Table S3. Chloroplast haplotypes and defining variations

Haplotype	No. of accessions	Locus name													
		WCt1 (19, A)	WCt4 (39, T)	WCt5 (19, A)	WCt6a (31, T)	WCt6b (78, C)	WCt6d (113)	WCt8 (44, T)	WCt10a (49, A)	WCt12 (38, T)	WCt17a (39, T)	WCt19 (34, A)	WCt24a (104, A)	WCt24d (38)	*trn*LFc (276)
HT7-1	1	9	9	12	9	9	G	8	9	12	9	8	9	C	TTTAAAA
HT7-2	1	9	9	12	9	9	G	8	9	12	10	8	9	C	TTTAAAA
HT7-3	1	9	9	15	9	8	G	8	10	11	12	8	9	C	TTTTAA3
HT7-4	1	10	9	10	9	8	G	8	10	10	10	8	10	C	TTTAAAA
HT7-5	3	10	9	10	9	8	G	8	10	10	10	8	11	C	TTTAAAA
HT7-6	2	10	9	10	9	8	G	8	10	10	10	8	AAAAATAAAAA	C	TTTTAA
HT7-7	1	10	9	10	9	8	G	8	10	10	10	9	11	C	TTTAAAA
HT7-8	1	10	9	10	9	9	G	8	10	10	9	8	8	T	TTTTAA
HT7-9	3	10	9	11	8	8	G	8	10	11	11	8	9	C	TTTTAA
HT7-10	1	10	9	11	9	8	G	8	10	10	10	8	11	C	TTTAAAA
HT7-11	3	10	9	11	9	8	G	8	10	11	10	8	9	T	TTTAAAA
HT7-12	1	10	9	11	9	10	G	8	10	10	12	8	9	T	TTTAAAA
HT7-13	1	10	9	11	10	8	G	8	10	11	12	8	9	T	TTTAAAA
HT7-14	13	10	9	12	9	9	G	8	9	12	10	8	9	C	TTTAAAA
HT7-15	17	10	9	12	9	9	G	8	9	12	11	8	9	C	TTTAAAA
HT7-16	5	10	9	12	9	9	G	8	9	12	12	8	9	C	TTTAAAA
HT7-17	2	10	9	12	9	9	G	8	9	12	12	8	9	C	TTTTAA
HT7-18	1	10	9	12	9	9	G	8	9	12	13	8	9	C	TTTAAAA
HT7-19	1	10	9	12	9	8	G	8	10	10	10	8	11	C	TTTAAAA
HT7-20	1	10	9	12	9	9	G	8	10	12	10	8	9	C	TTTAAAA
HT7-21	1	10	9	13	9	8	G	9	10	10	11	8	9	C	TTTTAA
HT7-22	1	10	9	13	9	8	G	9	10	9	12	8	9	C	TTTTAA
HT7-23	1	10	9	13	9	8	G	9	10	10	11	8	9	C	TTTTAA
HT7-24	1	10	9	13	9	9	G	8	9	12	12	8	9	C	TTTAAAA
HT7-25	1	10	9	13	9	9	G	8	10	11	11	8	9	C	TTTTAA
HT7-26	1	10	9	13	9	9	G	8	10	11	12	8	9	C	TTTTAA
HT7-27	1	10	9	13	10	9	G	8	9	12	11	8	9	C	TTTAAAA
HT7-28	1	10	9	14	9	8	G	8	10	11	12	8	10	C	TTTTAA
HT7-29	1	10	9	14	9	8	G	8	10	11	13	8	9	C	TTTTAA
HT7-30	1	10	9	14	9	8	G	8	10	12	12	8	10	C	TTTTAA
HT7-31	1	10	9	14	9	8	G	9	10	10	11	8	9	C	TTTTAA
HT7-32	1	10	9	15	9	9	G	8	10	11	12	8	9	C	TTTTAA
HT7-33	1	10	9	16	9	8	G	8	10	11	10	8	10	C	TTTTAA
HT7-34	1	10	10	11	8	8	G	8	11	11	9	8	10	C	TTTTAA
HT7-35	15	10	10	11	8	8	G	8	11	11	9	8	11	C	TTTTAA
HT7-36	1	10	10	12	8	8	G	8	11	11	9	8	11	C	TTTTAA
HT16A	1	10	9	10	9	8	T	8	10	10	11	8	11	C	TTTTAA
HT16B	2	10	9	10	9	8	T	8	10	10	11	8	10	C	TTTTAA
HT16C	1	10	9	11	8	8	T	8	10	11	10	8	9	C	TTTAAAA
HT16D	7	10	9	11	9	8	T	8	9	10	10	8	9	C	TTTTAA
HT16E	1	10	9	11	9	8	T	8	10	10	9	8	9	C	TTTAAAA
HT16F	3	10	9	11	9	8	T	8	10	10	10	8	10	C	TTTTAA
HT16G	2	11	9	11	9	8	T	8	10	10	10	8	10	C	TTTTAA
HT16H	1	10	9	11	9	8	T	8	10	10	10	8	11	C	TTTTAA
HT16I	1	10	9	11	9	8	T	8	10	10	11	8	10	C	TTTTAA
HT16J	12	10	9	11	9	8	T	8	10	11	9	8	9	C	TTTAAAA
HT16K	7	10	9	11	9	8	T	8	10	11	9	8	10	C	TTTAAAA

HT16L	5	10	9	11	9	8	T	8	10	11	10	8	9	C	TTTAAAA
HT16M	1	10	9	12	9	8	T	8	9	10	11	8	10	C	TTTTAAA
HT16N	2	10	9	12	9	8	T	8	10	10	9	8	11	C	TTTTAAA
HT16O	1	10	9	12	9	8	T	8	10	11	11	9	9	C	TTTAAAA
HT16P	1	10	9	13	9	8	T	8	10	11	10	8	9	C	TTTTAAA

Locus positions, based on aligned sequences, counted from the nucleotide next to the 3' end of the forward primer are in parentheses. For microsatellite loci, their repeat units also are given.

The WCt17 locus was amplified using WCt17 forward and WCt18 reverse primers [14].

*trn*LFc is in the intergenic spacer region between the *trn*L (UAA) and *trn*F (GAA) genes [16].