

Agronomy Abstracts

1996 Annual Meetings

American Society of Agronomy
Crop Science Society of America
Soil Science Society of America

00253	AGRONOMY ABSTRACTS - ANNUAL MEETINGS
 0960220137025 SISAC	1996  0065-4671(1996);1-5
	28708466

Nov. 3-8, 1996

Identification of Molecular Markers for *ant 28*, a Gene thatEliminates Proanthocyanidins from Barley Seeds.

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Barley (*Hordeum vulgare* L.) seed proanthocyanidins can complex with proteins during beer making, resulting in undesirable haze formation. The barley *ant 28* gene eliminates the synthesis of proanthocyanidins during grain development, and imparts excellent haze stability to beer. Molecular markers for *ant 28* would greatly reduce the time required to introgress this gene into commercial malting barley cultivars. This paper reports the use of RAPD analysis to identify a set of molecular markers linked to *ant 28*.

J.E. Miller-Garvin, (607) 255-5043

Forage Yield Trials: Some Analyses Using Incomplete Blocks.

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Efficiency, coefficient of variation, and Spearman rank correlation between randomized complete block cultivar means and adjusted lattice means, were compared for balanced lattice (BL) and incomplete block (IC) designs of alfalfa yield trials. Because of high soil variability, the 4x4 and 5x5 BL have been used for New York forage yield trials. A lattice is balanced when each cultivar in a trial is placed in a block with every other cultivar only once. Treatment means are adjusted for block effects in a BL, allowing small differences in yield to be distinguished. Disadvantages in using 4x4 or 5x5 BL designs are the strict limitation on the number of varieties (16 or 25), replications (5 or 6), and cultivars per block (4 or 5). An IC design allows for a larger number of cultivars without losing the ability to adjust treatment means for block effects. In 1994, three trials were planted in IC designs where the only restriction was that any two varieties in a trial were placed together in a block either one or zero times. The three IC trials contained 52, 33, and 27 cultivars; 5, 4, and 6 replications; and 4, 3, and 3 varieties per block, respectively. Efficiencies, CV, and rank correlation from first production year yield data (3 harvests/year) from three IC and 26 BL alfalfa trials were comparable. For the IC and BL trials, efficiency, CV, and rank correlation averaged 188 and 194, 4.6 and 5.1, 0.86 and 0.82, respectively.

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Phenotypic Stability for and Environmental Influence on Ear MoistureLoss Rate in Corn.

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Genotype by environment interaction (GEI) is an important component of variation for ear moisture loss rate (EMLR) in corn (*Zea mays* L.), with strong implications in breeding/selection for this trait. A measure of phenotypic stability of each hybrid is important for hybrid selection. Experiments with commercial corn hybrids were conducted in several environments. Mixed model equations and restricted maximum likelihood method were used to estimate GEI variances for each hybrid and interpret phenotypic stability. GEI variances were significantly different from zero for most of the hybrids, indicating lack of stability for EMLR. Stability and mean performance were not related, suggesting the possibility of selection of hybrids with stable fast dry down rate. Rainfall and growing degree days from planting to maturity were the most important environmental factors that influenced GEI for EMLR. The response of hybrids to removal of the effects of environmental factors varied.

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Evaluation of Transgenic Corn for Resistance to Fall

Armyworm and Southwestern Corn Borer. W.P. WILLIAMS*, J.B. SAGERS, J.A. HANTEN, F.M. DAVIS, and P.M. BUCKLEY. USDA-ARS, Mississippi State, MS and Northrup King Co., Stanton, Mn.

Fall armyworm, *Spodoptera frugiperda* (J.E. Smith), and southwestern corn borer, *Diatraea grandiosella* Dyar, are important pests of corn, *Zea mays* L., in the southern United States. Germplasm lines with moderate levels of resistance to leaf feeding by these pests have been developed and released; however, techniques for transforming

corn have expanded opportunities for developing corn lines with higher levels of resistance to these insect pests. Transgenic corn hybrids with insecticidal protein from *Bacillus thuringiensis* var. *kurstaki* were evaluated for resistance to fall armyworm and southwestern corn borer in field tests and laboratory bioassays. The transgenic hybrids sustained significantly less leaf-feeding damage than the resistant check hybrids. Both survival and larval growth were reduced. Growth was also reduced when larvae were fed laboratory diets comprised primarily of lyophilized leaf or husk tissue of the transgenic corn hybrids.

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Genetic Gain in the Narrow Midwestern Barley Gene Pool.

D.C. RASMUSSEN, Univ. of Minnesota.

Genetic diversity is limited in six-row barley breeding programs in the upper Midwestern USA. Breeding programs in the region share germplasm and strive to develop cultivars that satisfy common malting guidelines which are reinforced with market premiums. The dilemma can be seen in that two-thirds of new cultivar candidates in the cooperative regional nursery, 1994 and 1995, share parents from one breeding program. Fortunately, genetic diversity exceeds that predicted by pedigree and phenotypic analyses, as evidenced by recent cultivars which demonstrate incremental gains in malt extract, alpha amylase, grain yield, and lodging resistance. Recent studies at North Dakota by Horsley et al. showed that diversity for malting traits was greater than predicted by the coefficient of parentage. So how much genetic diversity exists within so-called narrow gene pools? I put forward the hypotheses that genetic diversity exceeds expectation, newly generated genetic variation is important, and that gene interaction, epistasis, is more important than commonly viewed.

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Pest Resistance and Agronomic Evaluations of *Aegilops tauschii*.

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Aegilops tauschii (DD), a wild diploid species, is the D-genome progenitor of bread wheat. A collection of 346 *Ae. tauschii* accessions, maintained by the Wheat Genetics Resource Center at Kansas State University, was evaluated for resistance to the pathogens that cause tan spot, leaf rust, stem rust, powdery mildew, and leaf blotch; the greenbug, Hessian fly, and Russian wheat aphid insect pests; and the wheat curl mite. Winterhardness was evaluated under natural field conditions near Manhattan where accessions with an 80% survival rate were considered tolerant. The percent of accessions tested with resistance to each pathogen or pest were: tan spot (64%), leaf rust (19%), stem rust (6%), powdery mildew (12%), leaf blotch (40%), greenbug (61%), Hessian fly (59%), wheat curl mite (19%), and the Russian wheat aphid (0.4%). Thirty-six percent of the accessions were considered cold tolerant. Depending on the pest, 51 to 98 percent of the *Ae. tauschii* collection is evaluated.

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Synthetic Hexaploids of the A, B, and D Genomes of the TriticeaeResistant to *Septoria tritici* Leaf Blotch.

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The Triticeae species of the A, B, and D genomes within the primary, and secondary gene pools offer a potent avenue that facilitates pyramiding of diverse stress resistances for wheat improvement. We have produced a wide array of genetic stocks using the above genomic accessions. These hexaploid amphiploids (2n=6x=42) are AAAABB, AABBBB and AABBBDD and were derived from crosses of the A, B, or D genome diploid accessions onto various durum wheats. Screening these germplasms in Toluca, Mexico, for *Septoria tritici* led to the identification of several resistant entries. Diagnostic parameters were disease damage during three grain filling stages and 1000 grain weight. The germplasm provides unique diversity for improving both bread and durum wheat cultivars through bridge crosses as one option. Some descriptors of the above germplasms are mentioned.

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