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Final Program & Abstracts Guide

P5 MAPPING GENES ASSOCIATED WITH HUMAN FLAVOR PREFERENCES IN SWEET CORN.

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This study was conducted to ascertain the number, chromosomal location and magnitude of quantitative trait loci (QTL) associated with human flavor preferences for sweet corn. RFLP analysis was performed on 102 F_3 families derived from a cross between two inbreds that differed greatly in their eating quality (W6786*su1* and IL731*su1se1*). A series of 94 genomic clones distributed throughout the sweet corn genome were used. F_3 sib-pollinated ears were harvested at 20 days after pollination, frozen in liquid nitrogen and stored at -80°C for subsequent evaluation. Sensory evaluation of these 102 sibbed F_3 families by a trained descriptive panel (21 panelists) was conducted to determine intensity of attributes associated with sweet corn eating quality (sweet corn aroma, sweetness, starchiness, grassiness, crispness, tenderness and juiciness). Panelists were also asked to evaluate the samples for overall liking. Single factor analysis of variance revealed significant QTLs for all the eating quality characteristics ($p < 0.01$). Sweet corn aroma, sweetness, starchiness, grassiness, crispness, tenderness, juiciness and overall liking were significantly associated with 7, 9, 9, 3, 6, 6, 5 and 5 loci distributed throughout the maize genome, respectively. Multiple regression models consisting from 3 to 5 loci on different chromosomes for each of the attributes explained from 20 to 60% of the phenotypic variation. The use of molecular markers in combination with sensory evaluation will allow for the identification of DNA markers associated with human flavor preferences. This information will be used to conduct molecular marker assisted selection to improve eating quality in sweet corn.

P6

LINKAGES BETWEEN RFLP, RAPD, ISOZYME, DISEASE-RESISTANCE, AND MORPHOLOGICAL TRAITS IN NARROW AND WIDE CROSSES OF CUCUMBER.

Kennard, W., Poetter, K., Dijkhuizen, A., Meglic, V., Bacher, J., Staub, J., Havey, M. USDA, ARS, University of Wisconsin, Madison, WI 53706.

A 58 point genetic map was constructed using RFLP, RAPD, isozyme, morphological and disease resistance markers spanning 766 cM on ten linkage groups for a wide cross (Gy14 x PI432860) within cultivated cucumber, *Cucumis sativus* var. *sativus*. Relatively few DNA polymorphisms were detected (around 10% of probes and primers screened resulted RFLP or RAPD polymorphisms with 91% and 60%, respectively, segregating in expected ratios at $P<0.05$), agreeing with previous studies documenting a narrow genetic base for cucumber. A second linkage map was constructed using RFLP, isozyme, morphological and disease resistance markers spanning 480 cM on ten linkage groups for a wide cross between cultivated cucumber and the wild *Cucumis sativus* var. *hardwickii* (Gy14 x PI183967) Unlinked markers and more linkage groups than chromosome pairs indicated that both maps are not saturated. Twenty-one markers segregated in both mapping populations and regions of colinearity were identified. A 100 point map is under construction using primarily RAPD markers for two more closely related cultivated cucumber lines (G421 x H19). The data from the three maps will be merged using a set of 50 sequence characterized amplified regions markers (SCARs). Genes controlling plant height (*de*), sex expression (*F,M*), and QTLs for multiple branching, sequential fruiting and late flowering are being identified and mapped in the G421 x H19 cross using a combination of near isogenic lines and bulk segregant analysis. Markers linked to target traits will be used for marker assisted selection of potentially high yielding cucumber lines suitable for once-over mechanical harvesting (i.e., lines with stable female sex expression, determinate plant architecture, multiple lateral and sequential fruiting habits, as well as other horticulturally desirable traits).

P7

S-RELATED SEQUENCES ARE NOT SUFFICIENT TO PRODUCE SELF-INCOMPATIBILITY IN *LYCOPERSICON ESCULENTUM*

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Stylar proteins involved in the self-incompatible (SI) response of *L. hirsutum* have been identified and mapped to the locus that controls SI (*S*-locus). *L. esculentum*, self-compatible (SC) cultivated tomato, does not display these proteins. Hybrids between SC *L. esculentum* and SI *L. hirsutum* are self-sterile despite these individuals bearing pollen containing the *S*-allele of *L. esculentum*. In progeny derived from backcrossing the hybrids to *L. esculentum*, there was strong correlation between the presence of the *S* allele from *L. hirsutum* and self-infertility. However, this relationship was uncoupled in a number of backcross (BC) progeny. The SI response appeared to be non-existent in two self-fertile BC individuals that were heterozygous for the *S*-allele of *L. hirsutum*, based on Mendelian segregation of of a tightly linked DNA marker, CD15, in selfed progeny. Self-fertile individuals in these progeny that were homozygous for the *L.hirsutum* allele of the linked marker were also determined to be homozygous for the *S*-related proteins of *L. hirsutum* through testcrosses with *L. esculentum*. In other words, plants were produced that were homozygous for a functional *S*-allele, but were self-fertile. To further clarify the role the *S*-locus and flanking chromosome regions play in SI, the *S*-locus was finely mapped relative to 14 *chromosome 1* RFLP markers covering a distance of approximately 53 cM. These markers are being used to introgress varying lengths of *chromosome 1* segments from *L. hirsutum* into *L. esculentum* and from *L. esculentum* into *L. hirsutum*. The SI response of the different partial substitution lines is being investigated.

P8 PROGRESS IN DEVELOPING BREAD WHEAT RESISTANT TO BARLEY YELLOW DWARF VIRUSES USING SEROLOGICAL, MOLECULAR MARKER AND MOLECULAR CYTOGENETIC TECHNIQUES

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Barley yellow dwarf viruses (BYDVs) are the most important viral pathogens in small grain cereals worldwide. Resistance to BYDVs (restricted infection and/or replication and/or invasion) [*sensu* J. I. Cooper and A. T. Jones, Phytopathology 73:127-128 (1983)] has not been found in any true wheats. Recently, resistance has been transferred to bread wheat from *Thinopyrum intermedium* (Host) Barkworth & D. R. Dewey [Larkin, P. J. et al. Acta Hort. 336 (in press) (1993)]. This germplasm is being characterized, genetically analyzed, and advanced at the International Maize and Wheat Improvement Center (CIMMYT). Genetic stocks are being developed for making the germplasm available to wheat improvement programs. In collaboration with other institutions, several innovative techniques are being exploited to characterize this germplasm and to develop tools for marker-assisted selection. Homozygous resistant lines were produced and identified by testing inoculated progenies with DAS-ELISA. It was confirmed by tissue-blot ELISA that the resistance of these lines to four BYDVs confers low virus concentrations but not immunity. Results of the detection of an RFLP (A600) in EcoRV-digested DNA of segregating, normally pairing hexaploid lines and of their parents correlated well with the presence of the resistance. A non-radioactive protocol was developed for the use of A600. Even if in most cases, resistant lines could be easily identified by using the A600, its slight cross-reaction with wheat DNA emphasizes the need for a more specific polymerase chain reaction-based marker assay for marker-assisted selection. DNA from *Th. intermedium* was physically mapped with fluorescent *in-situ* hybridization (FISH). Different translocation families were analyzed by FISH. Based on ELISA, A600 and FISH results, conclusions are drawn regarding the most appropriate way to transfer the resistance into a desired agronomic background.