International Adaptation Trial: Using probe and reference genotypes to characterize global spring wheat production environments.

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Abstract

Results are presented from a nursery (International Adaptation Trial - IAT) to investigate environmental stresses in spring-wheat production areas. These illustrate concepts of using probe and reference genotype sets to characterize environments. A probe pair compares presence/absence of the *Rht1* dwarfing gene in a Nesser background with results presented on maps. A reference genotype set of twenty-one broadly adapted CIMMYT-derived lines, grouped seventy-eight trials into three main groups, Australian rain-fed, high-yielding irrigated international trials and lower yielding irrigated or rain-fed international trials.

Media summary

Experiments in global and Australian locations aims to assist Australian wheat breeders to select germplasm for improved yield in our wheat industry.

Key Words

Genotype-by-environment interaction, probe genotypes, reference genotypes

Introduction

Genotype-by-environment interaction (GEI) complicates the interpretation of multi-environment trials (METs) in plant breeding, (e.g. Peterson and Pfeiffer, 1989; DeLacy et al., 1996). After estimating GEI effects, the next step is to characterize where trials are grown in an attempt to identify the repeatable sources of genotype-by-environment variation. Breeding strategies can then be designed to account for or to exploit GEI. Direct methods to characterize environments use data on the climate, trial management practices and soil parameters. Cooper and Fox (1996) discuss the use of 'probe' and 'reference' genotype sets to indirectly characterize environments. Probe sets aim to reveal specific environmental challenges (e.g. a disease or soil chemical problem), whereas reference sets are random-effects bioassays to investigate the relationships among environments. The International Adaptation Trial (IAT) is an investigative spring wheat nursery distributed globally by the International Centre for Wheat and Maize Improvement (CIMMYT). It contains probe genotypes to assess biotic and abiotic stress and a reference set of broadly adapted germplasm from CIMMYT and Australia to determine relationships among Australian and CIMMYT breeding and testing locations. The concepts of both probe and reference genotype sets in characterising global spring-wheat environments are illustrated using the IAT.

Methods

Treatment and experiment design

The IAT contains 60 bread and 20 durum wheat lines, primarily of CIMMYT and Australian origin, chosen for their drought adaptation characteristics and, their ability to identify soil borne problems (abiotic and biotic) and agronomic traits (Table 1). In many cases there are isogenic pairs (usually derived by

backcrossing) available for trait comparisons. Where an isogenic pair does not exist, the contrast consists of lines with similar genetic backgrounds but known different reactions for a key trait. There are about 40 contrasts, including 'replicate' contrasts for several traits.

Table 1. Trait contrasts in the International Adaptation Trial using probe and reference genotype sets.

Agronomic	Soil Constraints	Disease	Adaptive
Plant height (Rht1 or 2)	Boron toxicity	Crown rot	Terminal drought (¹ ME4A)
Vernalisation/earliness	Zn deficiency	Common root rot	Pre-anthesis drought (ME4B)
Drought adaptation	Mn deficiency	Cereal cyst nematode	Residual moisture (ME4C)
	Acid soil	Root lesion nematode	Irrigated environments (ME1)
		Major rust genes	High rainfall (ME2)

¹ ME = Mega-environment classification as defined by CIMMYT (Calhoun et al., 1994)

Twenty-one CIMMYT-derived lines are used here to investigate relationships among environments. These lines were included for their drought adaptation to spring wheat growing environments or their broad adaptation to both drought and irrigated or high rainfall conditions (Table 2).

Table 2. Broadly adapted CIMMYT-derived genotypes with trait descriptions.

Code	Genotype Name	Trait Description
ATTL	ATTILA	Adaptation to drought & irrigation conditions (ME4 & 1) (India)
CETT	CETTIA	Global adaptation to drought (ME4)
CHIL	CHIL/PRL	Global adaptation to drought (ME4)
CNDO	CNDO/R143//ENTE/MEXI _2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER	Synthetic derivative with good drought tolerance in Mexico
DHAR	DHARWAR DRY	Adaptation in monsoonal India (Rajastan)
GLVZ	GALVEZ DWARF	Rht1 isoline - long term drought check at CIMMYT

HXL	HXL7573/2*BAU	Adaptation to drought tolerance (Heilongjiang, north east China)
INQA	INQALAB 91	World's greatest acreage; early maturing (Pakistan)
JUN	JUN/BOMB	Global adaptation to drought (ME4)
KAUZ	KAUZ DWARF	Rht1 isoline - released in South Asia - high yield potential
NESS	NESSER DWARF	Rht1 isoline – widely released in West Asia
PAVN	PAVON DWARF	Rht2 isoline – widely released for dry and irrigated systems
PFDL	PROINTA FEDERAL	Bobwhite line - tolerant to pre-anthesis stress (Argentina)
PRL	PRL/SARA//TSI/VEE#5	Hessian fly resistant
PSTO	PASTOR*2/OPATA	Global adaptation to drought & high rainfall (ME4 & 2)
PSTR	PASTOR	Global adaptation to drought, high rain & irrigation (ME4, 2 & 1)
SITT	SITTA	Global adaptation to drought conditions (ME4)
SON	SONALIKA	Very early maturing; Green Revolution variety in South Asia
SSER	SUPER SERI #1	SERI plus Ir19 gene - widely adapted and released
TUI	TUI	Global adaptation to drought & high rainfall (ME4 & 2)
URES	URES/JUN//KAUZ	Global adaptation to drought & irrigation (ME4 & 1)

In most cases, the bread and durum lines were grown in separate two-replicate α -lattice designs under local agronomic practice. Where fungicide was not applied, trials that either reported a severe score for foliar disease or had a significant contrast for leaf or stem rust were removed. The remaining 78 trials were sown between 2000 and 2003 (25 were in Australia, 14 at CIMMYT's research station northwestern Mexico and the rest in major spring wheat production areas) (Fig. 1). Assuming replicate, replicate x block and variety effects to be random, trait contrasts were made to test the importance of the presence/absence of each trait (SAS Proc Mixed). Best linear unbiased predictors (BLUPs) were calculated for each trial and averaged for lines representing the presence or absence of the trait. Thus, "contrast averages", were mapped on the basis of statistical significance, (P < 0.10).

Extended factor analytic techniques (Smith et al. 2001) were applied in the across site analysis using ASREML (Gilmour et al 2002). Factor analytic models are the random effect equivalent of the fixed AMMI (additive main effects and multiplicative interactions) models and allow fitting of separate genetic variances to each environment and genetic covariances among environments. Best spatial models (i.e. row and column effects) where possible, otherwise incomplete block analysis was used with replicate, replicate ? block and variety considered as random effects. Design terms with a variance component of zero were removed to achieve a more parsimonious model. A biplot created from the factor analytic loadings and scores assists interpretation of the genetic correlations among environments. The circle in a biplot indicates 100% of trial genetic variance explained, i.e. trials whose vector length equals the radius of the circle have 100% of their genetic variance explained by the two factors on this biplot (Smith, A., 2004, pers comm.)

Results and discussion

Probe genotype set

An example map for Rht genes (Fig. 1) shows that the yield difference between semi-dwarf and tall types in a Nesser background is generally not significant. In one trial the tall genotype yields more than the semi-dwarf and in high input trials in Mexico, several trials in Australia and trials in Pakistan, Argentina, Spain and Ecuador, the semi-dwarf out yielded the tall type. The green revolution was based on the yield advantage of semi-dwarf types when combined with optimum agronomy and inputs. This preliminary analysis shows that following substantial improvement of breeding in a semi-dwarf backgrounds, the re-introduction of the 'tall' allele does not have as large a negative impact as might be expected, i.e. in the absence of lodging, the breeders were able to make significant progress for other adaptive traits. In a smaller set of trials, Singh et al (2001) noted that the value of the dwarfing gene in a large set of backgrounds was 0.66 t/ha. Further analysis of our data will investigate this effect in a large number of locations and in several genetic backgrounds.



Figure 1. Distribution of International Adaptation Trial, 2000-2003. The contrast shown is for the Nesser near-isogenic Rht1 pair.

The centre point of the biplot approximates 'average' yield in all environments, while the cosine of the angle between any two vectors is the genetic correlation between the two environments. Hence, in this dataset relationships between pairs of environments span the full range of highly correlated (coincident lines) to uncorrelated (angle = 90?) to negatively correlated (90 < angle < 180?). In the vertical direction, factor 1 was correlated with average yield in each environment (r = 0.47).

The centre group (partially correlated with Australian environments) contains the higher yielding southern European trials and the irrigated trials from CIMMYT. Most of the environments in the largely irrigated Indo-Gangetic plains and the non- or partially irrigated trials of CIMMYT are grouped toward the left hand side. The strong correlation between Obregon and the rice-wheat environments of South Asia confirms CIMMYT's historical success in developing spring wheat germplasm that is well adapted to this huge area of irrigated wheat production. However, these environments to the left were poorly correlated with the rain-fed Australian environments. The exceptions were: 1) two high-yielding Australian sites (Tamworth and Willowtree) located in the irrigated group; and 2) an irrigated CIMMYT trial, C149, that was grown in irrigation on melgas, a planting system similar to the Australian flat system with which it clusters.

Across the dataset, Inqalab has the broadest adaptation, being toward the centre upper part of the biplot, i.e. except for environments A4 and A11, this cultivar has a positive score when a perpendicular projection is made on to any environment vector. Nesser is the most poorly adapted in broad terms. Tui, Prointa Federal and the early maturing Sonalika have broad adaptation to international environments while Dharwar Dry, Attila and Kauz are the most broadly adapted to Australian environments.

Reference genotype set





Conclusion

Probe and reference genotype sets are useful to indirectly characterise environments, thereby explaining repeatable genotype-by-environment interaction. In conjunction with maps, probe genotypes assist breeders to identify locations or regions which allow the phenotypic expression of specific adaptation for a particular trait. Reference genotype sets allow a broader interrogation of the relationships among environments. These 21 lines classified the environments into three loosely geographical groups: rain fed Australian, irrigated high yielding CIMMYT and southern European locations and the non-irrigated CIMMYT and irrigated South Asian locations. A more direct result for Australian breeders is that CIMMYT international nurseries where Attila and Kauz perform well could be a source of new germplasm for yield adaptation in Australia.

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