

# Microsatellite analysis in the genome of *Acanthaceae*: An *in silico* approach

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Submitted: 09-01-2014

Revised: 19-05-2014

Published: 21-01-2015

## ABSTRACT

**Background:** *Acanthaceae* is one of the advanced and specialized families with conventionally used medicinal plants. Simple sequence repeats (SSRs) play a major role as molecular markers for genome analysis and plant breeding. The microsatellites existing in the complete genome sequences would help to attain a direct role in the genome organization, recombination, gene regulation, quantitative genetic variation, and evolution of genes. **Objective:** The current study reports the frequency of microsatellites and appropriate markers for the *Acanthaceae* family genome sequences. **Materials and Methods:** The whole nucleotide sequences of *Acanthaceae* species were obtained from National Center for Biotechnology Information database and screened for the presence of SSRs. SSR Locator tool was used to predict the microsatellites and inbuilt Primer3 module was used for primer designing. **Results:** Totally 110 repeats from 108 sequences of *Acanthaceae* family plant genomes were identified, and the occurrence of dinucleotide repeats was found to be abundant in the genome sequences. The essential amino acid isoleucine was found rich in all the sequences. We also designed the SSR-based primers/markers for 59 sequences of this family that contains microsatellite repeats in their genome. **Conclusion:** The identified microsatellites and primers might be useful for breeding and genetic studies of plants that belong to *Acanthaceae* family in the future.

**Key words:** *Acanthaceae*, microsatellites, molecular markers

*Acanthaceae* is one of the major groups in angiosperms and the plants, which belong to this family are mostly tropical herbs, shrubs, and rarely trees.<sup>[1]</sup> *Acanthaceae* family has about 202 genera and 3520 species, and most of this family members are well-known medicinal plants (e.g. *Acanthus ilicifolius*, *Andrographis paniculata*, *Asteracantha longifolia*, *Hemigraphis birta*, *Justicia adhatoda*, *Nelsonia canescens*, etc.) used in traditional medicine as they possess biologically active phytochemicals.<sup>[1-3]</sup> The medicinal plants of this family are enriched with secondary metabolites such as alkaloids, flavanoids, glycosides, steroids, saponins, phenols, and tannins. The phytochemicals obtained from these plants are used to treat diarrhea, snake bite, fever, inflammation, hypertension, diabetes, malaria, jaundice, and rheumatism.<sup>[1,3,4]</sup>

Simple sequence repeats (SSRs) or microsatellites are the short DNA sequences with 1-6 base pairs of length.<sup>[5]</sup>

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### Access this article online

#### Website:

www.phcog.com

#### DOI:

10.4103/0973-1296.149731

#### Quick Response Code:



Several studies suggest that the abundance of SSRs were present in noncoding regions of the genome sequences.<sup>[6]</sup> These repeats have a wide application in the field of plant genetics and breeding as they have multi-allelic, reproducible and co-dominant inheritance properties.<sup>[7]</sup> The microsatellites were identified in the genomes of many medicinal plants such as *Humulus lupulus* (hop),<sup>[8]</sup> *Ocimum basilicum* (basil)<sup>[9]</sup> and also for some economically important plants including *Oryza sativa* (rice),<sup>[10]</sup> *Glycine max* (soybean),<sup>[11]</sup> *Hordeum vulgare* L. (barley), *Triticum aestivum* (wheat), *Solanum lycopersicum* (tomato), *Vitis vinifera* (grape), and *Helianthus annuus* (sunflower).<sup>[9]</sup> The SSRs also provide basis for the development of SSR-based markers that have a wide range of application in genetic research including studies of genetic variation, linkage mapping, gene tagging, and evolution.<sup>[7]</sup>

The objective of this study includes identification of microsatellites and its associated primers in the genome of *Acanthaceae* family. In the current study, the different types of SSRs and its distribution from 108 sequences and 59 associated primers were identified. We also reported that the amino acid isoleucine was enriched in all the above SSRs in the genome sequences of *Acanthaceae* family.

## MATERIALS AND METHODS

### Nucleotide sequence retrieval

Totally 4077 nucleotide sequences were retrieved from National Center for Biotechnology Information for *Acanthaceae* family plants.<sup>[12]</sup>

### Identification of simple sequence repeat motifs

In order to identify the microsatellites from the genome of *Acanthaceae* family, the SSR Locator computing tool was used.<sup>[13]</sup> It is integrated with the functions such as primer design and PCR simulation.<sup>[14]</sup> The sequences were searched for mono-, di-, tri-, tetra-, penta- and hexa-types of SSR motifs with number of repeats 20, 10, 7, 5, 4, and 4, respectively. The enriched amino acids in the predicted SSRs were also identified using the above mentioned SSR Locator tool.

### Simple sequence repeat-based primer designing

The *in silico* based primers for each microsatellite containing nucleotide sequences were designed using Primer3, the interface module in the SSR Locator.<sup>[14]</sup> The default parameters such as length of the primer (15-25 base pairs), melting temperature (45-55°C) and GC content (45%) were specified for primer designing.

## RESULTS

### Simple sequence repeat identification and distribution in the genome

The SSR motifs were identified from 4077 nucleotide sequences of the *Acanthaceae* family plants with 31,41,420 base pairs. Totally we found 110 SSR motifs from 108 nucleotide sequences using SSR Locator tool. The microsatellites such as mononucleotide (32%), dinucleotide (50%) and tetranucleotide (11%) were found abundant in number in *Acanthaceae* family plants. The trimer, pentamer and hexamer motifs occurred comparatively less (about 2%) in the nucleotides. A summary of the predicted SSRs in the sequences was shown in Table 1. The distribution of SSR motifs in the *Acanthaceae* genome was shown in Figure 1.

The mononucleotides, including A and T were found abundant in the *Acanthaceae* family genomes. We also found eight different dinucleotide repeats (TG, AC, CA, AG, GT, TC, GA, and CT), which were found in about 50% of this genome. TCA, ATC, CAT were identified as trinucleotide repeats and the ATC repeat showed a higher frequency. There were nine tetranucleotide repeats such as AGAC, TATG, ATAC, ACAT, GTAT, TAGA, TATT, CTAT and ATAG with the frequencies of 5, 12, 9, 11, 8, 5, 5, 7, and 5, respectively. The occurrences of pentanucleotide and

hexanucleotide are comparatively less in number. TTGAT, a pentanucleotide and two hexanucleotides TTTCTT and TATATC were found in the *Acanthaceae* family genomes with frequencies of 8, 4, and 5, respectively. The distribution of above mentioned repeats (from mono- to tetra-) were shown in Figure 2.

### Frequency of amino acids in the microsatellites

The combination of three nucleotides/triplet codon generally codes for a specific amino acid type. In this study, we found that the trinucleotide repeat ATC was enriched in this genome and it predominantly codes for the essential amino acid isoleucine. The other SSR motifs encode the amino acids including histidine, serine, tyrosine, phenylalanine, leucine, arginine, and lysine that occupied the next levels of this genome. The types of SSRs along with codon and its specific amino acids were shown in Table 2.

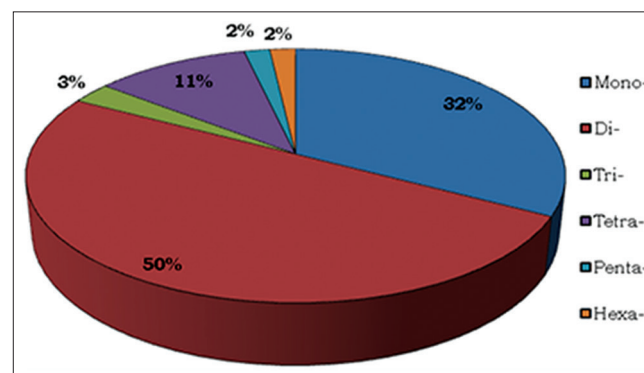
### Simple sequence repeat-based primers/markers

The designing of SSR-based primers/markers through experiments are costly and time consuming as well. Hence, using *in silico* primer designing methods, 59 out of 108 nucleotide sequences exhibited the primers. The designed

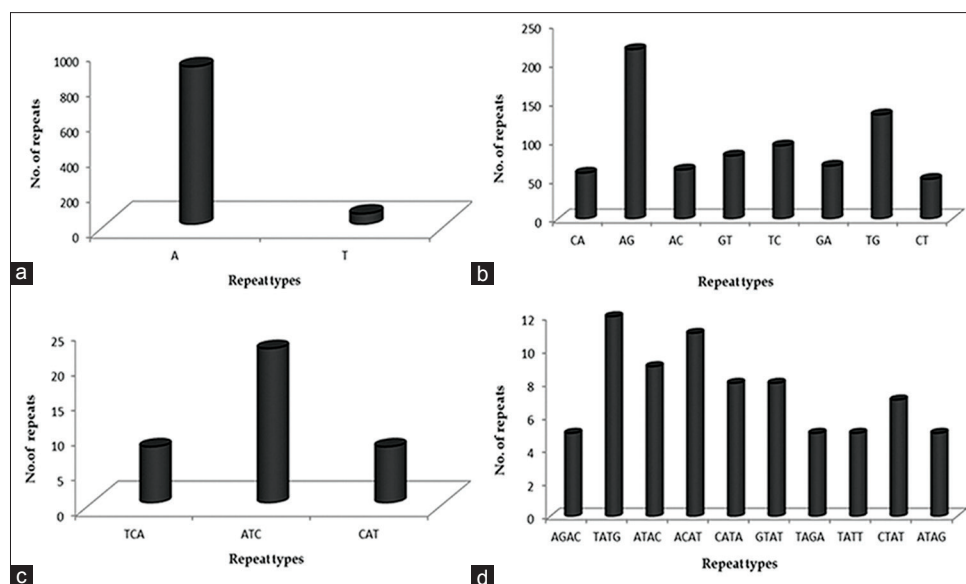
**Table 1: Summary of the screened microsatellites in the genome of *Acanthaceae***

Parameters	Values
Total number of sequences examined	4077
Total size of examined sequences (bp)	31,41,420
Total number of identified SSRs	110
Number of SSR containing sequences	108
Number of sequences containing more than 1 SSR	2
Mono-repeats	36
Di-repeats	55
Tri-repeats	3
Tetra-repeats	12
Penta-repeats	2
Hexa-repeats	2

SSRs: Simple sequence repeats



**Figure 1: Frequency of simple sequence repeat motifs in the nucleotide sequences of *Acanthaceae* family plant genomes**



**Figure 2:** Frequency distribution of (a) mononucleotide, (b) dinucleotide, (c) trinucleotide, and (d) tetranucleotide repeats in the genome of *Acanthaceae*

**Table 2: Microsatellites and its corresponding amino acids in the genome sequences of *Acanthaceae* family plants**

Microsatellite	Number of bases	Number of repeats	Codon	Amino acid
ATC	3	22	AUC	Ile
CAT	3	8	CAU	His
TCA	3	8	UCA	Ser
TATATC	6	5	UAU/AUC	Tyr/Ile
TTTCTT	6	4	UUU/CUU	Phe/Leu
ATATATAGA	9	3	AUA/ UAU/AGA	Ile/Tyr/Arg
TTCTAAAA	9	3	UUC/ UAA/AAA	Phe/Stop codon/Lys

forward and reverse primers of this genome also have adequate annealing temperature and GC content as well. The nucleotide accession numbers, forward and reverse primer sequences, melting temperature and product size of the designed primers were given in Table 3.

## DISCUSSION

The genome sequences of *Acanthaceae* family plants were retrieved and examined to know the occurrence of microsatellite types, characteristics and distribution. The length of microsatellites 1-6 base pairs were taken into consideration. Totally, we screened 110 SSRs from 108 out of 4077 nucleotide sequences. The occurrence of dinucleotide repeats was comparatively higher than all other repeat types including mono-, tri-, tetra-, penta-, and hexa-repeats and the same repeats pattern was reported in *Arabidopsis thaliana*.<sup>[15,16]</sup> Among mononucleotides, A/T repeat was found to be

abundant than C/T repeat in which repeat A (94%) is higher than T repeat. The dinucleotide repeat AG showed a higher frequency (28%) among eight other dinucleotide repeats such as TG (17%), TC (12%), GT (11%), GA (9%), AC (8%), CA (8%), and CT (7%) in the *Acanthaceae* family plants. The studies on medicinal plant *O. basilicum* and other plants, including *Arabidopsis thaliana*, *T. aestivum*, *H. vulgare* L., *O. sativa*, *Zea mays*, and *Prunus dulcis* also proposed that the frequency of AG repeats was higher than other dinucleotide repeats.<sup>[9]</sup> The trinucleotide repeat ATC (52%) was observed high in number than other trinucleotide repeats TCA (14%) and CAT (14%). The same trinucleotide repeat pattern was reported in *Gossypium* (cotton) (*Gossypium arboreum*, *Gossypium raimondii*, and *Gossypium hirsutum*) and *Arabidopsis thaliana* genomes.<sup>[16,17]</sup> The AT rich repeats were abundantly found in tetranucleotides of this family genome. The penta- and hexa-repeats were found in less frequency compared with other repeat types. We also identified that the repeat ATC, which codes for the essential amino acid isoleucine were found to be enriched in trinucleotide to hexanucleotide repeats and the amino acids serine and histidine were seen in less frequency in this genome. It was reported that the same amino acid distribution pattern was seen in the genome of *H. lupulus*.<sup>[8]</sup> The amino acid isoleucine plays a major role in maintaining blood sugar level. Therefore the *Acanthaceae* species such as *Adhatoda vasica*, *A. paniculata*, *A. longifolia*, *Barleria cristata*, *Barleria noctiflora*, *Barleria prionotis*, *Dipteracanthus prostrates*, *Jacobinia suberecta*, and *Strobilanthus crispus* have been used to treat diabetes in the traditional system of medicine as they contain enriched isoleucine in their genomes.<sup>[18]</sup> Moreover, the plants such as *Hygrophila auriculata*, *N. canescens*, and *Peristrophe bicalyculata* were also used to treat various infectious diseases such as diarrheal diseases, cholera,

**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	ATAAACAAATGCACCTCAAT	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	ATAAACAAATGCACCTCAAT	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	TTGGAAATCTTTTTGTTAC	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	CCAATTTTCATGTCATAGTTT	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	TATAGTCAATTCCGGCTACTC	49.757	199
gij78499517 gb DQ240221.1	TTCTTAGCGTGGTAAGTAAG	50.232	CCTGACAGTGTTATCCATTC	50.326	241
gij54292642 gb AY741808.1	ATTTTCACCTATATGAATGG	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	TGAAAAGAGAGAGATGTTTG	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.<sup>[19]</sup> 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 subvulvibilis*, *Ruellia ciliatiflora*, *Ruellia nitida*, *Ruellia eurycodon*, *Ruellia pedunculosa*, *Aphanosperma sinaloensis*, *Kalbreyeriella rostellata*, *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*.

## REFERENCES

- Alam AH, Rashid MH, Rahman MA, Baki MA, Sadik MG. Chemical constituents of *Hemigraphis hirta* T. Anders. (*Acanthaceae*). Pak J Biol Sci 2002;5:1264-6.
- Bhatt A, Naidoo Y, Nicholas A. The foliar trichomes of *Hypoestes aristata* (Vahl) Sol. ex Roem. and *Schult var aristata* (*Acanthaceae*) a widespread medicinal plant species in tropical sub-Saharan Africa: With comments on its possible phylogenetic significance. Biol Res 2010;43:403-9.
- Islam MT, Das PR, Kabir MH, Akter S, Khatun Z, Haque MM, et al. *Acanthaceae* and *Asteraceae* family plants used by folk medicinal practitioners for treatment of malaria in Chittagong and Sylhet Divisions of Bangladesh. Am Eurasian J Sustain Agric 2012;6:146-52.
- Sawadago WR, Meda A, Lamien CE, Kiendrebeogo M, Guissou PI, Nacoulma OG. Phenolic content and antioxidant activity of six *Acanthaceae* for Burkina Faso. Asian Netw Sci Inf 2006;6:249-52.
- Li C, Zhang Y, Ying K, Liang X, Han B. Sequence variations of simple sequence repeats on chromosome-4 in two subspecies of the Asian cultivated rice. Theor Appl Genet 2004;108:392-400.
- Sathishkumar R, Lakshmi PT, Annamalai A, Arunachalam V. Mining of simple sequence repeats in the Genome of *Gentianaceae*. Pharmacognosy Res 2011;3:19-29.
- Gupta PK, Varshney RK. The development and use of microsatellite markers for genetic analysis and plant breeding with emphasis on bread wheat. Euphytica 2000;113:163-85.
- Singh S, Gupta S, Mani A, Chaturvedi A. Mining and gene ontology based annotation of SSR markers from expressed sequence tags of *Humulus lupulus*. Bioinformatics 2012;8:114-22.
- Gupta S, Shukla R, Roy S, Sen N, Sharma A. *In silico* SSR and FDM analysis through EST sequences in *Ocimum basilicum*. Plant Omics J 2010;3:121-8.
- Rajendrakumar P, Biswal AK, Balachandran SM, Srinivasarao K, Sundaram RM. Simple sequence repeats in organellar genomes of rice: Frequency and distribution in genic and intergenic regions. Bioinformatics 2007;23:1-4.
- Li AQ, Zhao CZ, Wang XJ, Liu ZJ, Zhang LF, Song GQ, et al. Identification of SSR markers using soybean (*Glycine max*) ESTs from globular stage embryos. Electron J Biotechnol 2010;13:1-11.
- Available from: <http://www.ncbi.nlm.nih.gov/nuccore/?term=Acanthaceae>. [Last accessed on 2013 Jun 10].
- Available from: <http://www.minerva.ufpel.edu.br/~lmaia/faem/>. [Last accessed on 2013 Aug 05]
- Da Maia LC, Palmieri DA, de Souza VQ, Kopp MM, De Carvalho FI, Costa de Oliveira A. SSR Locator: Tool for simple sequence repeat discovery integrated with primer design and PCR simulation. Int J Plant Genomics 2008;2008:412696.
- Tóth G, Gáspári Z, Jurka J. Microsatellites in different eukaryotic genomes: Survey and analysis. Genome Res 2000;10:967-81.
- Cardle L, Ramsay L, Milbourne D, Macaulay M, Marshall D, Waugh R. Computational and experimental characterization of physically clustered simple sequence repeats in plants. Genetics 2000;156:847-54.
- Yuan D, Liang S, Lin Z, Zhang X. *In silico* comparative analysis of EST-SSRs in three cotton genomes. Afr J Biotechnol 2012;11:13269-371.
- Soumyanath A. Traditional Medicines for Modern Times: Antidiabetic Plants. USA: CRC Taylor and Francis Publication; 2006. p. 49.
- Nabere O, Adama H, Samson G, Kiessoum K, Patrice Z, Roland MN, et al. Antibacterial and phytochemical studies of three *Acanthaceae* species used in Burkina Faso traditional medicine. J Appl Pharm Sci 2013;3:49-55.

**Cite this article as:** Kaliswamy P, Vellingiri S, Nathan B, Selvaraj S. Microsatellite analysis in the genome of *Acanthaceae*: An *in silico* approach. Phcog Mag 2015;11:152-6.

**Source of Support:** Nil, **Conflict of Interest:** None declared.