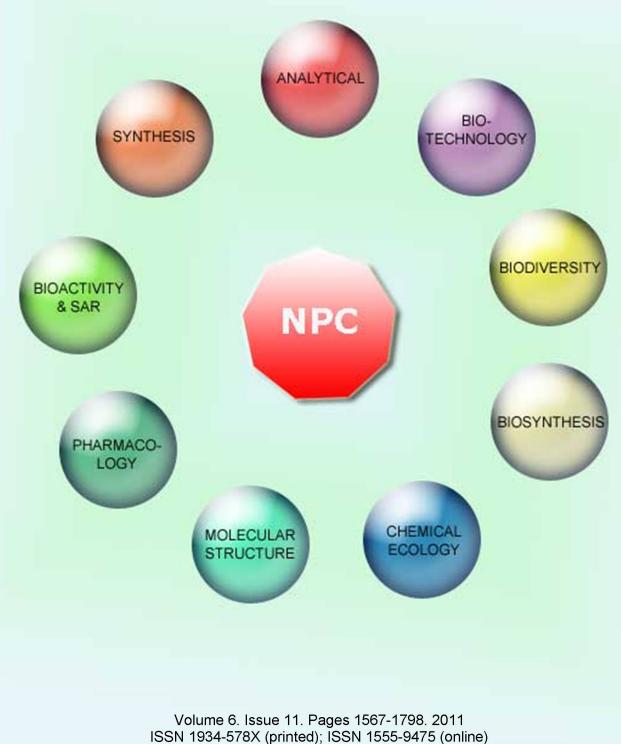
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AFLP Marking and Polymorphism among Progenies of *Gymnema sylvestre*: an Important Medicinal Plant of India

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The level of polymorphism among twelve selected progenies of *Gymnema sylvestre* was investigated through AFLP markers by multiplexing PCR reactions using 64 (8x8) primer combinations. Fourteen primer combinations were selected as the most suitable combination for *G. sylvestre*. Analysis of the 12 progenies with these 14 primer pairs produced 1689 fragments of which 972 (57.5%) were polymorphic and 485 (28.7%) were unique to a particular genotype. The number of fragments produced by individual primer pairs was in the range of 55 to 225. Out of these, polymorphic fragments were in the range of 34 (E-ACC/M-CAC) to 157 (E-AGG/M-CAG) and unique bands observed were 8 (E-ACC / M-CAC) to 69 (E-AGG/M-CAC). Different primer combinations detected different levels of polymorphism, ranging from 33% (E-AGG/ M-CAC) to 69.8% (E-AGG/ M-CAC). From the observations, it appears that the primer combinations E-AGG/M-CAC, E-AGG/CAG and E-ACA / CAT were the most informative for the detection of polymorphism among the progenies compared with others, since they produced a high number of unique fragments. The similarity coefficient ranged from 0.212 to 0.731. High similarity was observed between progeny S8 and S9 (73%) and high divergence between progenies S3 and S11. Among the selected progeny, S9 was found to be the most similar to the parent (63%), while genotype S11 was the most distant (36.9%).

Keywords: AFLP, DNA polymorphism, DNA markers, Gymnema sylvestre, Gurmar, triterpenoid saponins, glycosides, hypoglycemia.

Gymnema sylvestre R Br., (family Asclepiadaceae), is a large, stout, woody climber used as a stomachic, diuretic, and laxative, and for the treatment of sore throat and diabetes [1,2]. Leaves of this species, when chewed, have a unique property of antagonizing the sweet taste of sugar [3]. The leaf extract was found to contain glycosides of gymnemic acid possessing hypoglycemic activity [4,5]. The genetic variability in *G. sylvestre* (Chakkarakolli) was assessed using morphological and biochemical markers by Nair and Keshavachandran [6].

Advances in molecular biology during the last decade have provided a new class for studying variations at the DNA level through development of DNA markers. These genetic markers were found to be extremely useful in differentiating individuals compared with either phenotypic or protein markers. The DNA markers have been used to evaluate genetic diversity in different crop species [7]. They detect variations in the amplified DNA regions as in the case of RAPD (Random Amplified Polymorphic DNA), STSP (Sequence Tagged Site Polymorphism) and AFLP (Amplified Fragment Length Polymorphism). The AFLP technique combines the power of restriction fragment length polymorphism (RFLP) with the flexibility of PCR-based technology. The fingerprints are produced without prior knowledge of sequence by using a limited set of primers. This technique has been extensively used and well preferred to other DNA based markers because of its high multiplex ratio and nonrequirement of prior sequence information [8]. These markers consist largely of non coding DNA [9]. The AFLP markers that make up the fingerprint are often concentrated in the centromeric regions [10]. The patterns obtained from different strains are polymorphic due to mutations in the restriction sites, mutations in the sequences adjacent to the restriction sites and complementary to the selective primer extensions, and insertion and deletions within the amplified fragments [11].

AFLP markers have found genetic variation below the species level, particularly in the investigation of population structure and differentiation [12]. In this study, AFLP was employed to detect the genetic divergence of progeny of *G. sylvestre* from the parent. Therefore, the major objective of the present study was to investigate, the level of polymorphism among parent and progeny of *G. sylvestre* by AFLP.

Analysis of 12 *G. sylvestre* progenies with the 14 primer pairs revealed a total of 1689 bands (Table 1) of which 972 (57.5%) were polymorphic and 485 (28.7%) were unique

Serial No.	Primer combination EcoRI / MseI	Total number of bands	Number of polymorphic bands	Number of monomorphic bands	Number of unique bands	Percent Polymorphism
1	ACA/CAC	96	52	31	13	54.2
2	AGG / CAC	132	44	19	69	33.3
3	ACC / CAC	55	34	13	8	61.8
4	ACA / CTA	146	101	16	29	69.2
5	AGG / CTA	106	64	8	34	60.4
6	ACC / CTA	99	53	22	24	53.5
7	ACA / CAT	178	113	13	52	63.5
8	AGG / CAT	131	84	10	37	61.1
9	ACA / CAG	108	66	16	26	59.6
10	AGG / CAG	225	157	14	54	69.8
11	ACC / CAG	72	41	14	18	56.9
12	ACA / CTG	102	49	20	33	48.0
13	AGG / CTG	154	70	17	66	45.5
14	ACC / CTG	85	43	20	22	50.6
Total		1689	972	233	485	
Polymorphism%			57.5	13.8	28.7	

Table 1: AFLP primer combinations, total number of bands, unique, monomorphic and polymorphic fragments generated by each primer combination used in the study of *G. sylvestre* accessions

Table 2: AFLP similarity coefficients for twelve genotypes of G. sylvestre

	Р	S2	S3	S4	S 5	S 7	S8	S 9	S10	S11	S12	S13
Р	1.000											
S2	0.572	1.000										
S3	0.414	0.466	1.000									
S4	0.530	0.587	0.586	1.000								
S 5	0.535	0.642	0.519	0.705	1.000							
S7	0.546	0.476	0.354	0.498	0.607	1.000						
S8	0.589	0.531	0.435	0.570	0.548	0.689	1.000					
S9	0.630	0.555	0.454	0.538	0.567	0.629	0.731	1.000				
S10	0.438	0.495	0.335	0.508	0.561	0.498	0.528	0.610	1.000			
S11	0.369	0.346	0.212	0.368	0.412	0.435	0.390	0.429	0.462	1.000		
S12	0.549	0.505	0.401	0.482	0.594	0.577	0.567	0.610	0.452	0.473	1.000	
S13	0.473	0.539	0.332	0.482	0.484	0.362	0.429	0.478	0.489	0.321	0.432	1.000

to a particular genotype. The fragment sizes determined by comparing the amplicons with size standard DNA ranged from 30 - 400 bp and only a size more than 50 bp was considered for scoring the presence and absences of fragments. Data in Table I show that the total number of fragments detected by individual primer pairs ranged from 55 (E-ACA/ M-CAC) to 225 (E-AGG/M- CAG), and the number of polymorphic fragments from 34 (E-ACC/ M-CAC) to 157 (E-AGG/M-CAG). Also, individual primer combinations gave a range of 8 to 69 unique bands. Different primer combinations detected different levels of polymorphism ranging from 33% detected by primer combination E-AGG/ M-CAC to 69.8% for the combination E-AGG/M-CAC. From the results, it appears that the primer combinations E-AGG/M-CAC, E-AGG/CTG, E-AGG/CAG and E-ACA/CAT were most informative in detecting polymorphism among the genotypes compared with others since they have produced high numbers of unique fragments.

Genetic similarity and cluster analysis

A genetic similarity matrix was generated based on correlation coefficients using AFLP data for the assessment of genetic relatedness among the 12 progenies. The similarity coefficients ranged from 0.212 to 0.731. The high similarity was between progenies S8 and S9 (73%) and high divergence was between progenies S3 and S11 (Table 2). Among the selected progenies, S9 was found to be the most similar to Parent (63%), followed by

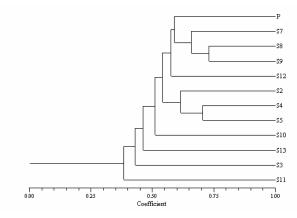


Figure 1: A dendrogram generated based on AFLP data using UPGMA cluster analysis among 12 genotypes of *Gymnema sylvestre*

progeny S8 (58%), while progeny S11 was the most distant (36.9%). Clustering of progenies based on genetic similarity is displayed in Figure 1, in which progeny S8 and S9 sub-cluster together sharing 73% of the fragments. Similarly, progeny S4 and S5 sub-clustered together sharing 70% of similarity. This study assessed the level of polymorphism among *Gymnema* progenies as well as the potential of the AFLP technique in analyzing the genetic variation in closely related genotypes.

The AFLP showed enough sensitivity to detect the polymorphism among parent and seed raised progenies of

G. sylvestre at the molecular level, which will be further used to discriminate the parent and progeny. AFLP has been proved to be the most powerful and reliable marker and revealed much higher levels of polymorphism irrespective of complexity of genome [13-15]. The results obtained will provide a basis for identification and development of molecular markers in this important antidiabetic plant of India, the natural resources of which are fast disappearing due to its overexploitation [16].

Experimental

Amplified fragment length polymorphism

Plant material and genomic DNA isolation: The plant materials comprised of twelve genotypes (one parent and 11 seed progenies) of *Gymnema sylvestre* maintained at CIMAP Conservatory, Lucknow, India. Leaves were collected from the plants and DNA isolated from leaf tissue according to the protocol described by Khanuja *et al.* [17] and quantified by loading on agraose gel together with known amounts of Lambda Hind III Eco RI DNA marker.

DNA restriction and ligation reactions: Genomic DNA was restricted with 2 restriction endonucleases, EcoRI and Tru 9I (an isoschizomer of MseI), and double stranded adaptor was ligated to the ends of DNA fragments, for subsequent generating template DNA PCR amplifications. Restriction and ligation reactions were carried out simultaneously in a single reaction [13]. To carry out the reaction, an enzyme master mix was prepared (for 10 reactions) containing 1 µL (10X) T₄ DNA ligase buffer, 1 µL (0.5 M) NaCl, 0.5 µL (1 mg/mL) BSA, 1 µL Tru 9I (10U/ µL), 4.25 µL EcoRI (12 U/µL), and 0.5 µL T_4 DNA ligase (20U/µL), and the volume was adjusted to 10 μ L by addition of 1.75 μ L double distilled water. The restriction-ligation reaction consisted of 300 ng of DNA (5.5 μ L), 1 μ L 10X T₄ DNA ligase buffer, 1.0 μ L 0.5 M NaCl, 0.5 µL (1mg/mL) BSA, 1 µL MseI Adaptors (Applied Biosystems), 1 µL EcoRI adaptors (Applied Biosystems) and 1 µL enzyme master mix, as described above. The reaction mix was incubated overnight at room temperature and subsequently diluted 20-fold with $T_{10}E_{0.1}$ (10 mM Tris and 0.1 mM EDTA) buffer. The ligated adaptors served as the primer binding site for the low-level selection in pre-selective amplification of the restriction fragments.

PCR amplifications

Preselective and selective amplification: The MseI complementary primer had a 3'- C and the EcoRI complementary primer a 3'-A. Only the genomic fragments having adaptor on each end amplified exponentially during PCR. The pre-selective amplification mixture was prepared by adding 4 μ L of 20 fold diluted DNA from the restriction ligation reaction, 0.5 μ L AFLP pre-selective primers (EcoRI, Applied Biosystems), 0.5 μ L AFLP pre-selective primer (MseI, Applied Biosystems), and 15 μ L AFLP core mix. The pre-selective amplification

was carried out in a thermal cycler programmed at 72°C for 2 min, followed by 20 cycles of 94°C for 20 sec, 56°C for 30 sec. 72°C for 2 min. 60°C for 30 min and finally incubated at 4°C. The amplified DNA was diluted 20 fold with $T_{10}E_{0,1}$ buffer and selective amplifications were carried out using different combinations of MseI and EcoRI primers. Sixteen out of the available AFLP primers (8 fluorescent labeled EcoRI and 8 unlabeled MseI) were chosen for amplifications. The EcoRI primers contained 3 selective nucleotides with the sequence 5' -[Dye-primer-Axx]- 3', and the MseI primers had the selective nucleotides starting with C 5' -[primer-Cxx]- 3'. The explorer gel for all 64 reactions was run with sample P (Parent) to determine the most responsive primer pairs that generate the greater number of fragments. Multiplexing PCRs was designed to set up all 64 (8 X 8) reactions in 24 tubes. Selective amplification reactions contained 3 µL of 20- fold diluted pre-selective amplification reaction products, 15 µL AFLP core mix, 1 µL MseI primer 5' -[primer-Cxx]- 3', 1.5 µL EcoRI primers 5' -[primer-Cxx]-3' (0.5 μ L of 3 primers each were pooled here). Selective amplification was carried out in a thermal cycler programmed at 94°C for 2 min, followed by 10 cycles of 94°C for 20 sec, 66°C for 30 sec and 72°C for 2 min with a subsequent hold for 30 min at 60°C and final incubation at 4°C.

Gel electrophoresis of PCR amplicons: Samples were loaded on 5% polyacrylamide gel on an ABI Prism 377 DNA sequencer (Applied Biosystem). The selective amplification reaction product $(3 \mu L)$ was mixed with $4 \mu L$ loading buffer (10% ROX 500 size standard, 10% blue dextran, 80% deionized formamide), from which 1.5 µL was finally loaded on the gel. The data for explorer gel was processed to determine the most efficient primer combinations providing the maximum number of fragments to carry out the AFLP reactions for the whole samples. The most suitable primer combinations for these samples under study were E-ACA /M- CAC. E-AGG/ M-CAC, E-ACC/ M-CAC, E-ACA/ M-CTA, E-AGG / M-CTA, E-ACC/ M-CTA, E-ACA/ M-CAT, E-AGG/ M-CAT, E-ACA/ M-CAG, E-AGG / M-CAG, E-ACC/ M-CAG, E-ACA/ M-CTG, E-AGG / M-CTG, E-ACC/ M-CTG. All samples were then subjected to selective amplification with these primer combinations, as above.

AFLP data analysis: Data were analyzed by scoring presence and absence of bands from the amplified products and similarity matrixes were obtained using software SPSS for windows (Jaccard correlations) and averages of the pooled similarity of the whole primers were used for clustering based on the UPGMA (Unweighted Pair Group Method with Arithmetic average) method using NTSY2.1 software program.

Analysis of amplified fragment length polymorphism: The AFLP data were converted from binary data matrix to a diagonal matrix format (Table 2) using SPSS v10.0 Software by calculating the similarities through Jaccard's coefficient (1908) [18]. The genetic similarities (GS) were estimated between the 8 primer combinations according to Jaccard's coefficient. These AFLP data were clustered using the NTSYS – pc statistical package v.17 [19]. A dendrogram was constructed employing the UPGMA (Unweighted Pair Grouping Method of Arithmetic averages) method according to Sneath and Sokal [20] to group the individuals into discrete clusters (Figure 1).

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Effects of pH, Sample Size, and Solvent Partitioning on Recovery of Soluble Phenolic Acids and Isoflavonoids in Leaves and Stems of Red Clover (<i>Trifolium pratense</i> cv. Kenland)	
Isabelle A. Kagan	1657
Arbutin Derivatives from the Seeds of <i>Madhuca latifolia</i> Shazia Khan, M. Nadeem Kardar and Bina S. Siddiqui	1661
Quinic Acids from <i>Aster caucasicus</i> and from Transgenic Callus Expressing a β-Amyrin Synthase Paola Pecchia, Maria Cammareri, Nicola Malafronte, M. Federica Consiglio, Maria Josefina Gualtieri and Clara Conicella	1665
Cytotoxic Activity and Cell Cycle Analysis of Hexahydro-curcumin on SW 480 Human Colorectal Cancer Cells Chung-Yi Chen, Woei-Ling Yang and Soong-Yu Kuo	1671
Does the Combination of Resveratrol with Al (III) and Zn (II) Improve its Antioxidant Activity? Karina Dias and Sofia Nikolaou	1673
Photosensitization Mechanisms of Triplet Excited Stateβ-Lapachone. A Density Functional Theory Study Liang Shen	1677
AFLP Marking and Polymorphism among Progenies of <i>Gymnema sylvestre</i> : an Important Medicinal Plant of India Magda Abbaker Osman, Sunita Singh Dhawan, Janak Raj Bahl, Mahendra P Darokar and Suman P S Khanuja	1679
Antioxidant Activity of Protein Hydrolysates from Aqueous Extract of Velvet Antler (<i>Cervus elaphus</i>) as Influenced by Molecular Weight and Enzymes	
Lei Zhao, Yang-Chao Luo, Cheng-Tao Wang and Bao-Ping Ji	1683
Effects of <i>Sideritis euboea</i> (Lamiaceae) Aqueous Extract on IL-6, OPG and RANKL Secretion by Osteoblasts Eva Kassi, Anna Paliogianni, Ismene Dontas, Nektarios Aligiannis, Maria Halabalaki, Zoi Papoutsi, Alexios-Leandros Skaltsounis and Paraskevi Moutsatsou	1689
In vitro Antiprotozoal Activity of Extracts of five Turkish Lamiaceae Species	1009
Hasan Kirmizibekmez, Irem Atay, Marcel Kaiser, Erdem Yesilada and Deniz Tasdemir	1697
Antimicrobial Investigation of <i>Linum usitatissimum</i> for the Treatment of Acne Pratibha Nand, Sushma Drabu and Rajinder K Gupta	1701
Chemical and Biological Diversity in Fourteen Selections of Four Ocimum Species Bhaskaruni R. Rajeswara Rao, Sushil K. Kothari, Dharmendra K. Rajput, Rajendra P. Patel and Mahendra P. Darokar	1705
Environmental Effect on Essential Oil Composition of <i>Aloysia citriodora</i> from Corrientes (Argentina) Gabriela Ricciardi, Ana Maria Torres, Ana Laura Bubenik, Armando Ricciardi, Daniel Lorenzo and Eduardo Dellacassa	1711
Essential Oil of Three Uvaria species from Ivory Coast Koffi A. Muriel, Tonzibo Z. Félix, Gilles Figueredo, Pierre Chalard and Yao T. N'guessan	1715
Composition of the Essential Oil of <i>Origanum tyttanthum</i> from Tajikistan Farukh S. Sharopov, Muhamadsho A. Kukaniev and William N. Setzer	1719
Volatiles of French Ferns and "fougère" Scent in Perfumery Didier Froissard, Françoise Fons, Jean-Marie Bessière, Bruno Buatois and Sylvie Rapior	1723
Volatile Constituents of Two Species of <i>Protium</i> from the Atlantic Rainforest in the State of Pernambuco, Brazil José Gildo Rufino de Freitas, Claudio Augusto Gomes da Camara, Marcílio Martins de Moraes and Henrique Costa Hermenegildo da Silva	1727
Volatile Constituents of Two Hypericum Species from Tunisia Karim Hosni, Kamel Msaâda, Mouna Ben taârit, Thouraya Chahed and Brahim Marzouk	1731
Chemical Composition and Possible <i>in vitro</i> Antigermination Activity of Three <i>Hypericum</i> Essential Oils	1.01
Aurelio Marandino, Laura De Martino, Emilia Mancini, Luigi Milella and Vincenzo De Feo	1735
Antioxidant, Antimicrobial Activities and Fatty Acid Components of Flower, Leaf, Stem and Seed of <i>Hypericum scabrum</i> Ali Shafaghat	1739
Composition of Three Essential Oils, and their Mammalian Cell Toxicity and Antimycobacterial Activity	1757
against Drug Resistant-Tuberculosis and Nontuberculous Mycobacteria Strains Juan Bueno, Patricia Escobar, Jairo René Martínez, Sandra Milena Leal and Elena E. Stashenko	1743
Antimicrobial and Antioxidant Activities of the Flower Essential Oil of <i>Halimodendron halodendron</i> Jihua Wang, Hao Liu, Haifeng Gao, Jianglin Zhao, Ligang Zhou, Jianguo Han, Zhu Yu and Fuyu Yang	1749
Composition and Antimicrobial Activity of the Leaf and Twig Oils of <i>Litsea acutivena</i> from Taiwan Chen-Lung Ho, Pei-Chun Liao, Eugene I-Chen Wang and Yu-Chang Su	1755
Chemical Composition and Antimicrobial Activity of the Volatile Oil from <i>Fusarium tricinctum</i> , the Endophytic Fungus in <i>Paris polyphylla</i> var. <i>yunnanensis</i>	
Ying Zhang, Jianglin Zhao, Jihua Wang, Tijiang Shan, Yan Mou, Ligang Zhou and Jingguo Wang	1759
Antifungal Activity of Essential Oil from Asteriscus graveolens against Postharvest Phytopathogenic Fungi in Apples Mohamed Znini, Gregory Cristofari, Lhou Majidi, Hamid Mazouz, Pierre Tomi, Julien Paolini and Jean Costa	1763
Interspecies Comparison of Chemical Composition and Anxiolytic-like Effects of Lavender Oils upon Inhalation Mizuho Takahashi, Tadaaki Satou, Mai Ohashi, Shinichiro Hayashi, Kiyomi Sadamoto and Kazuo Koike	1769
Essential Oils from the <i>Hyptis</i> genus- A Review (1909-2009) Megil McNeil, Petrea Facey and Roy Porter	1775

Natural Product Communications 2011

Volume 6, Number 11

Contents

<u>Original Paper</u>	Page
Antifungal Activity of Plumericin and Isoplumericin Dharmendra Singh, Umakant Sharma, Parveen Kumar, Yogesh K. Gupta, M. P. Dobhal and Sarman Singh	1567
A New Diacylated Labdane Diterpenoid from Andrographis wightiana Jalli Madhu Sudhana, Rachakunta Munikishore, Mopuru Vijayabhaskar Reddy, Duvvuru Gunasekar, Alain Blond and Bernard Bodo	1569
Triterpenoid Acids and Lactones from the Leaves of <i>Fadogia tetraquetra</i> var. <i>tetraquetra</i> (Rubiaceae) Dulcie A. Mulholland, Abdelhafeez M.A. Mohammed, Philip H. Coombes, Shafiul Haque, Leena L. Pohjala, Päivi S.M. Tammela and Neil R. Crouch	1573
Isolation of Friedelin from Black Condensate of Cork Ricardo A. Pires, Ivo Aroso, Susana P. Silva, João F. Mano and Rui L. Reis BIO	1577
Novel Microbial Transformation of Resibufogenin by Absidia coerules Jian Zheng, Dong-hai Su, Dong-sheng Zhang, Xiu-Lan Xin, Jun-ying Liu, Yan Tian, Qing Wei and Xun Cui	1581
Antidiabetic Activity of <i>Terminalia sericea</i> Constituents Nolitha Nkobole, Peter James Houghton, Ahmed Hussein and Namrita Lall	1585
X-ray Crystallographic Study of Ranaconitine Yang Li, Jun-hui Zhou, Gui-jun Han, Min-juan Wang, Wen-ji Sun and Ye Zhao	1589
Obscurine: a New Cyclostachine Acid Derivative from <i>Beilschmiedia obscura</i> Bruno Ndjakou Lenta, Jean Rodolphe Chouna, Pepin Alango Nkeng-Efouet, Samuel Fon Kimbu, Etienne Tsamo and Norbert Sewald	1591
Alkaloids from Papaver coreanum BIODIVERS Dong-Ung Lee, Jong Hee Park, Ludger Wessjohann and Jürgen Schmidt BIODIVERS	1593
Isolation, Structure Elucidation, and Biological Activity of a New Alkaloid from Zanthoxylum rhetsa Karsten Krohn, Stephan Cludius-Brandt, Barbara Schulz, Mambatta Sreelekha and Pottachola Mohamed Shafi	1595
Amplexicine, an Antioxidant Flavan-3-ol from <i>Polygonum amplexicaule</i> Mudasir A. Tantry and Aziz A. Rahman	1597
A New Flavonoid Glycoside from Vaccaria hispanica Haijiang Zhang, Kuiwu Wang, Jie Wu, Yao Chen and Peipei He	1599
Flavonoids from Algerian Endemic <i>Centaurea microcarpa</i> and their Chemotaxonomical Significance Souheila Louaar, Amel Achouri, Mostefa Lefahal, Hocine Laouer, Kamel Medjroubi, Helmut Duddeck and Salah Akkal	1603
On-line (HPLC-NMR) and Off-line Phytochemical Profiling of the Australian Plant, <i>Lasiopetalum macrophyllum</i> Michael Timmers and Sylvia Urban	S ₁₆₀₅
Chemical Fingerprint Analysis of Phenolics of <i>Albiziachinensis</i> Based on Ultra-Performance LC-Electrospray Ionization-Quadrupole Time-of-Flight Mass Spectrometry and Antioxidant Activity Abha Chaudhary, Pushpinder Kaur, Neeraj Kumar, Bikram Singh, Shiv Awasthi and Brij Lal	1617
Application to Classification of Mulberry Leaves using Multivariate Analysis of Proton NMR Metabolomic Data Eriko Fukuda, Motoyuki Yoshida, Masaki Baba, Yoshihiro Uesawa, Ryuichiro Suzuki, Osamu Kamo, Koji Tsubono, Kazunori Arifuku, Kazuhisa Yatsunami and Yoshihito Okada	1621
Phenolic Constituents of Knautia arvensis Aerial Parts Jaroslaw Moldoch, Barbara Szajwaj, Milena Masullo, Lukasz Pecio, Wieslaw Oleszek, Sonia Piacente and Anna Stochmal	1627
New Acylated Anthocyanins and Other Flavonoids from the Red Flowers of <i>Clematis</i> Cultivars Masanori Hashimoto, Toshisada Suzuki and Tsukasa Iwashina	1631
Prenylated Isoflavonoids from <i>Rhynchosia edulis</i> Ifedayo V. Ogungbe, Gabrielle M. Hill, Rebecca A. Crouch, Bernhard Vogler, Meenakshi Nagarkoti, William A. Haber and William N. Setzer	1637
Antiparasitic and Antimicrobial Isoflavanquinones from <i>Abrus schimperi</i> Aziz A. Rahman, Volodymyr Samoylenko, Surendra K. Jain, Babu L. Tekwani, Shabana I. Khan, Melissa R. Jacob, Jacob O. Midiwo, John P. Hester, Larry A. Walker and Ilias Muhammad	1645
Two New Rotenoids from <i>Boerhavia repens</i> Mamona Nazir, Muhammad Saleem, Naheed Riaz, Maria Hafeez, Misbah Sultan, Abdul Jabbar and Muhammad Shaiq Ali	1651
A Comparison of the Diastereoisomers, Silybin A and Silybin B, on the Induction of Apoptosis in K562 cells Jiyong Zhang, Qiuying Luan, Yanze Liu, David Y-W Lee and Zhao Wang	1653

(Continued inside back cover)