PEANUT SCIENCE

VOLUME 18 JULY - DECEMBER 1991 NUMBER 2

Inheritance of Seed Dormancy in a Cross Between Two Spanish Peanut Cultivars[1]

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ABSTRACT

Obtaining early maturing peanut (*Arachis hypogaea* L.) (spanish) with seed dormancy is a major objective in breeding programs. This study was conducted to determine the inheritance of seed dormancy in a cross between the only dormant, early maturing cultivar that is currently released (73-30) and a very early maturing non-dormant cultivar (Chico). Results showed that genetic control is not very complex (additive, dominance and digenic epistatic effects). Broad sense and narrow sense heritabilities ranged between 0.49 and 0.57. These results indicate that pedigree selection for dormancy could be successfully carried out in spanish type cultivars using 73-30 as a parent.

Key Words: *Arachis hypogaea* L., spanish type, dormancy, inheritance.

Obtaining early maturing peanut (*Arachis hypogaea* L.) cultivars with seed dormancy is a major objective in breeding programs involving spanish type cultivars. Once obtained, they would meet the requirements of widespread cropping situations in peanut producing countries, especially in Africa, where rain is likely to fall when some of the seeds have reached maturity. Such rainfall causes production losses estimated at 10 to 15% in spanish varieties due to sprouting in the field.

Physiologically, seed dormancy in peanut results from the hormonal balance between a germination inhibitor, abscisic acid, produced in the aerial part of the plant which then accumulates in the cotyledons and the seed coat, and a germination activator, ethylene, produced by the embryo through the action of the cytokinin during seed imbibition (8). During storage of dormant seed, oxidation of the inhibitor occurs which tips the hormonal balance in favor of the germination activator.

The data available on inheritance of seed dormancy in peanut are very limited. Stokes and Hull (13) reported that dormancy is mostly dominant. Hull (6) observed a normal phenotypic frequency distribution for segregating generations and suggested polygenic control. For four crosses, he obtained transgressions beyond the dormant parent. John *et al.* (7) did not observe any dominance in F_1 or F_2 seeds. F_2 and F_3 seeds revealed high performance variability, which led them to propose polygenic inheritance. Lin and Lin (9) determined the dormancy of seeds two weeks after harvesting from reciprocal crosses between virginia cultivars with different dormancy intensities. Based on F_2 and F_3 individuals, they suggested monogenic control with dormancy being dominant. Mauboussin (12) found a clear paternal influence between F_1 reciprocals which disappeared in the F_2 from two virginia x spanish crosses. He obtained narrow sense heritability estimates of 0.56 and 0.50 by regression of F_4 on F_3 values for two spanish x virginia crosses, with the spanish cultivar common to both crosses.

These few reports on the inheritance of heredity are contradictory. Most indicate polygenic inheritance with average heritability, whereas the study by Lin and Lin (9) suggested monogenic inheritance. These differences may be do Lin and Lin (9) using less diverse germplasm with crosses in a subspecies rather than between subspecies.

Many peanut breeders believe that earliness and dormancy are too closely linked to combine the two traits in the same cultivar. However, Mauboussin obtained an early (95 days) dormant cultivar (73-30) in 1973 by pedigree selection from a spanish x virginia cross (2). This result indicated that the association between the two characters is not physiological and that linkage could be broken. This cultivar is the only one of its type released to date, although many pedigree, bulk and single seed descent programs have been conducted since then with the same objectives. This exceptional character seems to indicate the existence of a strong linkage between genes conditioning cycle length and others responsible for dormancy.

The objective of this study was to determine the inheritance of dormancy in a cross between 73-30 and Chico which is a very early maturing spanish type cultivar.

Materials and Methods

The two parents used in this study (P_1, P_2) were 73-20 (2), a dormant early maturing spanish type cultivar released in Senegal, and Chico (1), a very early maturing spanish type cultivar released in the USA. Four hybrid generations where compared with the parents to determine the inheritance of dormancy as follow: F_2 generation, 200 F_3 families selected at random and 50 selfed families (B_{1s}, B_{2s}) from backcrosses to each parent.

[1]Support for this project was received from the EEC STD II program.

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Generations P_1, P_2, F_1, F_2, B_1 and B_2 were grown in 1984 in a randomized block design with five replications. Each block consisted of one row of the genotypically homogeneous generations P_1, P_2, and F_1, four rows of the segregating generation F_2, and a single row of genetically heterogeneous generations B_1 and B_2. The quantity of seeds available prevented the use of more plants, which would have provided a better indication of genetic variability with respect to within-plot variance. Each row contained twelve plants and two border plants, which were not analysed in the study. Out of the twelve plants, ten surrounded by four neighboring plants were monitored. The plants were spaced 50 cm apart.

At harvest, 10 mature pods were randomly sampled from each of the plants to obtain P_1, P_2, F_3, B_{1S} and B_{2S} seeds. Seeds were planted the next day in the same experimental design as indicated above. The number of seed which emerged on a per plant basis was counted each day. Germinated seed were then eliminated from the test. Monitoring continued until all the seeds had germinated. The dormancy criterion adopted was the number of days between planting and emergence, measured individually for each seed.

The study of the genetic effects governing the expression of dormancy was conducted using the additive-dominance and the digenic interaction models created by Mather and Jinks (11).

Dominance was evaluated by the deviation expressed as a percentage of the mean phenotype of the F_2 population as compared to the mean of the parents.

Broad sense heritability in F2 and F3 was estimated using the method of Mahmud and Kramer (10):

$$H_{Fg} = \frac{V_{Fg} - V_e}{V_{Fg}}$$

where : Fg = F_2 or F_3

V_{Fg} = Variance within block of the F_g

$V_e = 1/2(V_{P1} + V_{P2})$

where: P_1 and P_2 = Parent 1 and Parent 2.

Narrow sense heritability in F2 was evaluated by the intra-class coefficient of correlation (5):

$$h^2t\,(F_3) = 3/2 \quad \frac{V_{BF_3}}{V_{BF_3} + V_{WF_3}}$$

where: V_{BF_3} = F_3 between-families variance

V_{WF_3} = F_3 within-families variance

The factor 3/2 was applied to the intra-class coefficient of correlation to reduce the bias induced in the estimation of narrow sense heritability (3). The standard error in this estimation was obtained according to the method of Falconer (5).

The rates of legitimate descrimination (Rld) and favorable transgression (Rft) were assessed in the F_2 (4):

$$Rld = 1/2\sqrt{1 - H_{F_2}}$$

$$Rft = Proba\,(x > \frac{\left|\overline{P}_2 \pm 2\sqrt{V_R} - \overline{F}_2\right|}{\sqrt{V_{F_2}}})$$

where: V_R = residual variance, based on the analysis of variance of the parents.

Results and Discussion

Seed dormancy appears to result from the interaction between the maternal genotype, which determines inhibitor production in the aerial part of the plant (8), and the embryonic genotype, which determines activator production by the embryo (8). These genotypes are different in the first generation obtained from a cross, which is the case in this genetic study.

The residual variance values of the genetically homogenous parent generations, estimated from data in the orginal measurement scale, were significantly different ($P < 0.05$) (Table 1). A proportionality link occured between the residual variances and the means, which may be due to the absence of distribution normality in the original scale. Normalizing distributions by the logarithmic transformation (log (x +1)) eliminated the link between residual variances and means, and homogenized residual variances.

Table 1. Mean measurements[a] and variances for dormancy[b] in segregating generations.

Generation	Number of Plants	Mean	Standard Error	Total Variance	Within Block Variance	F Fisher	Within Families Variance	Between Families	CV (%)
P1	748	1.89	±.01	.035	.033	} *			10
P2	633	0.95	±.01	.045	.044				12
F2	837	1.43	±.01	.080	.076				20
F3	2825	1.40	±.01	.095	.089		.0620	.0327	22
B1s	596	1.61	±.01	.076	.060				17
B2s	716	1.19	±.01	.101	.092				27

(a) Original data transformated to logarithms for analysis.
(b) Number of days between planting and emergence.
* Non-significantly different at the .05 level of probability.

The additive - dominance model test indicated that the hypothesis of adequation to this model should be rejected ($P < 0.005$). The allelic digenic interaction model was then tested and found to be adequate to account for the observed means. According to this model, estimates of genetic effects (Table 2) indicated that the additive and dominance effects occur ($P < 0.001$). Additive x dominance ($P < 0.001$) and dominance x dominance ($P < 0.05$) type epistatic effects were also significant. Dominance and dominance x dominance have opposite signs. Therefore, digenic interactions are essentially duplicate in nature. No phenotypic dominance was seen in the F_2.

Table 2. Estimate, confidence intervals and significance tests of the genetic effects for seed dormancy according to Mather and Jinks' allelic digenic interaction model.

Genetic effects		Estimations	t test
d	additivity	0.468 ± 0.006	***
h	dominance	-0.211 ± 0.005	***
i	add.x add.	-	
j	add.x dom.	-0.197 ± 0.069	**
l	dom.x dom.	0.437 ± 0.177	*

* Significant at the 0.05 level of probability
** Significant at the 0.01 level of probability
*** Significant at the 0.0001 level of probability

In F_2 and F_3, broad sense heritability estimates were average (0.49 and 0.57) (Table 3). The slightly higher value in the F_3 came from an increase in genetic variance. The estimate of narrow sense heritability was also average, with high estimation accuracy (0.54 ± 0.04) (Table 3). Transgressive segregation in favor of dormancy intensity occured in the F_2, with good agreement between the calculated and observed rates (Table 3).

The dormancy character studied, as estimated by the number of days between planting seeds after harvest and seed emergence, is conditioned by genes exhibiting additive, dominance and duplicate digenic epistasic effects of the additive-dominance and dominance-dominance types. It can therefore be estimated that the genetic conditioning of dormancy is not very complex, which is corroborated by

Table 3. Estimates of broad sense and narrow sense heritabilities for seed dormancy, rates of legitimate dircrimination and calculated and observed rates of favorable transgression.

H_{F2} [a]	H_{F3} [b]	$h^2_{t\,(F3)}$ [c]	Rdl [d]	Rft [e]	
				Calculated	Observed
0.49	0.57	0.54 ± 0.04	36	3.0	3.7

(a) Broad sense heritability in the F_2
(b) Broad sense heritability in the F_3
(c) Narrow sense heritability in the F_3
(d) Rate of legitimate descrimination in the F_2
(e) Rate of favorable transgression in the F_2

broad sense and narrow sense heritability estimates which are average. This should enable successful pedigree selection in favor of dormancy based on the average performance of the families. Several selection programs involving spanish cultivars with this objective and using 73-30 as the dormant parent have begun at the National Agricultural Research Center in Bambey (C.N.R.A.), Senegal.

Literature Cited

1. Bailey, W. K., and R. O. Hammons. 1975. Registration of Chico peanut germplasm. Crop Sci. 15:105.
2. Bockelee-Morvan, A. 1983. Les différentes variétés d'arachide. Oleagineux. 38:81.
3. Cahaner A., and J. Hillel. 1980. Estimating heritability and genetic correlation between traits from generations F2 and F3 self-fertilizing species: a comparison of three methods. Theor. Appl. Genet. 58:33-38.
4. Ecochard, R., and J. Huet. 1961. Contribution á l'étucde de la génétque quantitative chez une plante autogame : le blé. I. Application expérimentale. Ann. Amélior. Plantes 11:25-59.
5. Falconer, D. S. 1961. Introduction to quantitative genetic. Oliver & Boyd (publisher), Edinburgh & London, pp. 166-185.
6. Hull, F. H. 1937. Inheritance of rest period of seeds and certain other characteristics in the peanut. Fla. Agric. Exp. Sta. Tech. Bull. 314.
7. John, C. M., R. M. Seshradi, and R. M. Bhanvanishankar. 1948. Dormancy in groundnut. Madras Agric. XXV. (8):1-9.
8. Ketring, D. L., and P. W. Morgan. 1972. Physiology of oil seeds IV. Role of endogenous ethylene and inhibitory regulators during natural and induced after-ripening of dormant Virginia type peanut seeds. Plant Physiol. 50:382-387.
9. Lin, H., and C. Y. Lin. 1971. Studies on the seed dormancy of peanuts. J. Agric. Res. (Taiwan) 20:49-53.
10. Mahmud, I., and H. H. Kramer. 1951. Segregation for yield and maturity following a soybean cross. Agron. J. 43:605-609.
11. Mather, K., and J. L. Jinks. 1982. Biometrical genetics. Chapman & Hall Ltd, London, pp. 65-94.
12. Mauboussin, J. 1966. Annual Report 1965. ISRA, National Agricultural Research Center, Bambey, 1966.
13. Stokes, W. E., and F. M. Hull. 1930. Peanut breeding. J. Amer. Soc. Agron., 22:1004-1019.

Accepted August 10, 1991