

International Journal of Plant Breeding

Abbreviation: Intl. J. Plant Breeding

Print: ISSN 1752-3478

Frequency and Peer status: Biannual, Peer reviewed

Scope and target readership: The *International Journal of Plant Breeding* deals with all issues related to plant breeding, in theory or in practice.

The primary themes that the journal covers include:

- 1) Understanding of plant reproductive systems that advance our knowledge of plant breeding concepts;
- 2) Breeding for disease resistance (and elucidation of immunity, resistance, susceptibility and tolerance);
- 3) Molecular markers and molecular techniques for selection of new traits (marker-assisted selection);
- 4) Breeding for innovative traits, improved quality (flavour, nutrition, aroma, or other);
- 5) Breeding for enhanced stress resistance (biotic and abiotic);
- 6) Gene flow from cultivated to wild populations, and screening of wild relatives for breeding programmes;
- 7) Effect of breeding systems on the environment and biodiversity;
- 8) Hormonal, physiological, environmental, genetic, biophysical, developmental or molecular approaches to the study of plants used in breeding systems

Editor-in-Chief

Jaime A. Teixeira da Silva, Kagawa University, Japan

Technical Editor

Kasumi Shima, Japan

Statistics Advisor

Marcin Kozak, Warsaw University of Life Sciences, Poland

Editorial Board and Advisory Panels (Listed alphabetically)

Niranjana Baisakh, Louisiana State University, USA
Ahmet Balkaya, University of Ondokuz Mayıs, Turkey
Harbans S. Bariana, University of Sydney, Australia
Saikat Kumar Basu, University of Lethbridge, Canada
Jer-Chia Chang, Council of Agriculture, Taiwan
Samir C. Debnath, Atlantic Cool Climate Crop Research Centre, Agriculture and Agri-Food Canada, Canada
Jai Gopal, Central Potato Research Institute, India
Pranab Hazra, Bidhan Chandra Krishi Viswavidyalaya, India
Aisha Saleem Khan, Kinnaird College for Women, Pakistan
Marcin Kozak, Warsaw University of Life Sciences, Poland
Sean Mayes, University of Nottingham, UK
Sisir Mitra, Bidhan Chandra Krishi Viswavidyalaya, India
Reda Moghaieb, Cairo University, Egypt
Sanjib Nandy, Lethbridge Research Centre, Agriculture and Agri-Food Canada, Canada
Christopher Ochieng Ojiewo, The World Vegetable Centre, Tanzania
Suprasanna Penna, Bhabha Atomic Research Centre, India
Salehi Jouzani Gholam Reza, Agricultural Biotechnology Research Institute of Iran, Iran
Nedeljka Rosic, University of Queensland, Australia
Hossein Sabouri, Gorgan University of Agricultural Sciences & Natural Resources, Iran
Kin-Ying To, Academia Sinica, Taiwan
Rajeev K. Varshney, International Crops Research Institute for the Semi-Arid Tropics, India

Global Science Books, Ltd.
Editorial Office
Miki cho Post Office, Kagawa ken, Kita gun
Miki cho, Ikenobe 3011-2, P.O. Box 7
761-0799, Japan



Head Office: Isleworth, United Kingdom
Accounting: Lagos, Portugal

GSB homepage: www.globalsciencebooks.info
Journals web-page: <http://www.globalsciencebooks.info/Journals/GSBJournals.html>
IJPB web-page: <http://www.globalsciencebooks.info/Journals/IJPB.html>
GSB Japan web-page: <http://www17.plala.or.jp/gsbjapan>
GSB™ is a trademark of Global Science Books, Ltd.

International Journal of Plant Breeding ©2009 Global Science Books, Ltd.

All rights reserved. No parts of this journal may be reproduced, stored in a retrieval system or transmitted in any form or by any means, electronic, mechanical, photocopying, microfilming, recording, or otherwise without written permission from Global Science Books, Ltd.

For additional copies, photocopies, bulk orders, or copyright permissions, please refer requests in writing to the above address, or apply online.

Cover photos/figures: Left: Infection type variation observed among F₃ families derived from the 'Kalka'/'Bansi' cross (Qamar *et al.*, pp 99-102). Top right: Amplification profile of the marker SCAR 937 (14f/r) in pigeon pea parents and bulks (Prasanthi *et al.*, pp 134-138). Bottom right: Variability in glory lily (*Gloriosa superba* L.) leaves and flowers (Rajagopal and Kandhasamy, pp 139-143).

Disclaimers: All comments, conclusions, opinions, and recommendations are those of the author(s), and do not necessarily reflect the views of the publisher, or the Editor(s). GSB does not specifically endorse any product mentioned in any manuscript, and accepts product descriptions and details to be an integral part of the scientific content.

Printed in Japan on acid-free paper.
Published: December, 2009.

CONTENTS

Ignacio Crippa, Carolina Bermejo, María A. Espósito, Eugenia A. Martín, Vanina Cravero, David Liberatti, Fernando S. López Anido, Enrique L. Cointry (Argentina) Genetic Variability, Correlation and Path Analyses for Agronomic Traits in Lentil Genotypes	76
Sergei Volis, Irina Shulgina (Israel), Samuel Mendlinger (Israel/USA), Mel Oluoch (Tanzania) Genetic Structure in Two African Vegetable Nightshade Species	81
Sergei Volis (Israel), Samuel Mendlinger (USA), Irina Shulgina (Israel), Mel Oluoch (Tanzania) Genetic Diversity in Tanzanian Accessions of <i>Brassica carinata</i> A. Braun	86
Mohammad Javad Yousefi, Mohammad Esmaeil Hassani, Gholamreza Salehi Jouzani, Hassan Maddah Arefi, Matin Mohammadipour (Iran) Genetic Variation of Some Iranian Black Henbane Accessions (<i>Hyoscyamus niger</i> L.) using RAPD and SDS-PAGE of Seed Proteins	92
Zia-ul Qamar, Urmil K. Bansal, Harbans S. Bariana (Australia) Genetics of Stem Rust Resistance in Three Durum Wheat Cultivars	99
Abdullah Abdulaziz Al-Doss, Khaled Ahmed Moustafa, Eid Ibrahim Ahmed, Adel Ahmed Elshafei, Mohamed Najeb Barakat (Saudi Arabia) Assessment of Genetic Diversity in Saudi Wheat Genotypes under Heat Stress Using Molecular Markers and Agronomic Traits	103
Danial Kahrizi (Iran) Study of Androgenesis and Spontaneous Chromosome Doubling in Barley (<i>Hordeum vulgare</i> L.) Advanced Lines Using Isolated Microspore Culture	111
Mudasir Hafiz Khan, Abdul Nayeem Dar (India) Heterosis in Soybean [<i>Glycine max</i> (L.) Merrill]	115
A. K. Atwal, Manoj Kumar, Pratibha Chauhan, Chhaya Atri, J. S. Kular, Sarwan Kumar, Surinder S. Banga (India) Myrosinase-Glucosinolate System in Crop <i>Brassica</i> species: Variation and Association with Defensive Responses to <i>Pieris brassicae</i> Infestation	121
Abdel-Tawab Fatthy Mohamed, Eman Mahmoud Fahmy, Abd-Elwahab Ismael Allam, Sabry Abdalla Khatab, Ahmed Ibrahim Abdel Fatah, Osama Ezzat El-Sayed, Rashad Mahmoud Mohamed Shoaib (Egypt) Molecular Genetic Characterization of Some Promising Sugarcane Varieties under Smut Disease	126
Lakki Reddy Prasanthi, Bommu Veera Bhaskara Reddy, Kokkanti Rekha Rani, Yeturu Siva Prasad, Thovi Rajeswari, Kondreddy Raja Reddy (India) Development of Sequence Characterized Amplified Region (SCAR) Marker for Fusarium Wilt Resistance Gene in Pigeon Pea (<i>Cajanus cajan</i> L. Millsp.)	134
Chitra Rajagopal, Rajamani Kandhasamy (India) Genetic Variability, Heritability and Scope of Improvement for Yield Components in Glory Lily (<i>Gloriosa superba</i> L.)	139
Mani Ramakrishnan, Lingaiah Rajanna, Narayanaswamy Papanna (India), Luke Simon (India/UK) Assessment of Genetic Relationship and Hybrid Evaluation Studies in Tea (<i>Camellia</i> sp.) by RAPD	144
Néji Tarchoun, Abdelaziz Mougou (Tunisia) Combining Ability and Heterosis for Earliness Flowering and Fructification on Pepper (<i>Capsicum annuum</i> L.) Grown Under Low Night Temperature	149

Ignacio Crippa, Carolina Bermejo, María A. Espósito, Eugenia A. Martin, Vanina Cravero, David Liberatti, Fernando S. López Anido, Enrique L. Cointry (Argentina) Genetic Variability, Correlation and Path Analyses for Agronomic Traits in Lentil Genotypes (pp 76-80)

ABSTRACT

Original Research Paper: Lentil (*Lens culinaris* Medik) is a diploid, autogamous species and is one of the oldest crops in the world. In Argentina, one of the most common problems is the narrow genetic base which must be broadened to provide greater production stability. The objectives were to study the genetic variation for different agronomic traits, the phenotypic and genotypic correlation coefficients among these traits and the direct and indirect effects of these traits on seed yield and to characterize the germplasm for use as parents in a breeding program. Thirty genotypes were evaluated. The collected data were analyzed to determine significant varietal differences by employing Principal Component Analysis (PCA). Genotypic and phenotypic correlation coefficients were estimated and Path coefficient analysis was calculated. Highly significant differences among genotypes for all traits recorded were found indicating the presence of genetic variability; thus broad-sense heritability estimates were high for all traits under study indicating little environmental influence. Correlation analysis indicated that the values of genotypic correlations were slightly higher, in general, than the phenotypic correlations. Different morphological traits showed significant direct and indirect effects on number of pods per plant. Number of branches had the greatest direct effect on number of pods per plant ($p = 0.40$) followed by total number of nodes ($p = 0.27$); height of first pod showed a highly negative direct effect on pod number per plant ($p = -0.37$) and the highest moderate indirect negative effects via number of nodes at the first pod ($p = -0.24$). PCA allowed the discrimination of four groups of cultivars with higher similarity. Our results provide better insight regarding the relationship between various characters determining either timing of flowering or productivity, and provide information on the likely interest of a particular accession as a parent in initial crosses for breeding stable and high-yielding varieties.

Sergei Volis, Irina Shulgina (Israel), Samuel Mendlinger (Israel/USA), Mel Oluoch (Tanzania) Genetic Structure in Two African Vegetable Nightshade Species (pp 81-85)

ABSTRACT

Original Research Paper: Fifty one accessions from two African vegetable nightshade species, 29 accessions of *Solanum scabrum* and 22 accessions of *S. villosum* were collected in Tanzania and examined for the extent and structure of genetic variation within and among accessions and between species using random amplified polymorphic DNA (RAPD) markers. The two species are important leafy vegetables and are important contributors to the nutritional well being of small-scale subsistence farmers in much of sub-Saharan Africa. The two main research questions were: 1) can RAPDs efficiently distinguish two morphologically distinct species of *Solanum*? and 2) what is the spatial structure of the genetic variation in these two species? In this study the efficiency of RAPDs in clustering accessions by species was very high, further encouraging the use of RAPDs for inter- and intraspecific comparative studies. The spatial structure of genetic variation in the two species was distinctly different. *S. scabrum* accessions were genetically similar for a distance up to 50 km and regionally structured, possibly indicating an exchange of seeds among neighboring farms combined with genetic differentiation due to selection for distinct ecological niches. In *S. villosum* no spatial structure was found even at a scale of a few kilometers.

Sergei Volis (Israel), Samuel Mendlinger (USA), Irina Shulgina (Israel), Mel Oluoch (Tanzania) Genetic Diversity in Tanzanian Accessions of *Brassica carinata* A. Braun (pp 86-91)

ABSTRACT

Original Research Paper: We analyzed the extent and structure of genetic variation in *Brassica carinata*, an important sub-Saharan African leafy vegetable using RAPD markers. Sixty one accessions from 49 sites were collected in Tanzania over an area of almost 0.8 M km². Most variation, 88%, was among accessions, 4% was among regions and 8% within accessions. This pattern was reflected in the AMOVA, PCA and cluster analysis which failed to segregate accessions into regional or ecogeographic groups. We did find a pattern of spatial genetic structure at shorter distances with a significant relationship between genetic and geographic distance among accessions as revealed by a Mantel test combined with a significant autocorrelation effect at three geographic distances, 1, 5 and 7 km. This result corresponds well to the known exchange and sale of *B. carinata* seeds among neighbors, friends and family members in Tanzania. The recommended collection strategy

based on results of this study is concentrating on collecting a larger number of accessions in a few, easily to collect areas and fewer accessions in less accessible areas.

Mohammad Javad Yousefi, Mohammad Esmaeil Hassani, Gholamreza Salehi Jouzani, Hassan Maddah Arefi, Matin Mohammadipour (Iran) Genetic Variation of Some Iranian Black Henbane Accessions (*Hyoscyamus niger* L.) using RAPD and SDS-PAGE of Seed Proteins (pp 92-98)

ABSTRACT

Original Research Paper: Genetic diversity of 20 accessions of Iranian black henbane (*Hyoscyamus niger* L.) collected from various agro-ecological regions was studied using RAPD DNA markers and SDS-PAGE of seed proteins. Application of 16 RAPD arbitrary primers resulted in a total of 208 bands, in which 196 bands were polymorphic (94.31%). Comparisons, based on Jaccard's coefficient and UPGMA clustering, revealed a considerable level of genetic diversity among accessions. Maximum similarity was observed between Roodbar-2 and Siahkal-1 accession with 80% similarity, while maximum differences were observed between the Isfahan accession and other accessions, placing it in a separate group. Electrophoresis of total seed proteins also revealed polymorphisms among accessions and resulted in three main clusters. Seed protein profiles of black henbane accessions showed a relatively high level of intraspecific variability which coincides with the results of RAPD analysis. An average genetic similarity of 0.52 (ranging from 0.16 to 1.0) was found among the accessions. Cluster 1 divided in two subgroups in which Khalkhal and Roodbar-2 accessions with 100% similarity were in one subgroup, even though they originated from different geographical regions. Finally, the results of this study indicate that RAPD DNA markers and seed protein profiles seem to be suitable for assessing genetic diversity among *H. niger* accessions for future breeding programs.

Zia-ul Qamar, Urmil K. Bansal, Harbans S. Bariana (Australia) Genetics of Stem Rust Resistance in Three Durum Wheat Cultivars (pp 99-102)

ABSTRACT

Original Research Paper: Durum wheat cultivars 'Kalka', 'Gundaroi' and 'Tamaroi' were crossed with the susceptible landrace 'Bansi' to study inheritance of stem rust resistance. Seedling screening of F₃ populations using the *Puccinia graminis* f. sp. *tritici* (Pgt) pathotype 34-1,2,3,4,5,6,7 suggested monogenic control of resistance in cvs. 'Kalka', 'Gundaroi' and 'Tamaroi'. The pathotype 34-1,2,3,4,5,6,7 was avirulent for stem rust resistance genes (*Sr8b*, *Sr9e* and *Sr13*) reported in durum wheat cultivars. Tests with *Sr9e*-virulent and *Sr9e*+*Sr8b*-virulent pathotypes, 40-1,2,3,4,5,6,7 and 40-1,2,3,4,5,6,7,8,9,10,11, respectively, indicated the absence of *Sr9e* and *Sr8b* in these cultivars. Genetic association between stem rust response segregation and the chromosome 6AL located marker gwm427 led us to conclude the presence of *Sr13* in 'Kalka', 'Gundaroi' and 'Tamaroi'. The absence of segregation for susceptibility in the 'Kalka'/'Tamaroi' cross further supported the presence of a common gene for stem rust resistance in these cultivars. 'Gundaroi' and 'Tamaroi' are likely to carry the same resistance gene based on their pedigree. These results indicated a narrow genetic base of stem rust resistance in these durum cultivars. Incorporation of diverse sources of resistance into future durum cultivars is necessary.

Abdullah Abdulaziz Al-Doss, Khaled Ahmed Moustafa, Eid Ibrahim Ahmed, Adel Ahmed Elshafei, Mohamed Najeb Barakat (Saudi Arabia) Assessment of Genetic Diversity in Saudi Wheat Genotypes under Heat Stress Using Molecular Markers and Agronomic Traits (pp 103-110)

ABSTRACT

Original Research Paper: The objectives of this study were to compare the application and utility of random amplified polymorphic DNA (RAPD) and inter-simple sequence repeat (ISSR) marker techniques for analysis of genetic diversity among Saudi wheat genotypes under heat stress, to compare genetic diversity estimated using molecular markers with agronomic performance under heat stress and to establish the degree of association between these techniques and develop heat tolerance-associated DNA markers. Twelve wheat genotypes were used in this study. They were evaluated phenotypically for heat tolerance and were planted on two sowing dates (20th December and 20th January) over two seasons to expose genotypes to different levels of heat stress during the grain-filling period. The UPGMA dendrogram generated from standardized agronomic data separated the 12 wheat genotypes into three main groups. RAPD and ISSR markers were assayed to determine the genetic diversity of the 12 wheat genotypes. In RAPD analysis, 336 out of 343 bands (98%) were polymorphic while in ISSR analysis, 199 out of 254 bands (75.98%) were polymorphic. The dendrogram based on RAPD markers differed from that based on ISSR markers. The combined dendrogram agreed better with the groups of wheat

genotypes based on pedigree analysis. The correlation coefficient between RAPD and ISSR matrix was highly significant (0.53**, $p > 0.001$). Specific RAPD and ISSR markers were developed successfully to identify heat-tolerant 'Ksu106' from heat-sensitive 'Yecora Rojo'. Thus, the markers identified in this study should be applicable for marker-assisted selection for heat tolerance in wheat breeding programs.

Danial Kahrizi (Iran) Study of Androgenesis and Spontaneous Chromosome Doubling in Barley (*Hordeum vulgare* L.) Advanced Lines Using Isolated Microspore Culture (pp 111-114)

ABSTRACT

Original Research Paper: This research investigated androgenesis and spontaneous chromosome doubling of six barley advanced lines and Igri genotype using isolated microspore culture. Statistical analysis of embryogenesis and cytogenetic results showed that genotype significantly affected haploid embryogenesis and spontaneous chromosome doubling. Igri showed the highest potential to develop haploid embryos (1625 embryos from 100 anthers) whereas genotypes BAL012, followed by BAL056, BAL073, BAL041, BAL018 and BAL022 were low, forming 397, 381, 363, 325, 264 and 172 embryos from 100 anthers, respectively. The highest percentage of spontaneous chromosome doubling was observed for the genotype that had the lowest embryogenesis (BAL022) and the lowest was observed for the genotype with the highest embryogenesis (Igri). Andro-embryogenesis showed also comparatively higher genotypic and phenotypic coefficients of variation, heritability and genetic advance indicating pre-dominance of additive gene action for the control of this character in the material studied. A negative relationship ($r=-0.87$) was found between embryogenesis and spontaneous chromosome doubling in these barley genotypes. All large embryos used had high regenerability and formed normal plantlets.

Mudasir Hafiz Khan, Abdul Nayeem Dar (India) Heterosis in Soybean [*Glycine max* (L.) Merrill] (pp 115-120)

ABSTRACT

Original Research Paper: Ninety soybean hybrids derived from a line \times tester analysis along with their parents were evaluated at the Research Farm of Kisan (PG) College, Simbhaoli, to estimate heterosis over mid- and better-parent. Heterosis was positively significant for yield in 15 hybrids over better-parent and in 24 hybrids over mid-parent. Heterosis for yield was generally accompanied by heterosis for number of seeds/pod, number of pods/plant and pod length. For protein 16 and for oil 31 hybrids exhibited significant positive heterosis over better parent. In view of the availability of genetic male sterility, the study revealed good scope for commercial exploitation of heterosis for yield and oil contents in soybean.

A. K. Atwal, Manoj Kumar, Pratibha Chauhan, Chhaya Atri, J. S. Kular, Sarwan Kumar, Surinder S. Banga (India) Myrosinase-Glucosinolate System in Crop *Brassica* Species: Variation and Association with Defensive Responses to *Pieris brassicae* Infestation (pp 121-125)

ABSTRACT

Original Research Paper: A diverse *Brassica* germplasm collection (128) was assayed for myrosinase activity and glucosinolate content in different plant tissues/organs. Significant genotypic variation was observed. Myrosinase activity was highest in leaves, followed by developing seeds and least in the mature seeds. *B. napus* leaves had the maximum mean value (1.29 ± 0.59 nmole glucose released $\text{mg}^{-1} \text{min}^{-1}$), followed by *B. juncea* (0.63 ± 0.05), *B. nigra* (0.52 ± 0.09) and *B. rapa* (0.30 ± 0.03). Genotypes with very low myrosinase activity were *B. napus* ACN 40 (0.68), *B. juncea* KH 2099 (0.09), *B. rapa* VKS 11/29 (0.08) and *B. nigra* FRG 2 (0.17). Glucosinolate values were substantially higher in mature seeds than in the green tissues. Land races in general possessed higher glucosinolate content. Leaf myrosinase activity was negatively correlated with total glucosinolate content. Correlation with but-3-ethyl glucosinolate (gluconapin) was negative while a positive correlation occurred with 2-OH-but-3-ethyl glucosinolates (progoitrin). Variation was recorded for resistance to cabbage caterpillar (*Pieris brassicae*) in *B. nigra*, where genotypes namely Assam, N 17, N24, Pakistan and Mozambique showed an antibiosis reaction. Increased myrosinase activity was correlated with resistance to herbivore. This was evident from a negative correlation between larval mortality and myrosinase content. Leaf glucosinolates, on the other hand, were negatively correlated with larval mortality.

Abdel-Tawab Fathy Mohamed, Eman Mahmoud Fahmy, Abd-Elwahab Ismael Allam, Sabry Abdalla Khatab, Ahmed Ibrahim Abdel Fatah, Osama Ezzat El-Sayed, Rashad Mahmoud Mohamed Shoaib (Egypt) Molecular Genetic Characterization of Some Promising Sugarcane Varieties under Smut Disease (pp 126-133)

ABSTRACT

Original Research Paper: The aim of the present study was to genetic characterize some identified promising sugarcane cultivars resistant to smut fungus (*Ustilago scitaminea*) at an early stage of the breeding program. Ten cultivars were used in this study, including seven promising cultivars: 'G99-165', 'G95-19', 'G95-21', 'G98-28', 'G98-24', 'G84-47', 'G85-37', one susceptible cultivar 'NCo310', and two commercial cultivars, 'GT54-9' and 'PH8013'. The performance of the 10 cultivars that were artificially infected with a teliospore suspension was assessed under greenhouse conditions and the results revealed that nine cultivars were relatively resistant. Random amplified polymorphic DNA (RAPD) analysis using 20 10-mer primers showed that 182 of 233 total amplified fragments were polymorphic with 78.1% polymorphism. Nine-anchored inter simple sequence repeat (ISSR) primers revealed 102 polymorphic fragments with 69.9% mean polymorphism from a total of 146 amplified fragments under smut infection. Using four SSR markers, 15 polymorphic fragments with 88.2% mean polymorphism from 17 total amplified fragments were detected. No specific SSR markers were determined among the 10 sugarcane cultivars. A total of 29 and 9 specific fragments existed in the resistant cultivars and not in the susceptible cultivar 'NCo310' were detected for RAPD and ISSR, respectively.

Lakki Reddy Prasanthi, Bommu Veera Bhaskara Reddy, Kokkanti Rekha Rani, Yeturu Siva Prasad, Thovi Rajeswari, Kondreddy Raja Reddy (India) Development of Sequence Characterized Amplified Region (SCAR) Marker for Fusarium Wilt Resistance Gene in Pigeon Pea (*Cajanus cajan* L. Millsp.) (pp 134-138)

ABSTRACT

Original Research Paper: Fusarium wilt resistance in pigeon pea is controlled by a single dominant gene. Bulked segregant analysis (BSA) was applied to identify molecular markers linked to a major resistant gene using the F₂ population of two crosses i.e. LRG-41 x ICPL-87119 and ICPL-7035 X ICPL-8863. A total of 195 random oligonucleotide primers were surveyed. Primer OPG08₉₅₀ was found to produce a consistent marker, which differentiated resistant from susceptible parent and bulk. Co-segregation analysis of the putative marker in the F₂ population confirmed the association of OPG08₉₅₀ produced by primer OPG08 with the resistance gene. An identified random amplified polymorphic DNA (RAPD) marker, OPG08, linked to fusarium wilt resistance in pigeon pea was cloned and sequenced. Their end sequences were used to design an allele-specific sequence characterized amplicon region (SCAR) primer SCAR937(14f/r), which was found promising in all generations. The marker designed was amplified at a specific site of 937 bp in resistant parents, F₁s and only in resistant F₂ plants. This would help to identify the transfer of the Fusarium wilt resistance gene to susceptible lines.

Chitra Rajagopal, Rajamani Kandhasamy (India) Genetic Variability, Heritability and Scope of Improvement for Yield Components in Glory Lily (*Gloriosa superba* L.) (pp 139-143)

ABSTRACT

Original Research Paper: Genetic variability, heritability (%) in a broad sense and genetic advance as per cent of mean (GA) were studied among 21 morpho-economic traits in 18 genotypes of glory lily (*Gloriosa superba* L.) during two seasons (2007 and 2008). The highest dry seed yield/plant was recorded for GS 15 followed by GS 06, GS 18 and GS 03. Promising genotypes were identified for multiple desirable morpho-economic traits viz., plant height, number of leaves, number of flowers/plant, number of pods/plant, number of seeds/pod and fresh yield/plant were GS 15, GS 06, GS 18 and GS 03 which can be utilized directly or included in a hybridization programme as a donor for the improvement of respective traits in desirable genotypes. The highest phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for fresh seed yield/plant followed by dry seed yield/plant and fresh pod yield/plant in both seasons. The higher estimates of heritability and genetic advance as per cent of mean were obtained per plant for number of leaves, fresh pod yield and fresh seed yield. Thus, selection for these traits is likely to accumulate more additive genes leading to further improvement in their performance.

Mani Ramakrishnan, Lingaiah Rajanna, Narayanaswamy Papanna (India), Luke Simon (India/UK) Assessment of Genetic Relationship and Hybrid Evaluation Studies in Tea (*Camellia* sp.) by RAPD (pp 144-148)

ABSTRACT

Original Research Paper: The genetic relationships among 12 tea accessions representing three species in the genus *Camellia* were studied using random amplified polymorphic DNA (RAPD) markers. The genetic distance matrix based on Euclidian Distances showed a minimum genetic distance of 2.24 between 'UPASI-2' and 'UPASI-3' clones and the maximum

was 4.47 between 'TRF-1' and 'TRI-2025'. The dendrogram based on Ward's method of cluster analysis clearly characterized all 12 tea varieties into three clusters based on their types namely China, Assam and Cambod. Pair-wise genetic similarity index between parent and hybrid clones generated showed a highest mean of 0.59 between 'TRI-2025' and 'BSS-1' and a lowest of 0.34 between 'UPASI-10' and 'BSS-1'. This study revealed that all the varieties analysed fall the present taxonomic framework of *Camellia* species and that the hybrid is of Cambod type. RAPD markers can thus be successfully applied in this taxon for the study of relationships and to confirm hybrid origin. The study offers a sound platform for future tea breeding programmes in tea as well as evolution of hybrids in the commercially important tea varieties.

Néji Tarchoun, Abdelaziz Mougou (Tunisia) Combining Ability and Heterosis for Earliness Flowering and Fructification on Pepper (*Capsicum annuum* L.) Grown Under Low Night Temperature (pp 149-153)

ABSTRACT

Original Research Paper: We investigated the combining ability and heritability of flowering and fruit setting earliness in diallel crossing of 6 divergent pepper parents. The first bifurcation height was used as the earliness indicator. The magnitudes of variance due to general (GCA) as well as specific combining ability (SCA) were highly significant for all traits indicating the importance of both additive and non-additive gene action. The high GCA/SCA ratio for the height of the first bifurcation (15.10) and fruit number (7.87) would explain that these traits are predominantly controlled by additive gene action. Broad and narrow sense heritability was high for the height of the first bifurcation (69 and 62%) as well as for the fruit number at this first branching (60 and 46%). General combining ability analysis revealed that PM797 (hot pepper) has the best precocity; GCA effect was negative (-3.11*) for height of the first bifurcation, positive and highly significant for flower and fruit number (0.20**, 0.32**, respectively), while local hot pepper cultivars 'Baklouti' and 'Beldi' showed opposite values and were too late. A reciprocal cross did not show a significant effect on precocity parameters. Genetic effects analysis (Sij) of the crosses, in which 'PM797' was one of their parents, revealed their efficiencies to fruit setting at low night temperature, as is the case of PM/Bel. The latter has a high value of the Sij effect (0.61*) and heterotic effect (0.92*). The ability to flowering and fruit setting at low temperature was also noted in some crosses having sweet pepper as a parent, such as Foid/Bel, Bel/Glac, Glac/Marc and Glac/Bak.