

Evaluation of Ploidy Indicators in Dactylis subsp.

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Utilization of diploid *Dactylis* subsp. in orchardgrass breeding via colchicine doubling, triploid intermediates, or meiotic mutants requires rapid and reliable identification of the ploidy level. Cytological methods are not suitable for screening a large number of genotypes. Genotypes of defined ploidy (2x, 3x, 4x) and inbreeding level were evaluated for dry matter yield, visual vigor rating, leaf length, and leaf dimensions. Four experiments conducted in a greenhouse using a RCB design, repeated four times during successive growth periods. No significant differences existed between genotypes for characters studied. In linear contrasts between genotypes, significant differences existed between diploids and triploids for all characters studied. Triploids and non-inbred tetraploids differed significantly for all characters except dry matter yield. Significant differences also were detected between inbred and non-inbred tetraploid genotypes for visual vigor rating and leaf length. Genotype x period interaction and its implication for screening will be discussed. Data on variance component estimation and allocation of resources will also be presented.

Maternal Half-sib Families Number Useful to Estimate Additive Variance in Maize Populations.

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Seventeen basic maize germplasms were evaluated in Palmira, Colombia, during 1980-B and 1981-A semesters, to determine if they had enough additive genetic variance to permit response to selection, and to determine the minimum number of maternal half-sib families, necessary to get additive variance and heritability estimations useable in predicting genetic advance from selection. Those parameters were studied for yield, prolificacy, plant and upper ear height. Using an average of 50 open-pollinated ears per population, we runed a combined analysis among half-sib families. The best estimations, free from genotype-environment interaction, were obtained from the combined rather than from the individual analysis. There were sufficient additive genetic variability and heritability in all the characters measured in all the population evaluated, to permit gain from selection. We finally concluded that 120 half-sib families were the most proper number to estimate the additive variance, independently from the genotype studied, as shown by a progressive analysis starting with five families in two random chosen populations.

Performance and Potential of Interspecific Wheatgrass Hybrids in the Central Great Plains.

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'Slate' intermediate wheatgrass (*Agropyron intermedium*), 'Ruff' (*A. cristatum*) and 'Nordan' (*A. desertorum*) crested wheatgrasses, 'RS-1' and 'RS-2' (*A. repens* x *A. spicatum* hybrids), and AR\*AD (*A. desertorum* x *A. repens* hybrid) were evaluated at Mead and Alliance, NE (35 and 562 km west of Omaha, NE, respectively) which differ markedly in climate. Slate yielded 2 Mg/ha more forage than the other grasses at Mead; Ruff, Nordan, RS-1, and RS-2 had similar yields. Slate, Ruff, and Nordan had the highest yields at Alliance. AR\*AD had the lowest yields at both locations. Slate had the highest forage digestibility at both locations. In 1983, at Mead there was variation among strains for cell wall components and their digestibility. In their present state of development, the interspecific hybrids are inferior to intermediate wheatgrass in the Central Great Plains.

Genotypic Variability for Grain Growth in Triticale.

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To complement the routine screening for reduced grain shrivelling and higher test weight in triticale (x *Triticosecale* Wittmack) at CIMMYT a detailed evaluation of the grain filling pattern of 29 earlier genotypes from the triticale crossing block was undertaken in two contrasting Mexican environments, the cooler rainfed site El Batán and the warmer irrigated site CIANO. Selected lines were also exposed to post-anthesis

water stress at CIANO. Triticale grain filling patterns were categorised into three groups depending on their similarity to bread wheat. Substantial variability in filling patterns was detected between the triticales. The earliest lines tended to be least like bread wheat. Although the grain filling period was shorter at CIANO, with few exceptions, the no stress grain filling patterns were similar at the two sites for individual genotypes. No broad relationship between a bread wheat-like filling pattern and improved filling performance under post-anthesis could be detected in the earliest lines. These lines were identified that show promise for reduction of early triticales less prone to post-anthesis drought.

Natural Selection during the Mating Cycle in Barley.

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856 progeny from a series of reciprocal backcrosses were assayed for four esterase loci marking linkage groups 1 and 3 in cultivated barley (*Hordeum vulgare* L.) Five parents homozygous for *Est-1*, *Est-2*, *Est-3*, and *Est-4* were crossed as males and females to individuals heterozygous for all four loci. The experimental design allowed a test for natural selection acting on male and female components of F1 individuals. One of the loci, *Est-4*, produced segregation ratios significantly different from Mendelian expectation ( $\chi^2=34.06$ ,  $p<0.001$ ) indicating strong selection favoring one of the alleles at this locus in both male and female gamete production or function. Since this is not a unique example of natural selection during the mating cycle, breeding programs might gain efficiency by capitalizing on naturally favored alleles.

Intergeneric and Interspecific Hybridization AmongPerennial Diploid Species of the Triticeae Tribe in Greenhouse.

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To enhance and manipulate the germplasms of perennial forage grasses in the Triticeae tribe, diploid species in the genera *Agropyron*, *Thinopyrum*, *Pseudoroegneria*, *Hordeum*, *Criticon*, *Psathyrostachys*, and *Secale* were vernalized at 5°C under short-day (8 hours of illumination) for various lengths of time (from 2 to 10 weeks). Subsequently, most species, except those of *Psathyrostachys*, were induced to flower by long-day conditions (18 hours) in the greenhouse. Controlled pollination followed by a GA<sub>3</sub> application the next day plus embryo culture technique were used to achieve hybridization. From emasculated crosses, plants were obtained in diploid combinations of *T. bessarabicum* x *T. elongatum*, *T. elongatum* x *A. mongolicum*, *T. elongatum* x *P. inermis*, *T. elongatum* x *P. stipifolia*, *A. mongolicum* x *S. montanum*, and *T. elongatum* x *C. violaceum*. Unemasculated crosses yielded plants in *A. cristatum* x *S. montanum*, *P. libanoticum* x *S. montanum*, *P. inermis* x *S. montanum*, and *A. mongolicum* x *S. montanum*. Germinated embryos were observed in *T. elongatum* x *S. montanum*, and *C. californicum* x *C. violaceum*. The significance of these new hybrid combinations on taxonomy and plant improvement will be discussed.

Screening of Aegilops species for karnal bunt (Neovossiaindica) resistance and their practical utilization forTriticum aestivum improvement.

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Several *Aegilops* species, accessions obtained from the Plant Breeding Institute, Cambridge, U. K., were screened under greenhouse conditions for resistance to karnal bunt (*Neovossia indica*) using the boot inoculation technique. The infection ranged from 0 to 100 per cent (%) over a scale of 0 (zero infection) to 5 (completely bunted kernel). The species observed to be resistant are *Ae. umbellulata*, *Ae. ovata*, *Ae. colummaris*, *Ae. biuncialis*, *Ae. variabilis*, *Ae. speltoides*, *Ae. crassa*, *Ae. vavilovii*, *Ae. ventricosa* and *Ae. juvenalis*. The *Aegilops* species *triaristata*, *triuncialis*, *cylindrica*, *longissima* and *squarrosa* showed 10 per cent or less infection. Intergeneric hybrids of some of these species have been produced with *Triticum turgidum* and *T. aestivum*. Resistance is expressed in backcross progenies of *T. aestivum*/*Ae. triaristata*/*T. aestivum* and of *T. aestivum*/*Ae. variabilis*/*T. aestivum* (1). These results and the greenhouse screening technique is discussed, as are methodologies for utilizing this resistant germplasm for the improvement of *Triticum aestivum* via subtle genetic transfers.