190.5 Exploiting Agrobiodiversity to Meet New Challenges to Agricultural Production in 21st Century.

Tuesday, November 3, 2009: 11:15 AM Convention Center, Room 402, Fourth Floor

Hari D. Upadhyaya, St. Dwivedi, S. Gopalakrishnan and C. L. L. Gowda, Intl. Crops Res. Inst. for the Semi-Arid Tropics (ICRISAT), Hyderabad, Andhra Pradesh, India

Parallel demand for food, feed, and energy from agricultural crops coupled with climate change will pose major challenge to feed the increasing global population. Hunger and malnutrition has affected over 900 million people worldwide. Access to diverse genetic resources is vital in plant breeding to provide genetic traits to deal with new challenges to sustain agricultural production and meet demand for nutritionally-rich food worldwide.

ICRISAT genebank holds 116,966 cultivated and 2725 wild relatives' accessions from 144 countries. To date, 1500 microorganisms including phosphate solublizers, siderophore producers, callulose degraders, nitrogen fixers, antagonists, entomopathogens and fluorescent *Pseudomonads* have been assembled, characterized and preserved.

Core (10% of entire collection) and mini core (1% of entire collection) germplasm subsets have been developed in chickpea, pigeonpea, groundnut, sorghum, pearl millet, finger millet and foxtail millet, and are available for researchers globally. In addition, genotype-based 'reference sets', which also included mini core subsets, are also available for discovering new sources of variation, allele mining, association genetics, and mapping and cloning gene(s). Evaluations of these subsets have led to the identification of diverse germplasm for grain yield, early maturity, large-seed size, seed quality, resistance to biotic and abiotic stresses in chickpea, pigeonpea and groundnut; and with high-stalk sugar content for ethanol production in sorghum. Wild relatives offer additional source of variability. Introgression of useful traits from wild to cultivated species is in progress in chickpea, groundnut and pigeonpea. Utilization of these genetically diverse resources in applied breeding should lead to the development of broad-based elite breeding lines/cultivars

with superior yield and enhanced adaptation to diverse environments.

Several agriculturally beneficial microorganisms with specific attributes have been identified and possibly will have potential to enhance crop adaptation.

Taken together, both plant and soil microbial genetic resources provide immense opportunity to identify potential sources of genetic variability to meet new and emerging challenges to agricultural production.

See more of: Genetic Resources and Responding to New Challenges/Div. COS Bus. Htg.: II