

RICHARD C. CRONN, RANDALL L. SMALL, TAMARA HASELKORN, AND JONATHAN F. WENDEL.
2002. Rapid diversification of the cotton genus (*Gossypium*: Malvaceae) revealed by analysis of sixteen nuclear and chloroplast genes. *American Journal of Botany* 89(4): 707-725

Appendix 2. Gap character description and data matrix for indel data set.

Gap character	Data set	Aligned position ^a	Character state 0	Character state 1	Character state 2
1	<i>ndhF-1</i>	1456-1464	ACATTA	2-codon deletion	-
2	<i>rpL16-1</i>	2198-2199	T + 1 bp gap	2-bp gap	TT
3	<i>rpL16-2</i>	2333	C	1-bp gap	-
4	<i>rpL16-3</i>	2500-2504	CATTT	5-bp gap	-
5	<i>rpL16-4</i>	2830	1-bp gap	T	-
6	<i>rpL16-5</i>	2968-2973	6-bp gap	TTATAC	-
7	<i>rpL16-6</i>	3196-3197	2-bp gap	CA	-
8	<i>rpL16-7</i>	3200	1-bp gap	C	-
9	<i>trnTL-1</i>	3261	G	1-bp gap	-
10	<i>trnTL-2</i>	3385-3395	11-bp gap	TTAATRTAANC	-
11	<i>trnTL-3</i>	3410-3417	8-bp gap	TAAATATA	-
12	<i>trnTL-4</i>	3435-3439	TAATA	5-bp gap	-
13	<i>trnTL-5</i>	3807-3811	TAATA	5-bp gap	-
14	<i>trnTL-6</i>	3869-3875	7-bp gap	ATTTTAG	-
15	<i>trnTL-7</i>	4057-4061	ATGAT	5- bp gap	-
16	<i>trnTL-8</i>	4581-4585	CTGAT	5-bp gap	-
17	<i>trnTL-9</i>	4633	gap	1-bp G	-
18	<i>trnTL-10</i>	4762-4772	11-bp sequence	11-bp gap	-
19	<i>matK-1</i>	4960	1-bp gap	T	-
20	<i>matK-2</i>	4980	1-bp gap	A	-
21	<i>matK-3</i>	7073	T	1-bp gap	-
22	<i>matK-4</i>	7081-7087	7-bp gap	TCAATTA	-
23	<i>matK-5</i>	7208	1-bp gap	T	-
24	<i>matK-6s</i>	7314-7315	TA	2-bp gap	-
25	<i>AdhA-1</i>	918	1-bp gap	T	-
26	<i>AdhA -2</i>	1021	1-bp gap	T	-
27	<i>AdhA -3</i>	1659-1666	4-bp gap	CATT	-
28	<i>CesAlb-1</i>	2981-3029	49-bp gap	49-bp insertion	-
29	<i>CesAlb-2</i>	3234-3236	3-bp gap	TCA	-
30	<i>CesAlb-3</i>	3575-3578	2-bp gap + AT	TTAT	4-bp gap
31	<i>CesAlb-4</i>	3595	1-bp gap	A	-
32	<i>CesAl-1</i>	4345-4346	TT	2-bp gap	-
33	<i>CesAl-2</i>	4744-4751	MCTGAAGC	8-bp gap	-
34	<i>AdhC-1</i>	5140-5142	TAC	3-bp gap	-
35	<i>AdhC-2</i>	5158	T	1-bp gap	-
36	<i>AdhC-3</i>	5175-5179	5- bp gap	TATGA	-
37	<i>AdhC-4</i>	5192-5195	4-bp gap	TAGC	-
38	<i>AdhC-5</i>	5198-5199	2-bp gap	AT	-
39	<i>AdhC-6</i>	5661-5662	AA	1- bp gap	-
40	<i>AdhC-7</i>	5712-5715	TTAG	4- bp gap	-
41	<i>AdhC-8</i>	5742-5752	GAGTTK	6-bp gap	-
42	<i>Al341-1</i>	6081	A	1-bp gap	-

43	<i>A1341-2</i>	6246-6247	2-bp gap	AC	-
44	<i>G1121-1</i>	7428-7430	AAG	3- bp gap	-
45	<i>G1121-2</i>	7431-7460	30-bp sequence	30-bp gap	-
46	<i>ITS-1</i>	9222	1-bp gap	T	-
47	<i>ITS-2</i>	9132-9133	TT	2-bp gap	-
48	<i>ITS-3</i>	9139	G	1- bp gap	-
49	<i>FAD2-1</i>	10297-10300	TTYT	4-bp gap	-

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A-genome  1001111101 011011111? 1101110111 1110111110 101010111
B-genome  1001111110 1111100111 1000111111 1110111110 101010111
C-genome  0111111111 1101000111 1010110112 1111111111 111011111
D-genome  0001111110 1100000111 1?00000112 1110110110 001010110
E-genome  1201111110 1110000110 1000110112 111??1???? ?01110111
F-genome  0001111101 1100001111 1101111111 1110111110 101011111
G-genome  0111111110 1101000101 1010110112 1111011111 111110111
Gkb      00000000?0 0000000000 0000010000 0000000000 00000000?
Kdb      0000000000 00??010000 0000000000 0000000000 000000000
    
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^a Aligned positions correspond to concatenated cpDNA or nDNA data sets

^b Abbreviations for outgroup taxa are *Gk* = *Gossypoides kirkii* and *Kd* = *Kokia drynarioides*.