SAMPLE SIZE IN THE ESTIMATION OF GENETIC PARAMETERS FOR ERGOT AND SMUT OF *Pennisetum typhoides* (Burm f.) S. & H.

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Following the North carolina Design-I in pearl millet at Punjab Agricultural University, Ludhiana, it was concluded that in case of ergot and smut disease. at least 76 males be used to construct this design.

The genetic analysis in any crop or population involves estimation of variances and covariances between relatives. These estimates are interpreted on the basis of population but are measured from a sample. An inadequate sample leads to inappropriate conclusions which can not be rectified later. Thus an adequate sample size is a pre-requisite for estimating genetic parameters for any biometrical analyses. This study has been made to specify the minimum sample size (number of males) to compute genetic variance through NCD-I of comstock and Robinson (1948, 1952)

MATERIAL AND METHODS

Ninety-six plants taken at random from the base population (PSB-7) of Pearl Millet *Pennisetum typhoides* (Burm. f.) S. & H. were designated as 'males'. Each 'male' plant was mated to four randomly chosen 'female' plants resulting into four full-sib families in a half-sib family.

The same way 96 half-sib families were or 384 full-sib families were developed. This material was raised in 24 sets each having 4 half-sib families and were randomized in each of the two replications. Each full-sib family in each replication of a set was assigned a single row plot of 2m length with interplant distance of 15 cm and interplot distance of 50 cm.

The experiment was raised in three environments by creating one at Punjab Agricultural University experimental area Ludhiana with 100kg of Nitrogen per hectare and with required irrigation (E₁); the second with 50 kg of Nitrogen per hectare which was kept rainfed (E₂). The third environment was provided at Regional Research Station, Faridkot with 100kg Nitrogen per hectare and was irrigated when required (E₃). The Observations were recorded on five rondom plants in each full-sib family in each replicate for ergot (*Claviceps microcephala*) and sumt (*Tolyposporium penicillariae*). Incidence of ergot disease was recorded at milk stage after grain set and smut incidence was observed at maturity. The following effective workable scoring system for the classification of disease reaction was utilized for these diseases :

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1 — No disease

2 — Less than 5 per cent disease

3 — From 6 to 10 per cent disease

4 = From 11 to 20 per cent disease

5 — From 21 per cent and more disease

The analyses of variance for individual environment and pooled over all the environments under NCD-I were carried out following Lindsey et al. (1962) by varying the experimental size in order to investigate the effects of different number of males. The lowest number of sets used for statistical analyses was kept as eight sets (32 male combinations) which was successively increased by the addition of one set comprising of four males till the maximum size of 24 sets (96 male or half-sib families) was obtained. Additive and dominance genetic variances along with their standard errors were estimated following sprague and Eberhart (1977). A Comparisons for the magnitude of parameters and their standard errors was made by computing its values for each sample. The 't' values of the parameters were calculated as follows :

$$t = \frac{\text{Estimate for Additive or Dominance Variance}}{\text{Standard Error of the same estimate}}$$

RESULTS AND DISCUSSION

The estimates of different genetic parameters obtainable from NCD-I differ in precision when experimental size is varied. They were determined by varying the number of males for each experimental size separately. The magnitude of standard error shows the precision of the estimate. The smaller the standard error the more is the precision. Table 1 for the traits, ergot and smut showed that in general the 't' values become almost constant after 19 sets. When the experimental size (number of males) was varied. wide fluctuations were observed for non-additive variance which showed greater variation over environments.

Comstock and Robinson (1948, 1952) gave a standard design namely NCD-I to study the components of variance in maize populations. A study on sample size has been reported in sugarcane (Wu et al. 1978), but their sample size different from the present study. From the results of the present study it is clear that atleast 76 males be used in constructing the NCD I in parel millet populations. This may serve as a guide line to the workers conducting biometric studies in pearl millet.

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Table 1. S. E. and 't' values for σ^2 A and σ^2 D for Ergot and Smut (pooled over three environments

Sets	Ergot				Smut			
	σ^2A		σ^2D		σ^2A		σ^2D	
	S. E.	't'	S. E.	't'	S. E.	't'	S. E.	't'
8	±0.03	0.04	±0.02	0.03	±0.03	0.05	±0.05	0.06
9	±0.03	0.04	±0.02	0.05	±0.03	0.05	±0.06	0.06
10	±0.03	0.05	±0.04	0.04	±0.02	0.03	±0.05	0.08
11	±0.03	0.05	±0.04	0.06	±0.02	0.03	±0.05	0.07
12	±0.03	0.04	±0.05	0.07	±0.03	0.04	±0.04	0.07
13	±0.04	0.05	±0.03	0.04	±0.04	0.05	±0.03	0.04
14	±0.03	0.06*	±0.02	0.03	±0.03	0.05	±0.04	0.07
15	±0.03	0.05	±0.02	0.03	±0.03	0.04	+0.05	0.08
16	±0.04	0.07	±0.03	0.04	±0.03	0.02	+0.03	0.05
17	+0.04	0.07	±0.03	0.05	±0.04	0.05	±0.03	0.04
18	±0.05	0.09	±0.04	0.07	±0.04	0.06	±0.03	0.07*
19	+0.04	0.11**	+0.03	0.06*	±0.04	0.09*	±0.02	0.06**
20	±0.04	0.09*	±0.03	0.06*	±0.03	0.07*	+0.03	0.06*
21	±0.03	0.09**	±0.03	0.06*	±0.02	0.06**	±0.03	0.07*
22	±0.04	0.08*	±0.03	0.07*	±0.03	0.05*	±0.02	0.04*
23	±0.04	0.08*	±0.05	0.10*	±0.03	0.06*	±0.03	0.07*
24	±0.04	0.08*	±0.04	0.09*	±0.03	0.06*	±0.03	0.07*

*, ** significant at 5 and 1 percent levels, respectively.