

Variation in agronomically important traits in natural populations of wild emmer wheat, *Triticum dicoccoides*, in Israel

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Abstract

Diversity in agronomically important traits of wild emmer wheat, *Triticum dicoccoides*, the progenitor of most cultivated wheats, was examined in 160 genotypes representing 16 populations derived from a wide ecogeographical spectrum of climate, soil and water availability in Israel and Turkey. The analysis included 14 quantitative economic characters including heading date, culm length, biomass, grain yield and its components, and grain protein percentage. The results led to two major conclusions: (i) agronomically important traits varied genetically: ecogeographic diversity in these traits is dramatically displayed when populations are grown in a relatively standardized environment; and (ii) genetic diversity is revealed not only between, but also within populations. Thus, genotypes excelling in some of these characters were found in several populations.

Keywords: agronomic traits; genetic diversity; *Triticum dicoccoides*; wheat breeding; wild emmer wheat

Introduction

The rich genetic diversity of wild emmer wheat, *Triticum dicoccoides*, the progenitor of cultivated wheat, is still largely untapped by breeders (Nevo *et al.*, 1984). The exploration, conservation and utilization of these important genetic resources is important for the future improvement of both tetraploid and hexaploid wheats (Nevo *et al.*, 2002). This study examines variation in agronomic traits for 160 *T. dicoccoides* accessions, representing 15 populations from Israel and one from Turkey.

Materials and methods

A full description of the material, along with its geographic origin and climatic conditions, has been provided by Nevo and Beiles (1989). Seeds from individual plants (genotypes) were taken at random for planting in two 80-cm long rows per accession (inter-row spacing 25 cm, inter-plant spacing 3.2 cm). Combined seasonal rainfall

and irrigation amounted to 895 mm. Phenotype was assessed in 2001/2 at the Aaronsohn Experimental Station, Atlit (Mediterranean coast of Israel). The leading Israeli *durum* cv. Inbar, two *durum* breeding lines, C-9-21 and 2097, and the leading Israeli *aestivum* cv. Galil were included as controls. Fourteen characters (Table 1) were measured from plants in the central 50 cm of each row.

Results and discussion

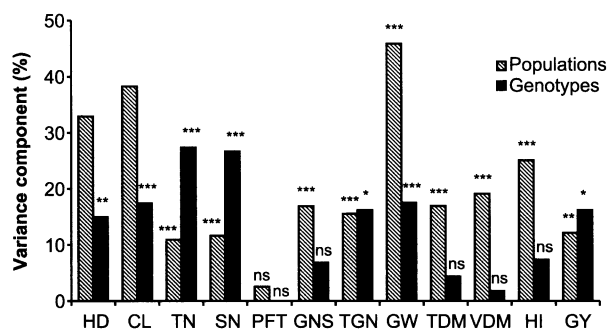
Significant diversity among the wild populations was found for all 12 traits tested in individual genotypes, except for PFT (Fig. 1; abbreviations are explained in Table 1). The diversity *between* genotypes *within* populations was significant for HD, CL, GY and for almost all GY components, but not significant for PFT, GNS, TDM, VDM and HI.

The means of 16 wild wheat populations ranged widely for all traits, except for PFT (Table 1). The highest HD was obtained in a population from a high altitude, semi-arid cold environment, Mt Hermon. The Gamla

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Table 1. Range of means for 14 agronomic traits in 160 accessions representing 16 wild emmer wheat populations from Israel and Turkey, and for four cultivated lines

Trait	Abbreviation	Range of population means	Range of cultivar means
Days to heading	HD	118–128	94–95
Culm length (cm)	CL	90–115	64–69
Number of tillers per m ²	TN	429–718	245–341
Number of spikes per m ²	SN	358–641	225–290
Percentage of fertile tillers	PFT	82–93	85–93
Grains per spike	GNS	13–18	35–42
Number of grains per m ²	TGN	4624–10,225	8328–12,188
1000 grain weight (g)	GW	23–35	39–52
Total amount of above-ground dry matter (g/m ²)	TDM	1071–1901	828–1075
Vegetative amount of above-ground dry matter (g/m ²)	VDM	906–1627	415–610
Harvest index	HI	0.12–0.19	0.45–0.53
Grain yield (g/m ²)	GY	144–306	387–536
Grain protein percentage	GPP	15.2–19.2	8.3–9.9
Grain protein yield (g/m ²)	GPY	25.7–46.4	32.1–51.4

**Fig. 1.** Relative values (% of total) of the populations and genotypes within population variance components (σ^2) for 12 agronomic traits (abbreviations are explained in Table 1) of *Triticum dicoccoides* from Israel and Turkey. ns, not significant; *, **, *** significant variation at $P < 0.05$, $P < 0.01$ and $P < 0.001$, respectively.

population showed the highest mean GY, 306 g/m², resulting from relatively high GNS, TGN, GW and HI. The relatively high GY, 273 g/m², of the Mt Gerizim population resulted from relatively high SN, TGN and HI. GPP was recorded from a seed sample of all genotypes in each population, and in three individual genotypes that were superior in their GY. The protein content (Kjeldhal nitrogen $\times 5.71$) was expressed on a 10% water content basis. The Givat Koach and Mt Gilboa populations showed the highest mean GPP, 19.2 and 18.4%, respectively. By contrast, the Gamla and Mt Hermon populations were characterized by the lowest GPP, 15.2 and 15.4%, respectively. In general, GPP was lower than that reported by Nevo *et al.* (1986). Our results, generated from relatively well-watered experiments, are in accordance with those obtained by

Rharrabti *et al.* (2001). As GPY is the product of GY and GPP, the highest values of 46.4 and 42.6 g/m² were obtained (similar to GY) in the populations of Gamla and Mt Gerizim, respectively.

All the cultivated lines showed a higher GY than the means of all wild populations (Table 1). The cultivated lines have low GPP compared with the wild populations. Despite this, *durum* cv. Inbar had a higher GPY than the means of all the wild populations. Almost all the individual wild genotypes delivered lower GY than the cultivated lines. However, three wild individuals were superior for GY: two from the Mt Gerizim population and one from the Gamla population (Fig. 2L). These high GYs derived generally from a combination of relatively high SN, GNS, TGN, GW and HI. GPP of the three genotypes was 16.3, 13.7 and 16.5%, respectively. As a result, these genotypes produced high levels of GPY, 91.1, 71.4 and 85.2 g/m², even compared with those of the four cultivated wheat lines (Table 1).

Analysis revealed a negative genetic correlation (r_G), estimated according to Beharav *et al.* (1998 and references therein), between HD and CL, DM and GY (Table 2), a slightly positive one between CL and GY, derived from a positive r_G between CL and both GNS and GW, and a highly positive one between GY and TGN, derived from positive r_G between GY and both SN and GNS. A positive r_G was also observed between GY with both GW, DM (total and vegetative) and HI.

Analysis of Spearman rank correlation of the 14 agronomical traits and 17 ecogeographical variables (see Table 1 of Nevo and Beiles, 1989) exhibited a trend of higher HD with lower temperature, but higher humidity conditions. The analysis reflects an increase in tillering

Fig. 2. Frequency distribution for 12 agronomic traits of *Triticum dicoccoides* in 160 accessions from Israel and Turkey. Cultivated lines: G, Galil; I, Inbar; C, C-9-21; 2, 2097.

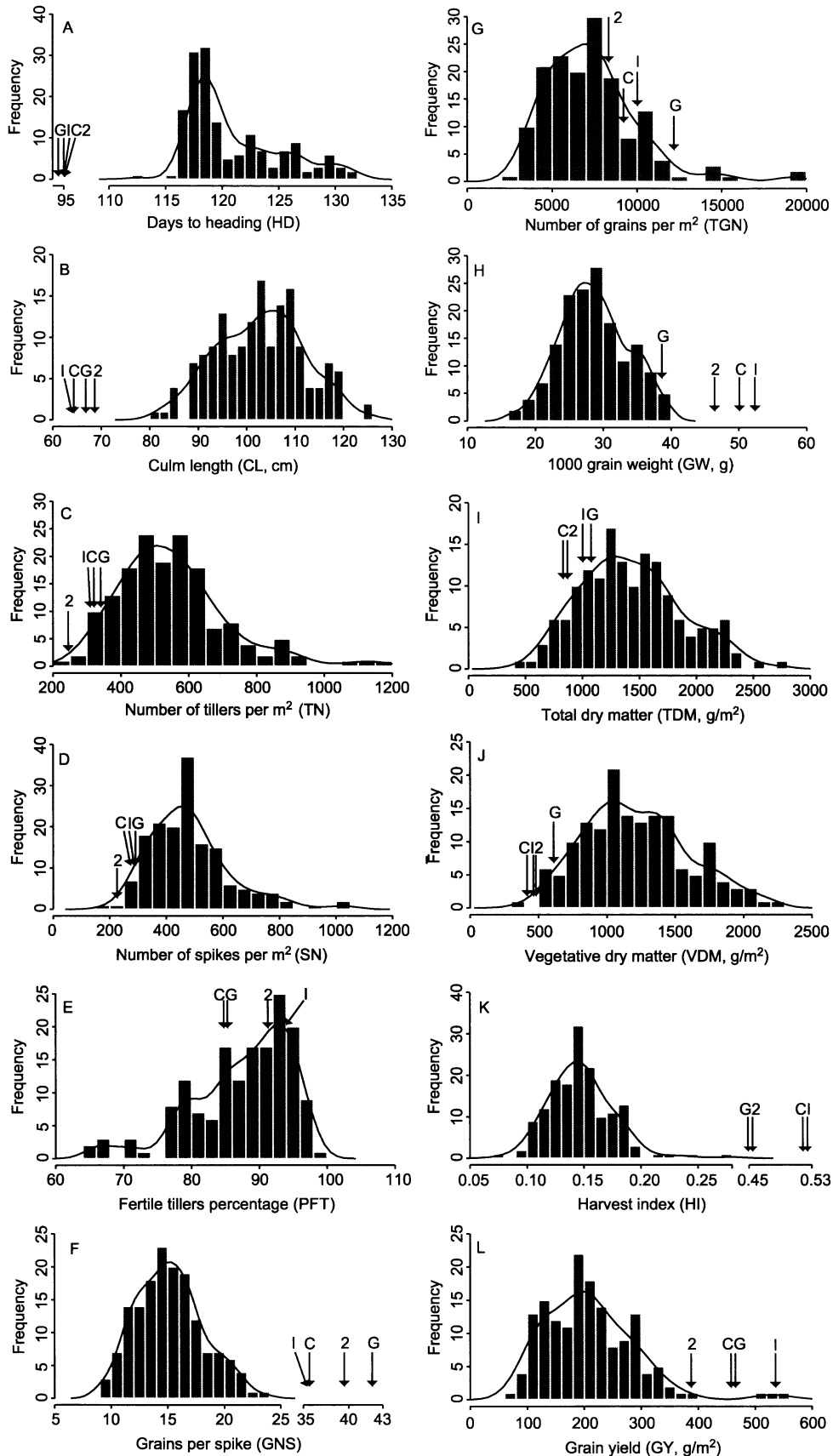


Table 2. Pairwise genetic correlation of HD, CL and GY with other traits (abbreviations are explained in Table 1) of 160 *Triticum dicoccoides* accessions from Israel and Turkey

Trait	GY	HI	VDM	TDM	GW	TGN	GNS	SN	TN	CL
HD	-0.355	-0.185	-0.378	-0.391	-0.669	-0.028	-0.497	0.146	0.157	-0.312
CL	0.326	-0.455	0.839	0.762	0.314	0.181	0.538	-0.033	-0.079	
GY		0.698	0.763	0.841	0.380	0.808	0.620	0.593	0.512	

and spike production with lower temperature; GW and GPP showed the same trend of increase with higher temperature but lower water availability. Stepwise multiple regression analysis showed that latitude, temperature factors, water availability factors and soil type, singly or in combination, explained a significant proportion of the diversity in the 14 agronomical characters. HD was the most predictable trait: a three-variable combination, involving temperature (Tm), geographic (Lt) and moisture (Rn) factors, accounted ($P < 0.001$) for 0.88 of the variance in HD.

Conclusions

The agronomically important characters studied vary genetically. Genetic diversity was revealed not only between but also within populations. Based on our analysis, it should be possible to select wild genotypes combining disease resistance, high grain protein percentage, improved baking quality, earliness, long culm, with a special emphasis on elite yield genotypes, combining high grain number per unit area coupled with high grain weight.

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