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Heritability of grain yield, plant height and test weight of a population of winter wheat adapted to Southwestern Ontario

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Summary. Grain yield, plant height and test weight were studied in a population of winter wheat (*Triticum aestivum* L.). The population consisted of F_2 bulk populations of 42 crosses among 11 genotypes adapted to S. W. Ontario. Heritabilities were: 0.30 ± 0.32 for yield, 0.77 ± 0.15 for height and 0.98 ± 0.08 for test weight. Predicted genetic gain with 10% selection intensity was 0.15 t/ha for yield, 10.1 cm for height and 3.00 kg/hl for test weight. The low heritability for yield indicates that effective selection would require pedigree information and progeny tests, while the high heritabilities for height and test weight indicate that selection for these traits using single plots would be appropriate.

Key words: Wheat – Heritability – Yield – Height

Introduction

This study was undertaken to provide estimates of heritability of yield, height and test weight of a population of winter wheat adapted to Southwestern Ontario.

Heritability is the fraction of the observed variance caused by differences in heredity, and a dependable estimate of the heritability of a characteristic is perhaps the most important consideration in deciding which of several possible breeding plans is most likely to be effective (Lush 1940). If heritability is high, mass selection is best, while if heritability is low and there is little epistatic variance, selection on the basis of performance of relatives and progeny tests would be useful. Furthermore, an estimate of heritability is useful in establishing an attainable goal in breeding and in charting a course to reach that goal.

Heritability has also been defined as an expression of the reliability of the observed value (phenotype), as a guide to breeding value (Falconer 1960). It is a property, not only of the character, but also of the population and the environmental circumstances to which the individuals are subjected. This study, intended to provide data in applied breeding, therefore uses an adapted population and the limited environment to which the anticipated cultivar is intended. While the information is of special interest locally it may have broader use for breeders elsewhere who are working mainly with adapted populations and in a limited environment.

Materials and methods

The 11 cultivars and lines (Table 1) used in the crosses were all selected for superior yield in cooperative trials of the Ontario Cereal Crops Committee, and while their sources vary a little (New York, Michigan, Ontario) an examination of pedigrees reveals many common ancestors, such as 'Genesee', 'Brevor', 'Norin 10', 'Yorkwin' and 'Avon'.

Table 1. Parents and their pedigrees

Parent	Pedigree
1. 'Augusta'	GE/RCT(A2747)/YS
2. B2090	N10/BVR//YW/3/2*GE(A3141)/4/ GE*3/RCT(A5115)
3. CW 79-7	Unknown
4. 'Frankenmuth'	N10/B-14//YW/3/2*GE(3141)/4/ GE*3/RCT(A5115)
5. 'Fredrick'	WASH No. 1/GE// CD6707
6. 'Houser'	B/N10//82A1/3/H-HR/YW/4/GE// CI12658/ALASKAN/3/AVON
7. H1-11	FRED/YS
8. H1-46	FRED/YS
9. H1-87	FRED/YS
10. HG1	HALYT/YS
11. HG2	HALYT/YS

Table 2. Method of calculating heritability, h^2, and its standard error SE h^2, according to Becker (1964)

$$SS_D(XX) = \sum_i \sum_j X_{ij}^2 - \frac{\sum x_{i.}^2}{n\,i.}$$

$$SS_D(ZZ) = \sum_i \sum_j Z_{ij}^2 - \frac{\sum z_{i.}^2}{n\,i.}$$

$$SCP_D(ZX) = \sum \sum X_{ij} Z_{ij} - \frac{\sum Xi, Zi.}{n\,i.}$$

$$b_1 = \frac{SCP_D(ZX)}{SS_D(XX)}$$

$$b_2 = \frac{SCP_D(ZX)}{SS_D(ZZ)}$$

$$r^2 = b_1 \cdot b_2$$

$$h^2 = r$$

where ni = number of females[a] mated to i^th^ male

Xij = progeny mean of i^th^ male[a] mated to j^th^ female

Zij = j^th^ female mean mated to i^th^ male

Standard error

$$S_{b1}^2 = \frac{SS_D(ZZ) - \dfrac{SCP_D(ZX)^2}{SS_D(XX)}}{(D-S-1)\,(SS_D(XX))}$$

for S_{b2}^2 replace SS_D (XX) with SS_D (ZZ)

where D = number of crosses

S = number of males

$$\text{SE } h^2 \text{ (or r)} = \sqrt{2\sqrt{S_{b1}^2} \times 2\sqrt{S_{b2}^2}}$$

[a] It is of no consequence which parent is considered to be the male or female unless there are maternal effects

Forty-two of the 55 possible crosses among the 11 parents were achieved. Bulk F_2 seed was used in planting field plots of the progeny tests at two locations with three replications in randomized complete blocks at each location. Plots were 3.6 m long with four rows spaced 23 cm apart. All four rows were harvested. Parents were not included in this study.

Heritabilities were calculated by the method outlined in Table 2; taken from Becker (1964) and modified for the standard unit method advocated by Frey and Horner (1957).

Response to selection was calculated as:

$R = i\sigma_p h^2$ (Falconer 1960, p 193)

where R is the difference of mean phenotypic value between offspring of the selected parents and the whole of the parental generation before selection, i = intensity of selection (standardized, p 193, Fig. 11.3) and σ_p = phenotypic standard deviation.

Results and discussion

Population means, phenotypic standard deviations, heritabilities and estimates of genetic gain for 10% selection intensity are given in Table 3.

The population mean yield was 5.11 t/ha which compares favorably with the yield of 'Fredrick' the most commonly grown cultivar, which yielded a mean of 5.01 t/ha in other tests at the two test locations. A low phenotypic standard deviation of 0.29 t/ha, 5.67% of the population mean, combined with a low heritability for yield of 0.30 result in a low estimate of genetic gain of 0.15 t/ha, or about 3% of the population mean. This low heritability and high standard error for heritability (±0.32) bear comparison with a study on hard red spring wheat (Pesek and Baker 1971) in which the mean of five tests was 0.30±0.22. Comparing the estimated genetic gains with historical data in S. W. Ontario (Anonymous 1979, 1981), one finds that the last two cultivars released exceeded their predecessors by 0.26 t/ha. While this is almost twice as large as the estimated gains in this study, selection within crosses should result in additional genetic gain.

The population mean height, a trait of secondary importance, was 117 cm, well within the range of cultivars currently grown in S. W. Ontario. Reduction in height, which might increase resistance to lodging and facilitate harvesting, should not be difficult given heritability of 0.77±0.15. Heritabilities of similar magnitude have been found by others: 0.80 (Britts and Cassalett 1975), 0.55 to 0.97 (Wegrzyn and Pochaba 1977), 0.39 to 0.66 (Mustafaev et al. 1978), and 0.71 (Kassem 1977). With such high heritabilities calculated from replicated plots, heritability on a single plot basis would also be high, though less, and effective selection should not be difficult even with moderate phenotypic variation in plant height.

Population mean for test weight was high. This trait, a criterion for establishing market grade, is of such economic impact that low test weight cultivars are unacceptable to the trade. While no reports of heritabilities for test weight were found in the literature, it is commonly accepted that test weight is highly heritable.

Where heritability is low, such as for yield, it is difficult to effectively evaluate a potential cultivar by its performance in a single plot. Precision in evaluation increases with replication, test sites and test years. Pre-

Table 3. Population means, phenotypic standard deviations, heritabilities, and estimated genetic gain for 10% selection intensity

	Yield	Height	Test wt
Population mean	5.11 t/ha	117.42 cm	75.87 kg/hl
Phenotypic SD	0.29 t/ha	7.70 cm	1.80 kg/hl
Phenotypic SD in % of mean	5.67%	6.56%	2.37%
Heritabilities ± SE	0.30 ± 0.32	0.77 ± 0.15	0.98 ± 0,08
Genetic gain	0.15 t/ha	10.1 cm	3.00 kg/hl
Genetic gain in % of mean	2.94%	8.60%	3.95%

cision also increases with the use of information on performance of relatives (Lush 1940). A potential cultivar whose parents and sibs are highly productive is more likely to be productive than a line whose relatives are mediocre.

The principle of using the performance of relatives in selection is inherent in the method of using early generation bulk (a bulk of sibs) trials to identify those crosses most likely to contain highly productive potential cultivars. Cregan and Busch (1977) clearly demonstrated that testing F_2 and F_3 using bulk hybrid seed was an effective means of identifying crosses with a higher than average frequency of high yielding lines. Given the low heritability of yield found in this study this appears to be a most prudent means of facilitating selection for yield.

Several methods are available for estimating heritability such as (1) environmental and phenotypic components of variance, (2) variance and covariance of full-sib families and (3) regression of offspring on parents. Of these three the second has been shown to be superior (Cahaner and Hillel 1980) for self fertilizing species in one study, while in another study the third has been advocated for cereals (Frey and Horner 1957) and applicable to generations as early as F_2. The method of calculating heritability in this study contains elements of methods 2 and 3 and has certain limitations: (1) heritability may be a little inflated because it contains half of the dominance variance, (2) although heritability does include the genotype environment interaction associated with locations it does not include that asociated with year, and (3) strictly speaking, it is applicable to similar experimental designs, i.e. plot size, and location and replication number (Frey and Horner 1957). Heritabilities for single plant or single plot selection would be lower than those calculated here, but gain for a highly heritable trait such as height would still be considerable. A small plot would be required to furnish enough seed for evaluating and selecting for test weight.

References

Anonymous (1979) Progress report: barley, oats and wheat regional tests in Ontario. Crop Sci Dept, University of Guelph 118-01-79 110/34

Anonymous (1981) Progress report: barley oats and wheat regional tests in Ontario. Crop Sci Dept, University of Guelph 119-01-81 110/34

Becker Walter A (1964) Manual of procedures in quantitative genetics. Washington State University, Pullman Wash

Britts MR, Cassalette DC (1975) The inheritance and heritability of plant height and its correlation with other characters in wheat (*Triticum vulgare* L.) (in Spanish). Rev Inst Columbiano Agropecuario 10:255–268

Cahaner A, Hillel J (1980) Estimating heritability and genetic correlation between traits from generations F_2 and F_3 of self-fertilizing species: a comparison of three methods. Theor Appl Genet 58:33–38

Cregan PB, Busch RH (1977) Early generation bulk hybrid yield testing of adapted hard red spring wheat crosses. Crop Sci 17:887–891

Falconer DS (1960): Introduction to quantitative genetics. Ronald Press, New York

Frey KJ, Horner T (1957) Heritability in standard units. Agron J 49:59–62

Kassem AA (1977) Genetic studies of wheat traits in a diallel cross. Meld Nor Landbrukshoegsk 56:1–16

Lush Jay L (1940) Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics. 33rd Annu Proc ASAP, pp 293–301

Mustafaev ID, Figarova VV, Ali-Zade AV, Jafarova RG (1978) Variability and heritability of quantitative characters in wheat (in Russian). Genetica USSR 14: 1400–1408

Pesek J, Baker RJ (1971) Comparison of predicted and observed responses to selection for yield in wheat. Can J Plant Sci 49:187–192

Wegrzyn S, Pochaba L (1977) The inheritance of plant height and grain yield and its components in winter×spring hybrids (in Polish). Biul Inst Hodowli Aklimatyzacji Rosl 131:3–11