

analysis. The different methods of classification were consistent between them, with the exception of the cropping system (irrigated or upland). The information obtained allowing to breeders a better chooses of accesses and lines to your crosses. The results suggest a screening with SRM to classify accesses and the use of clustering analysis for *I/J* accesses and relationship studies. Financed by PADCT/CNPq and FAP-DF.

03-027 - CORRELATION BETWEEN GENETIC DISTANCE OF PARENTS AND HETEROSIS IN RICE (*Oryza sativa* L.). André Beló¹, Silvana Telles Cavalheiro¹, Zilneide Pedrosa Amaral¹, Márcio Elias Ferreira¹, Élcio Perpétuo Guimarães² e Paulo Hideo Nakano Rangel². ¹Laboratório de Genética, EMBRAPA – Recursos Genéticos e Biotecnologia. ²EMBRAPA – Arroz e Feijão. andbelo@hotmail.com.

Hybrid Rice is an alternative to create genotypic combinations more productive than the actual varieties. The main factors limiting the heterosis exploitation to Hybrid Rice production are the self-pollination habit of the specie and the difficulty in to test all the possible crosses. An efficient method in the prediction of the hybrid heterosis, based on characteristics of the parental lines, could aid the genetic breeding programs to accelerate the selection of hybrids and avoid time and resources consuming. The objective of the work was to verify the existence of correlation between genetic distance of parental lines with phenotypic traits and heterosis in F_1 hybrids, to predict the potential yield of new hybrid combinations. Ninety-eight RAPD markers was used in the evaluation of four cytoplasmic-genetic male sterile lines, 45 maintainers of sterility lines and 224 restorer of fertility lines from Cytoplasmic Male Sterility (CMS) Rice Hybrid Program developed by EMBRAPA. Four *indicaljaponica*-specific RAPD markers were utilized to classify the lines in the different subspecies. Pairwise genetic similarity among the genotypes was estimated by Dice coefficient and the restorer lines were classified in more similar, less similar and intermediary, in relation to the male-sterile lines. The restorer lines of the three categories of genetic similarity were crossed with the four male-sterility lines to produce 70 hybrids. These F_1 hybrids, its parental lines and four control varieties were evaluated to productive, productive compounds and agronomic traits in an experimental design with four randomized complete blocks, being these results used to estimate the heterosis for rice hybrids. Significant statistic differences were detected in some specific genotype combinations. However, the data do not allow a clear relationship between genetic distance and heterosis in this germoplasm. The results showed that this correlation occurs in specific combinations of markers with genotypes, suggesting that the formation of heterotic groups can play an important role in Hybrid Rice production, including a new difficulty to technology. Financed by PADCT/CNPq and FAP-DF.

03-028 - CARACTERIZACION MOLECULAR EN *Prosopis* (MEZQUITE) Y ANALISIS DE SU COMPORTAMIENTO IN VITRO. Abraham Rubluo; Guillermo Carrillo; Juana Juárez; Elizabeth Arriaga; Ingrid Brunner. UNAM. Laboratorio de Cultivo de Tejidos. E-mail : rubluo@ibiologia.unam.mx

INTRODUCCION. *Prosopis*, género multipropósito de zonas áridas de México no ha sido caracterizado con fines de mejoramiento, proceso lento dada su condición arborea. Estas dificultades pueden superarse más rápidamente analizando sus relaciones genéticas mediante marcadores moleculares y explorando su respuesta *in vitro* para posteriormente seleccionar y clonar individuos élite. **OBJETIVOS.** Sentar las bases para

una caracterización molecular de las 9 especies mexicanas de *Prosopis* para patrones de proteínas totales y ADN así como explorar condiciones para su micropropagación *in vitro*. **MATERIALES Y METODOS.** Para el análisis de proteínas y ADN se usaron cotiledones. Las proteínas extraídas se analizaron por el método de Lowry, se separaron en gel de acrilamida y sus bandas se registraron. El ADN se aisló por el método de Dellaporta amplificándose por PCR con 25 iniciadores. Los productos amplificados fueron separados por electroforésis y sus bandas registradas. El peso molecular de proteínas y fragmentos de ADN se calculó usando curvas estandar. Se construyeron matrices de similitud con el coeficiente de Jaccard y el método UPGMA usando el programa NTSYS. Semillas de *P. pubescens* se germinaron y diferentes explantes se cultivaron *in vitro* en medio MS adicionado de reguladores del crecimiento a varias concentraciones. Segmentos nodales de plantas adultas fueron también utilizados como explante para su cultivo *in vitro*. **RESULTADOS Y CONCLUSIONES.** De las bandas proteicas observadas, dos fueron comunes a todas las especies. Con RAPDS se obtuvieron 1573 bandas con un fragmento de 850 pb común a todas las especies, y otros particulares para las secciones Algarrobia y Stombocarpa. Los patrones de RAPDS mejor que los de proteínas mostraron las diferencias entre especies. Los dendogramas de relaciones genéticas dieron una fuerte correlación con la clasificación taxonómica clásica. La germinación en *P. pubescens* se logró en tratamientos con H_2SO_4 . Los explantes con mayor potencial regenerativo fueron cotiledones con hipocótilo en presencia de Kin y ANA a 0.05 y 0.1 mg/l, los cuales favorecieron la multiplicación y el porcentaje morfogénico de los brotes, estos se enraizaron en presencia de IBA y se establecieron en invernadero. Los segmentos nodales de plantas adultas no prosperaron.

03-029 - DEVELOPMENT OF A *Chenopodium quinoa* GENETIC MAP – A TEAM APPROACH. Mikel R. Stevens¹; Alejandro Bonifacio²; Brian W. Gardunia¹; Susan E. Parkinson¹; Eric N. Jellen¹; Craig E. Coleman³; Hong-Bin Zhang⁴; K. Arumuganathan⁵; Daniel J. Fairbanks³. ¹Agronomy and Horticulture Department, Brigham Young University, Provo, UT 84602; ²The Foundation for the Promotion and Investigation of Andean Products (PROINPA), La Paz, Bolivia; ³Botany and Range Science Department, Brigham Young University, Provo, UT 84602; ⁴Department of Soil and Crop Sciences, Texas A&M University, College Station, TX 77843;

⁵Center for Biotechnology, University of Nebraska-Lincoln, Lincoln, NE 68588. E-mail: daniel_fairbanks@byu.edu

Of all the New World crops, *Chenopodium quinoa* Willd., commonly known as quinoa is one of the most under utilized, given its superb seed protein composition and yield potential. Its cultivation is mostly limited to the high Andean of South America, where it is principally grown as a staple crop. In an effort to increase the productivity and uses of quinoa in Bolivia, a multi-disciplinary approach has been developed to facilitate quinoa breeding in the Bolivian highlands. This project uses a three-pronged approach: first, to develop microsatellites (simple sequence repeats [SSRs]) for use in PCR-based testing; second, to develop an amplified fragment length polymorphism (AFLP)-SSR genetic map of the genome; and third, to develop a bacterial artificial chromosome (BAC) library for physical mapping and eventual gene isolation. We have already identified over 550 SSRs from over 2,600 quinoa DNA sequences of a "AG repeat" enriched cv. 'Real' DNA library. Our early testing has revealed that there are 26 SSR markers out 48 primer pairs tested that demonstrate polymorphisms among the set of ten breeding lines that we have used for parents to develop segregating populations