

Relationship Between Heritability, Progeny Size and Effectiveness of the Classification of Inbred Progenies by Simulation

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Introduction

ONE OF THE ADVANTAGES of simulation, as compared to conventional testing, is the large amount of results attainable in a **short** period of **time** and the possibility of circumventing the problem of sample size, overcoming the limitations due to large number of replications.

Specially in **plant breeding** simulation is very interesting and studies have been made with this approach (ABREU *et al.*, 2010).

Objectives

THE AIM OF THIS STUDY was evaluating the relationship between the **heritability** of a trait, **progeny size** and the effectiveness in the **ranking** of progenies considering selection of the **5% superior ones**.

Material and Methods

THE CORRECT identification of the 5% superior progenies was investigated, considering:

- One hundred $F_{6:7}$ progenies;
- Quantitative trait, controlled by **100 independent loci** with equal **additive effects** (two alleles);
- Variable number of **individuals** per progenies (**4, 16, 64 and 256**);
- Coefficients of **heritability** on a plant basis (h^2) ranging from **0.01 to 0.99**; and
- Each scenario was **repeated 500 times**.

ALL ANALYSIS were performed and/or implemented using the **software R** (R Development Core Team, 2011).

Results and Discussion

IN ORDER TO EVALUATE the precision of the simulation algorithm, average values of the parameters were obtained for all simulations, as given in table 1.

Heritability mean values of the 500 simulations were **consistently close** to the chosen parameter (h^2).

Table 1: Mean (\bar{x}) and standard deviation (σ) of the 500 simulations for the heritability (h^2) on a plant basis within F_6 and $F_{6:7}$ populations.

F_6	0.01		0.25		0.50		0.75		0.99	
n	\bar{x}	σ	\bar{x}	σ	\bar{x}	σ	\bar{x}	σ	\bar{x}	σ
4	0.010	0.002	0.252	0.036	0.514	0.058	0.754	0.081	0.986	0.021
16	0.010	0.001	0.255	0.038	0.506	0.064	0.751	0.072	0.987	0.020
64	0.010	0.002	0.258	0.034	0.504	0.060	0.754	0.068	0.993	0.020
256	0.010	0.001	0.254	0.037	0.510	0.061	0.762	0.073	0.990	0.024
$F_{6:7}$	0.01		0.25		0.50		0.75		0.99	
n	\bar{x}	σ	\bar{x}	σ	\bar{x}	σ	\bar{x}	σ	\bar{x}	σ
4	0.010	0.001	0.252	0.016	0.501	0.035	0.758	0.034	0.991	0.010
16	0.010	≤ 0.001	0.252	0.007	0.498	0.014	0.748	0.018	0.990	0.005
64	0.010	≤ 0.001	0.251	0.004	0.500	0.007	0.750	0.010	0.990	0.003
256	0.010	≤ 0.001	0.250	0.002	0.501	0.004	0.750	0.004	0.990	0.001

FOR LOW HERITABILITIES larger progeny sizes **increased the effectiveness** of the classification process.

For $h^2 = 0.25$, with 4 plants per progeny, the average of the 500 simulations indicated that the effectiveness of the classification was **half of that obtained with 64 individuals**. When $h^2 = 0.75$, the effectiveness achieved with 4 plants was about 80% of the precision obtained using 64 plants (**Figure 1**).

For a range of heritabilities between 0.25 and 0.75 the percentages of correct classification of the superior progenies varied from 0.79 to 0.94, respectively, when 64 individuals were evaluated per progeny. With 16 plants per progeny the percentage varied between 0.67 to 0.87.

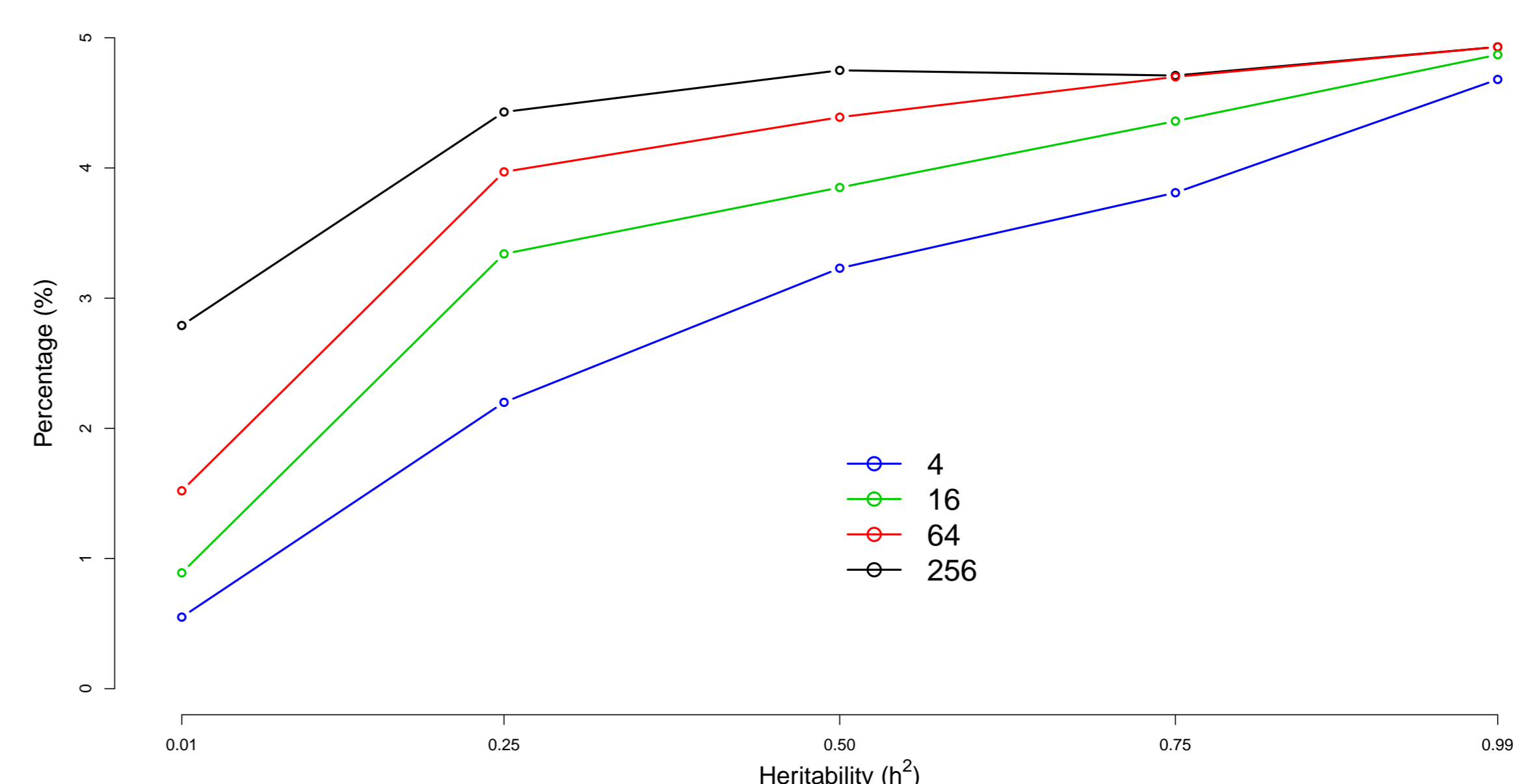


Figure 1: Average percentage of progenies correctly selected for each progeny size among different heritabilities (h^2).

References

- ABREU, G. B. *et al.* Strategies to improve mass selection in maize. **Maydica**, Bergamo, v. 55, p. 219–225, 2010.
- R Development Core Team. **R: A Language and environment for statistical computing**. Vienna, Austria, 2011.



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