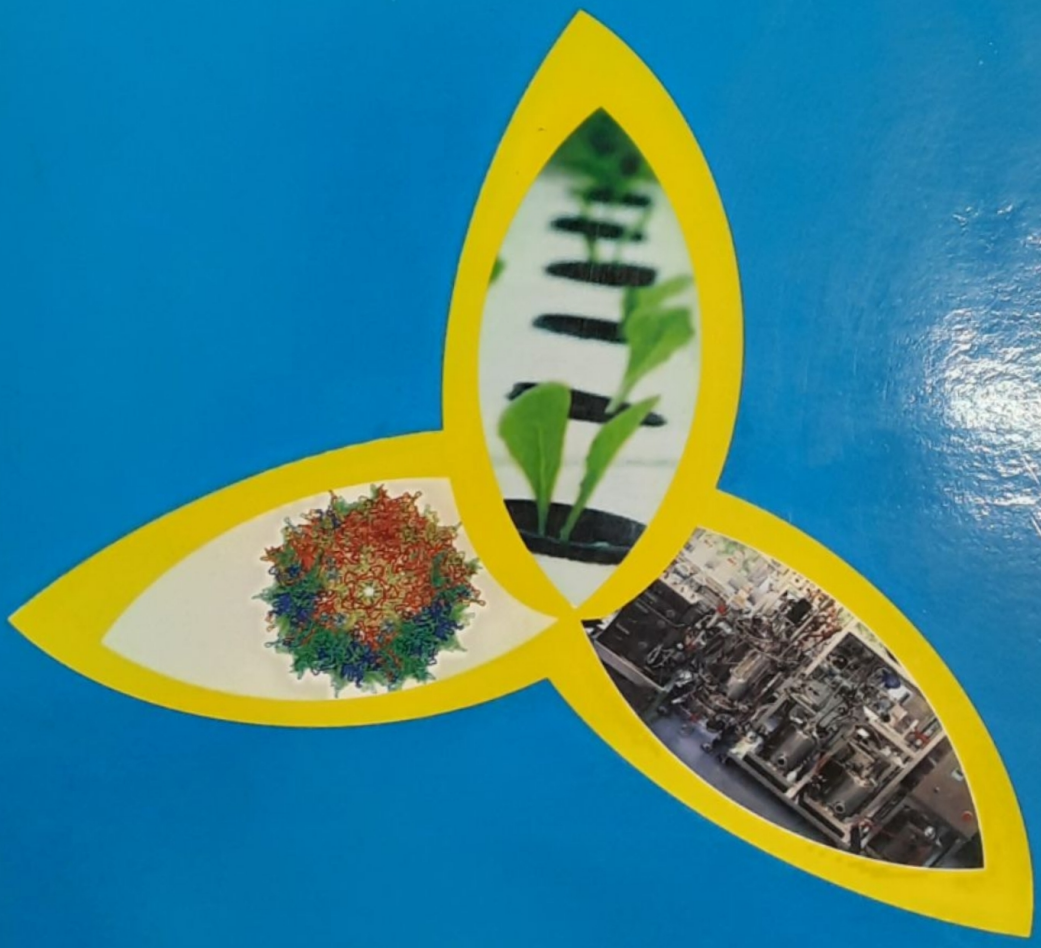
ABSTRACTS

28-29 June 2013

First International and Third National Conference

BIOTECHNOLOGY, BIOINFORMATICS AND BIOENGINEERING



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western plains zone (NWPZ) which is wheat bowl of India. Stripe (yellow) rust of wheat caused by *Puccinia striiformis* is one of the most important foliar diseases of wheat (*Triticum aestivum* L.) grown in cool regions covering maximum acreage under wheat in India. Hence considerable attention is desired to identify resistant genotypes against these two very important foliar diseases to sustain the wheat yields. Seven hundred CIMMYT germplasm accessions including Sonalika and Ciano as highly susceptible checks and Francolin and Chiraya 3 as moderate and highly resistant checks, respectively were screened for spot blotch severity creating epiphytotic conditions following the standard procedures. The accessions showing spot blotch resistance were also observed for stripe rust resistance on phenotypic basis. The forty accessions showing high resistance to spot blotch as well as stripe rust were subjected to molecular marker analysis. The linked markers Xpsp3000 and Xgwm273 to two highly effective stripe rust resistant genes, Yr10 and Yr15, respectively were deployed to confirm the resistance. Out of forty, 11 accessions were found possessing Yr10, 19 accessions Yr15 and 7 accessions were found possessing both the genes, Yr10 and Yr15. The germplasm accessions possessing spot blotch resistance as well as stripe rust resistant gene(s) could be used in pyramiding and ultimately in developing the high yielding resistant varieties of wheat.

Biochemical markers of pollen-stigma interaction in sugarcane (*Saccharum* sp.)

S. Alarmelu, R.M. Shanthi
Division of Crop Improvement, Sugarcane Breeding Institute, Coimbatore 641007, Tamil Nadu, Email: alarmelu.s@gmail.com

Enzymes detected in sugarcane pollen have been found to play a crucial role in the control of incompatibility and among them esterase isozyme has been shown to be of both sporophytic and gametophytic origin and provide a source of markers for studying development of pollen pistil interaction. The present study reports a biochemical approach to identify isozyme markers that control incompatibility reaction operating in sugarcane. Two isoenzyme systems, namely, esterase and glutamate dehydrogenase were studied to assess the variation in the protein content and their expression in the pistils, pollen and stigma of compatible and incompatible sugarcane clones that are used as parents in breeding programmes. Esterase and glutamate dehydrogenase isozyme patterns were studied in the anthers of six pollen parents and stigmas of two pistil parents. In general, the anther esterase pattern of Co 86011, Co 62198, Co 91004, Co 99002 and Co 1148 on the stigmas of Co 88028 indicated qualitative differences among them. Co 86011 had one intense band which was not present in other pollen parents might be the cause for the compatible reaction in crosses effected using Co 86011 as pollen parent. Esterase activity was found to be high in Co 86011 pollen on Co 88028 stigma in comparison with Co 88025 stigma and pollen of Co 62198, Co 91004 and Co 99002. Three fast migrating GDH bands were detected in the anther and stigma extracts of the parents studied. The isozyme pattern of GDH indicated that GDH 2 was common for pollen and pistil parents, GDH 1 found only in self incompatible parents, viz. Co 62198, Co 91004 and Co 99002 and GDH 3 only in the compatible parent Co 86011. The presence of esterases and its activity suggest that pollen esterases complexes with stigma enables pollen tube entry into the stigma and similarily the high esterase activity in the mature stigma of compatible parents suggests a possible role for these enzymes in compatible and GDH for incompatible pollinations.

Validation of allele specific associated primer linked to H1 locus and SSR markers linked to H2 locus of fusarium wilt resistance in selected Chickpea genotypes

A.S. Jayale, Pavankumar Jingade, R.L. Ravikumar
Department of Plant Biotechnology, UAS, GKVK, Bangalore, Karnataka, Email: shu8386@gmail.com

Chickpea (*Cicer arietinum* L.) has been described as the world's third most important pulse crop and a major pulse crop in the Indian subcontinent and the Mediterranean region. Several biotic and abiotic factors affect productivity of this crop in India; among which Wilt caused by *Fusarium oxysporum* f. sp. *ciceris*, is very important. High level of resistance is available in the cultivated taxa. However screening for wilt resistance in the segregating populations is a limitation to develop high yielding wilt resistant genotypes. Identification of molecular markers linked to resistant locus will be useful for easy and quick selection of resistance in breeding programmes. Two major independent loci H1 and H2 determine the resistance to race-1 in chickpea. The dominant alleles at both H1 and H2 loci result in susceptible early wilting and recessive at any one (h1h1H2_ or H1_h2h2) produce susceptible late wilting and recessive at both the loci (h1h1h2h2) result in resistance. Molecular markers linked to wilt resistance loci H1 and H2 have been identified by several workers co-dominant SSR markers TA- 72,

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Society for Applied Biotechnology
1/115, Puliyur, Krishnagiri,
Tamil Nadu 635201, South India
www.sabt.org.in

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13-6-771/20, Opp. APSRTC Bus Stand
Tirupati, Andhra Pradesh 517501, South India
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