How many test locations and replications are needed in crop variety trials for a target region?

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Introduction

- Crop variety trials are essential for plant breeders to select and for agronomists to recommend crop cultivars to growers.
- How many test locations and replications are needed in crop variety trials are questions everyone conducting variety trials has to ask.
- The purpose of this work was to develop simple formulas for estimating the optimum number of replicates within a trial and the optimum number of test locations for a target region.

The optimum number of replications within a trial

- The effectiveness of variety trials is measured by the heritability achieved in them. The solution for the optimum numbers residues in the definitions of heritability.
- The heritability within a trial is determined by (DeLacy et al, 1996):
- $H = \dfrac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_\varepsilon^2}{N_r}}$,
- where H is the heritability of the trial for the trait of interest, σ_g^2 is the genotypic variance, σ_ε^2 the error variance, and N_r the number of replicates in the trial. This formula can be written as:
- $N_r = \left(\dfrac{\sigma_\varepsilon^2}{\sigma_g^2}\right)\dfrac{H}{1-H} = Q_r\dfrac{H}{1-H}$
- The relationships between N_r and H is depicted in Figure 1. The increase in the number of replications N can effectively improve H only when H is smaller than certain level, say H = 0.75, beyond which the effect gradually diminishes.
- Assuming H = 0.75 is the target trial heritability, the number of replicates needed is determined by
- $N_{r,H=0.75} = 3\left(\dfrac{\sigma_\varepsilon^2}{\sigma_g^2}\right)\dfrac{H}{1-H} = 3Q_r$ [1]

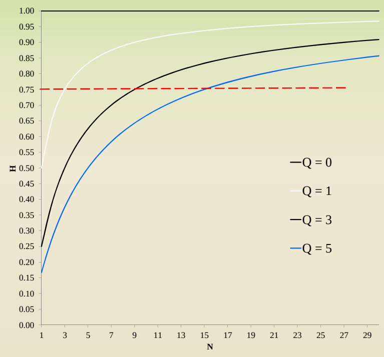

Fig. 1. Relationship between trial heritability (H) and number of replications at different trial noise levels (Q)

The optimum number of test locations for a target region

- Likewise, the heritability at multilocation trial level is defined as:
- $H = \dfrac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_{ge}^2}{N_e} + \frac{\sigma_\varepsilon^2}{N_e N_r}}$,
- where σ_g^2 is the genotypic variance, σ_ε^2 the experimental error variance, σ_{ge}^2 the genotype-by-location interaction variance, N_e the number of test locations, and N_r the number of replicates within trials. This equation can be written as:
- $N_e = \left[\dfrac{\sigma_{ge}^2 + \sigma_\varepsilon^2/N_r}{\sigma_g^2}\right]\dfrac{H}{1-H}$.
- Given the relationship between H and N_e (Fig. 1), the number of test locations needed to achieve H = 0.75 may be considered as the optimum number of test locations for a target region and can be determined by
- $N_{e,H=0.75} = 3\left[\dfrac{\sigma_{ge}^2 + \sigma_\varepsilon^2/N_r}{\sigma_g^2}\right] = 3Q_e$
- Assuming each trial is properly replicated this formula can be simplified to:
- $N_{e,H=0.75} = 1 + 3\left(\dfrac{\sigma_{ge}^2}{\sigma_g^2}\right)$ [2]

Case study

Table 1. Number of replicates used (N) and number of replicates needed to achieve a heritability of 0.75 (N_H75) estimated using Eq. [1] for different traits in the oat registration trials at Ottawa, Ontario from 2008 to 2012.

Year	Number of Reps	Days to heading	Plant Height	Test weight	1000-kernel weight	Grain yield
2008	N	4.0	4.0	3.9	3.9	4.0
	N_H75	4.0	2.1	1.7	1.5	1.4
2009	N	2.0	4.0	4.0	4.0	4.0
	N_H75	2.5	1.4	2.3	1.6	4.1
2010	N			4.8	4.8	4.8
	N_H75			1.8	1.3	1.8
2011	N	6.0	6.0	6.0	5.9	5.9
	N_H75	1.4	2.6	1.5	2.1	2.4
2012	N	6.0	6.0			6.0
	N_H75	2.2	3.0			3.1
Mean	N	4.5	5.0	4.7	4.7	5.0
	N_H75	2.5	2.3	1.8	1.6	2.6

Table 2 Number of test locations used (N) and number of test locations needed to achieve an H = 0.75 (N_H75) estimated using Eq. [2] for oat grain yield within each of two mega-environments in eastern Canada.

Year	Number of Locations	Southern mega-environment	Northern mega-environment
2006	N	4.0	5.0
	N_H75	7.6	5.1
2007	N	4.0	6.0
	N_H75	6.2	2.3
2008	N	5.0	8.0
	N_H75	4.8	6.6
2009	N	5.0	5.0
	N_H75	10.1	5.6
2010	N	5.0	5.0
	N_H75	27.7	8.8
2011	N	4.0	4.0
	N_H75	18.3	6.5
2012	N	3.0	4.0
	N_H75	9.0	4.5
Mean	N	4.3	5.3
	N_H75	12.0	5.6

References

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