



desi, *kabuli* and *gulabi* types, and as a result high yielding (1800-2000kg/ha) varieties viz., JG322 and JG218 were developed. A drought resistant, high yielding variety JG11 was released for south zone of India is the second mile stone achieved in 1999. To date, it is the most popular variety in Andhra Pradesh and Karnataka. Since then, a series of high yielding (2000-2200 kg/ha) and multiple disease resistant *desi* varieties have been developed for diversification, which include JG16, JG130, JG63, JAKI9218, JG412, JG226, JG12, RVG204, RVG205 and JG36, *gulabi* JGG1 and *kabuli* GK1, JGK2, JGK3, RVKG101, RVSGKG102, RVG201, RVG202, RVG203. A short duration high yielding, heat tolerant variety JG14 was developed for late sown condition under rice fallow which is mostly popularized in Northeastern states and Myanmar. Mechanization is important for making chickpea cultivation more profitable and attractive to farmers. In recent times, chickpea plant type has been reconstructed and RVG204 and JG 24 were developed, which are suitable for machine harvesting. These efforts led to both horizontal and vertical expansion of chickpea in Madhya Pradesh.

OP-4

Pre-breeding for genetic enhancement of grain legumes

SHARMA SHIVALI¹, KUMAR CV SAMEER², PRASANTHI L³, RAO P JAGANMOHAN⁴, THI PHYO PYAE⁵, WIN MAR MAR⁵, MUNISWAMY S⁶, PANWAR RK⁷, ARORA ANJU⁷, SINGH SARVJEET⁸, RAN UPASANA⁸, THUDI MAHENDAR¹, SHARMA MAMTA¹, NIMJE CHETNA¹ and VARSHNEY RK¹

¹International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad, TS, India; ²Regional Agricultural Research Station, Professor Jayashanker Telangana State Agricultural University, Palem, India; ³Regional Agricultural Research Station, Acharya N G Ranga Agricultural University, Tirupati, AP, India; ⁴Regional Agricultural Research Station, Professor Jayashanker Telangana State Agricultural University, Warangal, TS, India; ⁵Department of Agriculture, Yezin, Myanmar; ⁶Regional Agricultural Research Station, University of Agricultural Sciences, Kalaburagi, Karnataka, India; ⁷GB Pant University of Agriculture & Technology, Pantnagar, India; ⁸Punjab Agricultural University, Ludhiana, India; E-mail: Shivali.sharma@cgiar.org

Grain legumes such as chickpea (*Cicer arietinum* L.) and pigeonpea (*Cajanus cajan* (L.) Mill sp) play an important role in ensuring food and nutrition security and sustainable agriculture. Due to narrow genetic base, genetic enhancement in grain legumes is not adequate and the crops are prone to biotic (pests and diseases) and abiotic (drought, water-logging, salinity, heat and cold) stresses. As the high levels of resistance/tolerance sources are not available in cultivated genepool, this necessitates the exploitation of new variability for the genetic enhancement of pulse crops. Crop wild relatives (CWRs) harbor many useful genes/alleles and provide enormous genetic variability for crop improvement. Frequent utilization of these CWRs in breeding programs is stalled due to various cross-incompatibility barriers as well as due to linkage drag rendering it a time-consuming and resources-demanding research endeavor. Pre-breeding provides a unique opportunity to the crop breeders by creating new genepool having higher frequency of useful genes/alleles introgressed from wild species and with good agronomic background. At ICRISAT, pre-breeding populations derived from promising wild accessions of *Cicer*, and *Cajanus* as donors and popular cultivars of chickpea, and pigeonpea as recipients, respectively have been developed for further use in the crop improvement programs. Considerable variability has been generated in these populations for morpho-agronomic traits as well as for biotic/abiotic stress tolerance. Evaluation of these pre-breeding populations has resulted in the identification promising trait-specific introgression lines such as early maturing, high-yielding and disease resistant lines. These introgression lines are being shared with



breeding programs worldwide for their use either directly as a variety or as promising donors in the crossing programs to develop new cultivars with a broad genetic base. Further, efforts are in progress to use advanced backcross populations derived from wild species for mapping QTLs for important biotic stresses and agronomic traits following AB-QTL approach.

OP-7

Molecular mapping of QTLs for *Ascochyta* blight and *Botrytis* grey mould resistance in an inter-specific cross in chickpea

KUSHWAH ASHUTOSH¹, BHATIA DHARMINDER¹, RANI UPASANA¹, SINGH INDERJIT¹, BHARADWAJ C² and SINGH SARVJEET¹

¹Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana, Punjab; ²ICAR-Indian Agricultural Research Institute, New Delhi;

E-mail: sarvjeet62@pau.edu

Ascochyta blight (AB; caused by *Ascochyta rabiei* (Pass.) Lab.) and *Botrytis* grey mould (BGM; caused by *Botrytis cinerea* Pers. ex. Fr.) are the most devastating fungal diseases of chickpea worldwide. Development of varieties resistant to AB and BGM is considered as the most effective and sustainable approach. Thus, the present study deals with identifying the key genomic regions responsible for resistance to AB and BGM in a RIL mapping population developed from an inter-specific cross between GPF 2 x *C. reticulatum* acc ILWC 292 using ddRAD-seq based genotyping. Phenotyping for AB and BGM was done using artificial epiphytotic field/laboratory conditions for two years (2017-18 and 2018-19). Highly significant differences ($P < 0.001$) were observed for reaction to both the diseases, AB and BGM, in the RILs as well as the parents during both the years. SNP genotyping data were generated using ddRAD-Seq. Composite interval mapping revealed a total of five QTLs on three chromosomes (chromosome 4, 6 and 7) during 2017-18 and two QTLs on two chromosomes (chromosome 4 and 7) during 2018-19 for AB resistance while, a total of six QTLs on four chromosomes (chromosome 1, 3, 4 and 5) during 2017-18 and similar number of QTLs on three chromosomes (chromosome 4, 5 and 6) during 2018-19 for BGM resistance. Of these, two consensus QTLs namely, *qab-4.1* and *qab-7.1*, for AB resistance and three consensus QTLs namely, *qbgm-4.1*, *qbgm-4.2* and *qbgm-5.1*, for BGM resistance were found during both the years. QTLs for BGM resistance are being reported first time using most contrasting parents. High-throughput genotyping developed from candidate gene-based approach would give an opportunity of efficient marker-assisted selection for AB and BGM resistance.

OP-8

Transcriptome analysis for elucidating genes and pathways related to heat-stress tolerance in lentil (*Lens culinaris* L. Merrill)

KUMAR JITENDRA*, GUPTA DS, KESARI RAVI², BASU PS, GUPTA SANJEEV, SOREN KR, KONDA ARAVIND, TIWARI PRAVIN and SINGH NP

Division of Crop Improvement, ICAR-Indian Institute of Pulses Research, Kanpur, 208 024, UP, India;

²Department of Plant Breeding and Genetics, Bhola Paswan Shastri Agricultural College, Purnea, Bihar 854302,

E-mail: jitendra.kumar@icar.gov.in

Lentil is highly sensitive to abrupt increase in temperature during mid to late reproductive stage leading