

high yielding potential. The F₃ and F₄ populations from crosses involving AB resistant donors with ICARDA elite breeding lines, were advanced at Punjab Agricultural University, Ludhiana, India, respectively during main and off-seasons. The single plant F₅ progenies were exposed to AB infections under field conditions during 2006–2007 using disease rating scale of 1–9. Thirty two promising lines, bulked in F₇ generation, were evaluated for seed yield in multi-location trials (2009–2010 and 2010–2011) and for their reactions to AB under artificial inoculations along with susceptible check, LL147 (8 score). Six elite lines namely LL1187 (1.70 t ha⁻¹), LL1210 (1.75 t ha⁻¹), LL1197 (1.76 t ha⁻¹), LL1186 (1.76 t ha⁻¹), LL1201 (1.80 t ha⁻¹) and LL1205 (1.80 t ha⁻¹) recorded 9.6–16.1% yield advantage over the best check variety LL931 (1.55 t ha⁻¹). The level of resistance (≤ 4 score) of these lines to AB was also higher compared to check variety LL931 (5 score). Inheritance of AB resistance is simple and controlled by major genes; hence it is easy to incorporate stable resistance in high yielding background by selecting parents carefully for hybridization program.

Breeding faba bean for resistance to Ascochyta blight. F. MAALOUF¹, S. AHMED¹, S. KHALIL² and B. BAYAA³. ¹International Center for Agricultural Research in the Dry Areas (ICARDA), P.O Box 5466, Aleppo, Syria. ²Field Crop Research Institute, Agriculture Research Center, Giza, Cairo, Egypt. ³Faculty of Agriculture, Aleppo University, Aleppo Syria. *E-mail: F.maalouf@cgiar.org

Ascochyta blight (*Didymella fabae* Jellis and *Punithal-ingam*) is one of the most important foliar diseases that affect the quality and seed yield of faba bean (*Vicia faba* L.) worldwide. Breeding for resistance to Ascochyta blight is a major objective in many faba bean breeding programs. At ICARDA, systematic screening of germplasm accessions and elite breeding lines for resistance to Ascochyta blight is carried out at Tel Hadya Aleppo and Lattakia under artificial field inoculation with mixtures of aggressive isolates of the pathogen, since 1977. This has resulted in the identification of 120 resistance sources with origins mainly from Ecuador, Egypt, Ethiopia, Canada, China, Greece, Italy, Lebanon, Morocco, Peru, Spain, Syria and Tunisia. The resistance sources were inter-crossed with landraces adapted to diverse environments. More than 2000 breeding lines (F₄ to F₇ generations) emanating from the crosses involving resistant donors with landraces are screened for their reaction to Ascochyta blight on yearly basis. Only the identified resistant lines in advanced generations are tested under natural infestation in different locations under platform of international nurseries. From 2008 to 2011, 65 lines were tested in different locations in North Africa and west Asia. 28 lines maintained their resistance to ascochyta blight in all locations.

Allele diversity analysis for improvement of mycosphaerella blight resistance in pea. A.B. JHA*, G.C. ARGANOSA, B. TAR'AN and T.D. WARKENTIN. *Crop Development Centre/Department of Plant Sciences, University of Saskatchewan, Saskatoon, Canada.* *E-mail: ambuj.jha@usask.ca

The narrow available gene pool has slowed the development of pea cultivars with improved disease resistance. The objective of this study was to identify single nucleotide polymorphisms (SNPs) within the candidate genes associated with resistance to mycosphaerella blight as well as intrinsic seed compositions such as carbohydrate metabolism and protein deposition that can be used to aid selection in breeding program. A total of 169 diverse *Pisum sativum* accessions from eastern Europe, western Europe, Australia and Canada including two check cultivars, 'CDC Striker' (fair resistance) and 'Alfetta' (poor resistance) were initially screened for mycosphaerella blight resistance at mid-flowering and late pod filling stages. From the initial screening, 56 accessions with relatively higher resistance were selected. Additional four wild accessions of *P. sativum* ssp. *elatius* and *P. fulvum* with promising resistance were included for sequence analysis. Primer pairs of candidate genes associated with mycosphaerella blight resistance, carbohydrate metabolism and protein deposition were used to amplify DNA fragments from these accessions. Overall, 228 SNPs were detected within these candidate genes. Nine SNP loci were significantly associated with mycosphaerella blight score. Marker loci SS-273 and RGA-G3A-103 were significantly associated ($P \leq 0.01$) with mycosphaerella blight score at mid-flowering stage. At late pod filling stage, the association was significant ($P \leq 0.01$) for marker loci Gpt-116, Gpt-164, Agpl1-29 and highly significant ($P \leq 0.001$) for Agpl1-238, Gbsts1-137, Gbsts1-208 and Gbsts1-250. These marker loci explained 7 to 17% of the variation. The markers developed in this study have the potential to aid selection for development of pea cultivars with improved disease resistance.

Improving mycosphaerella blight resistance in pea. T.D. WARKENTIN¹*, Y. LIU¹, A. JHA¹, B. TAR'AN¹, A. SINDHU¹, M. MARWAN¹, A. SHARPE² and S. BAN-NIZA¹. ¹Crop Development Centre/Department of Plant Sciences, University of Saskatchewan, Saskatoon, Canada. ²Plant Biotechnology Institute, National Research Council, Saskatoon, Canada. *E-mail: tom.warkentin@usask.ca

Mycosphaerella blight is the most important pea disease in Canada, thus breeding for resistance is a major objective. Lack of strong resistance sources and the quantitative nature of resistance have resulted in slow breeding progress, however, cultivar ratings for resistance have generally improved from 'poor' to 'fair'