ANALYSIS OF GENOTYPE-BY-ENVIRONMENT INTERACTION IN WHEAT USING ANEUPLOID LINES WITH CHROMATIN INTROGRESSED FROM DASYPYRUM VILLOSUM


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The presence of genotype-by-environment interaction (GxE) impose additional efforts in selection of superior breeding lines, and an understanding of the type of GxE interaction is important in all stages of plant breeding especially for pursuing sustainable low-input agriculture aims. Crop production in low-input agriculture requires cultivated varieties showing resilience (low phenotypic plasticity or high stability over environments) to varying environmental effects in farmers’ fields. Breeding methods for low phenotypic plasticity require the assessment of the genotype x environment interaction pattern for both parental lines and selected progenies, and have an important bearing on usefulness of the resulting cultivated varieties. The most important genotype x environment interaction patterns in breeding materials can be divided in two categories: one of low genotypic variance, significant crossover interaction and genotypes endowed with environmental specialization, and the other that leads few genotypes to perform better than others in several environments (“universal” genotype).

Twelve inbred breeding lines (IBLs) derived from interspecific hybridization of *Triticum aestivum* cv “Chinese Spring” (CS) x *D. villosum* (Dv) were used to explore which genotype x environment interaction pattern will be expressed when tested in multienvironment low-input cropping system. Those lines have been selected from a population of 150 aneuploid lines developed through [(CS x Dv, F1) x CS] backcross, followed by three generation of selfing (BC1F1 S1 through S4), five generations of single-spike descent (from S4 through S8) and four generations of seed increase (S12 IBLs). S12 breeding lines traced to the same S4 plant were considered “sister lines”. Genetic uniformity within lines and differentiation among lines have been tested using AFLP and GISH. The lines have been tested in 7 different environments. In each cropping environment, off-farm inputs were minimized. The main genotype x environment interaction pattern displayed by the breeding lines is of the category “higher proportion of genotypic variance compared to the genotype x environment interaction variance component”. Multiplicative model and biplot invariably grouped similar genotypes (sister lines) in the same cluster and indicated the line CSxV_60 as the “ideal breeding line” in terms of genotypic main effects and stability for yield in
the tested environments. Good stability has been detected for time of anthesis and gluten strength. The observed results are compatible with the hypothesis that the main genotypic effects observed over environments are traceable to the direct and indirect effects of chromatin from *D. villosum*. These lines are ideal starting points for studying individual QTLs with a pre-tested environmental stability and for transferring those QTLs to commercial varieties.