

Supplementary Data

**Conservation of microsatellite regions across legume genera increases marker repertoire in pigeonpea.**

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**Table 1.** Properties of cross genera legume microsatellite markers amplifying alleles in pigeonpea.

S.No	Primer	Sequence (5'-3')	Motif	T <sub>m</sub> (C)	Size	Species	Nature
1.	TR1	FCGTATGATTTTGCCGTCTAT R ACCTCAAGTTCTCCGAAGT	(TAA) <sub>31</sub>	57.3	224	<i>C. arietinum</i>	Genomic
2.	TR20	FACCTGCTTGTTTAGCACAAT RCCGCATAGCAATTTATCTTC	(TAA) <sub>18</sub>	56.3	172	<i>C. arietinum</i>	Genomic
3.	TA59	FTCTAAAGAGAAATCAAATTTGTCGAA R AAATGTGAAGCATGTATAGATAAAG	(TAA) <sub>29</sub>	58.5	258	<i>C. arietinum</i>	Genomic
4.	TA96	F TGTTTTGGAGAAGAGTGATTC R TGTGCATGCAAATCTTACT	(AT) <sub>3</sub> (TTA) <sub>30</sub> (AT) <sub>3</sub>	55.4	275	<i>C. arietinum</i>	Genomic
5.	TA 76S	FTCCTCTTCTCGATATCATCA R CCATTCTATCTTTGGTGCTT	(AAT) <sub>7</sub> (AAT) <sub>4</sub> [ACT(AAT) <sub>11</sub> ] <sub>2</sub> ACT(AAT) <sub>3</sub> TAT(AAT) <sub>2</sub> (ATT) <sub>5</sub>	56.5	206	<i>C. arietinum</i>	Genomic
6.	AGLC16	F TTGGATATAACAGATGACGGGGAA R GAGTACTTGCCAACTAGCTTAGGA	-	62.0	365	<i>C. arietinum</i>	Genomic
7.	AGLC 34	F CTTTACCAAAAACCACCTTCACCAA R TCTCTCTCTCTCTCTCTGTTCCA	(AG) <sub>20</sub>	62.0	350	<i>C. arietinum</i>	Genomic
8.	AGLC52	F CGATCAAGAACCCAGTTTGGCAA R AAGATCGACAGGCGATCTGGTA	-	61.8	390	<i>C. arietinum</i>	Genomic
9.	TR26	F TCATCGCAGATGATGTAGAA R TTGAACCTCAAGTCTCTGG	(ATA) <sub>15</sub>	57.3	215	<i>C. arietinum</i>	Genomic
10.	NPS 2	F GACAAACAACCTCCCAAGAAA R GACGACAACAACAACAACA	(ATT) <sub>6</sub>	-	258	<i>C. arietinum</i>	Genomic
11.	NPS 5	F GAGCCCTGAAATGAAGAAAGAA R CACCTTTGAGCCCTAGTCTGTT	(AAAT) <sub>5</sub>	-	387	<i>C. arietinum</i>	Genomic
12.	NPS 7	F CACACACACAGACACACACACA R TGGTTCAGACATCACACCAAAT	(CA) <sub>33</sub>	-	136	<i>C. arietinum</i>	Genomic
13.	NPS 13	FATACGACGACGATCTGGATTT R TTCTCACATCTCTCTCTCTCTCTC	(GA) <sub>36</sub>	-	170	<i>C. arietinum</i>	Genomic

14.	NPS 35	F TGCTCATGCTTACTTCTTCCTG R GTCGGCTTGGCTCATGTAAT	(CAA) <sub>9</sub>	-	220	<i>C. arietinum</i>	Genomic
15.	BMd 26	F CTTGCCTTGTGCTTCCTTCT R TCCATTCCCAACCAAGTTTC	(GAT) <sub>6</sub>	56.3	141	<i>P. vulgaris</i>	Genic
16.	BMd 27	F GGACCCACCATCACCATAAC R TGGTGGAGGTGGAGATTGT	(CCA) <sub>6</sub>	61.4	151	<i>P. vulgaris</i>	Genic
17.	BMd 28	F TGCATCAACTTAGGAGCTTG R TCTTGTCTTATCAGCAGGTGGA	(GT) <sub>4</sub>	59.7	159	<i>P. vulgaris</i>	Genic
18.	BMd 35	F TCTCTTCCTTACCCTGTTCTGC R GCGTGGACTTGAATGGTTTC	(CAA) <sub>5</sub>	61.4	128	<i>P. coccineus</i>	Genic
19.	BMd 47	F ACCTGGTCCCTCAAACCAAT R CAATGGAGCACCAAAGATCA	(AT) <sub>5</sub>	59.4	150	<i>P. vulgaris</i>	Genic
20.	BMd 48	F CCCACCAACTCTTCTTCC R CAGAATTGACTTGGCGAGAA	(CT) <sub>5</sub>	60.4	131	<i>P. vulgaris</i>	Genic
21.	BMd 52	F TCTTGGTGCAGAAAGTTA R AAGGCTTTGTTTATTAAAGGTT	(ATT) <sub>4</sub>	57	151	<i>P. coccineus</i>	Genic
22.	BMd 53	F TGCTGACCAAGGAAATTCAG R GGAGGAGGCTTAAGCACAAA	(GTA) <sub>5</sub>	59.4	105	<i>P. vulgaris</i>	Genic
23.	BMd 55	F GTCCGTTTCATGGGTTTGACT R TCGAGATCTACGGAGGAGTTC	(AT) <sub>5</sub>	61.5	188	<i>P. coccineus</i>	Genic
24.	BMd 12	F CATCAACAAGGACAGCCTCA R CAGCTGGCGGTTAAAACAG	(AGC) <sub>7</sub>	62.4	167	<i>P. vulgaris</i>	Genomic
25.	BMd 33	F TACGCTGTGATGCATGGTTT R CCTGAAAGTGCAGAGTGGTG	(ATT) <sub>9</sub>	60.6	110	<i>P. vulgaris</i>	Genomic
26.	BMd 39	F CACCGAGGAGTTTCTGTGAA R TTAAGTCCTTGCAGCCCTTC	(CCA) <sub>4</sub>	60.4	126	<i>P. vulgaris</i>	Genomic
27.	BMd 40	F AACCTTCTTGCAGTATCTC R TAGTGGCCATTCTCGAT	(AT) <sub>6</sub>	60.4	197	<i>P. vulgaris</i>	Genomic
28.	BMd 41	F CAGTAAATATGGCGTGGATGA R TGAAAGTGCAGAGTGGTGGGA	(ATT) <sub>9</sub>	59.6	250	<i>P. vulgaris</i>	Genomic
29.	BMd 42	F TCATAGAAGATTCTGGAAGCA R TGAGACACGTACGAGGCTGTAT	(AT) <sub>5</sub>	59.9	149	<i>P. vulgaris</i>	Genomic
30.	BMd 43	F CAGCATCAAGAAGACCCAAG R CAGCACCACTATGGGAGGAC	(CCT) <sub>5</sub>	62.2	176	<i>P. vulgaris</i>	Genomic
31.	SSR13	F GAAACAACACCGAAATACAC R CGAAGTCAGATGAAGTTTG	(CA) <sub>6</sub>	53	150	<i>L. culineris</i>	Genomic
32.	SSR48	F CATGGTGAATAGTGTATGGC R CTCCATACACCACTCATTACAC	TG) <sub>13</sub>	57	165	<i>L. culineris</i>	Genomic
33.	SSR59-2	F CCAAATACTGCAACACACCG R GTTCCCATCAGGCAGAAGG	(CA) <sub>19</sub> (TA) <sub>19</sub>	58	175	<i>L. culineris</i>	Genomic
34.	SSR80	F CCATGCATACGTGACTGTC R GTTACTGTTGGTGTAAAGTG	(TC) <sub>14</sub> (AC) <sub>12</sub> (AT) <sub>2</sub>	56	155	<i>L. culineris</i>	Genomic
35.	SSR107	F GCGGCGAGCAAATAAAT R GGAGAATAAGAGTGAATATG	(TC) <sub>9</sub> (AT) <sub>5</sub> C(AT) <sub>3</sub> (GT) <sub>14</sub> A(TG) <sub>7</sub>	51	168	<i>L. culineris</i>	Genomic
36.	SSR130	F CCACGTATGTGACTGTATG R GAAAGAGAGGCTGAAACTTTG	(GT) <sub>9</sub>	55	196	<i>L. culineris</i>	Genomic
37.	SSR 167	F CACATATGAAGATTGGTCAC R CATTATGTCTCACACACAC	(TA) <sub>16</sub> (TG) <sub>21</sub>	54	160	<i>L. culineris</i>	Genomic
38.	SSR 199	F GTGTGCATGGCGTGTG R CCATCCCCCTCTATC	(GT) <sub>4</sub> GC(GT) <sub>8</sub> GC(GT) <sub>3</sub>	51	182	<i>L. culineris</i>	Genomic
39.	SSR 212-1	F GACTCACTGTTGTACCC	(AT) <sub>2</sub> (TC) <sub>26</sub> (AC) <sub>8</sub>	50	181	<i>L. culineris</i>	Genomic

40.	SSR 215	R GCGAGAAGAATGGGTG F CATTAAATATTTCTTTGGTGC R CTTTCTTCTCTTCCCC	(CA) <sub>15</sub> (TA) <sub>25</sub>	50	331	<i>L. culineris</i>	Genomic
41.	SSR 233	F CTTGGAGCTGTTGGTC R GCCGCCTACATTATGG	(GT) <sub>9</sub>	52	111	<i>L. culineris</i>	Genomic
42.	SSR 336	F GTGTAACCAACTGTTCC R GGCCGAGTTGTAACAC	(TAA) <sub>6</sub> AGA(TAA) <sub>4</sub>	54	253	<i>L. culineris</i>	Genomic
43.	PEAATPSYND	F CTCAGCCATCATAGTCGAAG R TCACAACCGAAGTCACAACC	(AC) <sub>6</sub>	58	-	<i>P. sativum</i>	Genic
44.	PSBLOX13.1	F GAACTAGAGCTGATAGCATGT R GCATGCAAAAAGAACGAAACAGG	(AT) <sub>17</sub>	54	-	<i>P. sativum</i>	Genomic
45.	PSGAPA1	F GACATTGTTGCCAATAACTGG R GGTCTGTCTCAATACAAG	(AT) <sub>17</sub>	51	-	<i>P. sativum</i>	Genic
46.	PSADHI	F GATGTGATAGGCCTAGAACAAAGC R CAGTCACACACTACAAGAGATC	(AT) <sub>10</sub>	54	-	<i>P. sativum</i>	Genomic
47.	PEACPLHPPS	F GTGGCTGATCCTGTCAACAA R CAACAACCAAGAGCAAAGAAAA	(AT) <sub>6</sub>	58	-	<i>P. sativum</i>	Genic
48.	CHPSTZPP	F TGAATAAAGGGCAGAGTTAATACA R GAATCACGGGACCAAAAACC	(AT) <sub>6</sub>	55	-	<i>P. sativum</i>	Genomic
49.	PSY14273	F AATTCGGCACGAGGAGAGA R TGCAGCCTTGAGCTGGTTAT	(TC) <sub>18</sub>	50	-	<i>P. sativum</i>	Genic
50.	PSU58830	F CACTCCATTTTCACCACCT R AGCATTGAAGAACAAAAGCACT	(TC) <sub>8</sub>	55	-	<i>P. sativum</i>	Genic
51.	PSARGDECA	F CTGTTCTCTTTCAAGCACTCC R GGGAAAGCAAAGCATGCGGATC	(TC) <sub>6</sub>	58	-	<i>P. sativum</i>	Genic
52.	PSP4OSG	F CAACCAGCATTATACACAAACA R GGCAATAAAGCAAAGCAGA	(AAT) <sub>36</sub>	58	-	<i>P. sativum</i>	Genomic
53.	PSAS	F GGTGATAACTATTTGGCTCATC R GTAGATTTCTCCATTACCTG	(AAT) <sub>6</sub>	54	-	<i>P. sativum</i>	Genic
54.	PSCAB66	F CACACGATAAGAGCATCTGC R GCTTGAGTTGCTTGCCAGCC	(CAT) <sub>5</sub>	55	-	<i>P. sativum</i>	Genomic
55.	PSBT2AGEN	F GCAGCAGAGCTTGCTTTGAG R GGAATCAGAAACAGCCTTGGG	(CCT) <sub>5</sub>	58	-	<i>P. sativum</i>	Genic
56.	PEAOM14A	F GGTGCCCTAGCATTTGCTG R TAGTAACAACCGCTCAAA	(CCT) <sub>5</sub>	60	-	<i>P. sativum</i>	Genic
57.	PSLEGKL	F CCATTCATACAGTATGCTCT R ATAGTTAGTACTATACACACC	(GAA) <sub>8</sub>	50	-	<i>P. sativum</i>	Genomic
58.	PSU51918	F GTCGTAACAGATCAATATGGC R CGATAGTGAGGTGGCGGTTG	(GAA) <sub>6</sub>	54	-	<i>P. sativum</i>	Genic

1-4, 9: Winter et al. 1999; 6-8: Buhariwalla et al. 2005; 10-14: Qadir et al. 2007; 15-30: Blair et al. 2003; 31-42: Hamweih et al. 2005; 43- 58: Burstin et al. 2001.

**Table 2.** Cross genera amplification of different SSR markers .

Marker	Genotypes						Allele Size (bp)	No.of Alleles	PIC value
	Asha	UPAS 120	Bahar	67 B	Type 7	Dholi dwarf			
TR 1	+	+	+	+	+	+	370	2	0.00
TR 20	+	+	-	-	-	-	370	2	0.64
TA 59	+	-	-	-	-	-	150	2	0.98
TA 96	+	-	-	+	+	-	380	1	0.75
TA 76 S	+	+	+	+	+	+	600	1	0.00
AGLC 16	+	+	+	-	+	+	210	1	0.31
AGLC 34	+	+	+	+	+	+	410	2	0.00
AGLC 52	+	+	+	+	+	+	400	1	0.00
TR 26	+	+	+	+	+	+	500	1	0.00
NPS 2	+	+	-	+	+	+	300	1	0.31
NPS 5	+	-	+	-	-	-	400	1	0.99
NPS 7	+	+	+	+	+	+	136	1	0.00
NPS 13	+	+	+	+	+	+	170	1	0.00
NPS 35	+	-	+	+	+	+	500	1	0.31
BMd 26	+	+	+	-	-	-	280	1	0.75
BMd 27	+	+	+	+	+	-	250	2	0.06
BMd 28	+	+	+	-	-	-	290	2	0.64
BMd 35	+	+	+	+	+	+	1000	3	0.75
BMd 47	+	+	+	+	+	+	300	2	0.00
BMd 48	+	+	+	+	+	+	140	2	0.66
BMd 52	+	+	+	+	+	+	300	1	0.00
BMd 53	-	-	-	-	-	+	200	1	0.97
BMd 55	+	-	-	+	+	+	200	2	0.45
BMd 12	+	+	+	+	+	+	460	3	0.72
BMd 33	+	-	-	-	+	+	290	1	0.75
BMd 39	+	-	-	-	-	+	490	2	0.89
BMd 40	-	-	-	-	-	+	300	1	0.97
BMd 41	-	-	-	-	-	+	900	2	0.94
BMd 42	+	-	-	-	-	-	200	1	0.97
BMd 43	+	-	-	-	-	+	700	1	0.89
SSR 13	+	+	+	+	+	+	500	1	0.00
SSR 48	+	+	+	-	-	-	150	1	0.75
SSR 59-2	+	+	+	+	+	+	400	1	0.00
SSR 99	+	+	+	+	+	+	500	1	0.00
SSR 107	-	+	+	+	+	+	180	1	0.31
SSR 130	+	+	+	-	+	+	500	1	0.31
SSR 167	+	+	+	-	-	-	300	1	0.75
SSR 199	+	+	-	-	-	-	500	1	0.89
SSR 212-1	+	+	+	+	+	-	150	1	0.31
SSR 215	+	+	+	-	-	-	200	1	0.75
SSR 233	-	+	+	+	+	+	250	1	0.31
SSR 336	+	+	+	-	-	-	200	1	0.75
PEAATPSYD	+	-	-	-	-	+	320	1	0.89
PSBLOX13.1	+	-	-	-	-	+	400	4	0.64
PSGAPA1	+	-	-	-	-	-	340	2	0.86
PSADH1	+	+	-	-	-	+	520	2	0.64
PEACPLHPPS	+	+	-	+	+	-	410	4	0.61
CHPSTZPP	+	-	-	-	-	-	550	2	0.78
PSY14273	-	-	-	-	-	+	800	2	0.95

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PSU58830	-	-	-	-	-	+	390	2	0.95
PSARGDECA	+	-	-	-	-	+	600	3	0.67
PSP4OSG	+	-	-	-	-	+	500	4	0.56
PSAS	+	-	-	-	-	+	350	1	0.89
PSCAB66	+	-	-	-	-	-	600	2	0.78
PEAATPSYD	+	-	-	-	-	+	600	2	0.64
PEAOM14A	+	-	-	-	-	+	700	2	0.83
PSLEGKL	+	-	+	-	+	-	230	2	0.64
PSU51918	+	+	+	+	+	+	180	2	0.11

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