



owing to a number of constraints. Among the biotic stresses, Fusarium Wilt (FW) and Sterility Mosaic Disease (SMD) cause severe yield losses in India particularly due to endemic prevalence in Telangana and Andhra Pradesh states of the country. Conventional breeding approaches though led to development of resistant varieties and hybrids for the two diseases, but in recent past break down of the resistance is an issue of major concern in crop improvement. Recent deciphering of genome sequence of pigeonpea in the year 2012 opened an avenue to utilize molecular breeding approaches to tag the genomic regions governing resistance for wilt and SMD diseases. ICRIAR along with other partners is involved in identification of the genomic regions governing resistance as well as important phenotypic traits. As a part of these efforts, two Recombinant Inbred Line populations (RIL P) (188 lines each) derived from the crosses ICP8863 \times ICPL20097 (RIL PI) (segregating for SMD alone) and ICPL332 \times ICPL20096 (RIL PII) (segregating for SMD and FW), were evaluated at the PJTS Agricultural University, for disease resistance as well as phenotypic traits during wet season 2012-13 and 2013-14. The best lines (18 lines from RIL PI and 22 lines from RIL PII) were further evaluated during 2015-16. Also 149 Introgression lines (ILs) derived from the cross ICPL 87119 \times ICPW 12 (*Cajanus acutifolius*) were evaluated for yield traits during 2013-14 and 2014-15. Twenty five ILs were again screened for wilt resistance during 2015-16. Among RILs, four lines showed both FW and SMD resistance, 11 lines had only FW resistance and 17 lines only SMD resistance whereas majority of ILs showed resistance to wilt. The yield parameters for the RILs are currently being recorded. The outcome of this study would be the identification of high yielding disease resistant lines which would be further evaluated in multi-location trials and promising lines would be promoted as varieties suitable to these two states as well as other parts of India.

PP59: Virulence and molecular diversity within *Ascochyta rabiei* in Moroccan population and evaluation of genotypic stability on chickpea

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Ascochyta blight (*Ascochyta rabiei* Lab.) is an economically important fungal disease on chickpea in Morocco, and in other parts of the world. Significant progress has been made in breeding chickpea for *Ascochyta* blight resistance in Morocco, but the plant resistance is typically overcome by the evolution of virulent pathotypes of the pathogen. In this study pathogenic variability among a population of *A. rabiei* isolates, collected from four different chickpea growing regions in Morocco (Doukkala-Abda, Chaouia, Gharb and Saiss), was assessed by screening over a set of chickpea differential genotypes. On the basis of the pathogenicity test, the isolates were classified into three pathotype groups. The most aggressive pathotype (PIII) was present in the majority of surveyed regions, however the weak aggressive pathotypes (PI and PII) were the most widespread. Genetic analysis with SSR fingerprinting of these isolates distinguished high variability within and among identified pathotype groups of *A. rabiei*, indicating low correlation between their virulence and the genetic pattern. The characterization of disease reaction of 6 Moroccan varieties and 18 selected chickpea genotypes against isolates from these three pathotype groups revealed a high variability. None of them were resistant to PIII and only one variety and one genotype were resistant to PII and PI together. Results of this study will be useful in breeding for *Ascochyta* blight-resistant chickpea cultivars and development of efficient screening strategies in Morocco.

PP60: Wide range of genetic variability for herbicide tolerance in Faba bean

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Weeds have emerged as major constraint to faba bean productivity. A study was carried out to evaluate faba bean lines to post-emergence herbicides with 210 g a.i./ha Metribuzin (photosynthesis inhibitor, PI),