

Table 3: SSR-based markers of *Acanthaceae* family genome sequences

Contigs	Forward primer	Temperature forward (°C)	Reverse primer	Temperature reverse (°C)	Product size (bp)
gij441482147 gb KC118349.1	TTTGCTTATCTCCATAAAG	50.105	TGAGATAATCTTTGGAATTG	50.305	275
gij147883767 gb EF214648.1	CTTCTTCCCTTTTTCTAAGT	49.881	CTTGAATTGCAAACAAAA	50.503	174
gij167595818 gb EU431055.1	AATTCCTTATTTGGCTATCT	50.127	GTCTATCCTCTCTGGTCTTT	49.896	138
gij167595792 gb EU431029.1	CAAAATCAACACAAAAGAGAT	50.166	GTAAGGAGTCTGTCTTCTC	50.331	225
gij167595823 gb EU431060.1	AATTCCTTATTTGGCTATCT	50.127	CCTCTCTGGTCTTTCTCTAT	50.124	130
gij158668364 gb EU081072.1	AAATGCATTGTGTAAGAATC	50.231	ATTCTCTATTCAAGCAACAA	50.123	117
gij307950703 gb HM470027.1	ATAAACAAATGCACCTTCAAT	49.944	CATAAGTTGCCTGTAAAAAT	49.886	263
gij307950699 gb HM470023.1	ACTAGAGCATAGCTTTTGTG	50.024	CTTTAAATTCATTGGTGATG	50.759	148
gij307950693 gb HM470017.1	CACAAAATGCACATAAATAA	49.829	ACTGAATGTCATAATGTGTG	48.677	229
gij307950691 gb HM470015.1	GTTCACTGCTTACTGTCATT	50.134	AAGGCCTTTCTATCATAAGT	50.082	271
gij307950689 gb HM470013.1	ATAAACAAATGCACCTTCAAT	49.944	CATAAGTTGCCTGTAAAAAT	49.886	263
gij307950683 gb HM470007.1	GAACAGTTGCTCTATACTGG	49.929	AGGAGAAATAAAAGTTGGTT	49.981	259
gij307950700 gb HM470024.1	ACTTCTTGATTCTAATGGGT	50.407	AACCAAGAACAAAACAGTAA	50.008	105
gij307950696 gb HM470020.1	ATATTCACAAGGAACAGTTG	50.022	AAGGAAATAAAAGTTGGTT	49.981	270
gij307950690 gb HM470014.1	TGAGAAGGATGTTAAAGAA	50.106	TAACACACGAAAGGTTAAAT	50.106	240
gij307950680 gb HM470004.1	GTTCACTGCTTACTGTCATT	50.134	AAGGCCTTTCTATCATAAGT	50.082	271
gij187950111 gb EU528996.1	AATTCCTTATTTGGCTATCT	50.127	CCTCTCTGGTCTTCTCTATT	50.124	159
gij87133115 gb DQ372453.1	TTGGAAATTCTTTTTGTTAC	49.791	CTCTTACTGCTATTTTTCCA	50.058	240
gij66815240 gb DQ059262.1	TTGAATAAAAAGCAGTCAAT	50.298	TTGTGTTGATATTGTTCAA	49.814	266
gij476002153 gb JX461339.1	GTATCCTATTGATTGTCAG	49.654	TACTAAAGGGGCATATACAG	49.839	272
gij401716762 gb JX445148.1	GTATCCTATTGATTGTCAG	49.654	TACTAAAGGGGCATATACAG	49.839	272
gij343530772 gb HQ172893.1	GATACCTTTGGTTACACAGA	50.022	CACTCATATCGGACAACAT	49.937	209
gij343530770 gb HQ172891.1	TCTCAACTGATTACCTCAAC	49.977	GGATAAACCACTTTGTATCA	50.073	206
gij343530771 gb HQ172892.1	CTCACAGTCCAAAATATAGC	49.982	ATATTCACACAGGTTGTTGT	50.082	266
gij343530769 gb HQ172890.1	CATGAATTGGAACAATAACT	50.073	CCAATCAAGATGCAAAAT	49.603	121
gij78499527 gb DQ240231.1	AATGCACAATAAAACAAATC	50.402	AATTTCTGCATACTTCTTGA	50.123	257
gij78499525 gb DQ240229.1	CCAATTTTATGTCATAGTTT	50.073	TTGAGTGATTTTCATTTCTT	49.882	173
gij78499523 gb DQ240227.1	GCAATGAAATTACAAAAGAG	50.298	ATTATTTGTTTGGAGTGTG	50.205	137
gij78499521 gb DQ240225.1	TCATGTCATAGTTTTTCTCC	50.03	TTGAGCTAAATATCATTCC	49.764	202
gij78499519 gb DQ240223.1	TAATTCTGAAGAAGAGTGGA	49.92	TATAGTCAATTTCGGCTACTC	49.757	199
gij78499517 gb DQ240221.1	TTCTTAGCGTGGTAAGTAAG	50.232	CCTGACAGTGTTATCCATTC	50.326	241
gij54292642 gb AY741808.1	ATTTTACACCTATATGAATGG	49.254	ACGTGCATATATTTTGTGAGT	49.993	168
gij54292640 gb AY741806.1	ATTATGACTAAAATGCTCCA	50.033	AATTAATAAAGGGAGAAGC	49.993	218
gij54292638 gb AY741804.1	AATCAAGTTGCTCAAGTAAA	50.254	TGTTAACAGGTTTTTCAAAT	50.058	222
gij54292636 gb AY741802.1	AACGCAGATAAATCCCT	50.241	TGAAAAGAGAGAGATGTTG	50.359	151
gij54292634 gb AY741800.1	TTTTCTCAGAGATGCTAGAC	49.592	CATATTAGGACTTGGAAACA	50.295	278
gij33439455 gb AY281862.1	AACAATGAAAGGATTTTGTA	49.928	TATGACAGAAGGTTTGTCTC	49.977	275
gij33439453 gb AY281860.1	ATTATCCTAACCAATCCTTC	50.043	GGACTAACAAACATGAGAAA	50.166	238
gij33439451 gb AY281858.1	GCTGAATATACCTTTCTGTG	49.982	GCTCATTATTGAAACTATGG	50.033	211
gij30961874 gb AY283927.1	TCCTTCTGTTCTTTAACTGT	49.06	CGACTTCTAGCAACTAACAC	50.257	211
gij78499528 gb DQ240232.1	AAGATTACCCCATTTATTTT	49.948	AACTTTCTATAAAGGGGAAG	49.802	194
gij78499526 gb DQ240230.1	TGTATGAAATCTAGGTGGAG	50.116	AAAGGACATTATTTATGGTG	49.389	251
gij78499524 gb DQ240228.1	CACCATCAAAGAATTACACT	50.022	GTTTAGCCTGATAAGTTGAG	49.375	183
gij78499522 gb DQ240226.1	TATGAATTACGGCAAGTATT	50.254	TACAATAGATCGATCACACA	49.514	152
gij78499520 gb DQ240224.1	TATTTGGTTGTATTTGGTTT	49.972	GATTGACCATTAGACTTGAA	50.03	279
gij78499518 gb DQ240222.1	TTGCTAGAATAGCAGAATTT	49.806	ACACAAATAACAATCCAAC	49.982	233
gij78499516 gb DQ240220.1	ACTTGAGATTCACATAGCAC	49.994	TGTATTCACCTATTTGATCC	49.94	257
gij54292635 gb AY741801.1	TGGCATTCTGTATTTATCT	50.033	AGCAACTACCAAGTGAGTAA	50.065	226
gij54292633 gb AY741799.1	CCTAATTTATTTGATGAAAA	49.796	CCTCAAGTGCATCTTATTAC	49.982	110
gij33439454 gb AY281861.1	CAGATGAAACTCAAGAGAAG	49.863	TACTGATTGAGACTGGTAGG	50.064	227
gij33439452 gb AY281859.1	TATTTTTCTTGTCTTTTTGG	50.004	GAGATATTTCAATCCATCCT	50.616	204
gij33439450 gb AY281857.1	GAAGGCTTTAAAATAGGATT	49.993	AAAATTTCAAATCACAAAGA	50.066	152
gij32966037 gb AY327547.1	AATACAGCGACAACAATAAT	49.993	GTAGGAAGGTCGGTATTTAT	50.213	138
gij158832352 dbj AB300577.1	AGAATTTGGCATCTGGT	50.834	GCGCTCTCTCTCTCTCT	49.994	126
gij30961873 gb AY283926.1	ATCTGGTGCATACTACTTGT	49.551	GTTGGGAGCTCTAGTGA	48.573	170
gij30961871 gb AY283924.1	CATGATAAAGTAGGGTTTTG	50.01	AAATAAGCTTAGTATTTGCG	49.769	174

Contd...

Table 3: Contd...

Contigs	Forward primer	Temperature forward (°C)	Reverse primer	Temperature reverse (°C)	Product size (bp)
gi 30961868 gb AY283921.1	TTATGAGTTCGATACGTAGG	50.531	GAAGAGTGAGTGTGTTTCTC	49.306	156
gi 30961872 gb AY283925.1	TTAGAAAAGTGGAGCAGTAG	50.008	TAAAACGACACCTTTTAAAT	49.576	167
gi 30961870 gb AY283923.1	GACTGAGTAAGCACACAGAT	49.938	CTCCAGCTGTAATCTTCATA	50.503	120

SSRs: Simple sequence repeats

typhoid fever, and tuberculosis.^[19] The SSR-based primers/markers have an extensive application in plant genetics and breeding. Hence, in our study, the potential SSR-based forward and reverse primers were designed for 59 out of 108 nucleotide sequences of the *Acanthaceae* species including *Avicennia germinans*, *Avicennia alba*, *Blepharis subvolubilis*, *Ruellia ciliatiflora*, *Ruellia nitida*, *Ruellia eurycodon*, *Ruellia pedunculosa*, *Aphanosperma sinaloensis*, *Kalbreyeriella rostollata*, *Aphelandra verticillata*, *A. paniculata*, and *A. ilicifolius*.

CONCLUSION

Microsatellites or SSRs play a major role in polymorphism analysis and in marker assisted selection. *In silico* approach for predicting SSRs in the whole genome, was found to be both cost and time effective and also helps to develop a new generation of molecular markers as well. In our study, the microsatellites and its associated primers were identified for the publically available *Acanthaceae* family genomes using computational methods. The identified microsatellites and markers might pave the way for further studies in the aspect of breeding and genetic studies of the plants that belong to the family *Acanthaceae*.

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