



NATALIA BARBOZA VARGAS: Costa Rica

Restriction-Site-Association DNA sequencing.



Natalia Barboza Vargas, a Costa Rican researcher and PhD student at the University of Costa Rica, began a project titled "Generation of Promising Strains of Beans through Induced Mutation in Calluses and Seeds to Increase Competitiveness" a few years ago under the supervision of Dr. Pilar Ramirez. The International Atomic Energy Agency (IAEA) sponsored this project, and is now sponsoring her three and a half month IAEA Fellowship at the University of California at Davis. The goal of this project is to contribute to the increase of the competitiveness of national bean production through the generation of promising bean lines and the effective transfer of technology to the agricultural sector of Costa Rica, thus promoting a better quality of life for farmers and strengthening national food security.

This project's research was divided into four main stages: a) generation of genetic diversity to try to find some tolerance/resistance to *Rhizoctonia solani* (web blight), b) the increasing of the promising lines in the greenhouse, c) morphological evaluation in the field and d) selection using molecular markers. Tests were conducted with elite bean varieties Bribri and Brunca, irradiated with cobalt-60. The plantlets were treated in 15Gy and 15% of *R. solani* extract.

The bean lines obtained were tested for different traits in the greenhouse and in the field in plots belonging to farmer experimenters in the Huetar Norte and Brunca Regions in Costa Rica. At present, bean lines obtained have been selected for significant agronomic traits such as growth habit, few tendrils and number of pods/plant, and tolerance to web blight.

During her current IAEA fellowship, Ms. Barboza Vargas has had the opportunity to work under the supervision of Dr. Paul Gepts. They have been using a next-generation DNA sequencing approach called restriction-site-associated DNA (RAD) sequencing, which allows them to generate thousands of sequences adjacent to restriction sites across the genomes of multiple individuals. Specifically, her fellowship is about the construction of DNA sequencing (Illumina HiSeq) of two libraries, each containing bar-coded DNA of 96 entries (192 accessions). The goal is to find interesting mutations that appear to co-segregate with the phenotype and do the evaluation of the sequence diversity across libraries. When the fellowship is complete, Ms. Barboza Vargas will have applicable knowledge as she returns to Costa Rica that will help to continue the IAEA project that has already been started at the University of Costa Rica.

Training period 9/11/2011 – 12/16/2011