sistant germplasm, breeding lines and cultivars, while some QTL were present only in kabuli lines (Ar2a, Ar2c, Ar4a, Ar5a) and others only in desi lines (Ar1a, Ar3c, Ar7a). Selected F_2 populations are being advanced to F_7 for fine mapping using single nucleotide polymorphism markers needed for effective pyramiding of QTL with complementary effect on the pathogen.

Genetic enhancement of resistance to ascochyta blight in chickpea. P.M. GAUR[1*], S. PANDE[1], T. KHAN[2,3], S. TRIPATHI[1,4], M. SHARMA[1], L. KAUR[5], J.S. SANDHU[5,6], S. SINGH[5], A. BASANDRAI[7], D. BASANDRAI[7], A.K. JUKANTI[1], C.L.L. GOWDA[1] and K.H.M. SIDDIQUE[2]. *[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad 502 324, AP, India. [2]The UWA Institute of Agriculture, The University of Western Australia, 35 Stirling Highway, Crawley, Western Australia 6009, Australia.[3]Formerly at Department of Agriculture and Food Western Australia, 3 Baron-Hay Court, South Perth, WA 6151, Australia. [4]Presently at Indian Agricultural Research Institute, New Delhi 110 012, India. [5]Punjab Agricultural University, Ludhiana 141 004, Punjab, India. [6]Presently at Indian Council of Agricultural Research, New Delhi 110 001, India. [7]Hill Agricultural Research and Extension Centre of CSKHPKV, Dhaulakuan 173 001, HP, India. *E-mail: p.gaur@cgiar.org*

Chickpea (*Cicer arietinum* L.) suffers significant yield losses from ascochyta blight (AB), caused by *Ascochyta rabiei*, in areas where the crop growing season is cool and wet. Developing chickpea cultivars with high and stable resistance to AB has been challenging because the resistance is controlled by several major and minor genes and the pathogen is known to be highly variable. Concerted efforts were made to develop breeding lines with enhanced resistance to AB in an international project that involved partnership between ICRISAT and Universities/Research Institutions in Western Australia and Northern India. The breeding strategy included use of diverse sources of AB resistance and multiple crosses for enhancing level of AB resistance. Over 250 crosses were made involving several sources of AB resistance (GL 90135, ICC 3996, ICC 12004, ICC 12965, ICC 14917, ICC 12964, ICC 18965, ICCV 98502, ICCV 98503, ICCV 04512, ICCV 04516, ICCV 04538, ICCV 04539, ICCV 05529, ICCV 05530, PBG 5) and popular cultivars/elite lines from Western Australia (Sona, Sonali, Rupali, WACPE 2098, WACPE 2099, WACPE 2113, WACPE 2114, WACPE 2125, WACPE 2131, WACPE 2152, WACPE 2162) and India (ICCV 10, ICCC 37, JG 11, JAKI 9218, JG 130). Top AB resistant lines derived from different crosses were intercrossed to further accumulate AB resistance genes from a number of sources. F_4 populations from bi-parental and multi-parental crosses were screened for AB resistance at seedling stage under artificial epiphytotic conditions in controlled environment growth room at ICRISAT-Patancheru. The AB resistant plants were transplanted to greenhouse and their progenies (>13,000) were subjected to preliminary evaluation for phenology, plant type and seed traits. Over 5,000 progenies were selected and evaluated for adult plant resistance to AB in the field at Ludhiana in northern India. Over 2,600 progenies were evaluated for AB resistance and agronomic traits under field conditions in Western Australia. A large number of breeding lines that show high levels of AB resistance (score 2–3 on 1–9 scale) in Western Australia and northern India have been developed. Majority of these lines also have desirable agronomic and adaptation traits and good seed quality. Some of the AB resistant lines also combine resistance to botrytis grey mould and fusarium wilt.

QTL identification for Ascochyta blight resistance and its application in chickpea breeding. M. IMTIAZ[1]*, A. HAMWIEH A.[1], S. AHMED[1], R. MALHOTRA[1], A. KHALIFEH[1], N.A. DOUBA[2] and S. SHEET[2]. *[1]International Center for Agricultural Research in the Dry Areas (ICARDA), Aleppo, Syria. [2]Aleppo University, Aleppo, Syria. *E-mail: m.imtiaz@cgiar.org*

Ascochyta blight (AB), caused by *Didymella rabiei* regularly occurs in epidemic form causing heavy yield and quality losses, and thus is a major biotic constraint to chickpea production, particularly in the cool and wet areas. Various chemical and cultural practices have been reported to control the disease, however, their usage is neither eco-friendly nor economical where the cultivated varieties possess low level of resistance. Therefore, development and deployment of resistant cultivars is the most viable alternative to overcome the impact of disease particularly in winter planted chickpea in West Asia and North Africa. ICARDA, being the hub for AB research, has made tremendous progress in the development of AB resistant germplasm through phenotypic selection, but significant difficulties are often encountered in phenotypic selection such as genotype by environment interactions, and expensive and unreliable screening methodologies. Therefore, to increase genetic gain and generate comprehensive knowledge, the chickpea breeding program at ICARDA started to map QTLs for AB resistance in different genetic backgrounds and use marker-assisted selection in early generations (F_2) as proof of concept. Recombinant inbred (RI) populations viz. FLIP98-1065 X ILC3279, FLIP98-1065 X ILC482, FLIP98-1065 X ILC1929, ILC3279 X ILC482, ILC3279 X ILC1929, and ILC482 X ILC1929 were developed to map and validate SSR markers associated with different putative sources of resistance in these populations. RI population derived from FLIP97-1065C x ILC1929 was phenotyped for three years and genotyped with 110 SSR markers. SSR markers GA-16, H5H-02, TA-194 and H1A-10b were found linked with

resistance under field and control conditions with phenotypic variation explained ranging from 10 to 20%. These markers and other publically reported markers were validated in the remaining 5 RI populations. The marker validation results showed that none of the markers alone differentiated resistance sources against different pathotypes in these populations. Thus a set of closely linked markers could be utilized to select for AB resistant genotypes until the availability of diagnostic markers for maker- assisted selection in future.

Validation of allele specific markers for detection of ascochyta blight resistance loci in chickpea. E. MADRID[1,4*], W. CHEN[2], P.N. RAJESH[2,3], J. RUBIO[4], P. CASTRO[4], T. MILLAN[1] and J. GIL[1]. [1]*Dept of Genetic, Córdoba University, Campus Rabanales, Edif. C5, 14071 Córdoba, Spain.* [2]*Grain Legume Genetics and Physiology Research Unit, USDA-ARS, Washington State University, Pullman, WA 99164, USA.* [3]*Trait Genetics and Technologies, Dow AgroSciences, Indianapolis, Indiana, 46268, USA.* [4]Área de Mejora y Biotecnología, IFAPA Centro "Alameda del Obispo", Apdo 3092, 14080 Córdoba, Spain.
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Although various candidate genes have been hypothesized to be responsible for blight resistance in chickpea, none have previously been found to be associated with QTLs for resistance to this disease so far. Recently a chickpea ethylene receptor-like sequence (*CaETR-1*), homologue to the *Arabidopsis thaliana* ethylene insensitive 4 gene (*EIN4*), has been reported to be associated with resistance and susceptibility to blight. The *CaETR-1a/b* locus was mapped in LGIV tightly linked to QTL_{AR1}, explaining up to 33.8% of the total phenotypic variation. Using this information an allele-specific associated primer (ASAP) was designed. With the aim of monitor the presence of blight resistance associated QTLs to avoid escapes and ambiguity in phenotype evaluation, more than 50 genotypes, including collection of landraces, cultivars, advanced breeding lines and wild relatives, were genotyped using the ASAP primer and the previously described SCAR marker $SCY17_{590}$, tightly linked to QTL_{AR2}. According with our results, in very few cases resistant genotypes was incorrectly predicted. Therefore, chickpea breeders could confidently use the markers to carry out selection of germplasm with high levels of resistance to blight in their breeding programmes, discarding genotypes with the susceptible allele for both QTLs.

Association Genetics Mapping of Referred QTLs Markers conferring resistant to ascochyta blight, earliness and seed size in chickpea. M. MARWAN[1*], B. TARAN[1], A. SHARPE[2], T. WARKENTIN[1] and A. VANDENBERG[1]. [1]*Crop Development Centre, University of Saskatchewan, Saskatoon, Saskatchewan, Canada S7N 5A8.* [2]*National Research Council-Plant Biotechnology Institute, Saskatoon, Saskatchewan, Canada.*
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Understanding genetic diversity and population structure in target populations is a prerequisite for association mapping. The current study used association mapping approach to identify molecular markers associated with resistance to ascochyta blight, earliness and seed size, three of important characteristics in chickpea breeding. A total of 136 genome-wide simple sequence repeat (SSR) markers were used to assess the genetic diversity and population structure of a set of 94 chickpea genotypes including cultivars, elite breeding lines and their progenitors and several landraces. These genetic materials have been used in chickpea breeding program at the University of Saskatchewan in the past 20 years. Analysis of population structure in combination with pedigree and breeding history grouped the chickpea genotypes into six subpopulations. Two subpopulations consisted of genotypes of different origins used mainly as sources for ascochyta blight resistance. The next three subpopulations were mostly genotypes used as sources for earliness. The last subpopulation consisted of genotypes used to improve seed quality. The association analysis using population admixture approach identified two new SSR markers associated with ascochyta blight resistance: H4G11 ($P<0.001$) and TR20 ($P<0.05$) markers accounted for 47% and 22%, respectively, of the variations for reaction to ascochyta blight. The current analysis also confirmed the association of previously mapped SSR markers such as TA2, TA8, TS19 and TA144 (1, 2) with ascochyta blight resistance. In addition, we identified two SSRs (TA2 and GA20) associated with seed size and another two (H3C11 and TA25) associated with earliness, which have not been detected in previous QTL studies. The results suggested that the current population may be useful for genome-wide marker–trait association study that has enabled the identification of new QTL for ascochyta blight resistance, earliness and seed size, three of most important characteristics in chickpea.

Combining Ascochyta blight resistance and high yield in lentil cultivars. S. SINGH[1*], S. KUMAR[2], R.K. GILL[1], L. KAUR[1], S. AHMED[2], J. KUMAR[3] and A. SARKER[2]. [1]*Department of Plant Breeding & Genetics, Punjab Agricultural University, Ludhiana 141004, India.* [2]*International Center for Agricultural Research in the Dry Areas, Aleppo, Syria.* [3]*Indian Institute of Pulses Research, Kanpur, India.*
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Ascochyta blight (AB), caused by *Ascochyta lentis* Bond and Vassil, is a major disease of lentil (*Lens culinaris* L. Medik.) causing 30–70% yield losses in Canada, USA, and Australia and northern parts of India. The aim of the present study was to combine AB resistance with