

Agronomical evaluation of the Spanish Barley Core Collection

S. Yahiaoui*, M.P. Gracia*, E. Igartua*, B. Medina*, F.J. Ciudad**,
P. Codesal**, J.L. Molina-Cano*** and J.M. Lasa*

*Department of Genetics and Plant Production, Aula Dei Experimental Station, CSIC,
P.O. Box 202, E-50080 Zaragoza, Spain

**ITA, Instituto de Tecnología Agraria, Junta de Castilla y León,
P.O. Box 172, E-47071 Valladolid, Spain

***Centre UdL-IRTA, Av. Rovira Roure 191, E-25198 Lérida, Spain

Introduction

A deep knowledge of the genetic resources is a prerequisite for their utilization in plant breeding programs. Local landraces are a potential source of new genes and alleles for plant breeding (Ceccarelli *et al.*, 1987, among others). Spanish barleys constitute an underused resource which shows distinct genetic, morphologic, and agronomic traits (Tolbert *et al.*, 1979; Lasa *et al.*, 2001). The Spanish Barley Core Collection (SBCC) was assembled as a manageable tool to study this genetic diversity. It is constituted by 159 landrace-derived inbred lines (148 six-row and 11 two-row), plus 16 old varieties (8 two-row, 8 six-row) extensively grown in Spain in the 20th century (Igartua *et al.*, 1998).

Material and methods

An extensive evaluation of the SBCC was carried out throughout the country across a range of environments (10 trials, from 5 locations across Aragón, Castilla y León, and Cataluña, over 3 years). A set of 10 modern cultivars was included in the trials as checks. A range of agronomic (yield, heading date, plant height, lodging, thousand kernel weight, test weight, spikes m⁻², kernels m⁻², kernels spike⁻¹), disease resistance (net blotch, leaf rust, powdery mildew), and malting quality traits (kernel plumpness, screening, malt extract and protein content) were evaluated. Not all traits were evaluated at all trials. Climatic data available from meteorological stations close to each trial were collected and used to interpret genotype by environment interaction by factorial regression.

Results and discussion

The distribution of relative frequencies for the traits measured is presented in Fig. 1, separately for the landraces (159) and the cultivars (26).

Large variability was observed for most of the traits studied, especially among the landrace material.

Landrace-derived inbred lines presented, on average, several negative traits compared to cultivars, such as excessive plant height, higher lodging, susceptibility to diseases, and later heading date. Most of these are typical changes observed when comparing old landraces and modern cultivars for the same region. However, later heading date for the landrace material was not expected. This shortening of the cycle may have to do with the much shorter time needed in modern agriculture to carry out harvesting operations.

Though cultivars outyielded landraces on average, when considering separately low- and high-yielding environments (Fig. 1, grain yield histograms on the first row), some Spanish inbred lines showed excellent yields under low productivity conditions. Also on the positive side, some landraces were as good as the best cultivars for each trait, but for plant height, which underscores their potential to contribute positive alleles for breeding programs. The excessive plant height of Spanish materials, and their propensity to lodging was expected, as they come from a period previous to generalizations of chemical fertilization. Regarding individual genotypes, 18 of the top 20 yielding genotypes at high

productivity environments were cultivars, whereas 16 of the top 20 were landrace-derived inbred lines at low productivity environments. This result stresses even more the differential responses recorded, consequence of an important genotype-by-environment interaction present in this study.

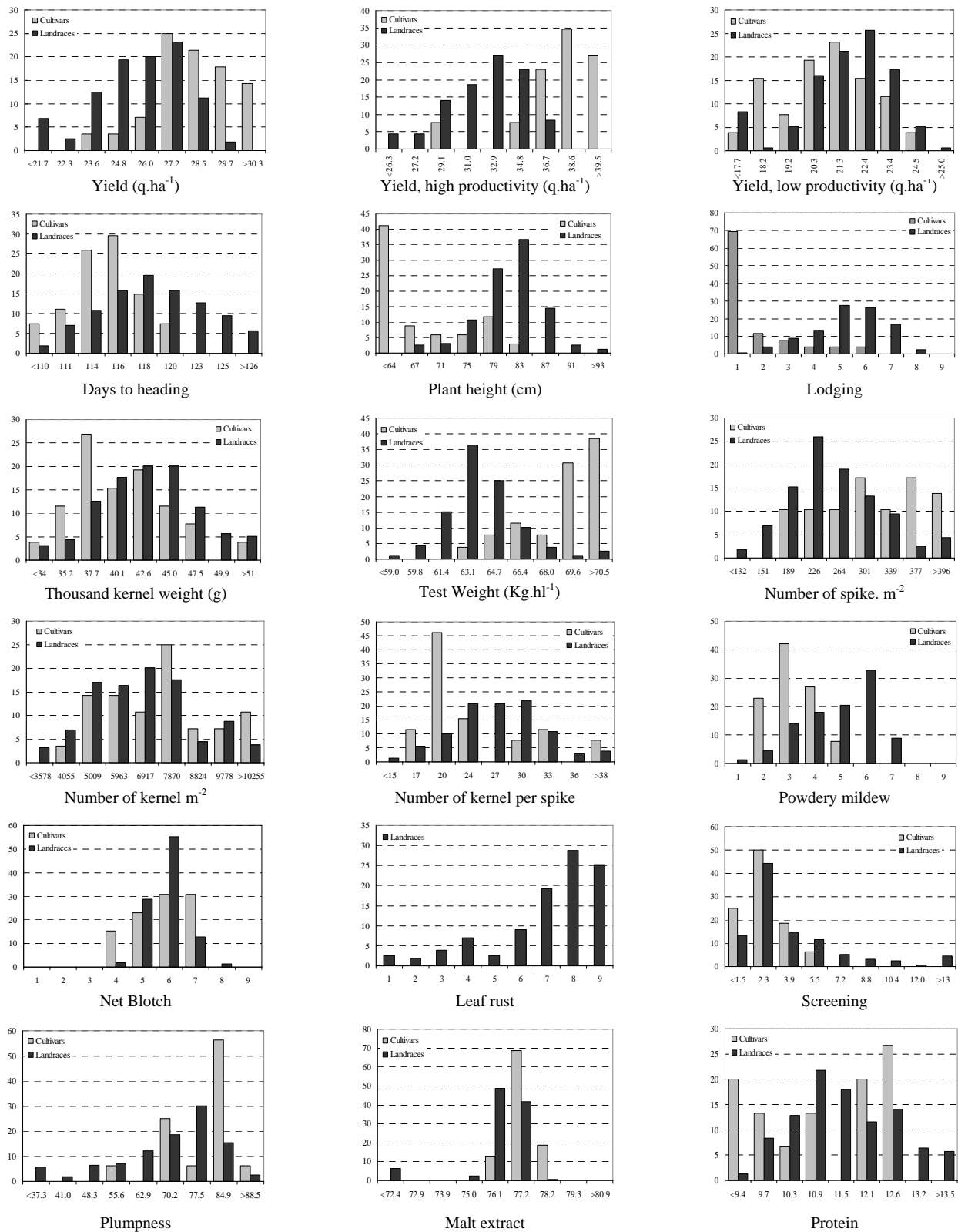


Fig. 1. Distribution of traits (relative frequencies) for 159 inbred lines derived from Spanish landraces, and 26 cultivars.

Genotype by environment (GxE) interaction sum of squares for grain yield doubled the sum of squares for genotypes (not shown). This large interaction was unequally distributed among genotypes. A substantial part of the interaction (for grain yield as well as for most traits) was accounted for by the seven genetic groups assembled after a molecular marker analysis (see contribution by Casas *et al.*, this volume).

Table 1 shows the most parsimonious GxE analysis, using factorial regression with genotypic and environmental variables. A total of 32% of GxE sum of squares was explained with only 0.7% of GxE degrees of freedom. Powdery mildew tolerance, heading date, and lodging were the three genotypic variables more closely related with grain yield GxE interaction. Powdery mildew attacks were evident at several environments. Many landraces were susceptible to powdery mildew, whereas most cultivars were resistant. The same could be said for lodging, cultivars being more lodging resistant than Spanish inbred lines, which caused a differential response in trials where lodging occurred. Heading date relationship with grain yield varies across trials. This is a common situation in Spain. In an average season, early genotypes do not have an advantage, as they do not benefit from spring rains. In seasons with lack of spring rains, early genotypes yield better than late ones. Interaction of heading date and powdery mildew with fall temperature mean a different effect of these genotypic variables on grain yield according to the temperatures experienced in the fall in the different environments.

Table 1. Break-down of grain yield genotype-by-environment interaction, after factorial regression with environmental and genotypic covariables

Source of variation	Degrees of freedom	Sums of Squares	Mean Squares	F	
Genotype-by-environment	1448	62942	43	5	**
Powdery mildew x Environment	8	10978	1372	169	**
Powdery mildew x Fall temperature [†]	1	8049	8049	991	**
Residual	7	2928	418	51	**
Heading date x Environment	8	6903	863	106	**
Heading date x Fall temperature [†]	1	5204	5204	641	**
Residual	7	1700	243	30	**
Lodging x Environment [†]	8	6539	817	101	**
Residual	1424	38522	27	3	**
Error	3276		8		

**Significant for $P < 0.01$

[†]Components of the most parsimonious model to interpret GxE interaction.

This work was supported by INIA (project RTA01-088-C3) and by the European Regional Development Fund (ERDF).

References

- Ceccarelli, S., Nachit, M.M., Ferrara, G.O., Mekni, M.S., Tahir, M., van Leur, J.A.G., Srivastava, J.P. (1987). Breeding strategies for improving cereal yield and stability under drought. In: *Drought Tolerance in Winter Cereals*, Srivastava, J.P., Porceddu, E., Acevedo, E. and Varma, S. (eds). John Wiley and Sons, New York, pp. 101-114.
- Igartua, E., Gracia, M.P., Lasa, J.M., Medina, B., Molina-Cano, J.L., Montoya, J.L., Romagosa, I. (1998). The Spanish barley core collection. *Genetic Resources and Crop Evolution*, 45: 475-481.
- Lasa, J.M., Igartua, E., Ciudad, F.J., Codesal, P., García, E.V., Gracia, M.P., Medina, B., Romagosa, I., Molina-Cano, J.L., Montoya, J.L. (2001). Morphological and agronomical diversity patterns in the Spanish barley core collection. *Hereditas*, 135: 217-225.
- Tolbert, D.M., Qualset, C.O., Jain, S.K., Craddock, J.C. (1979). A diversity analysis of a world collection of barley. *Crop Science*, 19: 789-794.