

IDT9-055 | Insights on host-pathogen interaction between groundnut (*Arachis hypogaea*) and *Aspergillus flavus*

Nayak SN¹, Agarwal G^{1,2,3}, Pandey MK¹, Sudini HK¹, Jayale AS¹, Purohit S¹, Bajaj P¹, Desai A¹, Wan L⁴, Guo B², Liao B⁴, Varshney RK^{1,5*}

¹International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India

²Crop Protection and Management Research Unit, USDA-Agricultural Research Service, Tifton, USA

³University of Georgia, Department of Plant Pathology, Tifton, USA

⁴Oil Crops Research Institute (OCRI), Chinese Academy of Agricultural Sciences (CAAS), Wuhan, China

⁵The University of Western Australia, Crawley, Australia

*E-mail: r.k.varshney@cgiar.org

Aflatoxin contamination, caused by fungal pathogen *Aspergillus flavus*, is the major quality and health problem delimiting the trade and consumption of groundnut (*Arachis hypogaea* L.) worldwide. Three types of aflatoxin resistance mechanisms namely, resistance to in-vitro seed colonization (IVSC), pre-harvest aflatoxin contamination (PAC) and aflatoxin production (AP) have been reported in groundnut. Transcriptome sequencing approach was used to study the differentially expressed genes that differ in-vitro seed colonization (IVSC) in resistant (J 11) and susceptible (JL 24) genotypes. A total of 1,344 million raw reads with an average of 84 million reads per sample were generated from 16 libraries from four different stages of fungal infection. A total of 737.75 and 770.83 million reads were mapped on the progenitor genomes- *A* subgenome (*A. duranensis*) and *B* subgenome (*A.*

ipaensis) of cultivated groundnut (*A. hypogaea*), respectively. In groundnut, defense related genes like senescence associated proteins, resveratrol synthase, seed linoleate 9s-lipoxygenases (9s-LOX), pathogenesis related proteins, peroxidases, glutathione-S-transferases, chalcone synthase, defensin and chitinases were differentially expressed. In *A. flavus*, the genes involved in growth and development of fungus, aflatoxin biosynthesis, binding and transporter proteins were found to be induced in compatible interaction. In addition to IVSC resistance, we have also carried out transcriptome sequencing for PAC and AP resistance. In summary, this study will provide greater insights on the resistance mechanisms and discovery of candidate genes for all the three mechanisms that can further be used as expression markers in genomics-enabled aflatoxin resistance breeding.

IDT9-056 | Iron acquisition and transport under aerobic and alkaline soil pH condition in rice (*Oryza sativa* L.)

Nisarga KN, Aftab Hussain IS, Sheshshayee MS, Udayakumar M*

University of Agricultural Sciences, GKVK, Bengaluru, 560065, Karnataka, India

*E-mail: udayakumar_m@yahoo.com

Iron (Fe) is an essential micronutrient for plant growth and development. Under aerobic rice cultivation Fe deficiency is a major problem resulting in low grain iron content and also under high soil pH condition iron acquisition is affected leading to iron deficiency chlorosis (IDC) resulting in substantial yield loss. To identify the superior rice genotype that adapts to aerobic cultivation system 24 different rice genotypes adapted to upland, low land and aerobic ecosystems were screened for shoot and grain Fe content and contrasts were identified. Further characterization of eight contrasting rice genotypes differing in shoot iron content under high pH (pH=8) condition showed chlorosis, reduction in growth and genetic variability for iron content was maintained. Similarly, these genotypes grown in agar media with high pH condition, extent of chlorosis

were more than low and neutral pH conditions. Further in two contrasting rice genotypes JBT 37/128 (high type) and CTH-1 (low type) the physiological and molecular mechanism of Fe acquisition, transport and plant responses to iron deficiency was studied. JBT 37/128 showed higher chlorophyll content, active iron (Fe²⁺) content, photosynthetic rate and shoot iron content. The iron deficiency responsive genes OsIRO2, OsIRT1, NAS1, OsNAS2, OsYSL2 and OsYSL15 were strongly up-regulated in JBT 37/128 than CTH-1 genotype indicates more tolerance to high pH condition/ Fe deficiency. The study demonstrates that the genotype JBT 37/128 has better adaptation under Fe deficiency due to the induced expression of Fe deficiency responsive genes that are involved in maintaining the cellular homeostasis.