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Evaluation of Seed Yield-Related Characters in Sesame
(*Sesamum indicum* L.) Using Factor and Path Analysis

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Abstract: Fifteen sesame genotypes were grown in a randomized complete block design with 3 replications during 2004, in experimental station of Agricultural College, Shiraz University in Badjgah, Iran. Many plant traits were scored in the field. Path coefficient analysis and factor analysis divided the 15 measured variables into 5 factors. The 5 factors explained 81% of the total genetic variation in the dependence structure. Factor 1 was strongly associated with number of capsules in the main stem, length of floral axis, number of capsules per plant and plant height. Other factors (2, 3, 4 and 5) explained the rest of genetic variations and may not be important in sesame breeding programs.

Key words: Sesame, plant traits, seed yield, factor analysis, path analysis

INTRODUCTION

Sesame (*Sesamum indicum* L.), from Pedaliaceae, is an important oil seed crop being cultivated in the tropics and the temperate zone of the world. It is increasingly becoming a popular oil seed crop in Iran, including Fars Province, due to its edible oil, protein content and quality vitamins and amino acids. Though Iran is one of the producers of sesame, its productivity is low due to lack of novel hybrids and therefore, varieties with suitable characters having high oil and protein contents are needed.

Factor analysis can be understood as a data-reduction technique by removing the duplicated information from among a set of correlated variables (Brejda, 1998; Kachigan, 1982). Factor analysis provides more information than a simple correlation matrix because it discriminates between groups of variables (Factors) and indicates percentage contribution of variables to each factor (Seiler and Stafford, 1985), but it is impeded by genotype through environmental interaction. The advantage of a genetic correlation matrix would be that, the sets of derived factors are free of environmental effects and, therefore, the genetic composition of a factor can be shown more clearly (Pandya *et al.*, 1996; Ashkani and Pakniyat, 2003; Ashkani *et al.*, 2007). Besides, inferences are made on a genetic basis, which is useful in a breeding program (Sieber *et al.*, 1988).

Factor analysis has been used by many researchers as Aquaah *et al.* (1992), Bramel *et al.* (1984), Denis and Adams (1978), Hamzehzarghania *et al.* (2005) and Seiler and Stafford (1985) for determination of dependent relationship among characters associated with seed yield in several crops. The objective of this research was to evaluate seed yield-related characters and their relationships to seed yield for determination of the best criteria for high-yield sesame genotype screening, using factor and path analysis.

MATERIALS AND METHODS

Fifteen sesame genotypes (Dezfool, T5-3, Darab-3 line, Yanma × Avaee, Chinese × 2882, BN × IS, Darab-1 Line, TN 223, Hajiabad, TN 234, Jiroft, Darab-2 Line, Borazjan-2, Darab-14, TN 238) were grown at the experimental station of Agricultural College, Shiraz University in Badjgah, Iran (29° 50' N, 52° 46' E) in 2004. These genotypes were selected from different geographical origins to provide enough variation for evaluation to the variables. The soil texture was clay loam (fine, mixed, mesic, calcixerollic xerochrepts).

The experiment was performed as a randomized complete block design with three replicates. Each plot consisted of 4 rows, 5 m long spaced 50 cm apart, with a plant to plant distance of 10 cm.

The two middle rows considered as boarder rows. The sowing date was June 4, 2004 and each genotype was harvested at plant maturity. Recorded traits were: seed yield (kg ha^{-1}), days to 50% flowering, physiological ripening, number of main stem capsules, number of

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capsules per plant, seed oil percentage, seed protein percentage, physiological yield and harvest index. All plots were irrigated as needed throughout the season. Also, plots were kept free of pests, diseases and weeds during the growing season. Fertilizer was applied at the rate of 120 kg N ha^{-1} and 50 kg ha^{-1} P_2O_5. Seed oil was estimated as the average of two measurements by Nuclear Magnetic Resonance (NMR) in each plot. Grain protein is rarely measured directly because of the difficult analytical procedures involved. Therefore, total nitrogen was measured in dry grain by the Kjeldahl and then converted to crude grain protein using a conversion factor (6.25). The path coefficient analysis using genotypic correlation coefficients was carried out as suggested by Dewey and Lu (1959). Factor analysis was performed according to the procedures outlined by Cattell (1965) and Guertin and Bailey (1982). All statistical procedures were carried out using the SAS software (2000, 2002).

RESULTS AND DISCUSSION

Factor analysis: Factor analysis was used for determination of high genetically variable traits as a beneficial criterion for use in suitable genotypes screening of sesame. Since no test of significance was performed for factor loadings, the decision was rather arbitrary as to how many factors should be extracted from the data set and what magnitude of loading coefficient a variable should posses to be considered meaningful. Factors whose values were greater than 1.0 were retained. Traits with loading greater than 0.6 in a factor were deemed major (Aquaah *et al.*, 1992). In this study factor analysis technique divided the 15 variables into 5 factors. The 5 factors explained 81% of the total genetic variation in the dependence structure (Table 1). Factor 1 was strongly associated with number of capsules in the main stem, length of floral axis, number of capsule per plant and

plant height. In this factor number of capsule in main stem, length of floral axis, number of capsule per plant and plant height loaded with positive signs (0.736, 0.852, 0.687 and 0.754, respectively), whereas, days to 50 % flowering, physiological ripening loaded with opposite sign (-0.783 and -0.664, respectively). The sign of the loading indicates the direction of the relationship between the factor and the variable. Thus, two variables with high magnitude of loading in the same factor would be expected to exhibit a high correlation (Seiler and Stafford, 1985). Thus, these traits may be influenced by the same gene or genes and may be beneficial for suitable sesame genotypes screening. Other factors (2, 3, 4 and 5) explained 15, 12, 12 and 7% of the total genetic variation, respectively and may be not important in sesame improvement programs. In this study factor analysis showed that, selection based on number of capsule in main stem, length of floral axis, number of capsule per plant and plant height may be more efficient for suitable sesame genotype screening, whereas, days to 50% flowering and physiological ripening may not be efficient in sesame improvement programs.

Path analysis: Path coefficient analysis has been widely used in crop breeding to determine the nature of relationships between grain yield and its contributing components and to identify those components with significant effects on yield for potential use as selection criteria (Mohammadi *et al.*, 2003; Milligan *et al.*, 1990; Williams *et al.*, 1990; Board *et al.*, 1997; Moghaddam *et al.*, 1998; Samonte *et al.*, 1998). A path coefficient is a standardized partial regression coefficient and measures the direct influence of a predictor variable on the response variable (Li, 1975). Results showed that the most important agronomic trait determining seed yield in the path coefficient analysis were biological yield (p = 0.647**), harvest index (p = 0.637**), 1000 seed weight (p = 0.197*), number of capsules in main stem

Table 1: Loading of the first five most principal from a factor analysis of physiological traits of sesame genotypes

| Variables	Factors (matrix of factor coefficient)					Communality
	1	2	3	4	5	
Height of first capsule from the soil surface	0.10	0.63	-0.36	0.58	-0.08	0.87
No. of capsules on main stem	0.74	0.23	0.48	-0.19	0.17	0.88
Length of floral axis	0.85	0.21	0.19	-0.25	0.08	0.87
No. of capsules per plant	0.69	-0.23	0.46	0.23	0.01	0.79
Length of the lowest capsules	0.57	-0.43	0.02	-0.20	0.45	0.74
Stem diameter	0.59	0.09	0.37	0.53	0.20	0.82
No. branches per plant	0.08	-0.61	-0.45	0.31	0.14	0.69
Biological yield	0.33	0.36	-0.65	-0.20	0.45	0.90
Harvest index	0.49	-0.71	0.10	0.09	0.35	0.89
1000 seed weight	0.46	-0.14	-0.22	0.70	-0.20	0.80
Days to 50% flowering	-0.78	0.03	0.23	0.37	0.04	0.80
Physiological ripening	-0.66	-0.07	0.06	0.25	0.45	0.70
Oil percentage	-0.46	0.48	0.55	-0.03	-0.17	0.77
Protein percentage	0.49	0.18	-0.39	-0.34	-0.48	0.76
Plant height	0.75	0.53	-0.07	-0.28	0.02	0.93
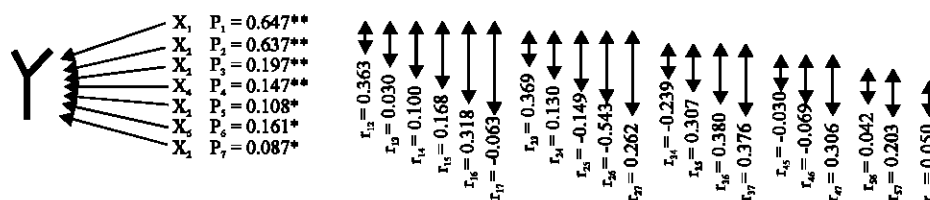
Fig. 1: Path diagram and coefficient of some agronomic traits affecting seed yield. One-directional arrow (→) represent direct path (p) and two-directional arrow (↔) represent correlations (r). X_1 = Biological yield; X_2 = Harvest index; X_3 = 1000 seed weight; X_4 = No. of capsules in main stem; X_5 = Height of first capsule from the soil surface; X_6 = Oil percentage; X_7 = Stem diameter; Y = Yield

(p = 0.147*) and height of the first capsule from the soil surface. These traits had a positive direct effect with seed yield (Fig. 1). These results are in agreement with those of Shi *et al.* (2001). In spite of the high positive direct effect among seed yield and the mentioned traits, oil percentage (p = -0.161*) and stem diameter (p = -0.087*), had a negative direct effect. According the results of our study, it can be concluded that to increase seed yield, selection should be carried out for higher biological yield, harvest index, 1000 seed weight, number of capsules in main stem and lower height of the first capsule from the soil surface. Also, selection for high oil content and stem diameter are contrary to achieve potential yield.

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