAGTTAATAGAC	67	GA(4)
		R	CATATGCCCTCTGCCTCTCTC	63	
Gh22	DQ907968	F	CAACTAAGGAAATGAAAAAGAAAAATC	60	AGA(8)
		R	GACTTAGTTTATCTAGGTTTCTCTTAGC	65	
Gh23	DQ907969	F	CCTCGGATCAACGCACTC	58	AT(4)
		R	GTATTTTCTCATCTAACACTAAGGTTGTGC	67	
Gh24	DQ907970	F	CATTTAATCAGTGGATGATTCAACCTTC	64	TTG(3)
		R	CTATTTTGATCGTCCCTCTCAATTCAG	65	
Gh25	DQ907971	F	CTACGTATCAATATTTTATTCCTTGATTTATACC	68	TCT(16)
		R	GGATATGATACAGTATGTTCTCTGAGG	66	
Gh26	DQ907972	F	CTAAACCCTAATCGCCAAATAATAGAGG	66	C(9)
		R	CGGTGGTCATGGAGAGGG	61	
Gh27	DQ907972	F	CACTAGCATTGCTTTTACTGG	61	CT(13)
		R	GAAAAATAATAGATAATGGAGGAGAACAAGG	65	
Gh28	DQ907973	F	CACATGATTTTACTCAAACTTAAAGCAAAC	66	T(8)
		R	GAAGTGACAAGGGGAGGG	62	
Gh29	DQ907974	F	CTTTATCCTTTTCTACTTTTCTCCCTTTTC	66	GT(5)
		R	GCATCCATCAAGCTTGCC	56	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
Gh30	DQ907975	F	CCAACCTAAGTATCTCTTGATCAAATAACTAAATC	67	T(11)
		R	CGTGAGTTTGAATTGAAAGCTTTAC	61	
Gh31	DQ907975	F	CAAAAGTAAGTAATTGCTTCATTGACC	62	CTT(3)
		R	CTTGAAGTGATGAGGATACTGCTTG	64	
Gh32	DQ907976	F	GAATCATAGTTTGGTGTTGAGG	61	AAG(15)
		R	CACATTCACCTCAAAGTCCATCAC	62	
Gh33	DQ907977	F	CAATTCCTTAGAAGTCTTTGGG	60	T(10)
		R	GGAAAACATCTCAAGATTGGG	57	
Gh34	DQ907978	F	CCCTTTTGTATCTAACTTCTGTACTCCTAAC	69	AAG(11)
		R	CCTTTTGTTAGCTCTTCTATACTTGAATTCC	67	
Gh35	DQ907979	F	GGGGAGAAGACTGAGATTGGG	63	GT(8)
		R	GCCAGGCTGCTATTAACCCC	63	
Gh36	DQ907980	F	CAAAATTCGAGAGACGGAGAAAG	63	AG(11)
		R	CCTTGGCGCTCCCTTTC	57	
Gh37	DQ907981	F	CAAATTCGTATATGCATNTATACATCTGTTC	65	TG(14)
		R	GACATCATCCAATGCGAGC	57	
Gh38	DQ907982	F	GCCATATTCGCATGGCTC	56	AT(4)
		R	GCTAATATGTATTTTGTTCAACTTTGAATATG	64	
Gh39	DQ907983	F	CCAGTTTATAATAAGAATCATAGTTTGGTGG	66	AAG(15)
		R	CACATTCACCTCAAAGTCCATCAC	62	
Gh40	DQ907984	F	GAACCACCACACTACCTCAGACTAGAC	70	CT(9)
		R	CCAAAAGGCATCTGTTTAGAATCTG	63	
Gh41	DQ907984	F	CAACCACACTACCTCAGGCTAGAC	67	TC(6)
		R	CCAAAGAGGCATCTGTTTGAATC	62	
Gh42	DQ907985	F	CAAGTAGGACCCACTTGCCC	63	AG(4)
		R	GAATTTACAAGTATTTATTAACCCCTTACACAC	66	
Gh43	DQ907986	F	GTCAACAACACTAGACATAAACCC	64	A(8)
		R	CTTTTGAACATTTTAAATGAGAATTTATGG	60	
Gh44	DQ907987	F	CATATCCGTCTCGGTGGC	58	CTT(4)
		R	CAAGGCGAAAATTCTCAAAGATG	60	
Gh45	DQ907988	F	GAGTTTACTTTATGAAAATTATGGGAAAAG	64	A(16)
		R	CTCCGAGGGTAACTTATCTTTTTTAAAG	66	
Gh46	DQ907988	F	GTGACTCACTGACTCGACTCGC	66	CTT(5)
		R	CATCACCAAAACGACGATTCTG	60	
Gh47	DQ907989	F	CAAGTTTTCTGATTCAAGCATCG	59	AAG(3)
		R	CATCCACTGTTTCATTCTACCAGTC	64	
Gh48	DQ907990	F	CTGTTTCTTAACATGGGTTTTTTCC	61	GAAAA(5)
		R	CAAAAACCTAATTGCAAAAATAAATTATATTTTG	62	
Gh49	DQ907991	F	GGATCTTGTTAGACATTGGATG	61	GT(8)
		R	GATTATGCTAAGAAAACCAGTGCC	62	
Gh50	DQ907992	F	TCTCAAGCACGTCTCTCACGAGC	67	AGA(16)
		R	CGCCAAATTAAGCAAAGAAGAC	58	
Gh51	DQ907993	F	GCACAATCACAGATTGGGA	55	AGA(4)
		R	GATTTTAGCTAACTGTATCGGTTTCG	63	
Gh52	DQ907994	F	CTTGATCCGGTAGAGGAGTGT	61	AGA(8)
		R	GCTTCCACAGAAACCAATGG	60	
Gh53	DQ907995	F	CCAGTTTCCCTTCAGTCTA	58	AG(13)
		R	GTTTCACCAATTCTTCCTCG	56	
Gh54	DQ907996	F	CAATGATGGTGGCAATGTG	58	GT(13)
		R	CTTCCCACATTTTCATCACAC	57	
Gh55	DQ907997	F	GAATCACGGTTGGCATCTC	57	TCT(16)
		R	GCACCAATTAAGGTTTAGGC	60	
Gh56	DQ907998	F	TCCATTAGACAAAGTTTTCTAAAGTTC	61	TC(21)
		R	TGAGACTTCCAACCAGATACAG	60	
Gh57	DQ907999	F	CTGACTTCTGAGAACCTAATTTC	62	CA(9)
		R	AGTTTGCATATTCAGCAATTTATCC	59	
Gh58	DQ908000	F	GACTTTGAGAGGGATTTTACAGTG	62	TCT(26)
		R	CACCCAATTAAGCAGAAATG	56	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
Gh59	DQ908001	F	CTGCTAAGGCTAAACAAGTAAGTATTGG	65	AG(12)
		R	CTTTCCTCAATTTTCCTCC	56	
Gh60	DQ908002	F	CATTCCCGTTCGATTTTCAG	55	TCT(19)
		R	ATGTTAAAGATCAAAGATCTGATAGGA	61	
Gh61	DQ908003	F	CCAAACGAGGCTTACATGAATTC	62	CA(5)
		R	GAATGCATAAGAGCACTATGTATGTG	63	
Gh62	DQ908004	F	GTCAAGGAATCGACGGCGAGA	62	TC(5)
		R	TGGCAACAGCGATAATGG	54	
Gh63	DQ908005	F	CCTGAACAACCTATTCCGG	57	GA(11)
		R	GTGAAGCAAGAAATAGAACGTAAAC	61	
Gh64	DQ908006	F	GAGAAGCCAATCCCATTTAAGA	58	CA(12)
		R	GATAGTGCATCTCTAGAGAAAGACA	64	
Gh65	DQ908007	F	TGTTTTGGCTGATTCTCTACTCT	59	TC(13)
		R	CGGCCAAACAACAAAATG	51	
Gh66	DQ908008	F	CATTACAAGGACCTACAGTAGCC	63	A(9)
		R	CGGATGTTGATCTCTTGAATTATC	60	
Gh67	DQ908009	F	CAAGAGGGAAATCGACAAGG	58	AG(12)
		R	CCCCTTCACCTATTAAGTCAACA	61	
Gh68	DQ908010	F	ACGAGACATGAAGCAGGA	54	A(14)
		R	CAAAGCAATGTGGAACATG	53	
Gh69	DQ908011	F	GCTGTCTCTGGTCCCATTG	60	CA(10)
		R	CGTATCTGCTTCAGTGGTTAAGTG	64	
Gh70	DQ908012	F	GCCATATCAGTAGTAATTTAGGGTT	61	AGA(24)
		R	GTTTAATAGGATTTACAGAGGAGGG	63	
Gh71	DQ908013	F	GTTTCATCACCATTTCATCAGC	57	AGA(13)
		R	GAATCCATAGCTTGTTCATTG	58	
Gh72	DQ908014	F	TGTAGGAGTTATTCATGCACTTG	59	TC(15)
		R	GCGTGAAAATGAGCTTGTC	55	
Gh73	DQ908015	F	GCTGACTGCATTGGTTCCG	56	TCT(16)
		R	TGGGTCTCTACCTAATAGCTGG	65	
Gh74	DQ908016	F	ACAGCCTATAATAAGATGCCACA	59	CT(11)
		R	CAGTAGCCAGAACTTAAGCTATG	62	
Gh75	DQ908017	F	CGTCTGGATTGAACAGTGATC	60	AGA(19)
		R	CAACTTGATCTAACTATTGCATACG	61	
Gh76	DQ908018	F	GAGTTCACATTCCTCCG	60	AAAAAG(3)
		R	GCCACATTTCTAAATCTCACAATTG	61	
Gh77	DQ908019	F	GTTGCGACGTTAGGTTTCAGTTAC	63	TCT(8)
		R	GAGTTGAAGAAAGCGAGTATCC	60	
Gh78	DQ908020	F	TCATAAACTGTGACTTACCGCA	58	AGG(5)
		R	GAGACCATAAGCCTCATTGGAG	62	
Gh79	DQ908021	F	CTGTTAGCTTGCCTGTGTCG	58	TCT(15)
		R	CAAAATGACTATGCCCTAGTTG	61	
Gh80	DQ908022	F	GAAATTAGATAACAGTGCAGAGAC	63	AG(13)
		R	TCACTCCTCCTTTGATCTCTGT	60	
Gh81	DQ908023	F	GAACCAACTATTCCAATTCATG	59	TCT(8)
		R	CACGAGTCAATTGGATCTGTG	60	
Gh82	DQ908024	F	GATACCTTTGTACGAAGCTG	60	AG(21)
		R	GCACCAATCAGTAAGTGCAAGTC	63	
Gh83	DQ908025	F	GGTTTGATCAGTTTGATGATTTAGC	61	TC(17)
		R	CCGCGGAATCGTCAAC	53	
Gh84	DQ908026	F	GTCCCCTCTTGAGTCCAC	60	CT(6)
		R	CCACTTGTTGTAGCTCTTCTTC	61	
Gh85	DQ908027	F	CCATGAATCTGAAATTGAGATACG	60	AG(10)
		R	CTACTCCAGATGAATATATTGGCC	62	
Gh86	DQ908028	F	GCTAAGTGATCCTTAACAGGCTTG	64	TCT(7)
		R	GTAAACTTCCATTGGGAAGTTGAG	62	
Gh87	DQ908029	F	GGCTACACGAACCTTTTCGATTATC	62	CA(9)
		R	CGATAATCCATATGATGTTATGTGC	61	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
Gh88	DQ908030	F	GCATGTGAGGCACCTTACAGA	62	CA(9)
		R	CATGATGAAGATTAATAAAATGGG	59	
Gh89	DQ908031	F	CCAGGAGGTTGAATCATCTACTC	63	AGA(9)
		R	CAATTGTAAGTTAGACTTTTCGCC	59	
Gh90	DQ908032	F	GTGCTGATTGGAGTATAGAAATTG	60	TG(5)
		R	CTCTAATCCCCAGGCTCTACC	63	
Gh91	DQ908033	F	GCAGGAGAGGAAGGCTGA	58	AG(6)
		R	CTTCCTTTCTGCTTCCTCACG	61	
Gh92	DQ908034	F	GATTTAAGCGCCGAGACAG	57	AGA(10)
		R	AGCCGGTCGATCAAATC	52	
Gh93	DQ908035	F	CAATGATTAACCGGATGGGT	57	TCT(7)
		R	GTGGACAAGTAGTCAAAGGGTC	63	
Gh94	DQ908036	F	CCTGAACAACCTCATTCCGG	57	GA(11)
		R	GTGAAGCAAGAAATAGAACGTAAAC	61	
Gh95	DQ908037	F	CCAAGTGTGAAGACAACATCC	60	AGA(7)
		R	TGTAGCTCGGACTCGACG	58	
Gh96	DQ908038	F	TCTCATAGACGTTCTGTTATAACAAG	62	AG(12)
		R	GCTGCCCATTCACCTCCTC	58	
Gh97	DQ908039	F	TCAGCTGACTGCATTGGT	54	TCT(6)
		R	GGAACCTCTACTGAATAGTCGGAG	65	
Gh98	DQ908040	F	CACCGCATCACCAAATAGTAG	62	AGA(4)
		R	TCTTCCATATCTTCTCTTCTCC	61	
Gh99	DQ908041	F	CCTGCCATTAAGATCCCGTGT	58	TCT(7)
		R	AGAGCCATGCCCTAGTCG	58	
Gh100	DQ908042	F	CTTCTTCATCCAGTTTCTGA	58	TA(8)
		R	CGTTTCAATGATAAACATGACG	56	
Gh101	DQ908043	F	GAAGAGGACGTTGTGTCTG	57	AGA(7)
		R	GACTTGGGTGCGGTGATAGT	60	
Gh102	DQ908044	F	GGAGAGGGAGACAAATAGACG	61	T(11)
		R	GGATGTGTAGTGGGAATTAGGG	62	
Gh103	DQ908045	F	GTCGACAGTCAGCAGGTTC	60	AGA(6)
		R	CTTCTGATATCGTGCTGTTGTTT	61	
Gh104	DQ908046	F	GAGCATGATTTCAATTGGCT	54	TA(6)
		R	CACTAAGTGTGCGTGGTTGA	58	
Gh105	DQ908047	F	ACCTCAATACATGCTTCATACACA	60	CA(6)
		R	GAGTCTGGAATATGATGAATTGTG	60	
Gh106	DQ908048	F	CCGAAGAAGTGAAGAGGAAGG	61	AG(7)
		R	TGTAGCCTTTCGTTGCTCTCT	57	
Gh107	DQ908049	F	CATATGTGACTTAACATTCATCGTC	61	CA(10)
		R	CTCACCCATGTTTGTTCGA	55	
Gh108	DQ908050	F	CTGCATGTTATTGATGGATGGA	58	T(15)
		R	ACATGTGCCTGCAACAAGT	55	
Gh109	DQ908051	F	CAAGAAGGAAATGGCTGAATTG	58	TCT(10)
		R	CAGACACCAGCTGTTGCC	58	
Gh110	DQ908052	F	ACCATCCCAAAGAATCATCCTC	60	TCT(16)
		R	ACTAAAACCAAGGCAATAAAGTG	58	
Gh111	DQ908053	F	GTGCAACCTTGGAACCA	55	AGA(30)
		R	GGGTTGCCGTTAGACCAG	58	
Gh112	DQ908054	F	GGTTGGGTTTCCACAATAGC	58	TCT(27)
		R	TGTTGCAACCTTGGAACCC	55	
Gh113	DQ908055	F	GAATTCGAAGGCAATATTGCT	56	TC(10)
		R	TGGGTAACCTAGGGTGTCAGG	63	
Gh114	DQ908056	F	CGCAGAAGAAGAAGAGGAAG	58	CGA(4)
		R	CCTCTCGTTCCTCTTCTCTCTC	65	
Gh115	DQ908057	F	AGAAGAGTAGTGAAGATGGTGACA	62	AGA(5)
		R	CTTATTCTCGAACTCATCCCT	58	
Gh116	DQ908058	F	GTCAAGAGTGTTCATCATATCCCT	62	GT(5)
		R	TCATGTCATATCGGATTGATCAC	60	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
<u>Gh117</u>	DQ908059	F	CGACTGAAGGTTGGCAGTAGTC	64	AGA(15)
		R	GATGGCCGACATTACTCAGAG	61	
<u>Gh118</u>	DQ908060	F	CGGAAGCTAGTGAAGGAGG	60	AG(16)
		R	TCTTTCCTTGTTCTGGAGT	56	
<u>Gh119</u>	DQ908061	F	GTTGAAGCAAGTGAGGATCC	58	AGA(16)
		R	CGGTIATTGGTTCATTAGTTCAGTCG	67	
<u>Gh120</u>	DQ908062	F	GTATGTTACACAGGCACTCAG	62	CA(11)
		R	TCTTGTACATTACTGTTGGCT	59	
<u>Gh121</u>	DQ908063	F	GTGAACATCATGGAGCAGACC	61	CA(10)
		R	TGAGGTAAGCTTATTACTTGTCCCTG	63	
<u>Gh122</u>	DQ908064	F	CTAGTGGTCACATCCTCTGCC	63	AGA(13)
		R	CTTCACTCGAACTTTCATCTTCC	61	
<u>Gh123</u>	DQ908065	F	CTTTGCCTAATTGCTGCACTG	60	AGA(13)
		R	CGTACTAATCAGTGGGCTAAGC	62	
<u>Gh124</u>	DQ908066	F	CGTTGGATAACATGCCATGT	56	TCT(11)
		R	GCAATTCTAATTCTGTCGATTACC	60	
<u>Gh125</u>	DQ908067	F	AGATCAGAAGACGGTCAATC	60	AG(9)
		R	AGCGATTGGGTGAATGG	52	
<u>Gh126</u>	DQ908068	F	GGAAGATCTTATGTGGAAGACC	60	AGA(6)
		R	AGAAAGAATTTCAACTTCAATGGA	57	
<u>Gh127</u>	DQ908069	F	CTGACCAATGTTAATCGGATCA	58	TC(11)
		R	TGTGAGAAGAAACCGATTGG	56	
<u>Gh128</u>	DQ908070	F	CCATGTCAGTTTGATCATTGGT	58	TCT(13)
		R	ACGAGTGGAACCTGAATGAGG	58	
<u>Gh129</u>	DQ908071	F	ACACAAGCGATCAACAAGG	55	CA(9)
		R	GAAATGATGTGAGCTCTTGTTC	59	
<u>Gh130</u>	DQ908072	F	GCTGTCTTGCCCTCAAATACC	61	CA(10)
		R	TGTCAGTGGTAAAACATCGTTACG	61	
<u>Gh131</u>	DQ908073	F	CAATGCCGAATGCCATTAG	55	CA(6)
		R	TGCTTATATGTGTATTCGGCCAG	61	
<u>Gh132</u>	DQ908074	F	TCATGGAACACCAAAGTTGGA	57	TCT(14)
		R	ACATGATAGATTATTCAGCAATGCA	59	
<u>Gh133</u>	DQ908075	F	TGTTTCTCTCGGAAACTATAGACCA	63	TG(11)
		R	CCAACCTAAGAAGGAAGAGATACCA	63	
<u>Gh134</u>	DQ908076	F	CTAAAGCTTCTGGGTCTGTTACAG	64	AAAG(3)
		R	ACCCAGAAGTTTAAACCCGAAGC	64	
<u>Gh135</u>	DQ908077	F	GGAGATCGGTAGGAGAGGAGAG	66	GA(8)
		R	GAATGCTTCTTCATCTCCCTCTTC	64	
<u>Gh136</u>	DQ908078	F	CACCAACCTCGAGCACC	57	TA(5)
		R	AACCCAAAGTTGTCAAATACCTT	58	
<u>Gh137</u>	DQ908079	F	TCCATTGAAACATCATGTCTTTAC	59	TCT(9)
		R	GACTTAAACCCAAACAGCGAAGAC	63	
<u>Gh138</u>	DQ908080	F	CCAGTGAACAACCTCATCAGACG	62	TCT(13)
		R	GAGAAGGACCAAATCTGTGGA	60	
<u>Gh139</u>	DQ908081	F	GACACCCTTGACTTGTTCAG	62	CA(8)
		R	CAGTTCAAAGAATCTTTGTCAATG	58	
<u>Gh140</u>	DQ908082	F	GGGAAACTAGTATGAGTTAGCGACT	64	GT(13)
		R	CCATGTTCAATCCACAATAATAAAC	59	
<u>Gh141</u>	DQ908083	F	TCTACCTAAGCAATCAGAACCTG	61	AG(11)
		R	GAAATGTTTCAGCCTCGTTTCT	58	
<u>Gh142</u>	DQ908084	F	GAGTCTCCTCCTCGCATG	58	GT(10)
		R	TCAACCACACATCATAAGACCA	58	
<u>Gh143</u>	DQ908085	F	CTTGATGCATGTTGACCTAGTC	63	TCT(7)
		R	CCTGATTGCATACTAATTGTAAGC	61	
<u>Gh144</u>	DQ908086	F	CCATCATGCATTTCATTGCTCT	57	GT(9)
		R	CGCTCCACCTTGTATCAGAG	61	
<u>Gh145</u>	DQ908087	F	CTCATTGCATAGCATTTTCATGA	58	CA(10)
		R	GATATCTTGTTGAACTGTGGCT	59	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
Gh146	DQ908088	F	GACCAGCACCGGAGTTTC	58	CA(10)
		R	CTACTTGCCTAGGTATTGAGGTG	63	
Gh147	DQ908089	F	GTGTTGCGACCCAAAAGTTTAC	60	TCT(9)
		R	TCAACCTCAATAACAGGCACC	60	
Gh148	DQ908090	F	AAATCTAGATCAGCACAGTAAAGCTC	63	TC(11)
		R	TTGATTGGCATTACAGCAAGATAGAG	63	
Gh149	DQ908091	F	GAGGCAGAGAGTCTTATCTATGGA	64	TC(10)
		R	GGAATCCATTTGAGACAATGTGA	59	
Gh150	DQ908092	F	CTGAGAGCCAAGCACTTCC	60	AGA(5)
		R	CCTGTGACTCACTGACTCGAC	63	
Gh151	DQ908093	F	CAACCAGGATGTAGACGTGA	58	A(12)
		R	CATTTGAACCCACGTTATCCTG	60	
Gh152	DQ908094	F	CCTGCCCTGAACAAAAGTTG	57	CT(5)
		R	TGCTAAACAAGACGGTGAGAAC	60	
Gh153	DQ908095	F	GGCTCAAATTTGCATTCCAG	56	CAT(7)
		R	CCATAGTTGGAAGCCATGAAG	60	
Gh154	DQ908096	F	AAGACTATTGATTTAACCTCGTTCA	59	TCT(11)
		R	GTATCAGAGCCTGGTTGCAAC	61	
Gh155	DQ908097	F	GTATCAGAGCCTGGTTGCAAC	61	AGA(11)
		R	CCTCGTTCAATAGAAAACTTTGA	58	
Gh156	DQ908098	F	GATCTTGACAGGGAAGACAGACA	63	TC(10)
		R	CATAACTTGACATCCATCCATGA	59	
Gh157	DQ908099	F	TCTCTGGAGGCTAACCTTGTG	61	CA(9)
		R	AGATTCATTGCAGTGGAAATATCC	59	
Gh158	DQ908100	F	GGTGCTCATGATGATGCTG	57	AG(16)
		R	GAGTCAATGACAAGAGGATCACC	63	
Gh159	DQ908101	F	CTTGCTCTTAGGCTTGAAGG	61	TCT(5)
		R	GTCTGTGAAAGGCACGGA	56	
Gh160	DQ908102	F	GATTTCCAGTCATCTCTCTCGTG	63	CTTT(5)
		R	ACTGGCTTTGAAACAACATCC	56	
Gh161	DQ908103	F	CTCATTCTCCATGATCAACC	60	AG(8)
		R	CGTTGAAGCTCACTTTTCTCG	60	
Gh162	DQ908104	F	CGATCCTACGCCCATTTAGAAGG	65	CTT(11)
		R	TCATATGTCGTTAGGTGCTCAAG	61	
Gh163	DQ908105	F	GAGATCAACATCCGGATTGTCT	60	GA(12)
		R	CTCTACGCCCTTATACCAGCAGG	64	
Gh164	DQ908106	F	TCATTGCCTCACTTCACTCTGT	60	T(13)
		R	TGGTGATATCTGATCCATCTATGC	62	
Gh165	DQ908107	F	TGTTGAGATAAGGAACTTGACACA	60	GAA(5)
		R	GGGATGTTACACTTTGGCTAGAG	63	
Gh166	DQ908108	F	CAGTTAACTCTGCATTCAACAGG	62	CTT(14)
		R	CTCCTTCTCGTTATCGGTC	60	
Gh167	DQ908109	F	CCATTACCTTTACACCTCAAATTC	63	CA(16)
		R	GAAAAGATGGATATGCACATATGC	59	
Gh168	DQ908110	F	GGAGAGCCAAGATTCGTTTC	57	CTT(6)
		R	GAAACTCAAAGCCAACCTCGG	60	
Gh169	DQ908111	F	AGACAAACATCCTAAGCCAAATATC	61	GA(16)
		R	GCGACATGCTGTGTAGCG	58	
Gh170	DQ908112	F	GTATTGCAGGCAACCACAATC	60	CTT(7)
		R	CTCCTTGGGTTGATTCGG	56	
Gh171	DQ908113	F	CCCTAAAGAGAAATCGGTATCCTC	64	CTT(12)
		R	CAAACCCAGAACTGGCTTC	57	
Gh172	DQ908114	F	CAATGCAGATCAATAATGAAGAATG	59	AGA(29)
		R	GGTGATCAACTTTCAATCAACAAG	60	
Gh173	DQ908115	F	GCCATAGCCGAAGCTTAGG	60	AT(6)
		R	ACACCATAACCCAAAGTTGTCA	58	
Gh174	DQ908116	F	CCTTCACTCATAAGTTGAGAAC	64	GT(11)
		R	CCTGAGCATGATTGTCTCTGG	61	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
Gh175	DQ908117	F	CAAGTGTGTATCTGCTTCAGTG	60	GT(9)
		R	CCACCAGACCAGCAGACC	61	
Gh176	DQ908118	F	CCACACTTGTGTCTATTATTCA	60	CTT(25)
		R	CCACAAGCATGTCGCAG	55	
Gh177	DQ908119	F	GAGATTGATTCGAGATCGATAACC	61	AG(6)
		R	CTGTAAAGGTATTCTCCAGACA	62	
Gh178	DQ908120	F	GCTCTGATTGATCTCGATATTGT	60	CTT(9)
		R	GGACCCTTATACTATGGAAACCAC	63	
Gh179	DQ908121	F	GGCAGAATCGCAGATTGG	56	GAA(10)
		R	CCAGTTGACTGCATTGGTTC	58	
Gh180	DQ908122	F	AGAAGAAGTCATTGTTGAGGCA	58	GAA(5)
		R	GGTCTTCTTTCTTAGCTCCTTCAC	64	
Gh181	DQ908123	F	GCTCGTATTTACACTTTACCGT	61	GT(9)
		R	CTCCTGTAATAGAGGTTGGCG	61	
Gh182	DQ908124	F	AGCGCTTAGAAGTTGTCAATGTC	61	GT(10)
		R	ACATGCCAACCTCTGACCTC	60	
Gh183	DQ908125	F	AGCCAGAACCTGATTGAATCA	57	GA(20)
		R	ACCGCTATATTTCTTTAAGCACC	59	
Gh184	DQ908126	F	CCAGTAACTTGCCACATTGG	60	GAA(5)
		R	AGACATGGAGTTTCAATGGCA	57	
Gh185	DQ908127	F	CAACTTGTTGACGTTTTGATAAAGG	60	TG(7)
		R	AGTCCAATTCTAGCTTGATCTTACC	63	
Gh186	DQ908128	F	CTTCTCGAACTTCTCAGGTCA	62	AC(9)
		R	GTTGATTCCATCCATAAGTTGC	58	
Gh187	DQ908129	F	CTCCTGCCTATGCTGCTATG	60	CTT(8)
		R	AGGAACTAGCACTGTCTACATTGA	63	
Gh188	DQ908130	F	CGCAACTGTAAGCTATCTCTTATGG	64	CT(15)
		R	TGCTTGTGGGAGTAATGGTG	58	
Gh189	DQ908131	F	GACGGCTCGTGCTAAGTG	58	CT(10)
		R	CTCAGTAAGCTCATCTATGGTGTC	64	
Gh190	DQ908132	F	CCTACCAAACGCTCCCTTAC	60	CT(11)
		R	AGAAAGGTCAAAGACGGAATC	60	
Gh191	DQ908133	F	GCAACATCTCACAAAAATTTCG	58	CA(12)
		R	TCCGTATTATATGCGCATGG	56	
Gh192	DQ908134	F	GATCACTTAATGATTCTCACGTCC	62	CTT(9)
		R	GCTTAAGGATGTCTAGGGTGCA	62	
Gh193	DQ908135	F	GGTTGTTGCTTGCTACCTTTC	60	GA(6)
		R	GGACCTTTCTCTTTCCTACGG	61	
Gh194	DQ908136	F	TGAATCGCAGCCTCCATC	56	CTT(5)
		R	CTTCCCTTTGTTTTCGATG	57	
Gh195	DQ908137	F	GCGAATTTCTTACTTAAACCCTTC	63	GAA(8)
		R	TCTATTCTCGAACTCATCCCT	59	
Gh196	DQ908138	F	CAATTCACATGACTTCCTTAGTTCC	63	CCT(7)
		R	CACCTGGTTTCTTCGCG	55	
Gh197	DQ908139	F	CTGCTGACAATGCCAAATAG	57	CTT(9)
		R	CATTGTGGGTGAGAGAGCG	60	
Gh198	DQ908140	F	TCTATTTACGATCGGGCAATACT	60	CTT(10)
		R	CAACGAGTTGAAGAAAAGTGAGG	60	
Gh199	DQ908141	F	CAAAAAGAATATGAATGAGTCAATAGAC	62	GA(10)
		R	CAATAAATGCCATAATCTTCAACTCAC	63	
Gh200	DQ908142	F	TCAAGTTCTTTTTTAAACCTCAACATTC	62	TCT(8)
		R	CTATTAGACTAGATCTTAGTTGATC	61	
Gh201	DQ908143	F	ATGCAAACGATGTAGCCACGTG	62	AGA(8)
		R	CTCTAGAACAATGGCTTTTATACCG	62	
Gh202	DQ908144	F	ACAATATAGGAGGATCAGAGAAAGA	61	CA(10)
		R	CGTAATAACTAACTCTTAAACCTC	61	
Gh203	DQ908145	F	GAATATTGAGAAGGTGAGAGACTC	63	GT(10)
		R	TCATGACTCATATTTATTACAAATCTATATG	62	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
Gh204	DQ908146	F	CATACAAACAGATACAAAGCAACATG	62	GA(12)
		R	CGAAGTCTGATAAGCTGAGGCA	62	
Gh205	DQ908147	F	CAACAAGAGCATGTGTGCGGAAGC	65	GA(14)
		R	CCTGTTTCATATCCAAAGTCAAATTTTCAG	64	
Gh206	DQ908148	F	AAGAGAGCGAAGGTGGAATATCAG	64	GA(11)
		R	CAACTCACCATTGTAAATACTAATACGC	64	
Gh207	DQ908149	F	TAGTCAAGATCAAGAAAGTTGAAACAG	62	TCT(8)
		R	CGTCGATCTGGGGAAGAACATG	64	
Gh208	DQ908150	F	GATTCATTACAACTCGAGCATTGTG	63	AG(13)
		R	TCAGTTTCCTCTCTTCAGGTC	62	
Gh209	DQ908151	F	GATTAAGTGAATGTGATAAGTAACTTACTC	64	GT(9)
		R	GCTACACGAACTTTTCGATTATCTTAC	64	
Gh210	DQ908152	F	CAGTGCAAATGAATCAATGGAGATTAC	64	ACA(14)
		R	TGAATTGTATCATAGTCCACTGTGGA	63	
Gh211	DQ908153	F	GATTGATAAAGTAGGGTTGTGTGCAC	63	GAA(24)
		R	CATTATGTGCCTTCAAATTCCTGGC	64	
Gh212	DQ908154	F	AGAAACGTCAAGCCGAGGACAG	64	GAA(8)
		R	CTCAAAAACTTGTTTACCTAACATTCAAC	64	
Gh213	DQ908155	F	GTTCTTATTCTGCTACTGTCTCCG	64	TC(18)
		R	CGCTCTTCATATTTTCATTTCACAAGC	63	
Gh214	DQ908156	F	GTAAAGACAGAATATCGGAAAGAGAG	64	AGGAGAAGA(16)
		R	CTTTCTGGTTCTTTTATTATCAATCTC	64	
Gh215	DQ908157	F	TCGGATACCACTTGTGGGAAGCA	63	CT(13)
		R	GTGTTAGTTATAAAAAAGAAAACTAGCAG	62	
Gh216	DQ908158	F	TCCACATTCCCATGCCTACTC	62	CT(15)
		R	CTAAAACCTTATACATACAAAAATGCAGC	63	
Gh217	DQ908159	F	CAACACGATGCGATTGACCCTC	64	CT(10)
		R	CAACACGATGCGATTGACCCTC	64	
Gh218	DQ908160	F	ACCCCTTTTGCCTTTATTGCTTGC	64	TC(14)
		R	CAAATCCAAGATGACAAACACACGTG	65	
Gh219	DQ908161	F	TACATTATTAGACCATAGAGAATGGAGA	63	CA(10)
		R	CATTATCATACGCTTAAGAGTAACC	63	
Gh220	DQ908162	F	CAATTATTCACCTCCAGGCTTCC	64	TCT(12)
		R	TGGATTTGAAAATCCATTGAACTCACC	64	
Gh221	DQ908163	F	TGCTTGAAAATTGAGAAGAATTGCGAG	64	AGA(9)
		R	GCCATAGCCGCTGTAGCTGC	65	
Gh222	DQ908164	F	CTAGTTTAGGCTTAGTTTCTCTAGG	64	TCT(15)
		R	AAAGTTGCTAGGAAATGTAATATTACAAC	63	
Gh223	DQ908165	F	CCTTCCTAGTTGTAATTTCCCTACTT	64	AG(18)
		R	TTTGTGCAACTGTGCATGCCAGA	64	
Gh224	DQ908166	F	TCCATTCTTTTCATTTCTCAAAGG	64	CT(22)
		R	TGAAACGAGAAGATGAGATTGGAGG	64	
Gh225	DQ908167	F	CCGAATTTGCTTCATTAGGACGC	63	C-rich repeat
		R	CTGCTGTGAAGAAATATTATGCCTG	63	
Gh226	DQ908168	F	CGATTATTCAGCATATAAACCAATTTGCC	64	GAA(9)
		R	CTTACTAAAGGATTATCATCAGGTCAG	64	
Gh227	DQ908169	F	GTAGTTCATCATTATACAAAACAACTAG	63	CA(10)
		R	GGGTTTTGGCATGTATATGTGGC	63	
Gh228	DQ908170	F	CGAAGAAAGTGAAGCCTATGAACC	64	AGA(7)
		R	GACTAACTTAACACATTGTTTCCTTCC	64	
Gh229	DQ908171	F	GACATGCCATTCATTAATTTTCATACATG	63	AGA(9)
		R	CTGAAACAACCAAGTCAAGCTCAG	63	
Gh230	DQ908172	F	CTACCTAGGCAATCAGAACCCTGA	63	AG(10)
		R	GTAATTTGTTGTTATCTGAGGTATTGTC	63	
Gh231	DQ908173	F	GAATAGTTGATAACAAAATAGAATGCAGAA	63	AG(8)
		R	ACGTTCACTTCCCCACTCC	63	
Gh232	DQ908174	F	TCTTCTCCTCAATTCCTCCCTC	64	TCT(14)
		R	GGGAACAAAAATAANCTTTAGTAATGAGG	64	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
Gh233	DQ908175	F	CTTTTAACTTAAACCCATTAAAGAGC	63	AGA(9)
		R	GGCAATCGCTGATACGAAGCTC	64	
Gh234	DQ908176	F	TTATGGTTCTCAAAGTGTGGATTATG	63	TC(12)
		R	AAGACTGACACTGAAGGCAGAAAC	64	
Gh235	DQ908177	F	CTGAAACTGAAGAGGTTGAGAAGG	64	AGA(7)
		R	GCACCATTAAACAGCAACAGGAGTC	65	
Gh236	DQ908178	F	CTTTTCCGTTTGCTTTTCTCAACTC	64	CT(12)
		R	ATACAACAATGATGGTGGCAATGTG	63	
Gh237	DQ908179	F	GACACTTGTTAAGTTTCGCTAAGAG	63	GT(14)
		R	GGAAAATAAACTTCCTCATGAACCCTTC	66	
Gh238	DQ908180	F	CAGGTAATTTCTTTTGGGAGATTATG	63	GT(11)
		R	TCAGCATATGAATCGATTATTC	65	
Gh239	DQ908181	F	TGAGGGCAGAGGTCTGTGGA	63	CT(17)
		R	GCAAAGATGACAAATATCAACAATAACC	63	
Gh240	DQ908182	F	ACATACTATGAATTCATTGTGCACCA	63	CA(7)
		R	GCGAGCCTCCTTGTTATCTTGC	65	
Gh241	DQ908306	F	TGTTGCTGGTGGTCACCATTTC	63	ACT(5)
		R	AACCATGTGCCCTGAAAGTGATG	63	
Gh242	DQ908183	F	TCCAATTGTTCTACACTTCTCCTCA	63	GA(11)
		R	TAACAAAACCAGAAAACAAACGCTCGA	64	
Gh243	DQ908184	F	CAGAAGTTATGCAACAACATGCA	63	AGA(14)
		R	CTAAACTCTCTGCTGTGTTC	63	
Gh244	DQ908185	F	GCTGAAAATTGAGTATCAAGTGCC	63	AGA(10)
		R	TAGAATCTTTCCTTACCAAACGAC	63	
Gh245	DQ908186	F	TACTGTCATTATACTCCAACAAGGATC	64	CA(9)
		R	GTCTAATGATGATAATTCTCAAACGG	63	
Gh246	DQ908187	F	GCATCTTGTTACGCTTATAGGG	63	AG(15)
		R	ACTTATCAAGTGATTGTCAGGTGAC	63	
Gh247	DQ908188	F	CTTCTCCGCCACGTAAGTCC	63	CT(13)
		R	CAGCCTAACCAAGAACCCAATCG	65	
Gh248	DQ908189	F	AGAACAACATGGACTTGTTCACG	63	GT(9)
		R	CACATAATATACATATATAAAACCCAAACC	64	
Gh249	DQ908190	F	ATATTGTTAAAATGAGTAATGAGCAAAGA	64	CT(10)
		R	GTTGGCATTTAATTAAGGTATTATGCCGA	65	
Gh250	DQ908191	F	AAAAAACCTTAACGATTTACAGTCTCTTC	64	TCT(12)
		R	CACGTTGGATATGTCCACGTGG	64	
Gh251	DQ908192	F	CCTCTATTATTGTTGTGCCTACAC	63	TCT(9)
		R	GCAATATAAGTAAAAGAGATGGTGCAC	63	
Gh252	DQ908193	F	GAAGCCTAAGCTAGGTTATACTGCT	64	CTT(11)
		R	TAGTGAAAATAGCAATATAATCTGTTACC	64	
Gh253	DQ908194	F	CCCAGCCATTACATGTCAGTTCG	65	GT(9)
		R	GATATTGCCCTCACCCCAACG	65	
Gh254	DQ908195	F	CACAATTAGACCTCTATCCAAGCTC	64	TC(13)
		R	ACGAATTTTACCCTAGAGGACAACC	64	
Gh255	DQ908196	F	CTAAACAAGACGGTGGCAGCGA	64	AGA(7)
		R	GAGCCAAGATTCGTTTCGATCGAC	65	
Gh256	DQ908209	F	GATTTTGTGTGATAGAGAATAATGGAAGG	64	TCT(9)
		R	GTCTTTTGAACCAATAGCTCTGAAG	63	
Gh257	DQ908197	F	GATCAAACAGTAGAAAATGAGAGCTC	63	TC(10)
		R	TTCTGAAAGTTCTCTTTGGGGTATC	63	
Gh258	DQ908198	F	AACAAGAAGAAAAGTTGCTAGGAAATGT	63	AGA(8)
		R	CTAGATCTGGACTACCATATCG	63	
Gh259	DQ908199	F	CACAAGCTGCTCCAATGGAGATC	65	CA(9)
		R	GGATTTTCGATGCTAAAACAGAAGGT	63	
Gh260	DQ908200	F	GCATGGAATAAATTATGAAGTCACAGAC	64	GT(10)
		R	GTATGGAAGAGTTGAGGATGGAAG	64	
Gh261	DQ908201	F	CTCTGCAATTATCTCACTTTTCACTCA	64	CT(18)
		R	CCTGGGAGAGAAAAGGTTTAGATC	64	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
<u>Gh262</u>	DQ908202	F	GTCAACAACCTTAAAATTGCCATAGGT	64	AGAAGG(5)
		R	TGGACTACCAATTAACCTTGCCACG	64	
Gh263	DQ908203	F	GTTCTTAGAGTGAGGGATTGGACG	65	TCT(7)
		R	CCTCATTTAAGAACCCTAGCTAGG	64	
Gh264	DQ908204	F	CTGCCATATCTCACTTAAAGATTGG	65	GAA(11)
		R	ACCGTATATCCAATCTTTGATCTTTGC	64	
Gh265	DQ908205	F	CAATCAATTCAGTGAGGAACTTCAC	63	CA(9)
		R	AACTTTCCATATGCATGCTTGGAAGA	63	
Gh266	DQ908206	F	CAATAGACCAGAACCAACAACAATGG	65	TCT(8)
		R	GTTTGAAGTAAACAACATTGGATTGTG	64	
Gh267	DQ908207	F	CAAAAAATGACACTGTCTCCGTAAATG	64	CA(16)
		R	GTGTTCTAGCTGTTGAATGGTGATG	64	
Gh268	DQ908208	F	CATTGATTTTTTGAATACCCCTGATTGG	65	TCT(11)
		R	CGAAGAAACCAACTCCGTATGTG	65	
Gh269	DQ908209	F	GTTTTCTTTAAGCACAGGGTGTATGG	65	TC(9)
		R	GTTCCCTAATGTTGCATCGCTGT	64	
Gh270	DQ908210	F	CAACGACGAGTTTCTCTTCCAC	65	CA(8)
		R	CGGTATAGAGATGAAGTTCATTAAGG	63	
Gh271	DQ908211	F	GTCCGCTCCTCTGATTTCGTC	63	TCT(12)
		R	CTAAACAAGCCGTTGCAGCGA	64	
<u>Gh272</u>	DQ908212	F	AACCGAAAAACCCCTAAATGTTGAG	63	GT(10)
		R	TTCAGAAAATATATCAAATGGGTAGTTC	63	
<u>Gh273</u>	DQ908213	F	TTGCTTCGTTTTCTCCCTGGTG	63	GA(9)
		R	AAGCAAAGACCAGCTTCTCTTCC	63	
Gh274	DQ908214	F	GACTTCCTATTGGCTGTAGATTAC	64	TC(12)
		R	CTGGATATCTCCCTGTACGAGC	64	
Gh275	DQ908215	F	TTGGGGACCATAAGCAAAGAGTG	63	AGA(9)
		R	ACGACAAGATCGTGCTGGAGG	63	
Gh276	DQ908216	F	CCATTGGCTGAGCCTACAAAGC	64	CT(16)
		R	GTGGTGGTGTGATTGCAAGTGA	63	
<u>Gh277</u>	DQ908217	F	TACTAAAACCAAGGCAATAAAGTGA	63	AGA(14)
		R	CACCACCTTCCATATATCTTGCTC	64	
Gh278	DQ908218	F	CATTTGAATGGCTTGTGTGGACAT	63	GT(8)
		R	AATGTTATCCATCCTTCAAACACACC	63	
Gh279	DQ908219	F	TCCAACAAGCTTCCAACCTAATCGA	63	CA(9)
		R	CTGCAATTAGCCTGGTAAAGTTCG	64	
Gh280	DQ908220	F	CAGGGCTTAATAGTCGTCGAACG	65	CA(10)
		R	TAGATTAATGTTAATGTGTGTTCTACTG	64	
Gh281	DQ908221	F	CGAGGAGCAGCAGCGGTTCTCT	65	TCT(7)
		R	ACATCAAACAATCAATCAACCAGTGG	63	
Gh282	DQ908222	F	CTGTAAAACCTAGAAACCGAATGCG	62	GT(10)
		R	CCAAAGATCAGACCTAGAAGTGCC	65	
<u>Gh283</u>	DQ908223	F	ACATGATAATAGCATAAATCTCAGATGC	63	TCT(7)
		R	GCAAGTTTTGATTGTTTGTATTGTAACC	63	
Gh284	DQ908224	F	CTCGCATTAGCATTCTTTCAATTACG	64	GA(14)
		R	TTGTGTATTATTACAGGTGCTCTACTG	64	
<u>Gh285</u>	DQ908225	F	GTAGATATTGGGACATCTGTAGCC	64	TC(7)
		R	GAACTAAACTTAAAGAGTTGTTATCCAC	63	
Gh286	DQ908226	F	TCTTGTGCTTAGCATTCAATTCTGC	63	TCT(7)
		R	CTGTGCGGGTCTTGAAAGAAACC	65	
Gh287	DQ908227	F	CTATTGATTTAACCTCGTTCAATAGAAAAAC	64	CTT(12)
		R	CAACTCGGCTGTGGATCGGGT	65	
<u>Gh288</u>	DQ908228	F	CTATTCCACAAGCTTCATTCTGCAG	64	GT(22)
		R	GGAGCACAATGAGGAAAGTATACTG	64	
Gh289	DQ908229	F	GGCATATGGAAGAAAAATGAGTCGG	64	TCT(8)
		R	CCTTGTTAGGGGCTTTGAATTGCG	65	
Gh290	DQ908230	F	TCATTGGAGTTGGGTGGAATAATCAC	64	GT(10)
		R	CAGATAATTACATGCAATAAGAGCAACC	64	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
Gh291	DQ908231	F	AGTTGAGATTGATCTTGAAGAGCG	63	TC(9)
		R	ACCTCTTCTCGATTGGTTGCATC	64	
Gh292	DQ908232	F	GAGAGGAAACAAAACAGAATATGCTG	63	AGA(9)
		R	CCGGTTCCTCCTTAATCCAGGT	64	
Gh293	DQ908233	F	CCTAATATGTATCAGATGCGGATACG	65	AGAAGAGGA(7)
		R	GGGGTGAGGAAGAAGATGGT	64	
Gh294	DQ908234	F	CATCGGACTTACATCATTTTCGAAGC	65	AGA(7)
		R	GTCTTCTCTCCCTCTCTTTCCCTG	66	
Gh295	DQ908235	F	CTAGGTCCCTCTGTGAAGTCC	64	TCT(8)
		R	GCCAAAAGCAAATGATGCGAGCTC	65	
Gh296	DQ908236	F	ACTAACCTGCACACTATCGATCTG	64	T(16)
		R	CTGAAAAGGACCCAAATATGTCACC	65	
Gh297	DQ908237	F	AACAATGGAGAGGGAGGAGGC	63	GA(13)
		R	CTCTTTCTTCTCTCTCATTCCCTC	64	
Gh298	DQ908238	F	TGTGACATCAAATCCAGATCAAAAAGG	64	AG(23)
		R	CATTCCATGGAAACATCACCTTTCC	64	
Gh299	DQ908239	F	AACAGAATAAGATGGTGACATATGGC	63	CTT(10)
		R	GAGGAGGGATTGAAGGGTTCC	64	
Gh300	DQ908240	F	GGAAAACCCAAAATACATAAGAACCC	63	AG(11)
		R	AGATTCTAACTTCCAGCAAGACATG	63	
Gh301	DQ908241	F	CTTACAGACCAGACAAGATTGGG	64	TTC(9)
		R	CCTTTTGTGTAACGATTAGGATCG	63	
Gh302	DQ908242	F	ACTAGTATCATTAGGGTCAGTGAGC	64	TCT(9)
		R	CACTGGATGTGAAGGAAATGCTATC	64	
Gh303	DQ908243	F	TGAACCATCATCCTCAAATGCCTG	64	CA(11)
		R	CAGTTGCAGAACTGATTGATAATCCC	65	
Gh304	DQ908244	F	GACCTATAGAAGCGAAGAGACTATG	64	GA(12)
		R	TTCTCCATTTAATCCTTATCGAATTTCC	63	
Gh305	DQ908245	F	TGTCTACTTCTGGGATGCTAAGG	63	CT(13)
		R	CAGCAATATGCAGATTCAGGGCT	64	
Gh306	DQ908246	F	CTGCTGGAGAAGAAATAGAGATAGG	64	C-rich repeat
		R	CTCTTTTCTTCTGCTCTTCTTCC	64	
Gh307	DQ908247	F	CTTGAGCTAGAGCTATGTAGAGC	63	AT(8)
		R	TGTGAATACCGAGGACATGTAGC	63	
Gh308	DQ908248	F	GAACCTGTGGCTTGGTGAATGTAG	64	TG(11)
		R	ACGTATCACATACTCATTGCATAGC	63	
Gh309	DQ908249	F	GTAACGGTGGTGGTGTGCTAG	63	TCT(10)
		R	GTATCCTTTCAGTCAAACCTTCTCAC	63	
Gh310	DQ908250	F	CGGCGTTTCTTGGCGTTTCTG	64	CT(10)
		R	GCTCATCTATGGTGTTCACATTTCC	64	
Gh311	DQ908251	F	CTTGCAGAAAAGCTAACCAATCTC	63	CA(14)
		R	CATGTAACCAATGAATTACTACTATAGTC	63	
Gh312	DQ908252	F	CTTGTGGGAGTAATGGTGAAAGATC	64	AG(15)
		R	CCATTTTCTGGATTGTTAAGGTAATC	64	
Gh313	DQ908254	F	TAATGATTAAGCACAAAAGAATTTGCTGC	63	GTA(6)
		R	GAAGCAGGAAGCATGGTATCTC	63	
Gh314	DQ908253	F	CCTTATCTTTGGAACATGATTGTTGTC	64	ATT(7)
		R	CATCGACCAGTTTCAAATCCTAGAC	64	
Gh315	DQ908254	F	GAGGGAATCCTGATTTCTCCCAG	65	AGA(12)
		R	CCTATGACTCCTGAAGCTGGTG	64	
Gh316	DQ908255	F	ACGCTTCTTCTCTTATCTTCC	61	CTT(30)
		R	TGAATCAAACAAGAACACAGCAGC	63	
Gh317	DQ908256	F	ACATCTTGTGATTTTCTGACTACAGG	64	GT(11)
		R	TCTGGACTATGATAATTGTCGATACTC	64	
Gh318	DQ908257	F	GACCATAGGCCCTGTAGTTATACC	64	CTT(16)
		R	CCTCAGAGAACATACTGTAATCATATC	64	
Gh319	DQ908258	F	TGGTGCTAGCAATGTTAAACAAGATG	63	CT(9)
		R	TCTTGCTTAGATCTGGACTAAAATAAATAG	64	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
Gh320	DQ908259	F	CTATGAAGTGTAACAAATAAAAGACAGC	63	AC(9)
		R	GTCCCCATCATGCATTCATTGTC	64	
Gh321	DQ908260	F	GATTTAACATTGGTCTTCTCCAC	63	CTCTTT(4)
		R	CAACTAGTATTGTATCCAATTGACG	63	
Gh322	DQ908261	F	ATATGCCATTAATTTCTGTGCTGAC	62	GT(10)
		R	ATGATTTGCAGATATTCATTAACAATATCC	63	
Gh323	DQ908262	F	AAGACAGAGATGAAGATGGAAACTG	63	AC(9)
		R	GGAAACCAGAAGGTAAGTTCTC	63	
Gh324	DQ908263	F	AACCTAAAACCATCCAAGCTACCC	64	GT(10)
		R	ATTCAATAATGAAATGGATGAGTTTTTCG	62	
Gh325	DQ908264	F	GTATGTGTGCACTGGATTCCAG	63	TC(16)
		R	GATACGAGACTAGATTCACAATCTTC	63	
Gh326	DQ908265	F	CGAGAGCTATCAATACCCAAACTC	64	AG(11)
		R	GCTTAAACATATGGATGTTCTAACCTG	64	
Gh327	DQ908266	F	GTTTTTCAACTTCTCTCTTCTGTTC	63	CTT(7)
		R	GTGGATTGCAAGATTGAGAAGCC	64	
Gh328	DQ908267	F	CCTAGTTCATCACCATTTCATCAGC	64	AGA(13)
		R	GTGAGGAATCCATAGCTTGTTC	63	
Gh329	DQ908268	F	CAGCAGGCAGAAATCTGTGATCG	65	AG(11)
		R	CTTAAATTTCTCTCCCTCAAACCATC	64	
Gh330	DQ908269	F	GATCATTCAAGCCCATAGTGTGC	64	CA(11)
		R	GTCAGGGCTTCAAAGAGGCTC	64	
Gh331	DQ908270	F	ACTAGTGTATAAGCTAGCTAAGACC	63	AG(15)
		R	CTTTGATTTCGTTGAATATTGAAGAAATGC	63	
Gh332	DQ908271	F	CACAAGCTTTGCCTAATTGTCTG	63	GAA(13)
		R	CTAATCAGTGAGCTAAGCCATGG	63	
Gh333	DQ908272	F	TACAATCTCTTCTTATTCTACTGCTGC	64	TTC(8)
		R	ACAGAACCCTGATGTGGCTAG	64	
Gh334	DQ908273	F	CAAGCACAATAACAAGTGAATTACACC	64	AG(17)
		R	CAGTTAGGATGGTTTACAATTCTCAC	63	
Gh335	DQ908274	F	TGGCGAGAGGGCTGAGAATCAG	64	AGA(9)
		R	AAGTCATGGAAGCCAAGTAGC	63	
Gh336	DQ908275	F	ACTAGGAGTTACATTGCAATTTGCC	63	AGA(9)
		R	CTAGCGCACAAGGGCTATTTTGC	65	
Gh337	DQ908276	F	CCCAAATTTATTTGAACCTAGCTC	63	CT(12)
		R	TGCCTTGGTAATCAACATTTGAGG	63	
Gh338	DQ908277	F	ACCGAAACAGTCCATAAAGTTC	64	CA(16)
		R	CGGTTATAAGTGACATTTAATAGGTGTAAC	65	
Gh339	DQ908278	F	CATATCAGTAGTAGTTAGGGTTTATACAG	65	AGA(17)
		R	CATCTGTTTATCTCCAAGCATCTCC	65	
Gh340	DQ908279	F	CCATACAACAATTTGAAGTCAGCTATG	64	AGA(16)
		R	TGCCAGCATGGATCCATTGGAG	64	
Gh341	DQ908280	F	CTGATACAGTAGGAACTCAATAGAG	63	AGA(9)
		R	CATCTTCTATCCGTAATTGTGTTTGG	63	
Gh342	DQ908281	F	ACTACCTCAATTTTCACTCATTTCCAC	64	CT(10)
		R	CTAAGTATTGGTTTATGAAAACAAGCAG	63	
Gh343	DQ908282	F	ACCCCAATTTAGATAAAGGTTTTTGA	62	CT(11)
		R	ACAACATAAAACAAAATGTCATCCTTGC	62	
Gh344	DQ908283	F	CAAAAACCTCTATTTTACTTGCTTCCC	64	CTT(7)
		R	ATCTGCTGTAATAGGAACCAAGG	64	
Gh345	DQ908284	F	ATTTGAGACTCCAACCAGATACAG	64	AG(20)
		R	TTCTAAAGTTCTCTCTCTCAAACC	63	
Gh346	DQ908285	F	CCATCTCTAAGTCTTAAATCCCTG	63	CT(14)
		R	TGAGATTGAGCTGAAGTGAAACCG	64	
Gh347	DQ908286	F	TATCGTCTACCCATGAGAGCG	64	AC(8)
		R	AACCCAAGTCAGGTCTGCCATG	64	
Gh348	DQ908287	F	CAAATGGGTTAGTTAGAATTCCTC	63	CTTTT(2)
		R	CATATATGGAATGAAATCGAGAGACG	63	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
Gh349	DQ908288	F	GATGCACTAGGCTAATCTGAAAAGG	63	CTT(11)
		R	CATTGCTTAAGCTATACACTAGATTTTCC	65	
<u>Gh350</u>	DQ908289	F	CAATCTGCATGTGCCAATACTG	64	AGA(22)
		R	TCCTCCATGTTACAGTTGAGGAC	64	
Gh351	DQ908290	F	CTGTTGATGTTGCTGTTTGCAG	64	GAT(8)
		R	GCAGTATGCTCAGAGAAATTGGTG	64	
Gh352	DQ908291	F	GAGTTGAGAAGAAGTATCAAATGCTC	63	GAA(13)
		R	CTCCTTAAATTGGCACTCGTTGG	63	
Gh353	DQ908292	F	GTGTAGTAGTTTGTGATCACATCAGC	64	CTT(22)
		R	CCGACCTATGCCTACGTTCTC	63	
<u>Gh354</u>	DQ908293	F	CTTACCCATAAAACCCCTAAATCTGAG	63	AGA(17)
		R	CTCTACATCCTTAAAGAATTTCTTCTCC	64	
Gh355	DQ908294	F	AACTTGCCACGTTGGGTGTCCA	64	AGA(7)
		R	GAATCATTGTTTGAACGGCTTCCG	64	
Gh356	DQ908295	F	CTACACGAACTTTTCGATTATCTACTC	64	CA(10)
		R	GATTAAGTGAATGTGATAAGTAACTACTC	64	
Gh357	DQ908296	F	CATAGCCCTAGCTGGGCAACA	63	AGA(20)
		R	GGTCGTAGCTAGGGTATGTCC	63	
Gh358	DQ908297	F	TCTTCTCGAATTTCTCAGGTCAG	64	AC(10)
		R	GTTGCATTTGATTAATCCATTACATAGC	63	
Gh359	DQ908298	F	CATAGCTTCCCATTTCTTACCA	64	CT(12)
		R	GGTATATGTATTGTTTTCGCCTCTG	63	
Gh360	DQ908299	F	CACTAAGCCTTGGTCGGTACTG	65	T(16)
		R	CCGAATAAATATACCGCTTACTTAACTG	64	
Gh361	DQ908300	F	TTCAACATGTAAACGTTGTGAATTAGG	63	CT(9)
		R	TTCTCTCAAATTAGCCCTCAATGTC	63	
Gh362	DQ908301	F	CAAACCTAGTCCAACAAATTGAAGC	63	AAG(7)
		R	TCCCACTCTGCTTTCTCCAAGG	64	
Gh363	DQ908302	F	CATTGATGACAAGCAGCTCATAACC	64	TC(7)
		R	TGGGATATCGTAGTTGAAATATCACAAG	64	
Gh364	DQ908303	F	CCATTTCTAGATTGTTAAGGTAATCC	64	TC(16)
		R	CTGTGGGAGTAATGGTAAAGATC	64	
Gh365	DQ908304	F	GGATATTCAGACCGTACTTAGACAG	64	GTA(3)
		R	CAACACAATTCTCAAATGTTCTGCATG	64	
Gh366	DQ908305	F	GCAAGATGGCGAGAATTGTGGAG	65	GT(10)
		R	CACAACCCAACACCCAAGCC	65	
Gh367	DQ908306	F	GAGGTCCCTATAAACAGGCTAAGG	65	GAA(9)
		R	AGCCAAATGGTATCTGAATATCTTCTC	64	
Gh368	DQ908307	F	GTGACGGAAATTGGGAAGAGGAAG	65	AGA(6)
		R	CCATCTCTCGTTCTTCATCCAGG	65	
<u>Gh369</u>	DQ908308	F	ATACACCTATTGATGTGTAATTCATTTGG	65	CTT(16)
		R	CGATATGAAGACTCACATTCACGTG	64	
Gh370	DQ908309	F	AAGAGCAAAACACAAAGCCCTAGG	64	AGA(13)
		R	GGTGGATGAATTATCTAAGTCGACC	64	
<u>Gh371</u>	DQ908310	F	GCTGACTGCATTGGTTTCGACC	63	TCT(9)
		R	CGAGTTGAAGAAAGCGAGTATCC	63	
Gh372	DQ908311	F	GCAATGCCCTAGCGATGGAG	63	CT(11)
		R	CAATTTTCAGAAATCAGTTTTTCAGAGACTG	65	
Gh373	DQ908312	F	GATAGCTTGCGGGCAACATGAG	64	CTT(13)
		R	CTTAAGGAGAAGGACCAAATCTGTGG	66	
Gh374	DQ908313	F	GCATCGGGCTTCCAGTTTCG	63	GCCTTTT(4)
		R	CCTGTATTGCGACGAACGGAG	63	
Gh375	DQ908314	F	TGGTTGAGGGAAGCATCATCAGT	63	TC(13)
		R	AGCTTTAATGAATATACTAGCAATTAGCA	62	
Gh376	DQ908315	F	GTTGCATCTCTATGGGATCTTCCG	63	CTT(29)
		R	GATGTTTAAAGATAACACCTCTACGG	63	
Gh377	DQ908316	F	AGAACCCTAGCTAGGCTGGG	63	GAA(7)
		R	TCCGTGATCTACAACCTCATGCT	63	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
Gh378	DQ908317	F	CTTCTATAAATGTCTTCAACATCTG	62	A(50)
		R	AGGTCGCGTTTCCAAGCGTGA	63	
Gh379	DQ908318	F	CTGAAATATTGAAAGACATGAAAGAGAAGC	65	GT(17)
		R	TGACACATCTGATTTTCTGGTCGTC	64	
Gh380	DQ908319	F	CAGTCCTCTTCATGCACAACTC	63	AGA(7)
		R	CCGTTTCAAGTTCGCATCAATGC	63	
Gh381	DQ908320	F	GAAATGGCTGAATTGAAAAGGTAAGG	63	TTC(10)
		R	CCATTCAGACACCAGCTGTTGC	65	
Gh382	DQ908321	F	CGTATTGGTATTGAAAGAATTATTGCG	62	GT(9)
		R	CTCACCTATATCATCATGATCACTC	63	
Gh383	DQ908322	F	CTTCTCTCAGCTCCGCCTCCA	65	TA(6)
		R	GCTTCAGACGTTTCTTGTTCGATTG	65	
Gh384	DQ908323	F	CCGCGAGAATATCAAACCTCGAACAC	66	AG(7)
		R	CTGGTCCCCTTTAATCTCTGCC	65	
Gh385	DQ908324	F	GAGATTTTCTCAATTGGCATTTGCC	63	TC(11)
		R	GGAAACTAAAGTATTGTATGGTATAATGAG	64	
Gh386	DQ908325	F	CGACGACGTTATATTCAAGCATGA	63	AGA(8)
		R	CCAACCTTATGCTTCTCTCCTTTG	64	
Gh387	DQ908326	F	ACTGCATTGGTTCGATCTTTGTGG	64	CTT(8)
		R	GACCTTTACTCTCTTCAACTCGTTG	64	
Gh388	DQ908327	F	CATCATCATCGTCGTCGCCG	63	CTI(5)
		R	GCAATGGAAGCTTTCGTCTCTTTC	64	
Gh389	DQ908328	F	AGGAGGTCCGGTTCACCCAGTG	65	GA(10)
		R	GACTAAAAGAGAGGATATACACAAACG	64	
Gh390	DQ908329	F	GGTAGTGGCAAGGATTAGCATCC	65	CTT(29)
		R	TCCAAAGCAAGCTATCGATTGTGG	64	
Gh391	DQ908330	F	CGTCCACATATTTGTGCATGTGC	63	AG(11)
		R	TCTGGTCTGGCACTACGGT	63	
Gh392	DQ908331	F	CTGCCAAATTCAACTTAATGCTTTAGG	64	AGA(5)
		R	GAAATTTTGTCTAGGTGCACGGC	64	
Gh393	DQ908332	F	CGGCAATAGTTCAGATGGTGAGG	65	CA(9)
		R	GGATACCCACTTATCCAAGAATGC	64	
Gh394	DQ908333	F	GTGAGCTTCAAGGAGACCGTG	63	ATACAT(3)
		R	GCAATACAAAGCCGATGAAGACG	63	
Gh395	DQ908334	F	AAACGGCGGACATTTCGAAGCG	64	CT(7)
		R	CGAAGCGTTTGGTGGAAGAGTG	64	
Gh396	DQ908335	F	GGTAAAAGCCCGAGCTAAGAACC	65	AAG(6)
		R	CTGCATTTCTTCTCTACTTGTTCATTG	64	
Gh397	DQ908336	F	GATTAACATCAACATCAGAGGAAGTG	63	AAG(7)
		R	CTTATCATCCTCATCATTATCATGCTG	64	
Gh398	DQ908337	F	GTGCTTCCTCACGTATCATAACC	62	GT(9)
		R	GGCTAGCTTGATATCATCCTCG	62	
Gh399	DQ908338	F	ACTCAAATAGTTAGGTGTGTATTCCG	63	GT(9)
		R	CTATTTACTCTACAATCTATAACTCCC	62	
Gh400	DQ908339	F	ACACATAGTAATTGTAAACGCCCTGA	63	GT(8)
		R	CAAAAGTGGAACCTGAACCCAAGAC	64	
Gh401	DQ908340	F	GACTATCGCAATCCACGTAAGTC	63	AC(9)
		R	CCATCGTGGTAGTGTGTAGTGG	64	
Gh402	DQ908341	F	GGTTAGAATGGTGCCCAAGTCTG	65	GT(8)
		R	CAATTTGAAAAGGTTGAATACTTAATAGTCA	63	
Gh403	DQ908342	F	GCAGAACTACAACATGCACAGATTC	64	AGA(6)
		R	GCTAGCAAATGTTATCAAGGGATGG	64	
Gh404	DQ908343	F	GAAATTTATCGCTTCTCTACTTTACC	62	CA(8)
		R	ACTGTTTATTACAGAGGAGGATGG	64	
Gh405	DQ908344	F	GAACTTCATGCAGTTTGGGGAATC	64	TCT(4)
		R	GAAAAACCCAGAATTCTCCATAAAAAATCC	65	
Gh406	DQ908345	F	CAAGCCCATGAGGTTGTTGCC	64	TCT(6)
		R	CTTTGCTTTGAATTTGGTAAACCTAGC	64	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
Gh407	DQ908346	F	TGGAGAAGCAAGAGTCTGAACTC	63	GT(9)
		R	CTAAAAGAAGCAACTATCTAAATTACAGG	63	
Gh408	DQ908347	F	CTATCTCTCCATCAACCACCTTG	63	CT(7)
		R	GGAATCCCTGTTCATCACACCTG	64	
Gh409	DQ908348	F	AGAAGGTAAAAGATGTGAAAACAGAGG	64	AG(16)
		R	CAGTGCAAGCAACGTGACTTAAACC	65	
Gh410	DQ908349	F	TACGACTGGAATATATGCTCTTC	62	GT(10)
		R	GTATCTACTGATCATTGCTCTGAC	62	
Gh411	DQ908350	F	GGACAAAAAGAGAGGAATGTAGACC	65	CA(15)
		R	CATCTCCCATTGATGTGATTGAGAG	65	
Gh412	DQ908351	F	CTTCAGCTTATTGGCATTGGTTCCG	64	TCT(6)
		R	CGAAACCACCTTCCCAGACTAGG	64	
Gh413	DQ908352	F	CTGATGGAGTTCTCTATTAAAGATGC	65	AG(14)
		R	CCTCTTCTCTTAAATTAATCACCCATC	65	
Gh414	DQ908353	F	TAGATCGAAATAGCTAATCAAGTGCTC	64	CTT(19)
		R	GTCGTAACGTATGCTTGGATCG	65	
Gh415	DQ908354	F	ACGGCGTAAGAAAGGGCTACC	63	CA(11)
		R	TCGAAATCTCCATTAACGGTTCCG	64	
Gh416	DQ908355	F	TCCTCATATTCATTGTCAAACACGAG	63	GT(14)
		R	CCACCTATTGTCTGAAATCCATGC	64	
Gh417	DQ908356	F	CTACCAGCACCATTTTAGGGTTAG	64	AGA(5)
		R	CACACTAGAATCACTTCAGGCATC	64	
Gh418	DQ908357	F	CCACATTTAATCCAAATTTGGAGCTC	64	AG(10)
		R	CATACTTTGAACTTCTTCTTGTCGTTTC	64	
Gh419	DQ908358	F	CTCATTAAGCTCTTGTATGATTTGG	63	TG(9)
		R	ATACCAACAATGCCATCAAATGC	63	
Gh420	DQ908359	F	TCTTGTCCACTCTGGAATAAACC	64	AG(9)
		R	ACAGGTTGGTCTTTGCTTCTTTC	64	
Gh421	DQ908360	F	TTTAAAGCAAAAGGCATCTGAAAGCTG	63	AG(9)
		R	TGTGTCTATAGATTCCATAATCTCC	63	
Gh422	DQ908361	F	ACTGAAAAGAGAGAATACGTATGGAG	63	AAG(8)
		R	GTGTTAGGTTTCGAGCTAGCTAC	63	
Gh423	DQ908362	F	TATCTCCGGTGAGAAAACCGATTC	64	TC(10)
		R	CCATTAGGGTTAGTAGTGGGTTTC	64	
Gh424	DQ908363	F	TCCAATCTCTCGTCTGCTTCTTC	64	TCC(7)
		R	GTTTCTTCGCGGTCGAAATTTGAG	64	
Gh425	DQ908364	F	GTTTCAATGGCAAAGAATCAGACCC	64	TCT(14)
		R	ACGTTGGATGTCCACAATGGAAAC	64	
Gh426	DQ908365	F	AATCTGAATGCGGATGTATTGGATAG	64	GAAAAAGAAA(3)
		R	GAAAAGCGTCGATTGTCTGCTG	64	
Gh427	DQ908366	F	CCTATTGGGTTCCATAAGAGCAC	64	TCT(8)
		R	GTGGATGTTGCGGTAGGATTG	63	
Gh428	DQ908367	F	AAAATCCCAGTCGTGCTCAACTC	64	AGA(6)
		R	ACAAAGGTTGTCTGTTTGATTCTGAAG	64	
Gh429	DQ908368	F	TGGACTAACATCGGAATCACAGTG	64	TCT(40)
		R	TTGAACATGATCGGATGCCACAGA	64	
Gh430	DQ908369	F	TCCCTCCAATTTTTCTGTCTGTTCC	64	TCT(13)
		R	GAGAAGAACTTGGGTTGAAGGAAG	64	
Gh431	DQ908370	F	GCACATCTTCAAATAAAATGTTAGCCC	64	AG(12)
		R	TTGTTTTGACCATGCCACTCATGTC	64	
Gh432	DQ908371	F	CCTAGTTCATAATCTGATTGTGTC	64	AG(12)
		R	CAACCACCTGCAATATAAGAGCAAC	64	
Gh433	DQ908372	F	TACCACATTGGATGTTTGCAAACCC	64	AGA(32)
		R	ATAGCAAACCTGGAATCACTCCAAGC	64	
Gh434	DQ908373	F	AGAGCTAGTAGGTGGCTTAAAGAG	64	AGA(18)
		R	GTTGGATGAATTATCTAAGTCGACCG	64	
Gh435	DQ908374	F	GGCGCTCACTAAAATCTCCAAAAG	64	AGA(14)
		R	AAGCCTGAGCTGACTTCAAACTC	64	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
Gh436	DQ908375	F	AATTTGAGGACTCAAGCAAGACAAG	63	GCA(3)
		R	AGGTCCTAAATGTTCCCTGTATTCC	63	
Gh437	DQ908376	F	ATCGTGTTTTGCTTGACCAACCTC	64	TC(5)
		R	ATTCGGCTAAACAAGGGAGGTAAC	64	
Gh438	DQ908377	F	AGGTGGGACTAAAGAGAATGAACC	64	GAA(6)
		R	ATTGTGGTCAACCTAAATAAACTCGTG	64	
Gh439	DQ908378	F	TTTAGCCTCTGTCTGTIACCACC	64	TC(6)
		R	GAGATTAGAGCTTGAAAGTGAGGG	64	
Gh440	DQ908379	F	TCTGGGTCATTTCGAAGATGGTAG	64	TC(14)
		R	TCTGGAGAAAAGACCAGGAAACAG	64	
Gh441	DQ908380	F	GATCGGTAATGTTTCGTAAACCTAC	64	AGA(21)
		R	AGAATTAGGTATAGAGGTGGTGCG	64	
Gh442	DQ908381	F	TTTTCAGACTGTGGAAAACGCAGG	64	GAGT(6)
		R	ACTCTTTGAAGGCGTTTTGTGTGC	64	
Gh443	DQ908382	F	TATCAGAATCAATATGCACAGGTTACG	64	TCT(22)
		R	CTAAAGAATTATTGTTGGAACCAGACG	64	
Gh444	DQ908383	F	TCTGTTCTACAGCAACGAGTTGAC	64	AGA(13)
		R	ACTGCATTGGTTCGATCTCTATGG	64	
Gh445	DQ908384	F	CAAAAACCTATAGACCTTTGCTGCTG	63	CTT(6)
		R	AACCATATTTATGTGAAAACGCCACC	63	
Gh446	DQ908385	F	CTATCGATCTGTTAGGGTTTTGGAG	64	AGA(6)
		R	GGCTGCCTTTCTACTATTACCTTG	64	
Gh447	DQ908386	F	CTAGTTTCTATGTTGTTAATGCAGAAGC	64	CT(11)
		R	GACTGATTACTTATATGATCGGAATCG	64	
Gh448	DQ908387	F	GGATTGAAAAGAGGTTTATAAAGCG	63	AG(9)
		R	GTCTCATGTGCTTAATGTTCTTAGC	63	
Gh449	DQ908388	F	CATTGCTGTAGACCATTGCTTTAAG	63	CA(12)
		R	GTTATGAATCGAAAGCTTGTTTAGGC	63	
Gh450	DQ908389	F	CCATTTAAGCAAATGGTGAATGTCC	63	TCT(14)
		R	GGTGCCTGTTCAATTACAATTATCAG	63	
Gh451	DQ908390	F	CGTTCATAATTTCCATCGAACGGC	64	CA(12)
		R	GAGAAAAGATCTGCGATTGGTGAAG	64	
Gh452	DQ908391	F	AAGACATGTTTGTCAATTTGGCAACC	63	AG(9)
		R	TATTCTCATGCACCTACTTTTCAGC	63	
Gh453	DQ908392	F	AAACAATGCCGGAAGCTAGTGAAG	64	AG(25)
		R	TGGTTCGTAACTCTCTCAGATC	64	
Gh454	DQ908393	F	GTTTCAAGCGAAGAAACCAACTC	64	AGA(7)
		R	CCCCTGTATTGGTTCTTTGATTCC	64	
Gh455	DQ908394	F	GGCTTAGTTTTCTCTAGGTTTTCTC	63	TCT(15)
		R	CAACTAAAGAAATGAAAATGAAGAACCC	63	
Gh456	DQ908395	F	AATGCTAATATGAGGATGGTGGTTAG	63	CTTT(4)
		R	CGAATGCAATTAAGAACTCACTTGG	63	
Gh457	DQ908396	F	CCTTGAGATATACCTATTCAACAC	63	TCT(14)
		R	GCAGGAATCGAAATGGATATGATTAC	63	
Gh458	DQ908397	F	CCAATGGAGATCTTATAAACCTGTTG	63	AC(9)
		R	TTCGATGCTAAAAACAGAAGGTTTAGG	63	
Gh459	DQ908398	F	AGGTGAGGAATCCATAGCTTGTTG	64	TCT(13)
		R	CCTAGTTCATCACCATTTCATCAGC	64	
Gh460	DQ908399	F	AAGGTAGGCTGTAGAATCAACTGAG	64	AGA(11)
		R	GTATCCAGGTTATATTCCTCATGAAAG	64	
Gh461	DQ908400	F	CGACCAAACCTTAAACAATGAAATGAG	64	AG(12)
		R	CACCTCCTATTTTTCTTTGACTGAAAG	64	
Gh462	DQ908401	F	GAAAGGTTTTAGCATATACCACTTAAGG	64	AGA(11)
		R	GTTAAATTCGGTTAAGGAAGATGGATC	64	
Gh463	DQ908402	F	CCATTTTCTAGATTGTTAAGGTAACCTCC	64	TC(16)
		R	AAAATGTTAACCAAGACTACCTGTG	64	
Gh464	DQ908403	F	CATGCCACTCACTTATGAAAGCTTC	64	AC(9)
		R	GCAGCATCACACTATCAAGTCATC	64	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
<u>Gh465</u>	DQ908404	F	AAGTCAAAAGGAAGAGACGCTTCG	64	AG(14)
		R	AAATTCACCTTCTGGCAGTGACAC	64	
<u>Gh466</u>	DQ908405	F	AATCTGCATGTGCCAATACACTGG	64	AGA(31)
		R	CATCACTCCATGTTACAGTTGAGG	64	
Gh467	DQ908406	F	TGCCAAGGAAATGTATGAAGCTGG	64	AG(16)
		R	TATGAGCCTTGTCCCTTAGTTCAG	64	
Gh468	DQ908407	F	TGCTTGAAAATTGAGAAGAATTGCGAG	64	AGA(9)
		R	GTAGCTGCTTTGTTTATCGCCTTTG	64	
Gh469	DQ908408	F	ATTTCCCAGCTGAGAAATCCATC	64	AG(18)
		R	ACAGAGTTTCTGAATGACATAAGAACC	64	
<u>Gh470</u>	DQ908409	F	ACATCAACTTTCAAACCGTTCAACC	63	CT(19)
		R	CTGGAAGCTAAATATACAGAGCAAG	63	
<u>Gh471</u>	DQ908410	F	CAGGCATCAACTAGCATTGAAAACG	64	TG(10)
		R	ATCTTCTGATCTCTATTAGCTACAACG	64	
Gh472	DQ908411	F	CGTGATTGTGGTTGTGATGAGTATG	64	TCT(9)
		R	TAATTTGCTTTCCAGGTGGCATGC	64	
Gh473	DQ908412	F	TGCCAAGGAAATGTATGAAGCTGG	64	AG(16)
		R	TGCTTTGTTGGTTGAATTCTAAGTTGC	64	
Gh474	DQ908413	F	ACGTATCACATACTCATTGCATAGC	63	CA(11)
		R	TGTGGCTTGGTGAATTGTAGAACC	64	
Gh475	DQ908414	F	TGGCTGAAAATTGAGTATTC AAGTGC	64	AGA(10)
		R	ATTGCCATCCCCTTGTAGCTAAC	64	
Gh476	DQ908415	F	GGACAAAATGTATGGGAAAAACATGTC	64	AAT(3)
		R	ATTCGGCCAAGAAACAATGAGAG	64	
Gh477	DQ908416	F	CAGAAAGGATCTGCTTGTATGAAGC	64	CA(6)
		R	CAAAGAGCTAGACAGATAGCTTGC	64	
<u>Gh478</u>	DQ908417	F	TCAATTCTGATTCTAACGCCATCAG	63	TCT(10)
		R	AGAATCGATGAGACACATGCTGAG	64	
Gh479	DQ908418	F	CCCTACTCAATTAGCCTCTCAATTG	64	GT(9)
		R	GAACATGTAGCAGCAGCATAACAAC	64	
Gh480	DQ908419	F	CTTTTATCTTTTCTGGGATAGCTTGG	63	TCT(14)
		R	CAATAGTTAAGGCTCTGGTTAAGAG	63	
Gh481	DQ908420	F	GAGAGTGGACACTTCTAAATAGTTTTG	64	TG(9)
		R	AATGCTCTATCAAGCCTGTAAAGAATG	64	
Gh482	DQ908421	F	CACACCGTTTCCAAGTAAGATTTCG	64	TCT(13)
		R	CTAGTTGAGGTCAACATATAAAAAGCAG	64	
Gh483	DQ908422	F	GAGTTGAGAAGAAGTATCAAATGCTC	63	AGA(12)
		R	GAGTAATTTAAGAGCAAGGACATATGC	64	
<u>Gh484</u>	DQ908423	F	CCTTTTGCCTTTATTGCTTGCTTGG	64	TC(15)
		R	CCAAGATGACAAAACACGCTGAATC	64	
Gh485	DQ908424	F	ATATGCAGGCAAAAACACGTGCAC	64	AGA(14)
		R	TAAAGTCTACTGCCAGCATGGATC	64	
<u>Gh486</u>	DQ908425	F	TTGTCACCCCTAAATTACATTGAATGGC	64	TCT(20)
		R	GTAAAGGCTTTGACTACAAGCACC	64	
Gh487	DQ908426	F	TGGGTAAACAAAACATTGCATCAATTCC	64	CA(17)
		R	TTCCATTCAATTAGACCTACTTCTTGG	64	
Gh488	DQ908427	F	GAAATTATACTCGAGCCATCCTCTG	64	AGA(12)
		R	TCACCATAATTTGGAGCATTGTGTGCT	63	
Gh489	DQ908428	F	TTAGACCATAGAGAATGGAGAAAATTC	63	CA(9)
		R	TTATCATCAGCTTAAGAGTAACCAG	63	
Gh490	DQ908429	F	AGGATGAGCAAACATAATGAACCTC	64	GT(9)
		R	CTCTCGAATCTTTGTATTTAGAGCTTC	64	
Gh491	DQ908430	F	AGAGAAAACGATGAAGAAGGAGTTC	63	CGT(3)
		R	AAAGGAACCCAGCTTTCCATCTC	63	
Gh492	DQ908431	F	AAGGCATGCTTTGTTTATATTCAAGCC	64	TCT(12)
		R	CCACTGTGATTAAACCCTTCTGATG	64	
Gh493	DQ908432	F	GAGCCTAGCTCAATGAGAAAACATG	64	CA(16)
		R	GTATGTTCAAAGTGAAGGGTGAG	64	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
Gh494	DQ908433	F	CCATTTTGAAGCTGAAAAGCTCGAG	63	AGA(4)
		R	AAACTCATCTTTACTCCATGGGTATC	64	
<u>Gh495</u>	DQ908434	F	AAACTCTTAGCCTTGTCCATGAAAG	63	CA(13)
		R	TGATCAAAGATGGGAGAAAAGAGTC	63	
Gh496	DQ908435	F	CAAGAGGAGATGGAGAAGAATAGAC	64	AAAAT(4)
		R	GGGATTCTGATTAGTAGAGGTGTAG	64	
Gh497	DQ908436	F	GTCTCACCCTTTCTTGGATACATG	64	AG(11)
		R	TCAAGGAGACAAACAAGCATGCAC	64	
<u>Gh498</u>	DQ908437	F	ATTTAGACTAGTTGATAGTGATAAGGAC	63	GT(14)
		R	ACAACATCAACCATATCTATATGCATTC	63	
<u>Gh499</u>	DQ908438	F	CCACAATAGCATATGAAATCATAATGGG	64	TCT(27)
		R	GTGCAACCTTGGAAACCATGAAAG	64	
Gh500	DQ908439	F	ACATTGGTTCGATCTCTATGGGATG	64	TCT(8)
		R	CAGCAACGTGTTAAAGAAAGTGAGG	64	
<u>Gh501</u>	DQ908440	F	CACAAATTGAAAGTACCCAGATCTTC	64	AGA(21)
		R	TCCTCATTCCTCGATTTCAG	64	
Gh502	DQ908441	F	CTCATATCTGTGGTAGATTTGGGC	64	TC(13)
		R	AGCTGCATGCTTCAACGTAATCTC	64	
Gh503	DQ908442	F	GGCATGTGATCAATTTATACACAAGTC	64	CA(16)
		R	TTATTTATACCAAGGATGTGGATGGAG	64	
Gh504	DQ908443	F	CTGGTACTAAAATAATGCCCGAGG	64	CA(7)
		R	AATAGGTGCAACAGACCCACATAG	64	
Gh505	DQ908444	F	GGTAAGAAAACGAGGAAGAATACGC	64	TCT(12)
		R	AAGGAGCTCAAACACTATGGATGG	64	
<u>Gh506</u>	DQ908445	F	TGGAGAATCCAAGTAAAGTAGCGAC	64	TCT(10)
		R	ATCTGCTGTAATAGGAACCAAGG	64	
Gh507	DQ908446	F	TTATCAGGCATACTCTTGAGATTGG	64	TCT(3)
		R	TTTTGGCACCTTAAGTAGACCACC	64	
<u>Gh508</u>	DQ908447	F	CTTTCTCCTTCAGGTTGTAGATCC	64	CT(12)
		R	CAATGAAAGATATAACACGTTCCAAGAC	64	
Gh509	DQ908448	F	TCCTCCTGATACCATTCTTCTCC	64	CTTTTT(3)
		R	ACTTGGTAGCAATCTTACGGTAGC	64	
Gh510	DQ908449	F	ATTTGGCGGGTCTGATTCTTTTC	64	TCT(6)
		R	ATACAAAGGGAGAGCCAAGTAG	64	
<u>Gh511</u>	DQ908450	F	GTTCCCATCATGCATTCTTGTTC	64	GT(9)
		R	GAAGTGTAACAAATAAAAGACAGCAGC	64	
Gh512	DQ908451	F	TGTCGAAAAAGGTTGGAAGAAGCG	64	AG(5)
		R	TTGTGCACATTTCATCCTCACCTTG	64	
<u>Gh513</u>	DQ908452	F	TAACTCTACAAGCGATGGGATCG	64	AG(12)
		R	TCTCAAAGCCGACAAACTGTTAG	64	
Gh514	DQ908453	F	AACCAACAAGCTTACCAAGATTTTCC	63	TCT(4)
		R	ATTTCAAGTAACTCGGTAATGCATCG	63	
<u>Gh515</u>	DQ908454	F	AACAGAGAGACCGGAAGAATTTCCG	64	AG(25)
		R	AGATCTGGACGGTTTCGTTTTTCAC	64	
Gh516	DQ908455	F	GGGTCCAAAATCATCATCGTTC AAG	64	CA(11)
		R	TTCTGGACTCGGTTATTGGCATG	64	
Gh517	DQ908456	F	GGATGGGAAAAATGCATACCATATATC	64	AGA(8)
		R	TGCAGGAGATGTAATTACAATGAAGG	64	
Gh518	DQ908457	F	CATGTCCACATATCCAGAAGTAGG	64	ATC(4)
		R	GTGTTTCTACAGGTATGATTCAGCC	64	
Gh519	DQ908458	F	CCCAAACCTATTTTGAAGTCAATGCTC	63	TC(12)
		R	TGCCTTGGTAATGCAACATTTGAGG	64	
Gh520	DQ908459	F	GGTAGAAAATTTGGGGAGTTACTTTC	64	GA(13)
		R	CTGAAATAAACTCCAAAGCATCAATGC	64	
Gh521	DQ908460	F	ACCTTATTTCTTATGACACTACTACC	64	AG(13)
		R	TTCTGGCTGGGTGTTTATTGATGATG	64	
Gh522	DQ908461	F	GATGGCTTGTGGGTTAAGTAGTG	64	AG(12)
		R	TAGTTCCTAATGGAACAAAATGAGTGC	64	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
<u>Gh523</u>	DQ908462	F	GGAACAATTGAAGAAGACGATATAAGG	64	CA(17)
		R	CTGGATGGACTATGGAAACTGTG	64	
Gh524	DQ908463	F	AGAGAGATGGAACATGGAGTGAATG	64	AGA(15)
		R	CTCCAAGTGTTACTTCTTCTCTTGG	64	
<u>Gh525</u>	DQ908464	F	ACCTTTACCAAAAATACAGGGATTGAC	63	AC(11)
		R	CTGTGATGATGTTCTCTGATG	63	
<u>Gh526</u>	DQ908465	F	CGCCTGCATTAACAAATACAATGAATAC	64	CA(12)
		R	GTTCAATTGCATATTGGATTGTCATCTC	64	
<u>Gh527</u>	DQ908466	F	AGCTGGAGGATTTAGCTTGATTC	64	TCT(6)
		R	ATGCCAGTTAACTTACCAGTTGG	64	
Gh528	DQ908467	F	GCGAAAAGAATTGTCTCAAAGATTGG	64	TCT(21)
		R	TCCGAATTTAGATGCTAGACAAACAG	63	
Gh529	DQ908468	F	CAGATTTCTGGTGATCGCCTAAAG	64	TCT(7)
		R	GCCATGAAGATGGCATCATAGATTC	64	
Gh530	DQ908469	F	TTACATCCAAAACGAGCTCGTACC	64	TCT(14)
		R	TAAGAATAGGAAGCATTGGAGAAGGTC	64	
Gh531	DQ908470	F	AACTGGAATCACTCCAAGCATCTC	64	TCT(15)
		R	ATTGGATGTTGCAAACCCTTAATACC	64	
<u>Gh532</u>	DQ908471	F	CACTAGAAACAGTTAGACACAACATTG	64	ATCT(5)
		R	TGCTAGTATTAGATTGTGCTTCTCTAC	64	
Gh533	DQ908472	F	TCCCTCCAATTTTCTGTCTGTTCC	64	TCT(14)
		R	CAATATTGGGGGAGAAGAACTTG	64	
Gh534	DQ908473	F	CTGCAAATCTTGACAACCTTCTG	64	CA(9)
		R	TATGGTGCTGAGTGCACATCATGT	64	
Gh535	DQ908474	F	GGACTAACTCAACTGAACCTTAAACAAG	64	TCT(7)
		R	CGATTTTCTTCCCTATAAAAATAGGTC	64	
Gh536	DQ908475	F	TCTACATTGAAATAGAGGGTGAGAAC	63	AGA(13)
		R	ACTTCGAACTCTTTCTAAAACCATCC	63	
<u>Gh537</u>	DQ908476	F	GTTGGGTGGCAATTCCTTTTAGATC	64	AGA(8)
		R	AAAGCTAATCCCTATACCTTTTCTTCG	64	
Gh538	DQ908477	F	ACGAGTTGAAGAAAGTGAGGATCC	64	AGA(13)
		R	ATTGCATCGGTTTCGATCTTTGTGG	64	
<u>Gh539</u>	DQ908478	F	AGTTCGTGCCTTTGATACTGAAGG	64	AC(13)
		R	CAAAACGAAGTGAATGTTAGTCTATTTCG	64	
Gh540	DQ908479	F	GTGTGGTTTTGTGTGAACACATGTG	64	AGA(14)
		R	GCAATCAATCTTACCATTTTCATGAC	64	
Gh541	DQ908480	F	CTAAGTAAATAGAGAATATCAACAAGGG	63	GA(15)
		R	CTTGTTCTATAAAGAAGTCATACCTTCC	63	
<u>Gh542</u>	DQ908481	F	TTCAATTCTGATTCTAACGCCATCAG	63	TCT(10)
		R	TACCCAGAATCGATGAGACACATG	64	
Gh543	DQ908482	F	ACGAAATCAGTCCAGTTTCGGATTC	64	ACA(4)
		R	TCCACTTTAGTAATCAGAAAGGGAAAG	64	
Gh544	DQ908483	F	TCAGTCTGCTGCTATCTTAACCAG	64	AG(13)
		R	GATTTAAGAAGAGAAATGGACGGTATG	64	
Gh545	DQ908484	F	ACACTCTTAAACAACAGTAACCACTTC	64	C(10)
		R	GGTCTTTTGCCTTCTCTCTATAGG	64	
Gh546	DQ908485	F	AATGGAGCTTGAAGCAATCACAGC	64	TA(4)
		R	CTTGGTCAAGGCTGTTTGTTC AAC	64	
Gh547	DQ908486	F	AGCAGGAAACGAGTTGGAAGAAAG	64	AGA(6)
		R	CGAAACATCCTCAGAAATATCACAATC	64	
Gh548	DQ908487	F	CCATCATATTTTACCTTTGCTCTC	63	TCT(8)
		R	GGTGGTTTTGCACCATCGTTAAG	64	
Gh549	DQ908488	F	TGCTATGACAATGTTTACATCAGAGTC	64	TCT(4)
		R	AGAAGGAAGCTGCTACTACAGAAG	64	
Gh550	DQ908489	F	ATTGGAGAACCTTACTGCACTGAC	64	AG(4)
		R	CTCCCACTATTTCATATTACCAC	63	
<u>Gh551</u>	DQ908490	F	TCTCACTTCAACGATTGGAGTGC	64	TC(10)
		R	CCGAAAGCTATGAGAATATGCTCC	64	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
Gh552	DQ908491	F	TACGGTTGAATTTCCAGCTCTGC	64	TC(7)
		R	CTACCTTTCCTTGTCTGTCTGTAAG	64	
Gh553	DQ908491	F	CTCTCTTTGTGTTATTGTGTAAGGG	64	CT(6)
		R	TGAGCTGAAAGAGGAGAACTACTC	64	
Gh554	DQ908492	F	GAGTGGAAGTGAATGAGGATTCTG	64	AAAAAGAAAAGAAG(2)
		R	TTCAACTGGCTGCATTGGTTCGAT	64	
Gh555	DQ908493	F	TGGCTCTTTCATTTCTCCATCATAG	63	TCT(10)
		R	TTGCTTACAGAAATAGCAACGAAGC	63	
Gh556	DQ908494	F	TGTCTAAGTATGCTATGAATTGTGCC	63	TG(5)
		R	GCAAATTGGCTTGGTAGATAGCCA	64	
Gh557	DQ908495	F	AATGGAGGACTCATTGGATTCTTTG	63	TC(4)
		R	TGGACAAGACATTCATTGCAATAGC	63	
Gh558	DQ908496	F	CACAAGCTTTTCTCCCTTCAACAC	64	AGA(8)
		R	CAAGACGTCCAAATTAGCTCCTCTA	64	
Gh559	DQ908497	F	TAGAAGCTTCCGCCAATATAGTAG	63	TTTTTTTTTTC(2)
		R	TAAGTTTCTCTGGTTTTTCTGGTC	63	
Gh560	DQ908497	F	TTTGACCAGGAAAAACCAGAGAAAAC	63	AGA(7)
		R	GTTCCAGATCTGCCTTTTCGATTTC	64	
Gh561	DQ908498	F	TATCTACACCGCTCGTCGAAACAT	64	GA(13)
		R	CAATGGGCAAAATGGAAGGAGATAG	64	
Gh562	DQ908499	F	AGAAATTAGATAACAGTGCAGAGAGAC	63	GA(14)
		R	CATTCACCTCCTTTGATCTCTG	64	
Gh563	DQ908500	F	CGTTTTTCTCATTTCCTCAGGTATCTC	64	CT(14)
		R	CAGCAAAAATATACGCTTAAACCCAG	64	
Gh564	DQ908501	F	CAATCTCAGTGTATTTCCCTCCTG	64	CT(11)
		R	CTAACAAAGTAAGTATTGGTAGAGTGG	63	
Gh565	DQ908502	F	AAAAGACTCGGGTACCACCTAATC	63	AG(15)
		R	GTCCTTCTCATTATCTGAATTCACC	63	
Gh566	DQ908503	F	AGGATGGTTTACAATTCTCACACAATG	64	CT(20)
		R	CAAGCACAATAACAAGTGAATTACACC	64	
Gh567	DQ908504	F	CCTAACATAAAACATCTATAAGTCCTC	64	TC(13)
		R	TGTATGATAATTTAGTGAAAGAAAAGGGC	63	
Gh568	DQ908505	F	GTCTTTGATCAACTGAATTGTGTGC	63	TA(7)
		R	TGAATGAAAGGGAAAACAGGTTTACC	63	
Gh569	DQ908506	F	TTTCTCCGCGAGGCAATTCAAAAC	64	TC(17)
		R	ATCCAAGAACCCTAATGAATTTCTGC	64	
Gh570	DQ908507	F	GTGGGAATTAGGCGAGAAGATAAG	64	ATTTT(3)
		R	GGAAAATAGAGTCAAAATTCGGTTATGG	64	
Gh571	DQ908508	F	CACTGCTCAATGATTTTCATATCTACC	63	TCT(8)
		R	AGGGGAAAAGTTGAAGAATTTTATAGGC	63	
Gh572	DQ908509	F	CTCAGCTCCATTACAAACCATCTAC	64	TCT(8)
		R	GGACCTTATAATGGTCCCAAAGTG	64	
Gh573	DQ908510	F	CCTTTTAGCACTAGTTTAGGGTTTAAAG	64	AGA(14)
		R	AGAAAGGGATTGGAATCAGGTCACG	64	
Gh574	DQ908511	F	CTCCGGTGATAACTCAATAGAAACC	64	TCT(7)
		R	CGTCTATCATATGCTAACAGCAA	64	
Gh575	DQ908511	F	TTGCTGTTAGCATGTGATAGGACG	64	A(10)
		R	GAGTTTGTTCACATCATAGGTAATAG	64	
Gh576	DQ908512	F	AACACAACTCACAAGAGAAGACAAC	64	AGA(13)
		R	TCCTTGTTAACTTCTCCGTTCCACC	64	
Gh577	DQ908513	F	CCTCATATTCATTGTCAAACACGAG	63	TG(13)
		R	AGGATATGATATTCCAAAGACCCTC	63	
Gh578	DQ908514	F	TAACGCAGACAGATTCATAGGTGC	64	CA(11)
		R	ATCAACGAAAGAATATTGATGCTGCAG	64	
Gh579	DQ908515	F	ATTGAATGGTAAATACGTGTTGGTATTG	63	TG(13)
		R	CTAACATTATCATCATGATCAATCCAC	63	
Gh580	DQ908516	F	ATCAATGCAGGCAAGTTTCAACTATC	63	TCT(12)
		R	CAGTGTATTGTGTGAGTTTTCATTG	63	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
Gh581	DQ908517	F	ATCGATAATCGATCATTACGCCAC	64	AG(9)
		R	CCTTTTATGAGCATTTCATACTCTGC	64	
Gh582	DQ908518	F	AACATGGAAAAGCGTTTGGTAAAGTAG	63	TC(11)
		R	CCCAATCAAGCCCATTTCATATAGTC	64	
Gh583	DQ908519	F	AATCTAAAGCCCAAGCTAGGTTGG	64	AGA(6)
		R	GTACAGTGAGCATGCTTAAACATGC	64	
Gh584	DQ908520	F	TTGCAACCTTGAAAACCATGAAAGG	64	AGA(27)
		R	AGCATATGAAATCATAATGGGTAGCC	63	
Gh585	DQ908521	F	AGCAATCAAGCATTCAACGCCAAG	64	AGA(5)
		R	CTTCAATTTGACCTTCCGGTTTTGG	64	
Gh586	DQ908522	F	GATCACTACTACCAATATGTATACATAC	63	GT(9)
		R	CTAGTTGCTTAGCTATGTCTTGTTTC	63	
Gh587	DQ908523	F	TCATCGCCATCTGTCAATTTTCACC	64	TC(14)
		R	GGGTAGAAAGTAGAATAATTGTTCCCTAG	64	
Gh588	DQ908524	F	GAAAGCTGAACCTATGCCTTACTC	64	TC(13)
		R	AGATACGAAAAGGTGATAGAATATGCG	64	
Gh589	DQ908525	F	GGTTTGGTTCTATTTGTAGCGCAG	64	AGA(3)
		R	ATGCTTGATTGCTCGTAGTCTCTG	64	
Gh590	DQ908525	F	AGCAATCAAGCATTCAACGCCAAG	64	AGA(5)
		R	CTTCAATTTGACCTTCCGGTTTTGG	64	
Gh591	DQ908526	F	GATTTGAAAACCTGGAGGCATCTCC	64	TCT(7)
		R	TCGGTTACCACCAATTTAACCAGC	64	
Gh592	DQ908527	F	TTGTTATCTAACTTCTGTTACTCCTAAC	63	AGA(11)
		R	TTGTTTAGCTCTTCTATACTTGAATTCC	63	
Gh593	DQ908528	F	TTGCTAAAGGTAGAGCTTGAACCC	64	CA(6)
		R	TGTATCTGCTTCAGTGATTAAGTATCC	64	
Gh594	DQ908529	F	TTGATAAAGATAGGGTCGCGTCAC	64	AGA(30)
		R	TGCCTTCAAATTCCTGGCATTGG	64	
Gh595	DQ908530	F	CCAAGTTTAGTGCATCTGATATTGTTAC	64	AG(12)
		R	AAGACTCCAAAAGCTTGCAAGTCC	64	
Gh596	DQ908531	F	ATAGCATTTCATTGCATCATTGCAATC	63	AG(11)
		R	TTTTTCACTCAACCGTGACCCTC	63	
Gh597	DQ908532	F	TGGAAAAGTGAACATTGAGAGACC	64	AG(9)
		R	GGCATGAAACTCAAGACAATCATC	64	
Gh598	DQ908533	F	CAATTAGACCTCTATCCAAGCTCAG	64	TC(13)
		R	CGAATTTTACCCTAGAGGACAACC	64	
Gh599	DQ908534	F	TTTAGCACCACCAACTCTTGCTTC	64	GT(9)
		R	TTGTGGCACAACAAGGTGTTCTAG	64	
Gh600	DQ908535	F	ACCAACTCACCTTAAATATTATGGTCC	64	CA(4)
		R	CTCTCATATCTCGTACTTGACGTG	64	
Gh601	DQ908536	F	GTTAGTGCATCTGATATTGTTACACC	64	AG(11)
		R	ACAAGACTCCAAAAGCTTGCAAGTC	64	
Gh602	DQ908537	F	AACACCGCACGGAATGTTGACG	64	TCT(8)
		R	CCAACAAGTCCGACGAGAACAC	64	
Gh603	DQ908538	F	CAAAGTTGTAAACGGGTGAGAAGTC	64	TCT(11)
		R	ATTAAGTATGCACCCATGTAGTCCC	64	
Gh604	DQ908539	F	CTGTAACTTGCCATAGTGGAACCC	64	AGA(4)
		R	AAGGAAAAGTTTGGATCTCTGATGG	63	
Gh605	DQ908540	F	CCTTTCATCCGCTAAGCTACGG	64	GT(8)
		R	TAGCAGTCCACACAGGTGTTGG	64	
Gh606	DQ908541	F	CAATAGCACATCGAAATCGCAGTG	64	TCT(5)
		R	CCCATTTTAGAAGAACTTACCTGG	63	
Gh607	DQ908542	F	CTTTTCTTGTGTCTATCTCCACTGC	64	CGT(4)
		R	ATACCGAAGAGTGGCAATTCATATC	63	
Gh608	DQ908542	F	GTCTCTTCTCAAAGCAACCCAC	63	AGA(8)
		R	GAGGAGGATTCAACTCCATCTTG	63	
Gh609	DQ908543	F	CAAGATGGAGTTGAATCCTCCTC	63	TA(5)
		R	GGATGAATGGTTGTGATGAGGTG	63	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
Gh610	DQ908544	F	GTAGCTTTATTGGTTCAATGTTTCCTAG	64	CA(10)
		R	CTGGACTAAAAGAACTATTGAAATGGG	64	
Gh611	DQ908545	F	CTCACGTTACCATTGATTCTTCAGG	64	CT(12)
		R	CTTGCTCTATCATTTACGTATATACATG	63	
Gh612	DQ908546	F	AGAACATACTAATTAGCCATTCTCACC	64	GT(10)
		R	ATCTTCTTTTCACCTGGGGCTATC	64	
Gh613	DQ908547	F	CTCGCGCATATATAAAACAATACAGTAG	64	C-rich repeat
		R	GGATCGTATTCATCGTCATTAGCTC	64	
Gh614	DQ908548	F	GTAGCTTTATTGGTTCAATTTTTCTAG	63	CA(8)
		R	GGAATTTTATAAGATCCACAAGAACTG	63	
Gh615	DQ908549	F	TTGTAGGGATGATTAGTTCATTACAGG	63	TTTTA(3)
		R	CTCATAGATGAACTAGGTCCACG	63	
Gh616	DQ908550	F	GTAATAAAACGAAGGCAGATGAGGC	64	AG(15)
		R	ATAAATGTAGGAGTTATTCATGCATTTG	63	
Gh617	DQ908551	F	CACCTATTGATGTGTAATTCATTGTGTTTC	65	TCT(17)
		R	CGATATGAAGACTCACATTCACGTG	64	
Gh618	DQ908552	F	CTCTAAAATAACAATCAACCCTTCTCTTC	64	TCT(7)
		R	CTACAAAATCCAAAGGTTGTGGAATC	63	
Gh619	DQ908553	F	CCATTTCAGAGCCCTGGGTAG	63	AGA(4)
		R	TTACGGTTTCAAGTTTTATTGCAGAAC	63	
Gh620	DQ908554	F	CTTCTGGCGTCTTTATCGACAC	64	TC(12)
		R	TACTAAGTCGATAGTCATCAAACCC	63	
Gh621	DQ908555	F	GGTTATTCTGAGCATTGAGTTTG	64	ACTC(3)
		R	GCAACTAAAGTTTCTGGCTTGGATC	64	
Gh622	DQ908556	F	AGGGTTTGGCATGTATATGTGGC	64	GT(11)
		R	GTATCTAAACACATATCTTTGTAGTTCATC	64	
Gh623	DQ908557	F	CATCTCATCGCATCATATTCATTCC	63	AC(14)
		R	CTGCTTCCAGGTTTTCTCATTCTC	64	
Gh624	DQ908558	F	AGTCGTTTCCCTGTCTTTAATTGATG	64	GT(11)
		R	CAAAAAAGTGCAACAGTAACAGCAG	63	
Gh625	DQ908559	F	ATCAGAGGCGAAAACAATACATATACC	64	TC(13)
		R	TATTTCTACTGTAGCGTGTATATGG	64	
Gh626	DQ908560	F	TTTTATCCGTTGAAGCTTGAAACTCC	64	TC(14)
		R	CTAAGGGGTTTTTGTGCCTTGAAG	64	
Gh627	DQ908561	F	CTATGTCCTAGTCGTTTCGTAAGAAG	64	AGA(8)
		R	ATGATAAAGCACGACTCTTGACCG	64	
Gh628	DQ908562	F	CATTCTTATATTGCTACCCACAGTTC	64	GT(11)
		R	TAAAGTGTCTGACATAGATAAGAAG	64	
Gh629	DQ908563	F	GGAACGACGACGTTATATTTCAAGC	64	AGA(8)
		R	TAACCCAACCTTATGCTTCTTCTCC	64	
Gh630	DQ908564	F	ATAGGCCTGTAGTTATACCTTTCAAC	64	TCT(16)
		R	CAGGAATCGAAATGGATATGATTACAG	64	
Gh631	DQ908565	F	TTGCCTTTGATCTCAACATAGTTCAG	63	AGA(21)
		R	CCATTGGTATGGATACTGAATATGAC	63	
Gh632	DQ908566	F	CCCATTACTGGATGTAAGGAAATG	64	AGA(6)
		R	ATTGGTGTATCGAGATAAGTGAGG	64	
Gh633	DQ908567	F	ATTGGCTTATCACACCTCTGATAC	64	TCT(11)
		R	CCATTAATAGGAGAATTAGCCCGAC	64	
Gh634	DQ908568	F	ATGGTAGTGGCAAGGATTAGCATC	64	TCT(29)
		R	TCCAAAGCAAGCTATCGATTGTGG	64	
Gh635	DQ908569	F	TGGATGGCAAGAACCTACTTAATCC	64	AGAAGG(45)
		R	CGCGTAAATTATCAAAGAATGTTCCAG	64	
Gh636	DQ908570	F	TCGATAGCAAAATCACGGTGACAAG	64	AGA(12)
		R	CTTCTTCTAGGTTCTGGTTACTG	64	
Gh637	DQ908571	F	ATTGCATCAGTTCGATCTGTGGG	64	TCT(17)
		R	AACGAGTTGAAGCAAGTGGATC	64	
Gh638	DQ908572	F	AAGATTTATCCGCTAGAGCAGCG	64	AGA(8)
		R	CTTGGGCTGTATATGTGAGTTACAC	64	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
Gh639	DQ908573	F	AAGATGTTAAGCTCGTGGAGTGC	63	AG(16)
		R	TTAACCTAAGGGCCTCTGCATAG	63	
Gh640	DQ908574	F	CTAGTTCATCGCCATTCATCAGC	64	AGA(13)
		R	GTGAGGAATCCATAGCTTGTGCA	64	
Gh641	DQ908575	F	GTGTTAACACCATACAATAGCTAATAGC	64	AC(10)
		R	TCCCATTGCAACTATTAAATACCCTTC	64	
Gh642	DQ908576	F	CTGCTTCAATAGTTAAGTGTCTGG	63	GT(4)
		R	AAACTGAGGGACTTGAACCCAAG	63	
Gh643	DQ908576	F	ATGTTAATTGGGGAGTTGGGAATATC	63	TTTTA(3)
		R	GGAACCAGAAAATGTTAAACAAAAGGG	64	
Gh644	DQ908577	F	CACTTATGTCAATGGAAGCATTTAGC	63	CA(6)
		R	CAACACTAAAAATGTTCCCTAGATGG	63	
Gh645	DQ908578	F	TCAACACTTCAAGCCTGTCTCAC	63	TC(14)
		R	AGGTTTTGGTTAGGGGAATATCATG	63	
Gh646	DQ908579	F	GTCTCGATTCAACAACCTCGAGC	64	AG(18)
		R	TTCTGCTCAGTTTCCCTCTTCA	64	
Gh647	DQ908580	F	AGGATGGTTTACAATTCTCACACAATG	64	TC(19)
		R	CAAGCACATAACAAGTGAATTACACC	64	
Gh648	DQ908581	F	AGGAAACAACACATGTATTCACCTG	63	AG(10)
		R	CAACAGCTCTGGATGTATGTGATG	64	
Gh649	DQ908582	F	CTGTGACTTTTGGTCCCATTCAAC	64	TC(12)
		R	ACCGTTACAACATCTGTAAGCTGAG	64	
Gh650	DQ908582	F	GATATCTAACCTAGATAAGCTTCTTGC	64	ATC(5)
		R	TTGAAACGTTATCAAAAGAGATGACGG	64	
Gh651	DQ908583	F	GTTCTCAGTTTGTAGCTTGTCCACC	64	AGA(4)
		R	TCATCTTACTCCGTGGGTATCAG	64	
Gh652	DQ908584	F	TAAATCTACTTGGAGAATGTAAGAGCC	64	AG(10)
		R	GAACCCTGTACCATTCTCTTTTCC	64	
Gh653	DQ908585	F	CTAAAGAATTATTGTTGGAACCAGACG	64	AGA(22)
		R	TATCAGAATCAATATGCACAGGTTTCCAG	64	
Gh654	DQ908586	F	TTTTGTGCCTTGAAGAGAAATGAAAGG	64	AG(15)
		R	TTTTATCCGTTGAAGCTTGAAAACTCC	64	
Gh655	DQ908587	F	GTTCCCTATCAGCACTGTTTACC	65	TC(19)
		R	AATCAATCAAATTCGCCAGTGGCTC	64	
Gh656	DQ908588	F	TTCTGAGAAACGGCATTCTGAGAAG	64	AG(16)
		R	GTCTCCACATCCCATGCACTAC	65	
Gh657	DQ908589	F	GTGGAGTCGAAAATATCAAAAATCAGC	64	C-rich repeat
		R	GTGTGTGACGTAAGGTAGATTTTCC	64	
Gh658	DQ908590	F	CTGCATTGGTTCGATCTTTGTGAG	64	TCT(11)
		R	AACGAGTTGAAGAGCAAGGATC	64	
Gh659	DQ908591	F	AAATTCACCTTCTGGCAGTGACAC	64	TC(16)
		R	AGTCAAAAGAAAGAGCCGTTCCGC	65	
Gh660	DQ908592	F	TTCGAAGCAGGAAGCATTGGTATC	64	ACT(6)
		R	CTTCTCGAATAGATTAATGATTAAGCAC	63	
Gh661	DQ908592	F	TTCTCCTTGATTTCTATCTTTCTTGC	64	TCT(8)
		R	GAACGACGACGTTATATTCAAGCATG	65	
Gh662	DQ908593	F	TATCCTCATATTCATTGTCAAACACGAG	64	TG(9)
		R	GTCCAAGGATATGATATTCCAAAGACC	65	
Gh663	DQ908594	F	AGTTAGGATGGTTTACAATTCTCACAC	64	CT(20)
		R	CAAGCACATAACAAGTGAATTACACC	64	
Gh664	DQ908595	F	GTGGATATGTCCACGTGGAACC	65	AGA(18)
		R	CCACAATAGCAACACTAAGGGAAG	64	
Gh665	DQ908596	F	GACTCAGCCCGATATAGTTAATAGG	64	CA(18)
		R	TAAGTGATTGAGGTGAGAATTCGAC	63	
Gh666	DQ908597	F	CCAGATCTGTAGAAACGTTATGCC	64	ACA(4)
		R	CACTATAAGCTTTGCCAAATTCCTCC	65	
Gh667	DQ908598	F	CTTCCAATGAATGAATCTTTTGAACACC	64	TC(23)
		R	ACGTGTTAGACATATGATTTTCATGTAAC	63	

Table 1A. continued

Primers ^s	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
Gh668	DQ908599	F	ACTGTCTCTCTGCAGTTTGTCTAC	64	C-rich repeat
		R	TIACTTGGTTCTACGCAGGTACTC	64	
<u>Gh669</u>	DQ908600	F	GCTTTACCAAATCTGAAATACCCAG	63	AGA(5)
		R	CATGATTCCAATTGCACGATTCTCG	64	
Gh670	DQ908601	F	GGACCGAGTAAAAAGTTTATCAAGG	64	AAT(3)
		R	GATCTGGACTAAAACTTGACCTTGTCT	65	
Gh671	DQ908602	F	CTACAGGATTGGAGGAGTTTATGG	64	AGA(7)
		R	ACAATCATGCCTGTCTTTCTCC	63	
Gh672	DQ908603	F	TCTGCTTTGGAAACTCTCATGTCAG	64	CTTT(4)
		R	ATTGCAATAAGATTACTCGTTGGGC	63	
Gh673	DQ908604	F	GCACACTAACAGTGGCTTCAAGG	65	TC(8)
		R	CATAGCCCATTAGGCAATCAATGG	64	
Gh674	DQ908605	F	CGGTTACTTGAGAACTTAGCTTAGG	64	T(9)
		R	CGTAGATGGTCTTAATGAATCCAAAGG	65	
Gh675	DQ908606	F	CTTTGCACAATTTTGTTCCTGTAACC	65	GT(10)
		R	CACTCCCGTTCCTTTGTTTCATTGC	65	
Gh676	DQ908606	F	CAATGAACAAAGGAACGGGAGTGG	65	GGC(4)
		R	GGTTTCCACTCGCTGCATCATAG	65	
Gh677	DQ908607	F	AGGAAGATTGAGAGCGAGAGCC	64	AG(16)
		R	GTGGGTGGCATTGAAGGTTACC	64	
<u>Gh678</u>	DQ908608	F	CTTCATTTTCAGCCGGTTCGATC	65	TCT(10)
		R	CCGAGACAGAGTCAATTGCTTCC	65	
Gh679	DQ908609	F	GGATCAGTATATAACATCTTGTCCATC	64	TCT(22)
		R	CAAGGCGTGAAATCAAATCCAATATTG	64	
Gh680	DQ908610	F	ACAGAGCTGAAGAAGCTCTAATGG	64	AGA(10)
		R	TATGTAAAGCCAACCATGCTCAGG	64	
<u>Gh681</u>	DQ908611	F	ACCCGGCCAAATTTAAGCAAAGAAG	64	TCT(9)
		R	CTTGCCACGTTGGATGTACACAG	65	
Gh682	DQ908612	F	CAATTTTGCCTCAAACGCTGATTCCG	65	TTTCCC(2)
		R	TTGCACCCTCATCTAAACCAACTC	64	
Gh683	DQ908612	F	ATGAGGGTGAATACGTCTGAAG	63	TTCC(3)
		R	TCAATGTGGGCAATAGCACTTCC	63	
<u>Gh684</u>	DQ908613	F	ACTAGGTCCCTCTTGTGAAGTCC	65	TCT(11)
		R	GCCAAAAGCAAATGATGCGAGCTC	65	
Gh685	DQ908614	F	GTAACAGAACGCAATTGATGAAAGC	63	AGA(9)
		R	CCCATGGCAATATTGGTATTTATACG	64	
Gh686	DQ908615	F	CTAGGGTAGAATATGGAGACAATGC	64	GT(8)
		R	CTGATTGAGGATAATTCCTTTCTCC	63	
Gh687	DQ908616	F	CTTCATCAGCATTGCTTGGTTTGC	64	TCT(10)
		R	CAAAGATCAAACCAAGCAAGGAGATG	65	
Gh688	DQ908617	F	GACTTCAGCTTATTGCATTGGTTCCG	64	TCT(6)
		R	CAATTTTGGGTTGTCACAAAGGATCC	65	
Gh689	DQ908618	F	ACAAAAGACCACGTAAAGTGTCTCG	64	CA(11)
		R	CATTCTTATATTTGCTACCCACAGTTC	64	
Gh690	DQ908619	F	GCGTTACACTCGTTAACATTTCCG	64	C-rich repeat
		R	TCATGACGGAAACTTCTGTAGCTG	64	
<u>Gh691</u>	DQ908620	F	ACTCCGTCTCTTTCAACAGATTCC	64	TC(14)
		R	ATTGAGAGCTTGAAAAATGATGCC	63	
Gh692	DQ908621	F	CTCATGTGCTTAATGTCTTAGCCC	64	TC(13)
		R	GGATTGGAAAGAGGTTTATAAAGCG	63	
Gh693	DQ908622	F	GCATACTTCTCCTATCGTTTTCCC	64	CTTTT(3)
		R	AAGAAAAAGGGTTTGTAGGCAGG	64	
Gh694	DQ908623	F	CTTAGGTTAAAAGATAACGGATTGCG	63	AGA(8)
		R	CCATTTCCAACCTGTCAGCTACTG	63	
Gh695	DQ908624	F	AAGAGATGGCAGCTTGACCTAGAC	65	ATG(6)
		R	CAAATCCAGTGTCCGACAAATCC	65	
Gh696	DQ908625	F	GAGGAAACAAACAACCTCGATCTG	64	AG(16)
		R	TTCTTGATCTCTTCGAGGAACTCC	64	

Table 1A. continued

Primers ^x	Acc. #		Forward (F) and reverse (R) primers	T _m ^y	SSR motif ^z
<u>Gh697</u>	DQ908626	F	TCCCTGAGCTCATATCTAACTCC	64	CA(8)
		R	GACTTACTAAGCTATTC AAGCTTCC	63	
Gh698	DQ908627	F	TCCTCTGCATTCTTTCCATACAGG	64	TC(9)
		R	ATCTCGTATCAGATCCTATCAGGG	64	
Gh699	DQ908628	F	CTTTTTTCCTATTTTTGTCTTCTCCTTG	64	TCCTCTTCTCT(2)
		R	TCGACAAATTGAGTCCTTAGAATCG	64	
Gh700	DQ908629	F	GAGAGCAACAGAGTTTCGGTAAGAG	64	GT(10)
		R	CCTATAAAAGACCATGATTTCTAAAGGG	64	

^x Primer pairs that amplify loci that are polymorphic between *G. hirsutum* TM1 and *G. barbadense* 3-79 are underlined (e.g. Gh22)

^y Salt (50 mM Na⁺)-adjusted melting temperatures of primers and simple sequence repeat motifs.

^z The number in parentheses indicates the number of times the indicated unit is repeated in cloned *G. hirsutum* cv. Tamcot Sphinx genomic DNA.