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BOOK OF ABSTRACTS



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L22

Bean improvement through genetic engineering towards the generation of the first commercial transgenic varieties

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Golden mosaic, caused by *Bean golden mosaic virus* (BGMV) is the major constraint to common bean production in Latin America, reducing yield from 40 to 100%. Due to the social and economic importance of common bean for more than 300 million people worldwide, we have tried to obtain BGMV-resistant lines since early 90's. We hypothesized that silencing the AC1 viral gene by sequence-specific degradation of target mRNA interfering with viral replication would prevent viral DNA accumulation and appearance of symptoms. Two transgenic lines exhibited immunity upon inoculation at high pressure at early stages of plant development. Field trials were carried out during 2007 and 2008 in Brazil. Results confirmed greenhouse observations and no infected transgenic plants were observed, while control plots showed up to 18% infection in 2007 and 83% in 2008. Biosafety evaluations are in progress in order to obtain authorization to commercially release the first transgenic bean varieties. All risk assessment data generated to date revealed no differences between transgenic lines compared to parental plants. In addition, no significant variations in the sequence from *rep* gene have been observed in viruses isolated from several parts of Brazil.

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Genomics-enabled chickpea improvement for drought tolerance

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To address terminal drought, the number one constraint to chickpea production in more than 70% chickpea growing areas, a prolific and deep root system has been shown to confer better plant growth and seed yield under terminal drought. In order to identify QTLs for root traits, a total of 1,655 novel SSRs have been isolated from a SSR-enriched library (311) and BAC-end sequences (1,344). These SSRs are being used to genotype the mapping population (ICC 4958 x ICC 1882) segregating for root traits. For identification of putative genes involved in drought tolerance, > 10,000 ESTs have been generated from the two parental genotypes using Sanger sequencing approach. In parallel, cDNA pools for the two parental genotypes, assembled from root tissues harvested at different time points after imposing drought stress, have been sequenced using Solexa gigabase sequencing approach. Half of a Solexa run on ICC 4958 and ICC 1882 cDNA pools provided 5.2 x 10⁶ and 3.6 x 10⁶ sequence reads of 36 bp length, respectively. Alignment of these Solexa tags with *Medicago*-IMGAG gene assembly and/or available transcriptome sequence data for chickpea and other related legumes has provided more than 700 high confidence SNPs. Primer pairs for these SNP containing genes designed based on the best reference genome are currently being used to validate SNPs using allele-specific sequencing. Genetic mapping of newly developed and already available SSRs together with identified gene-based SNPs should provide candidate markers/genes associated with QTLs for drought tolerance to use them in molecular breeding for chickpea improvement.

L23

Modifying soybean oil for feed and fuel

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The soybean biotechnology team at the University of Nebraska has developed soybean germplasm that produces unique oils for feed and fuel applications. Using genetic engineering strategies we have generated soybean that synthesizes oil with a fatty acid profile composed of approximately 4.0% palmitic acid, 2.7% stearic acid, 85.0% oleic acid, 4.3% linoleic acid and 3.9% linolenic acid. Over the last few years we have demonstrated that soybeans that produce this unique oil are not compromised in agronomic performance, including yield, total oil/protein, and the meal quality is substantially equivalent to conventional soybean. Moreover, the attributes of this oil for food applications, improved oxidative stability and reduced palmitate, are also desirable characteristics for biodiesel. A biodiesel with over 80% oleic acid will possess an increased tank life, for an oxidized biodiesel will gum-up engines. Also the reduction in palmitic acid will improve cold flow properties of biodiesel. In addition, we recently demonstrated that biodiesel derived from this novel soybean mitigates NOx, a gaseous emission that tends to be elevated in engines fueled with biodiesel, as compared to conventional biodiesel. More recently we developed a soybean that possesses approximately 60% omega-3 fatty acids. This soybean produces oil with approximately 30% linolenic acid and 30% stearidonic acid. While a soybean oil with high omega-3 fatty acids would be of great value for direct human consumption through a variety of food applications, we are currently investigating its potential as a feed ingredient for aquaculture.

L25

Using model and crop legumes to identify QTLs and candidate genes associated with increased seed mineral concentrations

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We and others have been interested in improving the mineral nutritional value of legume crops, especially for human essential minerals like iron, zinc and calcium, which are often limiting in the human diet. In developing world countries where legumes are often important staple foods, nutritional improvements in grain legume germplasm could have significant impacts on the health and well-being of consumers. In order to gain a better understanding of the extent of the genome that might harbor loci contributing to mineral nutritional traits, we have conducted several quantitative trait loci (QTL) analyses in model and crop legumes. Recombinant inbred (RI) populations of *Lotus japonicus*, *Medicago truncatula*, *Glycine max*, *Phaseolus vulgaris*, and *Pisum sativum* have been grown using nutrient replete conditions; seeds have been harvested and analyzed for concentrations of iron, zinc, copper, manganese, calcium, magnesium, potassium, phosphorus, and sulfur, in order to identify QTLs associated with elevated seed mineral concentrations. In general, one to several loci has been identified for each mineral in each species, demonstrating the quantitative nature of these traits. In this presentation, we will use available comparative genomic information amongst these species to highlight syntenic regions with potentially common seed mineral QTLs. We will also utilize sequenced species to identify candidate genes, located within these loci, which might contribute to the seed nutritional traits. This work was supported in part by USDA-ARS (No. 58-6250-6-001) and the HarvestPlus Project (No. 58-6250-4-F029) to MAG.