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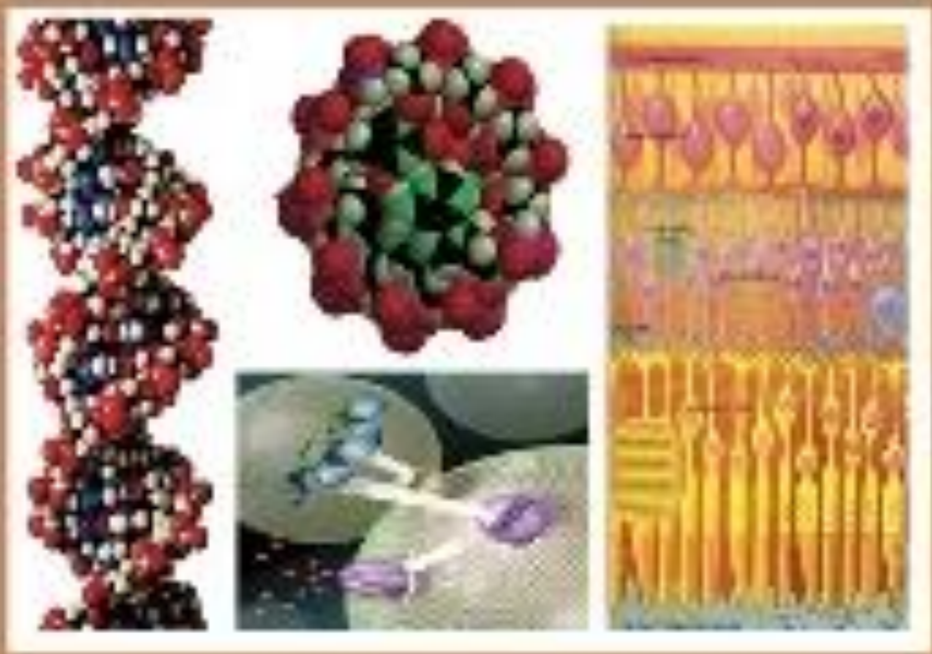

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Does GC Content of Random Amplified Polymorphic DNA (RAPD) Markers Influence Their Discrimination of Different Biological Specimens?

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ABSTRACT

A set of 2000 RAPD works involving different biological specimens was compiled and analyzed for the presence of discrete amplification to deduce the impacts of the percentage of nitrogenous bases (Guanine-Cytosine content) of RAPD markers on their discrimination of various biological specimens. Articles lacking data on RAPD amplification were excluded, while only 56 articles having a total of 761 decamer primers were subsequently subjected to logistic statistical analysis (Analysis of variance and correlation analysis). Results obtained revealed GC contents between 60-70%, 60-70%, 65%, 55% and 55-65% as the best for RAPD discrimination of bacteria, plants, insects, protozoans, and fungi, respectively. The bivariate correlation analysis also documents a significant relationship between GC contents of RAPD markers and their levels of polymorphisms. Our results, however, emphasize that the challenge faced with large-scale RAPD-PCR through several optimization techniques may be averted with judicious use of GC content as a predictor of the level of polymorphisms.

INTRODUCTION

The recent advances in PCR-based technology have revolutionized and simplified microbial diversity studies (Garcia *et al.,* 2004; Yutse-Lisbona *et al.,* 2011; Laursen *et al..,* 2017) due to their importance in uncovering several DNA markers (Bostein *et al.,* 1980; Tingey, 2003), that are significantly involved in the elucidation of the gene structure and functions (Erlich, 1989; Yutse-Lisbona *et al.,* 2011; Thomas *et al.,* 2016; Thomas *et al.,* 2019), in addition to their genomic and proteomic application (Chapman, 2003). This high-throughput technique, which is contingent upon amplification of nucleic acid (Zhang *et al.,* 2001; Vieux *et al.,* 2002) is a well-understood in vitro process (Mullis *et al.,* 1994) with several tools aimed at optimizing their product (Rozen and Skaletsky, 2000; McPherson and Moller, 2000).

For genetic diversity studies, the use of dominant molecular markers, including RAPD, inter-simple sequence repeats (ISSR), amplified fragment length polymorphisms (AFLP), among others, has been well studied (Garcia *et al.,* 2004; Vieira *et al.,* 2016), while their importance in profiling biological specimens has also been well emphasized (Laursen *et al.,* 2017).

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These molecular markers have consequently circumvented the past limitations associated with pedigree, morphological, and cytological markers, especially in accessing the genetic diversity of organisms (Garcia *et al.,* 2004), thereby enhancing the fine resolution required to score appropriate diversity of organisms (Amusa *et al.,* 2014; Thomas *et al.,* 2017).

However, the success of polymerase chain reaction (PCR) is highly dependent on the choice of primer used (Vieux *et al.,* 2002; Yuryev *et al.,* 2002); thus, a very strict primer selection strategy combined with stringent PCR conditions has earlier been proposed (Vieux *et al.,* 2002). In the use of both dominant molecular markers for deciphering genetic diversity of organisms, the selection of appropriate primers that would exhibit the right polymorphism is a major problem and antagonizing this problem is sequeled to several optimization procedures which could be time consuming and technical labour intensive thereby further increasing the cost of genetic diversity study using any of these dominant markers.

This study was therefore aimed at determining the influence of the GC content of RAPD markers on the discrimination power of dominant markers, especially in the characterization of different biological specimens, including Bacteria, viruses, fungi, protozoa, algae, and plants.

MATERIALS AND METHODS

In this study, a preliminary search of Random Amplified Polymorphic DNA (RAPD) analysis of various biological specimens across the globe was carried out on Google Scholar using www.scholar. google.com to screen for RAPD work done between 1992 and 2016. A set of 2000 RAPD works bordering different biological specimens was compiled and analyzed. These journals were screened down to 57 journals based on their relevance to the aim of this research. Out of these 57 journals that border on RAPD, 761 RAPD primers were obtained and analyzed for their GC content using the GC calculator (www.sciencebuddies.org). The GC content results obtained were subsequently aligned relative to their number of bands produced to deduce their impact on RAPD discrimination of the studied organisms. These results were subsequently subjected to statistical analysis using SPSS version 22.

RESULTS

Table 1 below represents the impacts of GC content on RAPD discrimination of various biological specimens. Results shown in this table reveal GC contents between 60-70%, 60- 70%, 65%, 55% and 55-65% as the best for RAPD discrimination of bacteria, plants, insects, protozoans, and fungi, respectively. The bivariate correlation analysis also documents a significant relationship between GC contents of RAPD markers and their levels of polymorphisms. Our results, however, emphasize that the challenge faced with large-scale RAPD-PCR through several optimization techniques may be averted with judicious use of GC content as a predictor of the level of polymorphisms**.**

Table 1: Influence of GC content on RAPD discrimination of various biological specimens

S/N	Name of Primer	Primer Sequence (5'-3')	G+C Content (%)	No of Bands	No of Base	Reference	Biological Specimens
1	OPF-2	GAGGATCCCT	60	12	10	(Kutty *et al*., 2006)	Plant
2	OPF-8	GGGATATCGG	60	13	10	(Kutty *et al*., 2006)	Plant
3	OPF-5	CCGAATTCCC	60	7	10	(Kutty *et al*., 2006)	Plant
4	OPF-6	GGGAATTCGG	60	6	10	(Kutty *et al*., 2006)	Plant
5	OPF-12	ACGGTACCAG	60	7	10	(Kutty *et al*., 2006)	Plant
6	OPF-13	GGCTGCAGAA	60	4	10	(Kutty *et al*., 2006)	Plant

7	OPE-1	CCCAAGGTCC	70	9	10	(Kutty *et al*., 2006)	Plant
8	OPE-3	CCAGATGCAC	60	7	10	(Kutty *et al*., 2006)	Plant
9	OPE-4	GTGACATGCC	60	10	10	(Kutty *et al*., 2006)	Plant
10	OPE-6	AAGACCCCTC	60	10	10	(Kutty *et al*., 2006)	Plant
11	OPE-14	TGCGGCTGAG	70	10	10	(Kutty *et al*., 2006)	Plant
12	OPE-18	GGACTGCAGA	60	8	10	(Kutty *et al*., 2006)	Plant
13	OPE-20	AACGGTGACC	60	8	10	(Kutty *et al*., 2006)	Plant
14	OPS-10	ACCGTTCCAG	60	16	10	(Kutty *et al*., 2006)	Plant
15	OPS-7	TCCGATGCTG	60	10	10	(Kutty *et al*., 2006)	Plant
16	A-02	TGCCGAGCTG	70	8	10	(Babi*et al*., 2009)	Plant
17	A-07	GAAACGGGTG	60	2	10	(Babi*et al*., 2009)	Plant
18	A-09	GGGTAACGCC	70	12	10	(Babi*et al*., 2009)	Plant
19	A-10	GTGATCGCAG	60	13	10	(Babi*et al*., 2009)	Plant
20	A-13	CAGCACCCAC	70	7	10	(Babi*et al*., 2009)	Plant
21	A-15	TTCCGAACCC	60	8	10	(Babi*et al*., 2009)	Plant
22	A-18	AGGTGACCGT	60	8	10	(Babi*et al*., 2009)	Plant
23	A-20	GTTGCGATCC	60	8	10	(Babi*et al*., 2009)	Plant
24	B-06	TGCTCTGCCC	70	8	10	(Babi*et al*., 2009)	Plant
25	B-10	CTGCTGGGAC	70	1	10	(Babi*et al*., 2009)	Plant
26	B-17	AGGGAACGAG	60	7	10	(Babi*et al*., 2009)	Plant
27	C-02	GTGAGGCGTC	70	9	10	(Babi*et al*., 2009)	Plant
28	C-05	GATGACCGCC	70	6	10	(Babi*et al*., 2009)	Plant
29	OPA-14	TCTGTGCTGG	60	11	10	(Sen *et al*., 2010)	Plant
30	OPC-09	CTCACCGTCC	70	9	10	(Sen *et al*., 2010)	Plant
31	OPJ-01	CCCGGCATAA	60	16	10	(Sen *et al*., 2010)	Plant
32	C-08	TGGACCGGTG	70	6	10	(Babi*et al*., 2009)	Plant
33	OPJ-02	CCCGTTGGGA	70	13	10	(Sen *et al*., 2010)	Plant
34	OPJ-03	TCTCCGCTTG	60	12	10	(Sen *et al*., 2010)	Plant
35	OPJ-04	CCGAACACGG	70	10	10	(Sen *et al*., 2010)	Plant
36	OPJ-05	CTCCATGGGG	70	15	10	(Sen *et al*., 2010)	Plant
37	OPJ-07	CCTCTCGACA	60	14	10	(Sen *et al*., 2010)	Plant
38	OPJ-08	CATACCGTGG	60	14	10	(Sen *et al*., 2010)	Plant
39	OPJ-09	TGAGCCTCAC	60	10	10	(Sen *et al*., 2010)	Plant
40	OPAC-15	TGCCGTGAGA	60	25	10	(Sen *et al*., 2010)	Plant
41	OPAD-06	AAGTGCACGG	60	9	10	(Carvalho *et al.,* 2004)	Plant
42	OPAD-14	GAACGAGGGT	60	8	10	(Carvalho *et al.,* 2004)	Plant
43	OPAK-15	ACCTGCCGTT	60	6	10	(Carvalho *et al.,* 2004)	Plant
44	OPAM-01	TCACGTACGG	60	9	10	(Carvalho *et al.,* 2004)	Plant
45	OPAR-02	CACCTGCTGA	60	9	10	(Carvalho *et al.,* 2004)	Plant
46	OPAR-04	CCAGGAGAAG	60	7	10	(Carvalho *et al.,* 2004)	Plant
47	OPAR-05	CATACCTGCC	60	7	10	(Carvalho *et al.,* 2004)	Plant
48	OPAR-11	GGGAAGACGG	70	4	10	(Carvalho *et al.,* 2004)	Plant
49	OPAR-15	ACACTCTGCC	60	4	10	(Carvalho *et al.,* 2004)	Plant

50	OPAR-16	CCTTGCGCCT	70	7	10	(Carvalho *et al.*, 2004)	Plant
51	OPAT-08	TCCTCGTGGG	70	10	10	(Carvalho *et al.*, 2004)	Plant
52	OPAU-12	CCACTCGTCT	60	7	10	(Carvalho *et al.*, 2004)	Plant
53	OPAV-03	TGTAGCCGTG	60	6	10	(Carvalho *et al.*, 2004)	Plant
54	OPAV-13	CTGACTTCCC	60	8	10	(Carvalho *et al.*, 2004)	Plant
55	OPAV-19	CTCGATCACC	60	6	10	(Carvalho *et al.*, 2004)	Plant
56	OPAW-07	AGCCCCCAAG	70	8	10	(Carvalho *et al.*, 2004)	Plant
57	OPAW-08	CTGTCTGTGG	60	6	10	(Carvalho *et al.*, 2004)	Plant
58	OPAW-10	GTTGTTTGCC	50	8	10	(Carvalho *et al.*, 2004)	Plant
59	OPAW-11	CTGCCACGAG	70	10	10	(Carvalho *et al.*, 2004)	Plant
60	OPAW-14	GGTTCTGCTC	60	7	10	(Carvalho *et al.*, 2004)	Plant
61	OPAW-19	GGACACAGAG	60	8	10	(Carvalho *et al.*, 2004)	Plant
62	OPAX-07	ACGCGACAGA	60	8	10	(Carvalho *et al.*, 2004)	Plant
63	OPAX-10	CCAGGCTGAC	70	8	10	(Carvalho *et al.*, 2004)	Plant
64	OPP-05	CCCCGGTAAC	70	11	10	(Carvalho *et al.*, 2004)	Plant
65	OPP-14	CCAGCCGAAC	70	4	10	(Carvalho *et al.*, 2004)	Plant
66	OPE-18	CGACTGCAGA	60	8	10	(Carvalho *et al.*, 2004)	Plant
67	OPW-08	GACTGCCTCT	60	10	10	(Carvalho *et al.*, 2004)	Plant
68	OPW-09	GTGACCGAGT	60	8	10	(Carvalho *et al.*, 2004)	Plant
69	OPW-13	CACAGCGACA	60	10	10	(Carvalho *et al.*, 2004)	Plant
70	OPY-04	GGCTGCAATG	60	13	10	(Carvalho *et al.*, 2004)	Plant
71	OPY-09	AGCAGCGCAC	70	8	10	(Carvalho *et al.*, 2004)	Plant
72	OPY-10	CAAACGTGGG	60	11	10	(Carvalho *et al.*, 2004)	Plant
73	OPA-04	AATCGGGCTG	60	10	10	(Kawar *et al.* 2009)	Plant
74	OPA-09	GGGTAACGCC	70	8	10	(Kawar *et al.* 2009)	Plant
75	OPA-11	CAATCGCCGT	60	9	10	(Kawar *et al.* 2009)	Plant
76	OPA-17	GACCGCTTGT	60	8	10	(Kawar *et al.* 2009)	Plant
77	OPA-19	CAAACGTCGG	60	10	10	(Kawar *et al.* 2009)	Plant
78	OPAB-02	TGATCCCTGG	60	6	10	(Kawar *et al.* 2009)	Plant
79	OPAB-06	TGCTCTGCCC	70	8	10	(Kawar *et al.* 2009)	Plant
80	OPAB-08	GTCCACACGG	70	14	10	(Kawar *et al.* 2009)	Plant
81	OPAB-11	GTAGACCCGT	60	5	10	(Kawar *et al.* 2009)	Plant
82	OPAB-14	TCCGCTCTGG	70	10	10	(Kawar *et al.* 2009)	Plant
83	OPAB-17	AGGGAACGAG	60	9	10	(Kawar *et al.* 2009)	Plant
84	OPC-03	GGGGGTCTTT	60	8	10	(Kawar *et al.* 2009)	Plant
85	OPC-04	CCGCATCTAC	60	6	10	(Kawar *et al.* 2009)	Plant
86	OPC-05	GATGACCGCC	70	10	10	(Kawar *et al.* 2009)	Plant
87	OPC-06	GAACGGACTC	60	15	10	(Kawar *et al.* 2009)	Plant
88	OPC-07	GTCCCGACGA	70	5	10	(Kawar *et al.* 2009)	Plant
89	OPC-08	TGGACCGCTG	70	8	10	(Kawar *et al.* 2009)	Plant
90	OPC-14	TGCGTGCTTG	60	8	10	(Kawar *et al.* 2009)	Plant
91	OPC-15	GACGGATCAG	60	8	10	(Kawar *et al.* 2009)	Plant
92	OPC-16	CACACTCCAG	60	9	10	(Kawar *et al.* 2009)	Plant

93	OPC-17	TTCCCCCCAG	70	9	10	(Kawar *et al.* 2009)	Plant
94	OPC-18	TGAGTGGGTG	60	12	10	(Kawar *et al.* 2009)	Plant
95	OPG-02	GGCACTGAGG	70	7	10	(Kawar *et al.* 2009)	Plant
96	OPG-03	GAGCCCTCCA	70	8	10	(Kawar *et al.* 2009)	Plant
97	OPG-04	AGCGTGTCTG	60	9	10	(Kawar *et al.* 2009)	Plant
98	OPG-05	CTGAGACGGA	60	10	10	(Kawar *et al.* 2009)	Plant
99	OPG-08	TCACGTCCAC	60	7	10	(Kawar *et al.* 2009)	Plant
100	OPG-09	CTGACGTCAC	60	3	10	(Kawar *et al.* 2009)	Plant
101	OPG-11	TGCCCGTCGT	70	5	10	(Kawar *et al.* 2009)	Plant
102	OPG-12	CAGCTCACGA	60	7	10	(Kawar *et al.* 2009)	Plant
103	OPG-17	ACGACCGACA	60	7	10	(Kawar *et al.* 2009)	Plant
104	OPG-19	GTCAGGGCAA	60	9	10	(Kawar *et al.* 2009)	Plant
105	OPK-03	CCAGCTTAGG	60	10	10	(Kawar *et al.* 2009)	Plant
106	OPK-04	CCGCCCAAAC	70	7	10	(Kawar *et al.* 2009)	Plant
107	OPK-08	GAACACTGGG	60	6	10	(Kawar *et al.* 2009)	Plant
108	OPK-11	AATGCCCCAG	60	9	10	(Kawar *et al.* 2009)	Plant
109	OPK-15	CTCCTGCCAA	60	5	10	(Kawar *et al.* 2009)	Plant
110	OPK-17	CCCAGCTGTG	70	6	10	(Kawar *et al.* 2009)	Plant
111	OPK-19	CACAGGCGGA	70	6	10	(Kawar *et al.* 2009)	Plant
112	OPK-20	GTGTCGCGAG	70	9	10	(Kawar *et al.* 2009)	Plant
113	OPC-01	TTCGAGCCAG	60	5	10	(Vieira *et al*., 2003)	Plant
114	OPC-06	GAACGGACTC	60	9	10	(Vieira *et al*., 2003)	Plant
115	OPC-08	TGGACCGGTG	70	8	10	(Vieira *et al*., 2003)	Plant
116	OPC-13	AAGCCTCGTC	60	6	10	(Vieira *et al*., 2003)	Plant
117	OPG-02	GGCACTGAGG	70	11	10	(Vieira *et al*., 2003)	Plant
118	OPG-04	AGCGTGTCTG	60	8	10	(Vieira *et al*., 2003)	Plant
119	OPG-05	CTGAGACGGA	60	7	10	(Vieira *et al*., 2003)	Plant
120	OPG-10	AGGGCCGTCT	70	10	10	(Vieira *et al*., 2003)	Plant
121	OPG-13	CTCTCCGCCA	70	17	10	(Vieira *et al*., 2003)	Plant
122	OPG-14	GGATGAGACC	60	10	10	(Vieira *et al*., 2003)	Plant
123	OPG-19	GTCAGGGCAA	60	7	10	(Vieira *et al*., 2003)	Plant
124	OPA-01	CAGGCCCTTC	70	21	10	(Gauer and Cavalli-Molina 2000)	Plant
125	OPA-02	TGCCGAGCTG	70	25	10	(Gauer and Cavalli-Molina 2000)	Plant
126	OPF-01	ACGCATCCTG	60	25	10	(Gauer and Cavalli-Molina 2000)	Plant
127	OPF-03	CCTGATCACC	60	22	10	(Gauer and Cavalli-Molina 2000)	Plant
128	OPF-05	CCGAATTCCC	60	22	10	(Gauer and Cavalli-Molina 2000)	Plant
129	OPF-14	TGCTGCAGGT	60	27	10	(Gauer and Cavalli-Molina 2000)	Plant
130	OPH-03	AGACGTCCAC	60	20	10	(Gauer and Cavalli-Molina 2000)	Plant
131	OPH-04	GGAAGTCGCC	70	22	10	(Gauer and Cavalli-Molina 2000)	Plant

132	OPH-05	AGTCGTCCCC	70	28	10	(Gauer and Cavalli-Molina 2000)	Plant
133	OPH-08	GAAACACCCC	60	21	10	(Gauer and Cavalli-Molina 2000)	Plant
134	OPH-12	ACGCGCATGT	60	22	10	(Gauer and Cavalli-Molina 2000)	Plant
135	OPH-13	GACGCCACAC	70	27	10	(Gauer and Cavalli-Molina 2000)	Plant
136	OPH-15	AATGGCGCAG	60	24	10	(Gauer and Cavalli-Molina 2000)	Plant
137	OPH-18	GAATCGGCCA	60	19	10	(Gauer and Cavalli-Molina 2000)	Plant
138	OPH-19	CTGACCAGCC	70	16	10	(Gauer and Cavalli-Molina 2000)	Plant
139	OPC-08	TGGACCGGTG	70	4	10	(Sharifova *et al.* 2013)	Plant
140	OPC-09	CTCACCGTCC	70	3	10	(Sharifova *et al.* 2013)	Plant
141	OPB-17	AGGGAACGAG	60	4	10	(Sharifova *et al.* 2013)	Plant
142	OPB-18	CCACAGCAGT	60	5	10	(Sharifova *et al.* 2013)	Plant
143	OPV-19	GGGTGTGCAG	70	8	10	(Sharifova *et al.* 2013)	Plant
144	OPG-17	ACGACCGACA	60	2	10	(Sharifova *et al.* 2013)	Plant
145	OPX-2	TTCCGCCACC	70	7	10	(Datta *et al*., 2012)	Plant
146	OPX-3	TGGCGCAGTG	70	11	10	(Datta *et al*., 2012)	Plant
147	OPX-4	CCGCTACCGA	70	13	10	(Datta *et al*., 2012)	Plant
148	OPX-5	CCTTTCCCTC	60	3	10	(Datta *et al*., 2012)	Plant
149	OPX-6	ACGCCAGAGG	70	8	10	(Datta *et al*., 2012)	Plant
150	OPX-9	GGTCTGGTTG	60	9	10	(Datta *et al*., 2012)	Plant
151	OPX-11	GGAGCCTCAG	70	9	10	(Datta *et al*., 2012)	Plant
152	OPX-13	ACGGGAGCAA	60	6	10	(Datta *et al*., 2012)	Plant
153	OPX-15	CAGACAAGCC	60	7	10	(Datta *et al*., 2012)	Plant
154	OPX-19	TGGCAAGGCA	60	13	10	(Datta *et al*., 2012)	Plant
155	OPX-20	CCCAGCTAGA	60	6	10	(Datta *et al*., 2012)	Plant
156	OPD-2	GGACCCAACC	70	6	10	(Datta *et al*., 2012)	Plant
157	OPD-5	TGAGCGGACA	60	11	10	(Datta *et al*., 2012)	Plant
158	OPD-7	TTGGCACGGG	70	17	10	(Datta *et al*., 2012)	Plant
159	OPD-8	GTGTGCCCCA	70	7	10	(Datta *et al*., 2012)	Plant
160	OPD-11	AGCGCCATTG	60	11	10	(Datta *et al*., 2012)	Plant
161	OPD-13	GGGGTGACGA	70	6	10	(Datta *et al*., 2012)	Plant
162	OPD-18	GAGAGCCAAC	60	8	10	(Datta *et al*., 2012)	Plant
163	OPD-20	ACCCGGTCAC	70	14	10	(Datta *et al*., 2012)	Plant
164	OPI-2	GGAGGAGAGG	70	5	10	(Datta *et al*., 2012)	Plant
165	OPI-3	CAGAAGCCCA	60	4	10	(Datta *et al*., 2012)	Plant
166	OPI-4	CCGCCTAGTC	70	8	10	(Datta *et al*., 2012)	Plant
167	OPI-6	AAGGCGGCAG	70	6	10	(Datta *et al*., 2012)	Plant
168	OPI-9	TGGAGAGCAG	60	2	10	(Datta *et al*., 2012)	Plant
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176	OPI-18	TGCCCAGCCT	70	7	10	(Datta *et al*., 2012)	Plant
177	OPF-1	ACGGATCCTG	60	7	10	(Datta *et al*., 2012)	Plant
178	OPA-1	CAGGCCCTTC	70	9	10	(Kumar *et al*., 2001)	Plant
179	OPA-20	GTTGCGATCC	60	12	10	(Kumar *et al*., 2001)	Plant
180	OPB-1	GTTTCGCTCC	60	12	10	(Kumar *et al*., 2001)	Plant
181	OPB-18	CCACAGCAGT	60	10	10	(Kumar *et al*., 2001)	Plant
182	OPC-11	AAAGCTGCGG	60	18	10	(Kumar *et al*., 2001)	Plant
183	OPC-12	TGTCATCCCC	60	12	10	(Kumar *et al*., 2001)	Plant
184	OPC-20	ACTTCGCCAC	60	17	10	(Kumar *et al*., 2001)	Plant
185	OPD-1	ACCGCGAAGG	70	14	10	(Kumar *et al*., 2001)	Plant
186	OPD-6	ACCTGAACGG	60	17	10	(Kumar *et al*., 2001)	Plant
187	OPD-7	TTGGCACGGG	70	18	10	(Kumar *et al*., 2001)	Plant
188	OPG-01	CTACGGAGGA	60	6	10	(Srivastava *et al*., 2011)	Plant
189	OPG-02	GGCACTGAGG	60	6	10	(Srivastava *et al*., 2011)	Plant
190	OPG-03	GAGCCCTCCA	70	3	10	(Srivastava *et al*., 2011)	Plant
191	OPG-04	AGCGTGTCTG	60	11	10	(Srivastava *et al*., 2011)	Plant
192	OPG-05	CTGAGACGCA	60	11	10	(Srivastava *et al*., 2011)	Plant
193	OPH-01	GGTCGGAGAA	60	10	10	(Srivastava *et al*., 2011)	Plant
194	OPH-02	TCGGACGTGA	60	12	10	(Srivastava *et al*., 2011)	Plant
195	OPH-03	AGACGTCCAC	60	4	10	(Srivastava *et al*., 2011)	Plant
196	OPH-04	GGAAGTCGCC	70	11	10	(Srivastava *et al*., 2011)	Plant
197	OPH-05	AGTCCTCCCC	70	11	10	(Srivastava *et al*., 2011)	Plant
198	OPI-01	ACCTGGACAC	60	9	10	(Srivastava *et al*., 2011)	Plant
199	OPI-02	GGAGGAGAGG	70	4	10	(Srivastava *et al*., 2011)	Plant
200	OPI-03	CAGAAGCCCA	60	9	10	(Srivastava *et al*., 2011)	Plant
201	OPI-04	CCGCCTAGTC	70	10	10	(Srivastava *et al*., 2011)	Plant
202	OPI-05	TGTTCCACGG	60	8	10	(Srivastava *et al*., 2011)	Plant
203	OPP-01	GTAGCACTCC	60	9	10	(Srivastava *et al*., 2011)	Plant
204	OPP-02	TCGGCACGCA	70	9	10	(Srivastava *et al*., 2011)	Plant
205	OPP-03	CTGATACGCC	60	12	10	(Srivastava *et al*., 2011)	Plant
206	OPP-04	GTGTCTCAGG	60	12	10	(Srivastava *et al*., 2011)	Plant
207	OPP-05	CCCCGGTAAC	70	8	10	(Srivastava *et al*., 2011)	Plant
208	OPQ-01	GGGACGATGG	70	11	10	(Srivastava *et al*., 2011)	Plant
209	OPQ-02	TCTGTGGGTC	60	9	10	(Srivastava *et al*., 2011)	Plant
210	OPQ-03	GGTCACCTCA	60	9	10	(Srivastava *et al*., 2011)	Plant
211	OPQ-04	AGTGCGCTGA	60	11	10	(Srivastava *et al*., 2011)	Plant
212	OPQ-05	CCGCGTCTTG	70	10	10	(Srivastava *et al*., 2011)	Plant
213	OPR-01	TGCGGGTCCT	70	9	10	(Srivastava *et al*., 2011)	Plant
214	OPR-02	CACAGCTGCC	70	10	10	(Srivastava *et al*., 2011)	Plant

215	OPR-03	ACACAGAGGG	60	8	10	(Srivastava *et al*., 2011)	Plant
216	OPR-04	CCCGTAGCAC	70	6	10	(Srivastava *et al*., 2011)	Plant
217	OPR-05	GACCTAGCAC	60	7	10	(Srivastava *et al*., 2011)	Plant
218	OPS-01	CTACTGCGCT	60	6	10	(Srivastava *et al*., 2011)	Plant
219	OPS-02	CCTCTGACTG	60	3	10	(Srivastava *et al*., 2011)	Plant
220	OPS-03	CACAGGTCCC	70	3	10	(Srivastava *et al*., 2011)	Plant
221	OPS-04	CACCCCCTTG	70	10	10	(Srivastava *et al*., 2011)	Plant
222	OPS-05	TTTGGGGCCT	60	6	10	(Srivastava *et al*., 2011)	Plant
223	OPT-01	GGGCCACTCA	70	10	10	(Srivastava *et al*., 2011)	Plant
224	OPT-02	GGAGAGACTC	60	14	10	(Srivastava *et al*., 2011)	Plant
225	OPT-03	TCCACTCCTG	60	3	10	(Srivastava *et al*., 2011)	Plant
226	OPT-04	CACAGAGGGA	60	9	10	(Srivastava *et al*., 2011)	Plant
227	OPT-05	GGGTTTGGCA	60	12	10	(Srivastava *et al*., 2011)	Plant
228	OPA-02	TGCCGAGCTG	70	9	10	Gajera *et al.* (2010)	Plant
229	OPA-03	AGTCAGCCAC	60	12	10	(Gajera *et al.* 2010)	Plant
230	OPA-13	CAGCACCCAC	70	10	10	(Gajera *et al.* 2010)	Plant
231	OPA-15	TTCCGAACCC	60	10	10	(Gajera *et al.* 2010)	Plant
232	OPA-18	AGGTGACCGT	60	6	10	(Gajera *et al.* 2010)	Plant
233	OPB-01	GTTTCGCTCC	60	6	10	(Gajera *et al.* 2010)	Plant
234	OPB-08	GTCCACACGG	70	8	10	(Gajera *et al.* 2010)	Plant
235	OPD-02	GGACCCAACC	70	11	10	(Gajera *et al.* 2010)	Plant
236	OPD-07	TTGGCACGGG	70	10	10	(Gajera *et al.* 2010)	Plant
237	OPD-08	GTGTGCCCCA	70	8	10	(Gajera *et al.* 2010)	Plant
238	OPD-11	AGCGCCATTG	60	6	10	(Gajera *et al.* 2010)	Plant
239	OPD-13	GGGGTGACGA	70	10	10	(Gajera *et al.* 2010)	Plant
240	OPE-03	CCAGATGCAC	60	8	10	(Gajera *et al.* 2010)	Plant
241	OPE-07	AGATGCAGCC	60	9	10	(Gajera *et al.* 2010)	Plant
242	OPE-14	TGCGGCTGAG	70	6	10	(Gajera *et al.* 2010)	Plant
243	OPE-15	ACGCACCAAC	60	7	10	(Gajera *et al.* 2010)	Plant
244	OPE-16	GGTGACTGTG	60	7	10	(Gajera *et al.* 2010)	Plant
245	OPF-10	GGAAGCTTCG	60	8	10	(Gajera *et al.* 2010)	Plant
246	OPF-13	GGCTGCACAA	60	10	10	(Gajera *et al.* 2010)	Plant
247	OPF-14	TGCTGCAGCT	60	11	10	(Gajera *et al.* 2010)	Plant
248	OPH-13	GACGCCAGGT	70	7	10	(Gajera *et al.* 2010)	Plant
249	SIGMA-D-O1	AAAACGCCGC	60	8	10	(Gajera *et al.* 2010)	Plant
250	SIGMA-D-14	TCTCGCTCCA	60	8	10	(Gajera *et al.* 2010)	Plant
251	SIGMA-D-19	CCCGCCTTTA	60	8	10	(Gajera *et al.* 2010)	Plant
252	SIGMA-D-B	TGCCGAGCTG	70	11	10	(Gajera *et al.* 2010)	Plant
253	SIGMA-D-I	CAGCACCCAC	70	7	10	(Gajera *et al.* 2010)	Plant
254	SIGMA-D-O	GTGAGGCGTC	70	8	10	(Gajera *et al.* 2010)	Plant
255	SIGMA-D-P	TGGACCGGTG	70	10	10	(Gajera *et al.* 2010)	Plant
256	SIGMA-D-U	AGGACCGGTG	70	10	10	(Gajera *et al.* 2010)	Plant
257	SIGMA-D-W	ACGCACACCC	60	8	10	(Gajera *et al.* 2010)	Plant

258	OPB-01	GTTTCGCTCC	60	9	10	(Bahurupe *et al.* 2013)	Plant
259	OPB-04	GGACTGGAGT	60	7	10	(Bahurupe *et al.* 2013)	Plant
260	OPB-05	TGCGCCCTTC	70	7	10	(Bahurupe *et al.* 2013)	Plant
261	OPB-07	GGTGACGCAG	70	7	10	(Bahurupe *et al.* 2013)	Plant
262	OPB-08	GTCCACACGG	70	6	10	(Bahurupe *et al.* 2013)	Plant
263	OPB-10	CTGCTGGGAC	70	5	10	(Bahurupe *et al.* 2013)	Plant
264	OPB-12	CCTTGACGCA	60	6	10	(Bahurupe *et al.* 2013)	Plant
265	OPB-14	TCCGCTCTGG	70	7	10	(Bahurupe *et al.* 2013)	Plant
266	OPB-15	GGAGGGTGTT	60	9	10	(Bahurupe *et al.* 2013)	Plant
267	IDT E 5	TCAGGGAGGT	60	14	10	(Pamidimarri *et al.*, 2009)	Plant
268	IDT E 12	TTATCGCCCC	60	21	10	(Pamidimarri *et al.*, 2009)	Plant
269	IDT E 4	GTGACATGCC	60	16	10	(Pamidimarri *et al.*, 2009)	Plant
270	IDT E 7	AGATGCAGCC	60	17	10	(Pamidimarri *et al.*, 2009)	Plant
271	IDT E 18	GGACTGCAGA	60	12	10	(Pamidimarri *et al.*, 2009)	Plant
272	OPJ-13	CCACACATAC	50	11	10	(Pamidimarri *et al.*, 2009)	Plant
273	OPJ-20	AAGCGGCCTC	70	16	10	(Pamidimarri *et al.*, 2009)	Plant
274	OPL-5	ACGCAGGCAC	70	10	10	(Pamidimarri *et al.*, 2009)	Plant
275	OPN-4	GACCGACCCA	70	10	10	(Pamidimarri *et al.*, 2009)	Plant
276	OPN-7	CAGCCCAGAG	70	4	10	(Pamidimarri *et al.*, 2009)	Plant
277	OPN-8	ACCTCAGCTC	60	7	10	(Pamidimarri *et al.*, 2009)	Plant
278	OPN-12	CACAGACACC	60	10	10	(Pamidimarri *et al.*, 2009)	Plant
279	OPN-14	TCGTGCGGGT	70	11	10	(Pamidimarri *et al.*, 2009)	Plant
280	OPN-16	AAGCGACCTG	60	12	10	(Pamidimarri *et al.*, 2009)	Plant
281	OPN-19	GTCCGTACTG	60	8	10	(Pamidimarri *et al.*, 2009)	Plant
282	OPN-20	GGTGCTCCGT	70	10	10	(Pamidimarri *et al.*, 2009)	Plant
283	OPO-2	ACGTAGCGTC	60	5	10	(Pamidimarri *et al.*, 2009)	Plant
284	OPO-5	CCCAGTCACT	60	9	10	(Pamidimarri *et al.*, 2009)	Plant
285	OPO-18	CTCGCTATCC	60	8	10	(Pamidimarri *et al.*, 2009)	Plant
286	OPO-19	GGTGCACGTT	60	9	10	(Pamidimarri *et al.*, 2009)	Plant
287	OPO-20	GGTGCACGTT	60	6	10	(Pamidimarri *et al.*, 2009)	Plant
288	OPP-2	TCGGCACGCA	70	6	10	(Pamidimarri *et al.*, 2009)	Plant
289	OPP-6	GTGGGCTGAC	70	6	10	(Pamidimarri *et al.*, 2009)	Plant

290	OPP-14	CCAGCCGAAC	70	4	10	(Pamidimarri *et al.*, 2009)	Plant
291	OPP-15	GGAAGCCAAC	60	7	10	(Pamidimarri *et al.*, 2009)	Plant
292	OPQ-7	CCCCGATGGT	70	10	10	(Pamidimarri *et al.*, 2009)	Plant
293	OPQ-9	GGCTAACCGA	60	14	10	(Pamidimarri *et al.*, 2009)	Plant
294	OPQ-15	GGGTAACGTG	60	6	10	(Pamidimarri *et al.*, 2009)	Plant
295	OPQ-2	TCTGTCGGTC	60	7	10	(Pamidimarri *et al.*, 2009)	Plant
296	OPA-03	AGTCAGCCAC	60	7	10	(Deshwal *et al.*, 2005)	Plant
297	OPA-10	GTGATCGCAG	60	5	10	(Deshwal *et al.*, 2005)	Plant
298	OPA-17	GACCGCTTGT	60	6	10	(Deshwal *et al.*, 2005)	Plant
299	OPA-18	AGGTGACCGT	60	5	10	(Deshwal *et al.*, 2005)	Plant
300	OPA-19	CAAACGTCGG	60	7	10	(Deshwal *et al.*, 2005)	Plant
301	OPB-5	TGCGCCCTTC	70	6	10	(Deshwal *et al.*, 2005)	Plant
302	OPC-6	GAACGGACTC	60	3	10	(Deshwal *et al.*, 2005)	Plant
303	OPC-8	TGGACCGGTG	70	7	10	(Deshwal *et al.*, 2005)	Plant
304	OPC-13	AAGCCTCGTC	60	4	10	(Deshwal *et al.*, 2005)	Plant
305	OPC-20	ACTTCGCCAC	60	4	10	(Deshwal *et al.*, 2005)	Plant
306	OPG-13	CTCTCCGCCA	70	5	10	(Deshwal *et al.*, 2005)	Plant
307	OPG-18	GGCTCATGTG	60	6	10	(Deshwal *et al.*, 2005)	Plant
308	OPI-3	CAGAAGCCCA	60	3	10	(Deshwal *et al.*, 2005)	Plant
309	OPI-10	ACAACGCGAG	60	5	10	(Deshwal *et al.*, 2005)	Plant
310	OPP-09	GTGGTCCGCA	70	12	10	(Padmesh *et al.*, 2006)	Plant
311	OPP-11	AACGCGTCGG	70	9	10	(Padmesh *et al.*, 2006)	Plant
312	OPP-13	GGAGTGCCTC	70	4	10	(Padmesh *et al.*, 2006)	Plant
313	C66	GAACGGACTC	60	8	10	(Padmesh *et al.*, 2006)	Plant
314	C67	GTCCCGACGA	70	5	10	(Padmesh *et al.*, 2006)	Plant
315	C68	TGGACCGGTG	70	9	10	(Padmesh *et al.*, 2006)	Plant
316	C69	CTCACCGTCC	70	8	10	(Padmesh *et al.*, 2006)	Plant
317	C70	TGTCTGGGTG	60	8	10	(Padmesh *et al.*, 2006)	Plant
318	C71	AAAGCTGCGG	60	8	10	(Padmesh *et al.*, 2006)	Plant
319	C72	TGTCATCCCC	60	5	10	(Padmesh *et al.*, 2006)	Plant
320	C73	AAGCCTCGTC	60	5	10	(Padmesh *et al.*, 2006)	Plant
321	C74	TGCGTGCTTG	60	5	10	(Padmesh *et al.*, 2006)	Plant
322	C75	GACGGATCAG	60	6	10	(Padmesh *et al.*, 2006)	Plant
323	C76	CACACTCCAG	60	4	10	(Padmesh *et al.*, 2006)	Plant
324	C77	TTCCCCCCAG	70	5	10	(Padmesh *et al.*, 2006)	Plant
325	OPA-02	TGCCGAGCTG	70	11	10	(Akbar *et al.*, 2011)	Plant
326	OPA-03	AGTCAGCCAC	60	5	10	(Akbar *et al.*, 2011)	Plant
327	OPA-04	AATCGGGCTG	60	11	10	(Akbar *et al.*, 2011)	Plant
328	OPA-09	GGGTAACGCC	70	17	10	(Akbar *et al.*, 2011)	Plant
329	OPA-10	GTGATCGCAG	60	12	10	(Akbar *et al.*, 2011)	Plant

330	OPA-16	AGCCAGCGAA	60	6	10	(Akbar *et al.*, 2011)	Plant
331	OPA-18	AGGTGACCGT	60	11	10	(Akbar *et al.*, 2011)	Plant
332	OPB-03	CATCCCCCTG	70	7	10	(Akbar *et al.*, 2011)	Plant
333	OPD-08	GTGTGCCCCA	70	7	10	(Akbar *et al.*, 2011)	Plant
334	OPK-04	CCGCCCAAAC	70	7	10	(Akbar *et al.*, 2011)	Plant
335	OPA-02	TGCCGAGCTG	70	9	10	(Iqbal. *et al.* 2010)	Plant
336	OPA-03	AGTCAGCCAC	60	6	10	(Iqbal. *et al.* 2010)	Plant
337	OPA-05	AGGGGTCTTG	60	7	10	(Iqbal. *et al.* 2010)	Plant
338	OPA-06	GGTCCCTGAC	70	6	10	(Iqbal. *et al.* 2010)	Plant
339	OPA-07	GAAACGGGTG	60	11	10	(Iqbal. *et al.* 2010)	Plant
340	OPA-08	GTGACGTAGG	60	8	10	(Iqbal. *et al.* 2010)	Plant
341	OPA-09	GGGTAACGCC	70	6	10	(Iqbal. *et al.* 2010)	Plant
342	OPA-10	GTGATCGCAG	60	3	10	(Iqbal. *et al.* 2010)	Plant
343	OPB-01	GTTTCGCTCC	60	7	10	(Iqbal. *et al.* 2010)	Plant
344	OPB-02	TGATCCCTGG	60	9	10	(Iqbal. *et al.* 2010)	Plant
345	OPB-03	CATCCCCCTG	70	5	10	(Iqbal. *et al.* 2010)	Plant
346	OPB-04	GGACTGGAGT	60	6	10	(Iqbal. *et al.* 2010)	Plant
347	OPB-05	TGCGCCCTTC	70	6	10	(Iqbal. *et al.* 2010)	Plant
348	OPB-06	TGCTCTGCCC	70	5	10	(Iqbal. *et al.* 2010)	Plant
349	OPC-18	TGAGTGGGTG	60	11	10	(Iqbal. *et al.* 2010)	Plant
350	OPD-02	GGACCCAACC	70	9	10	(Iqbal. *et al.* 2010)	Plant
351	OPD-04	TCTGGTGAGG	60	5	10	(Iqbal. *et al.* 2010)	Plant
352	OPD-05	TGAGCGGACA	60	8	10	(Iqbal. *et al.* 2010)	Plant
353	OPD-07	TTGGCACGGG	70	5	10	(Iqbal. *et al.* 2010)	Plant
354	OPD-08	GTGTGCCCCA	70	9	10	(Iqbal. *et al.* 2010)	Plant
355	OPD-10	GGTCTACACC	60	7	10	(Iqbal. *et al.* 2010)	Plant
356	OPD-11	AGCGCCATTG	60	4	10	(Iqbal. *et al.* 2010)	Plant
357	OPD-12	CACCGTATCC	60	9	10	(Iqbal. *et al.* 2010)	Plant
358	OPD-13	GGGGTGACGA	70	6	10	(Iqbal. *et al.* 2010)	Plant
359	OPD-14	CTTCCCCAAG	60	9	10	(Iqbal. *et al.* 2010)	Plant
360	OPD-17	TTTCCCACGG	60	5	10	(Iqbal. *et al.* 2010)	Plant
361	OPD-18	GAGAGCCAAC	60	5	10	(Iqbal. *et al.* 2010)	Plant
362	OPD-19	CTGGGGACTT	60	9	10	(Iqbal. *et al.* 2010)	Plant
363	OPD-20	ACCCGGTCAC	70	11	10	(Iqbal. *et al.* 2010)	Plant
364	OPE-01	CCCAAGGTCC	70	11	10	(Iqbal. *et al.* 2010)	Plant
365	OPE-02	GGTGCGGGAA	70	9	10	(Iqbal. *et al.* 2010)	Plant
366	OPE-04	GTGACATGCC	60	9	10	(Iqbal. *et al.* 2010)	Plant
367	OPE-05	TCAGGGAGGT	60	12	10	(Iqbal. *et al.* 2010)	Plant
368	OPE-06	AAGACCCCTC	60	9	10	(Iqbal. *et al.* 2010)	Plant
369	OPE-07	AGATGCAGCC	60	7	10	(Iqbal. *et al.* 2010)	Plant
370	OPE-08	TCACCACGGT	60	8	10	(Iqbal. *et al.* 2010)	Plant
371	OPE-09	CTTCACCCGA	60	6	10	(Iqbal. *et al.* 2010)	Plant
372	OPE-10	CACCAGGTGA	60	4	10	(Iqbal. *et al.* 2010)	Plant

373	OPE-12	TTATCGCCCC	60	7	10	(Iqbal. *et al.* 2010)	Plant
374	OPE-13	CCCGATTCGG	70	3	10	(Iqbal. *et al.* 2010)	Plant
375	OPE-15	ACGCACAACC	60	6	10	(Iqbal. *et al.* 2010)	Plant
376	OPE-17	CTACTGCCGT	60	10	10	(Iqbal. *et al.* 2010)	Plant
377	OPE-19	ACGGCGTATG	60	11	10	(Iqbal. *et al.* 2010)	Plant
378	OPE-20	AACGGTGACC	60	10	10	(Iqbal. *et al.* 2010)	Plant
379	A02	TGCCGAGCTG	70	3	10	(Ferriol *et al.* 2003)	Plant
380	A03	AGTCAGCCAC	60	10	10	(Ferriol *et al.* 2003)	Plant
381	A08	GTGACGTAGG	60	2	10	(Ferriol *et al.* 2003)	Plant
382	A10	GTGATCGCAG	60	2	10	(Ferriol *et al.* 2003)	Plant
383	A20	GTTGCGATCC	60	4	10	(Ferriol *et al.* 2003)	Plant
384	B17	AGGGAACGAG	60	5	10	(Ferriol *et al.* 2003)	Plant
385	287	CGAACGGCGG	80	4	10	(Ferriol *et al.* 2003)	Plant
386	W13	CACAGCGACA	60	6	10	(Ferriol *et al.* 2003)	Plant
387	AB23	CCAGATGCAG	60	4	10	(Ferriol *et al.* 2003)	Plant
388	AB24	GTGACATCCC	60	7	10	(Ferriol *et al.* 2003)	Plant
389	AB27	AGATGCAGCC	60	2	10	(Ferriol *et al.* 2003)	Plant
390	AB28	TCACCACGGT	60	3	10	(Ferriol *et al.* 2003)	Plant
391	AB29	CTTCACCCGA	60	5	10	(Ferriol *et al.* 2003)	Plant
392	AB211	GAGTCTCAGG	60	3	10	(Ferriol *et al.* 2003)	Plant
393	AB212	TTATCGCCCC	60	3	10	(Ferriol *et al.* 2003)	Plant
394	AB214	TGCGGCTGAG	70	3	10	(Ferriol *et al.* 2003)	Plant
395	AB215	ACGCACAACC	60	6	10	(Ferriol *et al.* 2003)	Plant
396	AB216	GGTGACTGTG	60	10	10	(Ferriol *et al.* 2003)	Plant
397	AB217	CTACTGCCGT	60	4	10	(Ferriol *et al.* 2003)	Plant
398	AB218	GGACTGCAGA	60	4	10	(Ferriol *et al.* 2003)	Plant
399	AB219	ACGGCGTATG	60	2	10	(Ferriol *et al.* 2003)	Plant
400	OPD-3	GTCGCCGTCA	70	4	10	(Sedra *et al.* 1998)	Plant
401	OPD-4	TCTGGTGAGG	60	2	10	(Sedra *et al.* 1998)	Plant
402	OPD-10	GGTCTACACC	60	2	10	(Sedra *et al.* 1998)	Plant
403	OPD-12	CACCGTATCC	60	5	10	(Sedra *et al.* 1998)	Plant
404	OPD-15	CATCCGTGCT	60	2	10	(Sedra *et al.* 1998)	Plant
405	OPD-16	AGGGCGTAAG	60	3	10	(Sedra *et al.* 1998)	Plant
406	OPD-19	CTGGGGACTT	60	2	10	(Sedra *et al.* 1998)	Plant
407	OPJ-4	CCGAACACGG	70	2	10	(Sedra *et al.* 1998)	Plant
408	OPJ-5	CTCCATGGGG	70	3	10	(Sedra *et al.* 1998)	Plant
409	OPJ-13	CCACACTACC	60	3	10	(Sedra *et al.* 1998)	Plant
410	OPJ-14	CACCCGGATG	70	4	10	(Sedra *et al.* 1998)	Plant
411	OPJ-18	TGGTCGCAGA	60	2	10	(Sedra *et al.* 1998)	Plant
412	OPJ-19	GGACACCACT	60	4	10	(Sedra *et al.* 1998)	Plant
413	OPL-6	GAGGGAAGAG	60	5	10	(Sedra *et al.* 1998)	Plant
414	OPM-5	GGGAACGTGT	60	2	10	(Sedra *et al.* 1998)	Plant
415	OPM-11	GTCCACTGTG	60	6	10	(Sedra *et al.* 1998)	Plant

416	OPN-1	CTCACGTTGG	60	2	10	(Sedra *et al.* 1998)	Plant
417	OPN-12	CACAGAGACC	60	1	10	(Sedra *et al.* 1998)	Plant
418	OPX-4	CCGCTACCGA	70	2	10	(Sedra *et al.* 1998)	Plant
419	OPA-05	AGGGGTCTTG	60	21	10	(Karishaloo*et al.* 2003)	Plant
420	OPA-07	GAAACGGGTG	60	14	10	(Karishaloo*et al.* 2003)	Plant
421	OPA-11	CAATCGCCGT	60	13	10	(Karishaloo*et al.* 2003)	Plant
422	OPA-12	TCGGCGATAG	60	17	10	(Karishaloo*et al.* 2003)	Plant
423	OPA-14	TCTGTGCTGG	60	12	10	(Karishaloo*et al.* 2003)	Plant
424	OPA-15	TTCCGAACCC	60	9	10	(Karishaloo*et al.* 2003)	Plant
425	OPA-16	TTCCGAACCC	60	15	10	(Karishaloo*et al.* 2003)	Plant
426	OPA-17	GACCGCTTGT	60	8	10	(Karishaloo*et al.* 2003)	Plant
427	OPA-18	AGGTGACCGT	60	12	10	(Karishaloo*et al.* 2003)	Plant
428	OPA-19	CAACGTCGG	60	12	10	(Karishaloo*et al.* 2003)	Plant
429	OPA-20	GTTGCGATCC	60	15	10	(Karishaloo*et al.* 2003)	Plant
430	OPB-10	CTGCTGGGAC	70	15	10	(Karishaloo*et al.* 2003)	Plant
431	OPB-20	GGACCCTTAC	60	16	10	(Karishaloo*et al.* 2003)	Plant
432	OPE-12	TTATCGCCCC	60	17	10	(Karishaloo*et al.* 2003)	Plant
433	OPF-09	CCAAGCTTCC	60	18	10	(Karishaloo*et al.* 2003)	Plant
434	OPF-15	CCAGTACTCC	60	7	10	(Karishaloo*et al.* 2003)	Plant
435	OPG-05	CTGAGACGGA	60	15	10	(Karishaloo*et al.* 2003)	Plant
436	OPG-11	TGCCCGTCGT	70	17	10	(Karishaloo*et al.* 2003)	Plant
437	OPH-20	GGGAGACATC	60	15	10	(Karishaloo*et al.* 2003)	Plant
438	OPI-19	AATGCGGGAG	60	4	10	(Karishaloo*et al.* 2003)	Plant
439	OPJ-06	TCGTTCCGCA	60	7	10	(Karishaloo*et al.* 2003)	Plant
440	OPK-10	GTGCAACGTG	60	6	10	(Karishaloo*et al.* 2003)	Plant
441	OPM-12	GGGACGTTGG	70	16	10	(Karishaloo*et al.* 2003)	Plant
442	OPW-11	GTGATGCGTG	60	13	10	(Karishaloo*et al.* 2003)	Plant
443	K1	TTGGCGGCCT	70	9	10	(Ercan *et al*., 2004)	Plant
444	K2	ACCTCGCCAC	70	18	10	(Ercan *et al*., 2004)	Plant
445	K4	TGCTGGTTCC	60	10	10	(Ercan *et al*., 2004)	Plant
446	K6	CTGCGCTGGA	70	10	10	(Ercan *et al*., 2004)	Plant
447	K8	GAGGTCCACA	60	14	10	(Ercan *et al*., 2004)	Plant
448	K9	GTCAGTGCGG	70	9	10	(Ercan *et al*., 2004)	Plant
449	K11	AGACCCAGAG	60	8	10	(Ercan *et al*., 2004)	Plant
450	OLP 6	GAGGGAAGAG	60	4	10	(Zare *et al*., 2019)	Bacteria
451	OLP 11	ACGATGAGCC	60	5	10	(Zare *et al*., 2019)	Bacteria
452	OLP 13	ACCGCCTGCT	70	15	10	(Zare *et al*., 2019)	Bacteria
453	A	AGCAGCGTGG	70	15	10	(Cocconcelli *et al*., 1995)	Bacteria
454	OPE-14	TCGGGCTGAG	70	11	10	(Araújo *et al*., 2004)	Bacteria
455	OPE-19	ACGGCGTATG	60	11	10	(Araújo *et al*., 2004)	Bacteria
456	OPE-20	AACGGTGACC	60	10	10	(Araújo *et al*., 2004)	Bacteria
457	OPX-09	GGTCTGGTTG	60	11	10	(Araújo *et al*., 2004)	Bacteria
458	OPX-16	CTCTGTTCGG	60	11	10	(Araújo *et al*., 2004)	Bacteria

459	OPE-12	TTATCGCCCC	60	10	10	(Araújo *et al*., 2004)	Bacteria
460	OPX-18	TGGCAAGGCA	60	10	10	(Araújo *et al*., 2004)	Bacteria
461	P1254	CCGCAGCCAA	70	8	10	(Madadgar *et al*., 2008)	Bacteria
462	23L	CCGAAGCTGC	70	8	10	(Betancor *et al*., 2004)	Bacteria
463	OPB-17	AGGGAACGAG	60	7	10	(Betancor *et al*., 2004)	Bacteria
464	OPA-14	AATCGGGCTG	60	8	10	(Betancor *et al*., 2004)	Bacteria
465	OPB-15	CCAGGGTGTT	60	7	10	(Betancor *et al*., 2004)	Bacteria
466	P1	GGGTAACGCC	70	3	10	(Zameer *et. al*., 2015)	Bacteria
467	P2	CCCGTCAGCA	70	4	10	(Zameer *et. al*., 2015)	Bacteria
468	OPA-17	GACCGCTTGT	60	4	10	(Tompkins *et al*., 1996)	Bacteria
469	OPB-16	TTTGCCCGGA	60	4	10	(Tompkins *et al*., 1996)	Bacteria
470	OPE-05	TCAGGGAGGT	60	3	10	(Tompkins *et al*., 1996)	Bacteria
471	OPA-17	GACCGCTTGT	60	7	10	(Saxena *et al*., 2014)	Bacteria
472	OPN-02	ACCAGGGGCA	70	12	10	(Saxena *et al*., 2014)	Bacteria
473	OPU	GGCTGGTTCC	70	11	10	(Saxena *et al*., 2014)	Bacteria
474	OPU-15	ACGGGCCAGT	70	9	10	(Saxena *et al*., 2014)	Bacteria
475	OPV-10	CAAACGTGGG	60	11	10	(Saxena *et al*., 2014)	Bacteria
476	OPV-14	GGTCGATCTG	60	16	10	(Saxena *et al*., 2014)	Bacteria
477	OPV-20	AGCCGTGAAA	50	14	10	(Saxena *et al*., 2014)	Bacteria
478	OPW-8	GACTGCCTCT	60	14	10	(Saxena *et al*., 2014)	Bacteria
479	OPW-11	CTGATGCGTG	60	14	10	(Saxena *et al*., 2014)	Bacteria
480	OPW-15	ACACCGGAAC	60	16	10	(Saxena *et al*., 2014)	Bacteria
481	OPW-20	TGTGGCAGCA	60	11	10	(Saxena *et al*., 2014)	Bacteria
482	OPX-20	TTCCGCCACC	70	14	10	(Saxena *et al*., 2014)	Bacteria
483	OPX-07	GAGCGAGGCT	70	10	10	(Saxena *et al*., 2014)	Bacteria
484	OPX-11	GGAGGCTGAG	70	14	10	(Saxena *et al*., 2014)	Bacteria
485	OPX-12	TCGCCAGCCA	70	15	10	(Saxena *et al*., 2014)	Bacteria
486	OPY-01	GTGGCATCTC	70	13	10	(Saxena *et al*., 2014)	Bacteria
487	OPY-10	CAAACGTGGG	60	6	10	(Saxena *et al*., 2014)	Bacteria
488	OPY-20	AGCCCTGGAA	60	15	10	(Saxena *et al*., 2014)	Bacteria
489	OPZ-01	TCTGTGCCAC	60	13	10	(Saxena *et al*., 2014)	Bacteria
490	OPZ-08	GGGTGGGTAA	60	14	10	(Saxena *et al*., 2014)	Bacteria
491	OPZ-10	CCGACAAACC	60	12	10	(Saxena *et al*., 2014)	Bacteria
492		AGCGGGCCAA	70	8	10	(Nanvazadeh *et al*.,2013)	Bacteria
493	1274	AAGAGGCCG	60	11	9	(Zahraei *et al*., 2008)	Bacteria
494	OP-C1	TTCGAGCCAG	60	14	10	(Shahaby *et al*., 2012)	Bacteria
495	OP-C6	GAACGGACTC	60	22	10	(Shahaby *et al*., 2012)	Bacteria
496	OP-C7	GTCCCGACGA	70	22	10	(Shahaby *et al*., 2012)	Bacteria
497	OP-C8	TGGACCGGG	70	18	9	(Shahaby *et al*., 2012)	Bacteria
498	OP-C9	CTCACCGTCC	70	18	10	(Shahaby *et al*., 2012)	Bacteria
499	OP-C10	TGTCTGGGTG	60	14	10	(Shahaby *et al*., 2012)	Bacteria
500	OP-D6	ACCTGAACGG	60	21	10	(Shahaby *et al*., 2012)	Bacteria
501	OP-D7	TTGGCACGG	60	18	9	(Shahaby *et al*., 2012)	Bacteria

502	OPD-D8	GTGTGCCCCA	70	21	10	(Shahaby *et al*., 2012)	Bacteria
503	1254	CCGCAGCCAA	70	11	10	(Akopyanz *et. al*., 1992)	Bacteria
504	1283	GCGATCCCCA	70	8	10	(Akopyanz *et. al*., 1992)	Bacteria
505	1247	AAGAGCCCGT	60	10	10	(Akopyanz *et. al*., 1992)	Bacteria
506	1281	AACGCGCAAC	60	10	10	(Akopyanz *et. al*., 1992)	Bacteria
507	1290	GTGGATGCGA	60	8	10	(Akopyanz *et. al*., 1992)	Bacteria
508	1253	GTTTCCGCCC	70	6	10	(Akopyanz *et. al*., 1992)	Bacteria
509	1252	GCGGAAATAG	50	5	10	(Akopyanz *et. al*., 1992)	Bacteria
510	1280	GAGGACAAAG	50	6	10	(Akopyanz *et. al*., 1992)	Bacteria
511	1288	GGGGTTGACC	70	4	10	(Akopyanz *et. al*., 1992)	Bacteria
512	1292	CCCGTCAGCA	70	2	10	(Akopyanz *et. al*., 1992)	Bacteria
513	1284	GTCAACGAAG	50	0	10	(Akopyanz *et. al*., 1992)	Bacteria
514	1285	AGCCAGTTTC	50	2	10	(Akopyanz *et. al*., 1992)	Bacteria
515	1287	CGCATAGGTT	50	3	10	(Akopyanz *et. al*., 1992)	Bacteria
516	1289	ACTTGCATCC	50	3	10	(Akopyanz *et. al*., 1992)	Bacteria
517	1248	TGCCGAATTC	50	3	10	(Akopyanz *et. al*., 1992)	Bacteria
518	1249	CGAACTAGAC	50	0	10	(Akopyanz *et. al*., 1992)	Bacteria
519	1250	GGCTTAACAC	50	2	10	(Akopyanz *et. al*., 1992)	Bacteria
520	1251	AAGACTGTCC	50	0	10	(Akopyanz *et. al*., 1992)	Bacteria
521	1255	CCGATCTAGA	50	3	10	(Akopyanz *et. al*., 1992)	Bacteria
522	1282	GACGACTATC	50	0	10	(Akopyanz *et. al*., 1992)	Bacteria
523	67AB1GO7	TTGGCACGGG	70	21	10	(Nishat *et. al*., 2015)	Bacteria
524	OPA 02	TGCCGAGCTG	70	15	10	(Nishat *et. al*., 2015)	Bacteria
525	OPB 08	GTCCACACGG	70	14	10	(Nishat *et. al*., 2015)	Bacteria
526	OPB 17	GACCGCTTGT	60	18	10	(Nishat *et. al*., 2015)	Bacteria
527	M1	GTTGGTGGCT	60	17	10	(Seppola *et. al*., 2006)	Bacteria
528	UBC-155	CTGGCGGCTG	80	16	10	(Seppola *et. al*., 2006)	Bacteria
529	OPC-08	CCCGTCAGCA	70	17	10	(Sadeghi *et al.,* 2012)	Fungi
530	OPC-19	GTAGACCCGT	60	38	10	(Sadeghi *et al.,* 2012)	Fungi
531	Cs1503	TGGACCGGTG	70	29	10	(Sadeghi *et al.,* 2012)	Fungi
532	P5	GAGTGGTGAC	60	28	10	(Sadeghi *et al.,* 2012)	Fungi
533	P6	CGGCCCACGT	80	19	10	(Sadeghi *et al.,* 2012)	Fungi
534	OPA-03	AGTCAGCCAC	60	16	10	(Bayraktar, 2010)	Fungi
535	OPA-04	AATCGGGCTG	60	11	10	(Bayraktar, 2010)	Fungi
536	OPB-18	CCACAGCAGT	60	13	10	(Bayraktar, 2010)	Fungi
537	OPE-01	CCCAAGGTCC	70	9	10	(Bayraktar, 2010)	Fungi
538	OPE-12	TTATCGCCCC	60	6	10	(Bayraktar, 2010)	Fungi
539	OPF-10	GGAAGCTTGG	60	8	10	(Bayraktar, 2010)	Fungi
540	OPF-12	ACGCTACCAG	60	12	10	(Bayraktar, 2010)	Fungi
541	OPH-02	TCGGACGTGA	60	9	10	(Bayraktar, 2010)	Fungi
542	OPH-05	AGTCGTCCCC	70	7	10	(Bayraktar, 2010)	Fungi
543	OPI-09	TGGAGAGCAG	60	9	10	(Bayraktar, 2010)	Fungi
544	OPK-12	TGGCCCTCAC	70	10	10	(Bayraktar, 2010)	Fungi

545	OPA 4	AATCGGGCTG	60	14	10	(Sahoo *et al*., *2011)*	Fungi
546	OPA 11	CAATCGCCGT	60	10	10	(Sahoo *et al*., *2011)*	Fungi
547	OPA 14	TCTGTGCTGG	60	14	10	(Sahoo *et al*., *2011)*	Fungi
548	OPC 8	TGGACCGGTG	70	16	10	(Sahoo *et al*., *2011)*	Fungi
549	OPC 11	AAAGCTGCGG	60	11	10	(Sahoo *et al*., *2011)*	Fungi
550	OPC 15	GACGGATCAG	60	12	10	(Sahoo *et al*., *2011)*	Fungi
551	OPC 19	GTTGCCAGCC	70	14	10	(Sahoo *et al*., *2011)*	Fungi
552	OPH 4	GGAAGTCGCC	70	9	10	(Sahoo *et al*., *2011)*	Fungi
553	OPH 8	GAAACACCCC	60	14	10	(Sahoo *et al*., *2011)*	Fungi
554	OPH 11	CTTCCGCAGT	60	11	10	(Sahoo *et al*., *2011)*	Fungi
555	OPH 15	AATGGCGCAG	60	13	10	(Sahoo *et al*., *2011)*	Fungi
556	OPY 2	CATCGCCGCA	70	14	10	(Sahoo *et al*., *2011)*	Fungi
557	OPY 20	AGCCGTGGAA	60	16	10	(Sahoo *et al*., *2011)*	Fungi
558	OPA 3	AGTCACCCAC	60	15	10	(Nath *et al.,*2012)	Fungi
559	OPA 17	GACCGCTTGT	60	13	10	(Nath *et al.,*2012)	Fungi
560	OPG 1	CTACGGAGGA	60	18	10	(Nath *et al.,*2012)	Fungi
561	OPG 8	TCACGTCCAC	60	14	10	(Nath *et al.,*2012)	Fungi
562	OPG 13	CTCTCCGCCA	70	15	10	(Nath *et al.,*2012)	Fungi
563	OPT 9	CACCCCTGAG	70	15	10	(Nath *et al.,*2012)	Fungi
564	OPT 11	TTCCCCGCCA	70	12	10	(Nath *et al.,*2012)	Fungi
565	OPT 15	GGATGCGACT	60	10	10	(Nath *et al.,*2012)	Fungi
566	91299	CGATTCGGCG	70	6	10	(Guo *et al*., 2003)	Fungi
567	X	GATAACGCAC	50	5	10	(Guo *et al*., 2003)	Fungi
568	Y	CGAGACACAC	60	12	10	(Guo *et al*., 2003)	Fungi
569	91300	CGAGGTTCGC	70	37	10	(Guo *et al*., 2003)	Fungi
570	OPR A-1	CAGGCCCTTC	70	9	10	(Guo *et al*., 2003)	Fungi
571	OPR A-3	AGTCAGCCAC	60	6	10	(Guo *et al*., 2003)	Fungi
572	OPR B-1	GTTTCGCTCC	60	14	10	(Guo *et al*., 2003)	Fungi
573	OPR B-2	TGATCCCTGG	60	37	10	(Guo *et al*., 2003)	Fungi
574	OPR B-4	GGACTGGAGT	60	9	10	(Guo *et al*., 2003)	Fungi
575	OPR B-5	TGCGCCCTTC	70	11	10	(Guo *et al*., 2003)	Fungi
576	OPR B-6	TGCTCTGCCC	70	8	10	(Guo *et al*., 2003)	Fungi
577	OPR B-7	GGTGACGCAG	70	11	10	(Guo *et al*., 2003)	Fungi
578	OPR B-8	GTCCACACGG	70	0	10	(Guo *et al*., 2003)	Fungi
579	OPR B-9	TGGGGGACTC	70	14	10	(Guo *et al*., 2003)	Fungi
580	OPR B-10	CTGCTGGGAC	70	14	10	(Guo *et al*., 2003)	Fungi
581	OPR B-11	GTAGACCCGT	60	58	10	(Guo *et al*., 2003)	Fungi
582	OPR B-12	CCTTGACGCA	60	0	10	(Guo *et al*., 2003)	Fungi
583	OPR B-13	TTCCCCCGCT	70	9	10	(Guo *et al*., 2003)	Fungi
584	OPR B-14	TCCGCTCTGG	70	9	10	(Guo *et al*., 2003)	Fungi
585	OPR B-15	GGAGGGTGTT	60	7	10	(Guo *et al*., 2003)	Fungi
586	OPR B-16	TTTGCCCGGA	60	5	10	(Guo *et al*., 2003)	Fungi
587	OPR B-17	AGGGAACGAG	60	9	10	(Guo *et al*., 2003)	Fungi

588	OPR B-18	CCACAGCAGT	60	9	10	(Guo *et al*., 2003)	Fungi
589	OPR B-19	ACCCCCGAAG	70	9	10	(Guo *et al*., 2003)	Fungi
590	OPR B-20	GGACCCTTAC	60	11	10	(Guo *et al*., 2003)	Fungi
591	OPA 03	AGT CAG CCA C	60	6	10	(Ciarmiello *et al*., 2015)	Insect
592	OPA 09	GGG TAA CGC C	70	25	10	(Ciarmiello *et al*., 2015)	Insect
593	OPB 12	CCT TGA CGC A	60	10	10	(Ciarmiello *et al*., 2015)	Insect
594	OPB 13	TTC CCC CGC T	70	28	10	(Ciarmiello *et al*., 2015)	Insect
595	OPC 20	ACT TCG CCA C	60	18	10	(Ciarmiello *et al*., 2015)	Insect
596	OPD 16	AGG GCG TAA G	60	7	10	(Ciarmiello *et al*., 2015)	Insect
597	OPE 20	AAC GGT GAC C	60	12	10	(Ciarmiello *et al*., 2015)	Insect
598	OPG 16	AGC GTC CTC C	70	8	10	(Ciarmiello *et al*., 2015)	Insect
599	OPH 11	CTT CCG CAG T	60	33	10	(Ciarmiello *et al*., 2015)	Insect
600	OPH 12	ACG CGC ATG T	60	13	10	(Ciarmiello *et al*., 2015)	Insect
601	OPM 06	CTG GGC AAC T	60	11	10	(Ciarmiello *et al*., 2015)	Insect
602	OPM 15	GAC CTA CCA C	60	24	10	(Ciarmiello *et al*., 2015)	Insect
603	OPM 16	GTA ACC AGC C	60	25	10	(Ciarmiello *et al*., 2015)	Insect
604	OPM 18	CAC CAT CCG T	60	9	10	(Ciarmiello *et al*., 2015)	Insect
605	ODP 01	GTA GCA CTC C	60	13	10	(Ciarmiello *et al*., 2015)	Insect
606	OPC 13	AAG CCT CGT C	60	36	10	(Ciarmiello *et al*., 2015)	Insect
607	OPB 2	TGA TCC CTG G	60	4	10	(Kamakshi *et al*., 2012)	Insect
608	OPB 7	GGT GAC GCA G	70	3	10	(Kamakshi *et al*., 2012)	Insect
609	OPB 17	GGA CCC TTA C	60	4	10	(Kamakshi *et al*., 2012)	Insect
610	OPB 20	AGG GAA CGA G	60	7	10	(Kamakshi *et al*., 2012)	Insect
611	OPJ 01	CCC GGC ATA A	60	10	10	(Moorthy *et al*., 2013)	Insect
612	OPJ 02	CCC GTT GGA	60	9	10	(Moorthy *et al*., 2013)	Insect
613	OPJ 03	TCT CCG CTT G	60	11	10	(Moorthy *et al*., 2013)	Insect
614	OPJ 04	CCG AAC ACC G	70	14	10	(Moorthy *et al*., 2013)	Insect
615	OPJ 05	CTC CAT GGG G	70	9	10	(Moorthy *et al*., 2013)	Insect
616	OPJ 06	TCG TTC CGC A	60	10	10	(Moorthy *et al*., 2013)	Insect
617	OPJ 07	CCT CTC GAC A	60	11	10	(Moorthy *et al*., 2013)	Insect
618	OPJ 08	CAT ACC GTG G	60	9	10	(Moorthy *et al*., 2013)	Insect
619	OPJ 09	TGA GCC TCA C	60	10	10	(Moorthy *et al*., 2013)	Insect
620	OPJ 10	AAG CCC GAG G	70	10	10	(Moorthy *et al*., 2013)	Insect
621	OPJ 11	ACT CCT GCG A	60	11	10	(Moorthy *et al*., 2013)	Insect
622	OPJ 12	GTC CCG TGG T	70	9	10	(Moorthy *et al*., 2013)	Insect
623	OPJ 13	CCA CAC TAC C	60	14	10	(Moorthy *et al*., 2013)	Insect
624	OPJ 14	CAC CCG GAT G	70	9	10	(Moorthy *et al*., 2013)	Insect
625	OPJ 15	TGT AGC AGG G	60	9	10	(Moorthy *et al*., 2013)	Insect
626	OPJ 16	CTG CTT AGG G	60	11	10	(Moorthy *et al*., 2013)	Insect
627	OPJ 17	ACG CCA GTT C	60	9	10	(Moorthy *et al*., 2013)	Insect
628	OPJ 18	TGG TCG CAG A	60	9	10	(Moorthy *et al*., 2013)	Insect
629	OPJ 19	GGA CAC CAC T	60	10	10	(Moorthy *et al*., 2013)	Insect
630	OPJ 20	AAG CGG CCT C	70	11	10	(Moorthy *et al*., 2013)	Insect

631	OPK 01	CAT TCG AGC C	60	9	10	(Moorthy *et al*., 2013)	Insect
632	OPK 02	GTC TCC GCA A	60	11	10	(Moorthy *et al*., 2013)	Insect
633	OPK 03	CCA GCT TAG G	60	10	10	(Moorthy *et al*., 2013)	Insect
634	OPK 04	CCG CCC AAA C	70	9	10	(Moorthy *et al*., 2013)	Insect
635	OPK 05	TCT GTC GAG G	60	10	10	(Moorthy *et al*., 2013)	Insect
636	OPK 06	CAC CTT TCC C	60	10	10	(Moorthy *et al*., 2013)	Insect
637	OPK 07	AGC GSG CAA G	60	11	10	(Moorthy *et al*., 2013)	Insect
638	0PK 08	GAA CAC TGG G	60	9	10	(Moorthy *et al*., 2013)	Insect
639	OPK 09	CCC TAC CGA C	70	9	10	(Moorthy *et al*., 2013)	Insect
640	OPK 10	GTG CAA CGT G	60	10	10	(Moorthy *et al*., 2013)	Insect
641	OPK 11	AAT GCC CCA G	60	12	10	(Moorthy *et al*., 2013)	Insect
642	OPK 12	TGG CCC TCA C	70	10	10	(Moorthy *et al*., 2013)	Insect
643	OPK 13	GGT TGT ACC C	60	9	10	(Moorthy *et al*., 2013)	Insect
644	OPK 14	CCC GCT ACA C	70	9	10	(Moorthy *et al*., 2013)	Insect
645	OPK 15	CTC CTG CCA A	60	9	10	(Moorthy *et al*., 2013)	Insect
646	OPK 16	GAG CGT CGA A	60	11	10	(Moorthy *et al*., 2013)	Insect
647	OPK 17	CCC AGC TGT G	70	10	10	(Moorthy *et al*., 2013)	Insect
648	OPK 18	CCT AGT CGA G	60	10	10	(Moorthy *et al*., 2013)	Insect
649	OPK 19	CAC AGG CGG A	70	9	10	(Moorthy *et al*., 2013)	Insect
650	OPK 20	GTG TCG CGA G	70	10	10	(Moorthy *et al*., 2013)	Insect
651	OPA 04	AAT CGG GCT G	60	12	10	(Belletti *et al.,*2008)	Insect
652	OPA 05	AGG GGT CTT G	60	10	10	(Belletti *et al.,*2008)	Insect
653	OPA 07	GAA ACG GGT G	60	14	10	(Belletti *et al.,*2008)	Insect
654	OPA 09	GGG TAA CGC C	70	8	10	(Belletti *et al.,*2008)	Insect
655	OPA 10	GTG ATC GCA G	60	8	10	(Belletti *et al.,*2008)	Insect
656	OPA 18	AGG TGA CCG T	60	12	10	(Belletti *et al.,*2008)	Insect
657	RAN-C 01	GAT GAC CGC C	70	9	10	(Anbalangan *et al.,* 2012)	Insect
658	RAN-C 02	GGC ACC ATT C	60	7	10	(Anbalangan *et al.,* 2012)	Insect
659	RAN-C 03	GGC ACG TAA C	60	7	10	(Anbalangan *et al.,* 2012)	Insect
660	RAN-C 04	GGC ATG ACC T	60	6	10	(Anbalangan *et al.,* 2012)	Insect
661	RAN-C 05	GGG TAA CGC C	70	5	10	(Anbalangan *et al.,* 2012)	Insect
662	RAN-C 06	GGT GCG CCT T	70	6	10	(Anbalangan *et al.,* 2012)	Insect
663	RAN-C 07	GTC AGA GTC G	60	5	10	(Anbalangan *et al.,* 2012)	Insect
664	RAN-C 08	GTC GCC GTC T	70	9	10	(Anbalangan *et al.,* 2012)	Insect
665	RAN-C 09	GTG CCA AAT G	50	5	10	(Anbalangan *et al.,* 2012)	Insect
666	RAN-C 10	GTG CCC GAT G	70	5	10	(Anbalangan *et al.,* 2012)	Insect
667	P1	GGT GCG GGA A	70	27	10	(Gadelhak and Enan, 2005)	Insect
668	P2	GTT TCG CTC C	60	25	10	(Gadelhak and Enan, 2005)	Insect
669	P3	GTA GAC CCG T	60	39	10	(Gadelhak and Enan, 2005)	Insect
670	P4	AAG AGC CCG T	60	61	10	(Gadelhak and Enan, 2005)	Insect
671	P5	AAC GCG CAA C	60	38	10	(Gadelhak and Enan, 2005)	Insect

672	P6	CCC GTC AGG A	70	35	10	(Gadelhak and Enan, 2005)	Insect
673	OPN-01	CTCACGTTGG	60	5	10	(Jain *et al*., 2015)	Virus
674	OPN-05	ACTGAACGCC	60	9	10	(Jain *et al*., 2015)	Virus
675	OPN-08	ACCTCAGCTC	60	3	10	(Jain *et al*., 2015)	Virus
676	OPN-09	TGCCGGCTTG	70	8	10	(Jain *et al*., 2015)	Virus
677	OPN-12	CACAGACACC	60	4	10	(Jain *et al*., 2015)	Virus
678	OPN-13	AGCGTCACTC	60	10	10	(Jain *et al*., 2015)	Virus
679	OPN-14	TCGTGCGGT	60	9	10	(Jain *et al*., 2015)	Virus
680	OPN-16	AAGCGACCTG	60	7	10	(Jain *et al*., 2015)	Virus
681	OPN-17	CATTGGGGAG	60	2	10	(Jain *et al*., 2015)	Virus
682	OPN-19	GTCCGTACTG	60	11	10	(Jain *et al*., 2015)	Virus
683	OPN-20	GGTGCTCCGT	70	12	10	(Jain *et al*., 2015)	Virus
684	OPQ-07	CCCCGATGGT	70	11	10	(Jain *et al*., 2015)	Virus
685	OPG-11	TCTCCGCAAC	60	6	10	(Jain *et al*., 2015)	Virus
686	OPQ-12	AGTAGGGCAC	60	6	10	(Jain *et al*., 2015)	Virus
687	OPQ-20	TCGCCCAGTC	70	12	10	(Jain *et al*., 2015)	Virus
688	F8	GGGATATCGG	60	96	10	(Brisse *et al.,* 2000)	Protozoa
689	N19	GTCCGTACTG	60	14	10	(Brisse *et al.,* 2000)	Protozoa
690	OPA-04	AATCGGGCTG	60	112	10	Cepicka *et al.,* (2005)	Protozoa
691	B13	TTCCCCCGCT	70	24	10	(Guo and Johnson, 1995	Protozoa
692	F6	GGGAATTCGG	60	23	10	(Guo and Johnson, 1995	Protozoa
693	UBC-703	CCCACAACCC	70	6	10	(Nath *et al.,* 2011)	Protozoa
694	UBC-704	GGGAGAAGGG	70	5	10	(Nath *et al.,* 2011)	Protozoa
695	UBC-707	GGAAGGAGGG	70	4	10	(Nath *et al.,* 2011)	Protozoa
696	UBC-708	GGTGGTTGGG	70	4	10	(Nath *et al.,* 2011)	Protozoa
697	UBC-710	CCCAACACCC	70	6	10	(Nath *et al.,* 2011)	Protozoa
698	UBC-712	GGGTTGTGGG	70	3	10	(Nath *et al.,* 2011)	Protozoa
699	UBC-713	GGTGGTGGGT	70	10	10	(Nath *et al.,* 2011)	Protozoa
700	UBC-714	GGGTGTGGGT	70	8	10	(Nath *et al.,* 2011)	Protozoa
701	UBC-717	CCCTCCCTCT	70	3	10	(Nath *et al.,* 2011)	Protozoa
702	UBC-718	GGGAGAGGGA	70	9	10	(Nath *et al.,* 2011)	Protozoa
703	OPN 21	CCCACACCCA	70	4	10	(Nath *et al.,* 2011)	Protozoa
704	OPN 22	GGGAGAGGGA	80	3	10	(Nath *et al.,* 2011)	Protozoa
705	OPD01	ACCGCGAACG	70	7	10	(Huh*et al*., 2006)	Algae
706	OPD02	CGACCCAACC	70	13	10	(Huh*et al*., 2006)	Algae
707	OPD03	GTCGCCGTCA	70	11	10	(Huh*et al*., 2006)	Algae
708	OPD04	TCTGGTGAGG	60	6	10	(Huh*et al*., 2006)	Algae
709	OPD05	TGAGCGGACA	60	12	10	(Huh*et al*., 2006)	Algae
710	OPD06	ACCTGAACGG	60	10	10	(Huh*et al*., 2006)	Algae
711	OPD07	TTGGCACGGG	70	8	10	(Huh*et al*., 2006)	Algae
712	OPD09	CTCTGGAGAC	60	7	10	(Huh*et al*., 2006)	Algae
713	OPD1	GGTCTACACC	60	10	10	(Huh*et al*., 2006)	Algae

714	P-2	ACAACTGCTC	50	8	10	(Gomez and Gonzalez, 2004)	Algae
715	P-3	TGACTGACGC	60	7	10	(Gomez and Gonzalez, 2004)	Algae
716	P-10	GCGATCCCCA	70	8	10	(Gomez and Gonzalez, 2004)	Algae
717	P-100	ATCGGGTCCG	70	5	10	(Gomez and Gonzalez, 2004)	Algae
718	OPA-01	CAGGCCCTTC	70	10	10	(Gomez and Gonzalez, 2004)	Algae
719	OPA-04	AATCGGGCTG	60	8	10	(Gomez and Gonzalez, 2004)	Algae
720	OPA-09	GGGTAAGCCC	70	8	10	(Gomez and Gonzalez, 2004)	Algae
721	OPA-11	CAATCGCCGT	60	5	10	(Gomez and Gonzalez, 2004)	Algae
722	OPA-13	CAGCACCCAC	70	5	10	(Gomez and Gonzalez, 2004)	Algae
723	OPA-18	AGGTGACCGT	60	8	10	(Gomez and Gonzalez, 2004)	Algae
724	OPD-11	AGCGCCATTG	60	11	10	(Gomez and Gonzalez, 2004)	Algae
725	OPD-18	GAGAGCCAAC	60	7	10	(Gomez and Gonzalez, 2004)	Algae
726	OPA-03	AGTCAGCCAC	60	8	10	(Eren *et al*., 2018)	Algae
727	OPA-09	GGGTAACGCC	70	9	10	(Eren *et al*., 2018)	Algae
728	OPA-12	CCTTGACGCA	60	10	10	(Eren *et al*., 2018)	Algae
729	OPB-13	TTCCCCCGCT	70	12	10	(Eren *et al*., 2018)	Algae
730	OPE-14	TGCGGCTGAG	70	10	10	(Eren *et al*., 2018)	Algae
731	OPG-16	AGCGTCCTCC	70	9	10	(Eren *et al*., 2018)	Algae
732	OPH-11	CTTCCGCAGT	60	13	10	(Eren *et al*., 2018)	Algae
733	OPH-12	ACGCGCATGT	60	8	10	(Eren *et al*., 2018)	Algae
734	OPM-15	GACCTACCAC	60	8	10	(Eren *et al*., 2018)	Algae
735	RAPD-1	ACAACTGCTC	50	7	10	(Mostafa *et al*., 2011)	Algae
736	RAPD-2	TGACTGACGC	60	6	10	(Mostafa *et al*., 2011)	Algae
737	RAPD-4	ATCGGGTCCG	70	8	10	(Mostafa *et al*., 2011)	Algae
738	RAPD-5	CAGGCCCTTC	70	11	10	(Mostafa *et al*., 2011)	Algae
739	RAPD-6	AATCGGGCTG	60	20	10	(Mostafa *et al*., 2011)	Algae
740	RAPD-7	GGGTAACGCC	70	10	10	(Mostafa *et al*., 2011)	Algae
741	RAPD-8	CAATCGCCGT	60	7	10	(Mostafa *et al*., 2011)	Algae
742	RAPD-9	CAGCAACCAC	60	6	10	(Mostafa *et al*., 2011)	Algae
743	RAPD-10	AGGTGACCGT	60	17	10	(Mostafa *et al*., 2011)	Algae
744	RAPD-11	AGGTGACCGT	60	17	10	(Mostafa *et al*., 2011)	Algae
745	RAPD-12	GAGAGCCAAC	60	11	10	(Mostafa *et al*., 2011)	Algae
746	S30	GTGATCGCAG	60	21	10	(Cui *et al*., 2016)	Algae
747	S31	CAATCGCCGT	60	26	10	(Cui *et al*., 2016)	Algae
748	S51	AGCGCCATTG	60	38	10	(Cui *et al*., 2016)	Algae
749	S52	CATCCGTGCT	60	19	10	(Cui *et al*., 2016)	Algae
750	560	ACCCGGTCAC	70	26	10	(Cui *et al*., 2016)	Algae

751	S80	ACTTCGCCAC	60	21	10	(Cui *et al*., 2016)	Algae
752	S104	GGAAGTCGCC	70	36	10	(Cui *et al*., 2016)	Algae
753	S112	ACGCGCATGT	60	12	10	(Cui *et al*., 2016)	Algae
754	S1501	CTACGGCCTTC	60	21	10	(Cui *et al*., 2016)	Algae
755	S1513	GGCTTGGCGA	60	22	10	(Cui *et al*., 2016)	Algae
756	S2110	GTGACCAGAG	60	21	10	(Cui *et al*., 2016)	Algae
757	S2111	GACGACCGCA	60	21	10	(Cui *et al*., 2016)	Algae
758	S2114	CCGCGTTGAG	70	11	10	(Cui *et al*., 2016)	Algae
759	S2115	ACGCGAACCT	60	26	10	(Cui *et al*., 2016)	Algae
760	S2116	AGGGTCCGTG	70	17	10	(Cui *et al*., 2016)	Algae
761	S2118	AGCCAAGGAC	60	16	10	(Cui *et al*., 2016)	Algae

DISCUSSION AND CONCLUSION

The importance of Random Amplified Polymorphic DNA markers in taxonomic identification, kinship relationship, assessment, mixed genome sample analysis as well as specific probes creation has been well established (Bardakci, 2001; Kumari and Thakur, 2014; Vieira *et al*., 2016; Thomas *et al.,* 2017; Nadeem *et al*., 2018). However, these applications are not without constraints including appropriate RAPD primer's selection which may further be difficult as a result of several optimization protocols (He *et al*., 1994; Vieux *et al*., 2002; Jiang, 2013). In this study, we achieved biological resolution through guided primer selection based on appropriate biospecific GC contents. According to our analysis, primer's GC content varies for all the biological specimens observed except for bacteria and plants that shares primer's GC content of between 60-70%. This observation is an indication that variation exists in the nucleotide content of different biological specimens in a correlated manner across all types of sites, including non-protein coding regions, synonymous and non-synonymous sites (Hershberg and Petrov, 2009, 2010, 2012) and such variations subsequently impact on the behavior of the biological specimen vis-à-vis their specificities to RAPD primers.

As for the bacteria, the observed best primer's GC content for their discrimination was 60-70%. This observation may not be unexpected, as bacteria have earlier been reported to harbor between as less as 15% GC contents to more than 75% GC contents (Bentley and Parkhill, 2004; Hildebrand *et al*., 2010; Lightfield *et al*., 2011). This observation may be an indication that these organisms have high AT rich genome in a case of less than 15% GC content and the opposite for high GC content of 75%. Such findings, however, therefore depicts that nucleotide composition of individual organisms is necessary in deciphering the appropriate RAPD primer to be used (Zakiyah *et al*., 2019; Amiteye, 2021). The above observation is correspondingly unvarying for plants studied.

Insects were also best resoluted by RAPD primer with a GC content of approximately 65%. This result further asserts that the corresponding GC content of biological specimen to be analyzed is crucial to the type of RAPD primer to be selected (Dieffenbach *et al*., 1993; Fritsch *et al*., 1993; Naheem *et al*., 2018). This is because most organisms with lower GC content and higher AT regions follow similar pattern of requiring GC rich RAPD primers. This may not be unconnected to the fact that such organisms needed complementary flanking primer sequences for proper annealing and subsequently good polymorphisms (Sharrocks, 1994; Yang *et al*., 2006).

Generally, insects have an average GC content of 31% to classify them in the region of AT rich organisms. It is thus imperative to note that the nucleotide composition of prospective organisms to be discriminated against may be as important as the RAPD primer selection in RAPD experiment designs (Ferita *et al*., 2013; Nadeem *et al*., 2018). Fungi, which are a group of eukaryotic organisms that include microorganisms such as yeast and moulds as well as the more familiar mushrooms, were also studied for best RAPD primers during discriminations and it was observed that the best GC content for their typing was between 55-65%. This observation is a further attestation to the impact of nucleotide composition on discrimination of biological specimen (Feng *et al*., 2009; Cao *et al*., 2015; Dwivedi *et al*., 2018).

Thomas *et al*. (2019) documented accumulation of mutations in polyketide synthase gene of *Aspergillus* section *Nigri* as a possible cause of variation in nucleotide composition. According to them, several levels of transition-transversion mutations were observed in the polyketide synthase gene and this was further corroborated by other studies that nucleotide composition of a genome is determined by mutational biases (Andersson and Sharp, 1996; Chen *et al*., 2004). These mutational biases not only impact nucleotide composition but also their behavior (Eduardo *et al*., 2006). The fact that the examined protozoans were best discriminated at 55% is an indication that their GC content is almost at equilibrium with their AT contents (Kubelik and Szabo, 1995; Worthey and Myler, 2005), hence requiring an average GC-rich RAPD primer. Results of our study therefore affirmed that the challenge faced with large scale RAPD-PCR through several optimization techniques may be averted with judicious use of GC content of primer as a predictor of level of polymorphisms.

Declarations:

Ethical Approval: This study did not involve human participants or animals. The research was limited to in vitro laboratory analyses of plant extracts and thus did not require ethical approval.

Informed Consent: Not applicable. The study did not involve human participants, patient data, or biological samples.

Declaration of Generative AI and AI-assisted Technologies in the Writing Process: The author has not used any of the generative AI or AI-assisted tool in the writing of this article.

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REFERENCES

Akbar, F., Rabbani, M.A., Masood, M.S. and Shinwari, Z.K. (2011). Genetic diversity of Sesame (*Sesamum indicum L.*) germplasm from Pakistan using RAPD markers. *Molecular Ecology,* 2, pp. 151-159.

Akopyanz, N., Bukanov, N.O., Westblom, T.U., Kresovich, S. and Berg, I. (1992). DNA diversity among clinical isolates of *Helicobacter pylori* detected by PCR-based RAPD fingerprinting. *Nucleic Acids Research*, 20(19), pp. 5137-514.

Amiteye, S. (2021). Basic concepts and methodologies of DNA marker systems in plant molecular breeding. *Heliyon*, 7(10), e08093.

Amusa, O., Adesoye, A., Ogunkanmi., A., Omoche, O., Olowe, O., Akinyosoye, S. and Omodele, T. (2014). Genetic diversity of Parkia biglobosa from different agroecological zones of Nigeria using RAPD Markers. *International Journal of Biodiversity,* pp 1-9.

Anbalagan, S., Bharathirja, C., Pandiarajan, J., Dinakaran, S. and Krishman, M. (2021). Use of Random Amplified Plymorphic DNA (RAPD) to study genetic diversity within a population of black fly, *Simulium gravely* from palnihills, Peninsullar India. *Biologia*., 67(6), pp. 1195-1203.

Araújo, W.L., Angellis, D.A. and Azevedo, J.L. (2004). *Direct RAPD Evaluation of Bacteria without Conventional DNA Extraction*, 47, pp. 375–380.

Babi, S., Dahot, M.U., Khan, I.A., Khati, A. and Navi, M.H. (2009). Study of genetic diversity in wheat (*Triticulum aestivum* L.) using Random Amplified Polymorphic DNA (RAPD) markers. *Pakistan Journal of Botany,* 41(3), pp. 1023-1027.

Bahurupe, J.V., Sakhare, S.B., Kulwal, P.L., Akhare, A.A and Pawar, B.D. (2013). Genetic diversity analysis in chilli (*Capsicum annum L.*) using RAPD markers. *International Quarterly Journal of Science.,* 8(3), pp. 915-918.

Bardakci, F. (2001). Random Amplified Polymorphic DNA (RAPD) Markers. *Turkish Journal of Biology,* 25, pp. 185-196.

Bayraktar, H. (2010). Genetic diversity and population structure of *Fusarium oxysporum* F. sp. *Cepae*, the casual agent of Fusarium basal rot on onion using RAPD markers. *Journal of Agricultural Sciences*, 16, pp. 139-149.

Belletti, P., Monteleone, I. and Ferrazzini, D. (2008). A population genetic study in a scattered forest species, wild service tree (*Sorbus torminінalis* L. *Grantz*), using RAPD markers. *European Journal of Forest Research,* 127, pp. 103-114.

Bentley, S.D. and Parkhill, J. (2004). Comparative genomic structure of prokaryotes. *Annu Rev Genet*., 38, pp. 771–792.

Betancor, L., Schelotto, F., Martinez, A., Pereira, M., Algorta, G.M., Rodríguez, A., Vignoli, R. and Chabalgoity, J.A. (2004). *Journal of Clinical Microbiology*, 42(3), pp. 1155-1162.

Botstein, D., White, R.L., Skolnick, M. and Davis, R.W. (1980). Construction of a genetic linkage map in man using restriction fragment length polymorphisms. *The American Journal of Human Genetics*, 32(3), pp. 314–331.

Brisse, S., Barnabé, C. and Tibayrenc, M. (2000). Identification of six *Trypanosoma cruzi* phylogenetic lineages by random amplified polymorphic DNA and multilocus enzyme electrophoresis. *International Journal for Parasitology,* 30, pp. 35-44.

Brown-Guedira, G.L., Thompson, J.A., Nelson, R.L. and Warburton, M.L. (2000). Evaluatiom of genetic diversity of soybean introductions and North America ancestors using RAPD and SSR markers. *Crop Science,*40, pp. 815-823.

Cao, X., Wu, Z., Zhou, R., Jiang, F.L. and Yang, Z.E. (2015). A novel random amplified polymorphic DNA-based strategy for genetic diversity analysis and identification of tomatoes. *Genetics and Molecular Research,* 14 (1), pp. 1650-1661.

Carvalho, V.P., Ruas, C.F., Ferreira, J.M., Moreir, R.M.P. and Ruas, P.M. (2004). Genetic diversity among maize (*Zea mays* L.) landraces assessed by RAPD markers. *Genetic and molecular biology*, 27(2), pp. 228-236.

Cepicka, I., Kutišová, K., Tachezy, J., Kulda, J. and Flegr, J. (2005). Cryptic species within the Tetratrichomonas gallinarum species complex revealed by molecular polymorphism. *Veterinary Parasitology,* 128 (1-2), pp. 11-21.

Chapman, T. (2003). Lab automation and robotics: Automation on the move. *Nature,* 421 (6923), pp. 661-663.

Ciarmello, L.F., Piccirill, P., Carillo, P., Luca, A. and Woodrow, P. (2005). Determination of the genetic diversity relatedness of fig (Ficus carica L.) accessions using RAPD fingerprinting and their agro-morphological characterization. *South African Journal of Botany*, 97, pp. 40-47.

Cocconcelli, P.S., Porro, D., Galandini, S. and Senini, L. (1995). Development of

RAPD protocol for typing of strains of lactic acid bacteria and enterococci. Letters in Applied Microbiology, 21, pp. 376-379.

Cui, C., Li, Y., Liu, Y., Li, X., Luo, S., Zhang, Z., Wu, R., Liang, G., Sun, J., Peng, J. and Tian, P.P. (2016). Determined of genetic diversity among *Saccharina* germplasm using ISSR and RAPD markers. *Comptes Rendus Biologies*., pp. 3473-3484.

Datta, S., Gangwar, S., Kumar, S., Gupta, S., Rai, R., Kaashyap, M., Sigh, P., Chaturvedi, S.K., Sigh, B.B. and Nadarajan, N. (2012). Genetic diversity in selected Indiana mungbean (*Vigna radiate* (L) *Wilczek*) cultivars using RAPD markers. *America Journal of plant sciences,* 3, pp. 1085-1091.

Deshwal, R.P.S., Singh, R., Malik, K. and Randhawa, G.J. (2005). Assessment of genetic diversity of genetic relationships among 29 population of *Azadiradita indica* A. Juss. Using RAPD markers. *Genetic Resources and Crop Evolution*, 52, pp. 285-292.

Dieffenbach, C.W., Lowe, T.M. and Dveksler, G.S. (1993). General concepts for PCR primer design. *PCR Methods and Applications,* 3(3), pp. 30–37.

Dwivedi, S., Singh, S., Chauhan, U.K. and Tiwari, M.K. (2018). Inter and intraspecific genetic diversity (RAPD) among three most frequent species of macrofungi (*Ganoderma lucidum*, *Leucoagricus* sp. and *Lentinus* sp.) of Tropical Forest of Central India. *Journal of Genetic Engineering and Biotechnology*, 16(1), pp. 133-141.

Eduardo, P.C., Touchon, M. and Feil, E.J. (2006). Similar compositional biases are caused by very different mutational effects. *Genome Research,*16(12), pp. 1537–1547.

Ercan, A.G., Taskin, M. and Turgut, K. (2004). Analysis of genetic diversity in Turkish sesame (*Sesamum indicum L.*) populations using RAPD markers. *Genetic Resources and Crop Evolution,* 51, pp. 599.607.

Eren, A., Lovinella, M., Yoon, H.S., Cennamo, P., Stefano, M., Catro, O. and Claudia, S. (2018). Genetic structure of *Galdieria* populations from Iceland. *Polar Biology,* http://dio.org/10.007/s00300-018-2308-3.

Erlich, H.A. (1989). PCR Technology: Principles and Applications for DNA Amplification, New York, Stockton Press.

Ferita, I., Fauza, H., Suliansyah, I. and Jamsari, G. (2013). Characterization of specific random amplified polymorphic (RAPD) DNA fragments related to catechin content for early detection methods in gambier plant (Uncaria gambir (Hunter) Roxb). *African Journal of Biotechnology*, 12(15), pp. 1736-1744.

Ferriol, M., Pico, M.B. and Nuez, F. (2003). Genetic diversity of some accessions of *Cucurbita maxima* from Spain. *Genetic Resources and Crop Evolution,* 50, pp. 227-238.

Gadelhak, G.G. and Enan, M.R. (2005). Genetic diversity among population of red palm weevil, *Rhynchophorus ferrigeneus* Olivier (Coleoptera curulionidae), determined by Radom Amplified Polymorphic DNA-Polymerase Chain Reaction (PAPD-PCR). *International Journal of Agriculture and Biotechnology*, 1560-8530/2005/07-3-395-399.

Gajera, B.B., Kumar, N., Singh, A.S. and Punvar, B.S. (2010). Assessment of genetic diversity in castor (*Ricinus communisL.*) using RAPD and ISSR markers. *Industrial crops and products.,* 32, pp. 491-498.

Garcia, A.F., Benchimol, L.L., Barbosa, A.M.M., Geraldi, I.O., Souza, C.L. and Dsouza, S.A.P. (2004). Comparison of RAPD, RFLP, AFLP and SSR markers for diversity studies in tropical maize inbred lines. *Genetics and Molecular Biology,* 27(4), pp. 579–588.

Gauer, L. and Cavalli-Molina, S. (2000). Genetic variation in natural populations of matea (*Ilex paraguariensis A. St.-Hil., Aquifoliaceae)* RAPD markers. *Heredity,* 84, pp. 647-656.

Gomez, P.I. and Gonzalez, M.A. (2004). Genetic variation among seven strains of *Dunaliella salina* (chlorophyta) with industrial potential based on RAPD banding patterns and on nuclear ITS or DNA sequences. *Auaticulture*, 233, pp. 149-162.

Guo, Z.G. and Johnson, A.M. (1995). Genetic characterization of Toxoplasma gondii strains by random amplified polymorphic DNA polymerase chain reaction. *Parasitology,* 111 (2), pp. 127-132.

Guo, Y.D., Yli-Mattila, T. and Pulli, S. (2003). Assessment of genetic variation in timothy (*Phleum pretense* L.). using RAPD and UP-PCR. *Heraditas.,* 138, pp. 101-113.

He, Q., Marjamäki, M., Soini, H., Mertsola, J. and Viljanen, M.K. (1994). Primers are decisive for sensitivity of PCR. *Biotechniques*, 17(1), pp. 82–84.

Hildebrand, F., Meyer, A. and Eyre-Walker, A. (2010). Evidence of Selection upon Genomic GC-Content in Bacteria. *PLoS Genet*., 6(9), e1001107.

Huh, M.K., Lee, B.K. and Lee, H.Y. (2006). Genetic diversity and phylogentic relations in five *porphyra* species revealed by RAPD analysis. *Prostitology,* 4(3), pp. 245-250.

Iqbal, A., Bushra, S., Khan, A.I., Faisal, A., Kainth, R.A. and Hafeez, S. (2010). Biodiversity in the sorghum (Sorghum bicolor L. Moench) germplasm of Pakistan. *Genetics and molecular research*, 9, pp. 756-64.

Jain, L., Rawat, M., Kumar, V. and Chachra, D. (2015). Characterization of Brucellophge using RAPD and microsatellite repeat marker. *Journal of Pure and Applied Microbiology*, 9, pp. 683-690.

Jiang, G.L. (2013) Molecular Markers and Marker-Assisted Breeding in Plants. In: Andersen, S.B., Ed., Plant Breeding from Laboratories to Fields, IntechOpen, London, 45-83.

Kamakshi, N., Sudhakar, P. and Muralishna, T. (2012). Analysis of genetic diversity of field bean genotypes showing resistance to pod borers and pod bugs using RAPD technique. *Current Biotica.,* 5(4), pp. 421-427.

Karishaloo, J.L., Dwivedi, Y.K., Archak, S. and Giakwad, A.B. (2003). Analysis of genetic diversity of Indiana mango cultivars using RAPD markers. *Journal of Horticultual Science and Biotechnology,* 79(3), pp. 285-289.

Kawar, P.G., Devarumath, R.M. and Nerkar, Y. (2009). Use of RAPD markers for the assessment of genetic diversity in sugarcane cultivars. *Indian Journal of Biotechnology*, 8, pp. 67-71.

Kumar, N.V.H., Narayanaswany, P., Prasad, D.T., Mukunda, G.K. and Sondur, S.N. (2001). Estimation of genetic diversity of commercial mango (*Magnifera indica L.*) cultivars using RAPD markers. *Journal of Horticultural Science and Biotechnology,* 76(5), pp. 529-533.

Kumari, N. and Thakur, S.K. (2014). Randomly amplified polymorphic DNA- A brief review. *American Journal of Animal and Veterinary Sciences*, 9 (1), pp. 6-13.

Kutty, M.S., Gowda, R.V. and Anand, L. (2006). Analysis of genetic diversity among Indian short-day onion (*Alium cepa* L.) cultivars using RAPD markers. *Journal of Horticultural Science and Biotechnology,* 81(4), pp. 774-778.

Laursen, M.F., Dalgaard, M.D. and Bahl, M.I. (2017). Genomic GC-content affects the accuracy of 16S rRNA gene sequencing based microbial profiling due to PCR bias. *Frontiers in Microbiology,* 8, pp. 1934.

Lightfield, J., Fram, N.R. and Ely, B. (2011). Across bacterial phyla distantly related genomes with similar genomic GC content have similar patterns of amino acid usage. *PLoS ONE*., 6, e17677.

Madadgar, O., Salehi, Z.T. and Tadjbakhsh, H. (2008). Genomic and phenotypic evaluation of Salmonella *typhimurium* and Salmonella *enteritidis* in Iran. *Comparative Clinical Pathology,* 17, pp. 229–235.

McPherson, M.J. and Moller, S.G. (2000). Polymerase Chain Reaction. BIOS Scientific Publishers Ltd., Oxford, pp. 1-18.

Moorthy, S.M., Rao, A.S.K., Kumar, V. and Bindroo, B.B. (2013). Genetic diversity analysis using RAPD marker in some Silkworm breeds breeds of *Bombyx mori L. Scholars Research Library Annals of Biological Research.*, 4(12), pp.82-88.

Mostafa, N., Omar, H., Tan, S.G. and Nepis, S. (2011). Studies on the genetic variation of the green unicellular algae *Haematococcus pluvialis* (Chlorophyceae) obtained from different geographical locations using ISSR and RAPD molecular markers. *Molecules,* 16: 2598-2608.

Mullis, K.B., Ferre, F. and Gibbs, R.A. (1994). The Polymerase Chain Reaction, Boston, Birkhauser. Accessed from https://books.google.com/ on the 23/04/2025.

Nadeem, M.A., Nawaz, M.A., Shahid, M.Q., Doğan, Y., Comertpay, G., Yıldız, M., Hatipoğlu, R., Ahmad, F., Alsaleh, A., Labhane, N., Özkan, H., Chung, G. and Baloch, F.S. (2018). DNA molecular markers in plant breeding: Current status and recent advancements in genomic selection and genome editing. *Biotechnology Equipment,* 32(2), pp.261–285.

Nanvazadeh, F., Dokht, A. and Reza, M. (2013). Genotyping of *Pseudomonas aeruginosa* strains isolated from burn patients by RAPD-PCR. *Burns*, 39(7), pp. 1409–1413.

Nath, B.S., Hassan, W., Rao, S.N., Prakash, N.B.V., Gupta, S.K., Mohanan, N.M. and Bajpai, A.K. (2011). Genetic diversity among microsporidian isolates from the silkworm, Bombyx mori, as revealed by randomly amplified polymorphic DNA (RAPD) markers. *Acta Parasitologica,* 56 (4), pp. 333-338.

Nath, V.S., Sankar, M.S.A., Hedge, V.M., Jeeva, M.L., Musra, R.S., Veena, S.S. and Raj, M. (2012). Analysis of Genetic Diversity in *Phytphthora colocasiae* using RAPD markers. *The Asian and Australasian Journal of Plant Science and Biotechnology,* 6(1), pp.38-43.

Nishat, S., Hamim, I., Khalil, M.I., Ali, A., Ali, M., Meah, M.B. and Islam, R. (2015). Comptes Rendus Biologies Genetic diversity of the bacterial wilt pathogen Ralstonia solanacearum using a RAPD marker. *Comptes Rendus Biologies.*, 338(11), pp. 757-767.

Padmesh, P., Reji, J.V., Dhar, M.J. and Seeni, S. (2006). Estimation of genetic diversity in varieties of *Macuna puriens* using RAPD. *Biologia Plantarum*, 50(3), pp. 367-372.

Pamidimarri, D.V.N.S, Mastan, S.G., Rahman, H. and Reddy, M.P. (2009). Molecular characterization and genetic diversity analysis of *Jatropha curcas L.* in India using RAPD and AFLP analysis. *Molecular Biology Reports,* 37, pp. 2249-2257.

Rozen, S. and Skaletsky, H. (2000). Primer on the WWW for general users and for biologist programmers. *Methods in Molecular Biology,* 132, pp. 365-386.

Sadeghi, L., Alizadeh, A., Safaie, N. and Jamali, S.H. (2012). Genetic diversity of *Gaumannomyces graminis* var. *tritici* populations using RAPD and ERIC markers. *Journal of Plant Pathology & Microbiology,* 3(7), pp.74-71.

Sahoo, P.K., Mohanty, J., Kumar, A., Bikash, G., Mohanty, R., Banyakar, J.J. and Prasanth, H. (2011). Genetic diversity and species identification of *Argulus* parasites collected from major aquaculture regions of India using RAPD. *Aquaculture Research, pp.* 1-11.

Saxena, S., Verma, J., Shikha, R.D. (2014). RAPD-PCR and 16S rDNA phylogenetic analysis of alkaline protease producing bacteria isolated from soil of India: Identification and detection of genetic variability. *Journal of Genetic Engineering and Biotechnology.*, 12(1), pp. 27–35.

Sedra, M.H., Lashermes, P., Trouslot, P., Combes, M.C. and Hamon, S. (1998). Identification and genetic diversity analysis of date palm (*Phoenix dactylifera L.)* varieties from Morocco using RAPD markers. *Euphytica*, 103, pp. 75-82.

Sen, S., Skaria, R., and Abdul Muneer, P.M. (2010). Genetic diversity analysis in *Piper* species (*Piperaceae*) using RAPD markers. *Molecular Biotechnology,* 46, pp.72-79.

Seppola, M., Erik, R., Sandaker, E., Kanapathippillai, P., Holzapfel, W., and Ringø, E. (2006). Random amplification of polymorphic DNA (RAPD) typing of carnobacteria isolated from hindgut chamber and large intestine of Atlantic cod. *Gadus morhua*, 29, pp.131–137.

Shahaby, A.F., Awad, N.S. and El Tarras, A.E. (2012). Mobile phone as potential reservoirs of bacterial pathogens. *African Journal of Biotechnology*, 11(92), pp. 15896–15904.

Sharifova, S., Mehdiyeva, S., Theodorikas, K., Roubos, K. (2013). Assessment of genetic diversity in cultivated tomato (*Solanum lycopersicum L.*) genotypes usimg RAPD primers. *Journal of Horticultural Research*, 21(1), pp.83-89.

Sharrocks, A.D. (1994). The design of primers for PCR. In: Griffin HG, Griffin AM, editor. PCR technology: current innovations. London, CRC Press. Pp.5–11.

Srivastava, P., Pandey, A. and Sinha, D.P. (2011). Genetic diversity analysis in different varieties of black gram using RAPD markers. *Journal of Plant Breeding and Crop Science,* 3(3), pp.53-59.

Thomas, A.C., Deagle, B.E., Eveson, J.P., Harsch, C.H. and Trites, A.W. (2016). Quantitative DNA metabarcoding: improved estimates of species proportional biomass using correction factors derived from control material. *Molecular ecology resources,* 16 (3), pp. 714-726.

Thomas, B.T., Ogunkanmi, L.A., Iwalokun, B.A. and Popoola, O.D. (2017). Genetic diversity of ochratoxigenic Aspergillus section Nigri, using RAPD and VCG techniques. *African Journal of Clinical and Experimental Microbiology,* 18 (4), pp. 205-209.

Tompkins, T.A., Stewart, R., Savard, L., Russell, I. and Dowhanick, T.M. (1996). RAPD-PCR characterization of brewery yeast and beer spoilage bacteria. *Journal of the American Society of Brewing Chemists*, 54(2), pp. 91–96.

Vieira, M.L.C., Santini, L., Diniz, A.L. and Munhoz, C.F. (2016). Microsatellite markers: what they mean and why they are so useful. *Genetics and molecular biology,* 39, pp. 312-328.

Viera, R.F., Goldsbrough, P. and Simon, J.E. (2003). Genetic diversity of basil (*Ocinum* spp.) is based on RAPD marker. *Journal of the American Society for Horticultural Science,* 128(1), pp. 94-99.

Vieux, E.F., Kwok, P.Y. and Miller, R.D. (2002). Primer design for PCR and sequencing in high-throughput analysis of SNPs. *Biotechniques,* 32, pp. S28-S32.

Worthy, E.A. and Myler, P.J. (2005). Protozoans' genomes: gene identification and annotation. *International Journal for Parasitology,* 35(5), pp. 495-512.

Yang, X., Scheffler, B.E. and Weston, L.A.

(2006). Recent developments in primer design for DNA polymorphism and mRNA profiling in higher plants. *Plant Methods*, 2, pp. 4.

Yuryev, A., Huang, J., Pohl, M., Patch, R., Watson, F., Bell, P., Donaldson, M., Phillips, M.S. and Boyce-Jacino, M.T. (2002). Predicting the success of primer extension genotyping assays using statistical modeling. *Nucleic Acids Research,* 30(23), pp. 1-11.

Yuste-Lisbona, F.J., Capel, C., Gómez-Guillamón, M.L., Capel, J., López-Sesé, A.I. and Lozano, R. (2011). Codominant PCR-based markers and candidate genes for powdery mildew resistance in melon (Cucumis melo L.). *Theoretical and applied genetic.,* 122 (4), pp. 747-758.

Zakiyah, N., Handoyo, T. and Kim, K.M. (2019). Genetic diversity analysis of Indonesian aromatic rice varieties (*Oryza sativa* L.) using RAPD. *Journal of Crop Science and Biotechnology,* 22, pp. 55-63.

Zameer, M., Mahmood, S., Mushtaq, Z., Tabasum, B. and Ali, Q. (2015). Detection of bacterial load in drinking water samples by 16s rRNA ribotyping and RAPD analysis. *Advances in Life Sciences*, 2(3), pp. 135-141.

Zare, S., Derakhshandeh, A., Haghkhah, M., Naziri, Z. and Broujeni, A.M. (2019). Molecular typing of Staphylococcus aureus from different sources by RAPD-PCR analysis. *Heliyon.*, 5(8), e02231.

Zhang, J., Zheng, H.G., Aarti, A., Pantuwan, G., Nguyen, T.T., Tripathy, J.N., Sarial, A.K., Robin, S., Babu, R.C., Nguyen, B.D., Sarkarung, S., Blum, A. and Nguyen, H.T. (2001). Locating genomic regions associated with components of drought resistance in rice: comparative mapping within and across species. *Theoretical and Applied Genetics,* 103 (1), pp. 19-29.