Advances in Arachis
Through Genomics & Biotechnology

AAGB-2015

Program

8th International Conference of the Peanut Research Community

Brisbane, Australia
November 4 – 7, 2015

Organized by:
The Peanut Foundation
The Peanut Company of Australia

Screening of groundnut interspecific derivatives for resistance to *Sclerotium rolfsii*

M. Balaraju[1], P.V. Kenchangoudar[1]*, B.N. Motagi[1], S.S. Adiver[1], M.V.C. Gowda[1], S. Pujer [1]

[1]Oilseeds Scheme, Main Agricultural Research Station, University of Agricultural Sciences, Dharwad-580 005, Karnataka, India
[2]ICRISAT, Kano, Nigeria
*pvkgoudar@gmail.com

Sclerotium rolfsii is a major constraint for production in most of the groundnut growing areas in India inflicting 28-30 per cent yield losses annually. Irrigated groundnut grown in the post-rainy and summer seasons in India is often infected by this pathogen. The 54 interspecific derivatives and 6 recombinant inbred lines (TAG-24 x R-9227 cross) along with 6 check varieties (Dh-86, Dh-216, ICGV 91114, Dh-3-30, R-9227 and TAG-24) were screened for *S. rolfsii* resistance in sick plots during summer and *Kharif* 2012 seasons. In summer 28 lines and 32 lines in *Kharif* showed highly resistant reaction to stem rot disease. High genetic variability and heritability was observed for disease and yield attributes viz., number of pods per plant, pod yield, harvest index, disease incidence at harvest, disease severity and disease spread irrespective of seasons. Per cent disease incidence at harvest was having strong significant negative association with dry pod yield per plant in both seasons. The interspecific derivatives viz., ICGV 3649-1, ICGV 4368-1, ICGV 3727-4, ICGV 34-1 and ICGV 4670-7 and recombinant inbred lines viz., RIL 3-14, RIL 6-1 and RIL 6-28 had desirable combination of high level of stem rot resistance and good agronomic attributes. These promising lines can been tested in trials over locations to confirm their superiority and utilized in breeding for Sclerotium disease resistance.

Molecular cloning and characterization of phospholipase D from peanut (*Arachis hypogaea*)

Silong Chen[1]*, Boshou Liao[2], Yurong Li[1]

[1]Hebei Provincial Laboratory of Crop Genetics and Breeding, Cereal and Oil Crop Institute, Hebei Academy of Agricultural and Forestry Science, Shijiazhuang, 050031, China. [2]Key Laboratory of Biology and the Genetic Improvement of Oil Crops, Ministry of Agriculture, Oil Crops Research Institute of the Chinese Academy of Agricultural Sciences, Wuhan, 430062, China.
*chsl99@163.com

Phospholipase D (PLD) is a kind of important enzymes in signal transduction of biological membrane and plays a crucial role in responding to drought stress in plant. Some evidences demonstrated the specificity of PLDs in signal transduction with plant species and cellular processes. In our previous studies, a novel *PLD* gene, *AhPLDα3*, was isolated from peanut (*Arachis hypogaea*) via cDNA library screening. The full-length cDNA and genomic DNA sequence of *AhPLDα3* were cloned; our data demonstrated that *AhPLDα3* cDNA was 2717 bp in length with a complete open reading frame of 2439 bp which encoded a polypeptide of 812 amino acids with a predicted molecular mass of 93.1 kD and a theoretical isoelectric point (*pI*) of 6.42, and its genomic sequence was 3031 bp. *AhPLDα3* was composed of three exons and two introns with typical GT-AG sequence at the splice sites. The two highly conserved catalytic HXKXXXXD (HKD) motifs, which are key amino acid residues related to the PLD activity, are encoded by two highly conserved exons. Phylogenetic analysis indicated *AhPLDα3* showed a low similarity to other PLDαs from plants, such as *Arabidopsis thaliana*, *Ricinus communis*, *Jatropha curcas* and *Glycine max*. The gene expression of *AhPLDα3* was strongly stimulated by water deficit. More importantly, *AhPLDα3* presented a remarkable stability of expression in conditions of progressive drought stress in peanut. Therefore, *AhPLDα3* could be greatly important for peanut to respond to drought stress. Additionally, *AhPLDα3* from peanut will provide an additional candidate gene for drought-tolerant crops improvement.