

EVALUATION OF GENETIC VARIABILITY AND THE NATURE OF GENE ACTION IN PEA.

I. YIELD CHARACTERS

Swidan, Suzan A.

Horticultural Crops Research Institute, Agricultural Research Centre, Cairo, Egypt.

ABSTRACT

The variability in thirty-six pea (*Pisum sativum* L.) genotypes which were represented by two local and four foreign varieties, fifteen derived F₁ hybrids and their reciprocals was used to evaluate the performance of yield and its attributes of these genotypes and the nature of gene action controlling this performance during the seasons of 1997/98 and 1998/99 at El-Kassasein Horticultural Research Station.

Both the mean performance of yield characters and gene action suggest that the high-yielded F₁ hybrids; Hunter x Ambassador and Ambassador x Mammoth could successfully be used in raising high yield promising new pea varieties.

However, additive gene effects without any genic interaction was found to be more important in controlling both number of seeds per pod and pod length. Meanwhile, non-additive gene action was demonstrated for number of pods per plant, pods weight per plant and pod diameter. Both additive and epistatic gene effects were observed for seeds weight per pod. Dominant gene effects were found to play the main role in controlling the expression of number of pods per plant and pods weight per plant.

Non-random gene distributions of the dispersion type was observed over parental genotypes for both number and weight of pods per plant, seeds weight per pod and pod diameter.

Keywords: Additive, Dominance, Gene action, *Pisum sativum*; Quantitative characters, Yield.

INTRODUCTION

Improving yield in any vegetable crop depends mainly not only on the availability of genetic variations but also the nature of gene action in loci controlling the expression of yield and its related characters for this crop.

However, performance is critical to identify the best genotypes which could be used in different types of breeding programmes to increase yield (Partap *et al.*, 1992). Many researchers dealt with yield characters and the nature of gene effects controlling these characters as an important purpose for improving pea cultivars (Partap *et al.*, 1992 and Ahmed *et al.*, 1998).

This study aimed to use the diallel crosses to evaluate and increase the genetic variability, hence, offer better material for raising new high-yielding pea varieties and to study the nature of gene action controlling yield characters in these parental genotypes.

MATERIALS AND METHODS

Six pea (*Pisum sativum* L.) varieties represented by four foreign and two local varieties; Arica (Van Waveren) as P₁, Hunter (Pflanzenzucht) as P₂,

Ambassador, Wav 505 (Vaver Top, Germany) as P₃, Master (Horticultural Crops Research Institute) as P₄, Mammoth (Elsoms Seeds) as P₅ and Little Marvel (Horticultural Crops Research Institute) as P₆, which differ considerably in respect of their quantitative traits, were used to achieve this study in El-Kassasein Horticultural Research Station.

Seeds of the six varieties were planted in October 1997 and were crossed in all possible combinations including reciprocals. In the season of 1998/1999, seeds of the six parental varieties, their F₁'s and reciprocals were planted in a randomized complete block design with three replications. Each replication comprised thirty-six entries (six parents and thirty hybrids). All agricultural treatments were similar for all entries under study and were in accordance with the recommended for pea plants.

Ten plants from each entry, over all replications, were randomly chosen for measuring yield characters. The characters of total yield were the weight of green pods per plant (g.) and number of pods per plant. Pod quality characters measured were average pod weight (g.), number of seeds per pod, seeds weight per pod (g.) pod length (cm.) and pod diameter (cm.).

The statistical analysis was carried out using the methods suggested by Hayman (1954) and Mather and Jinks (1971). The analysis involves grouping the data for each character into arrays, each consisting of one parent and all the crosses in which this parent is involved.

The graphical analysis was achieved by plotting the variance of each array (V_r) against the covariance of that array with the non-recurrent parents (W_r) and the regression line of W_r/V_r. Standardized deviations of both the parental measurements (Y_r) and the values of dominance order (W_r+V_r) were also plotted graphically in order to allocate parental genotypes with dominance and/or recessive genes expressing high or low values of the six characters.

RESULTS AND DISCUSSION

I. Performance of Parental and Hybrid Genotypes:

The mean performance of parental and F₁ hybrids over reciprocals for the studied characters, appeared in (Table 1), revealed a wide range of genetic variation among the six parental genotypes as well as F₁ crosses. However, such diversity in yield characters between parental genotypes ranged from 25.03 gm to 136.67 gm for pods weight per plant and from 5.67 to 33.0 for number of pods per plant in Hunter (P₂) and Mammoth (P₅), respectively. These ranges were found to be larger in the F₁ genotypes. It ranged from 5.66 to 139.0 for number of pods per plant and from 25.5 gm to 515.6 gm for pods weight per plant for the F₁ hybrids Arica (P₁) X Hunter (P₂) and Hunter (P₂) X Ambassador (P₃), respectively. Such, wide range of variability was also reported in parental and pea generations used by Ahmed (1999).

However, the highest scores for number of pods and pods weight per plant (Table 1) were observed in the F₁ hybrid Hunter (P₂) X Ambassador (P₃) followed by the F₁ hybrid Ambassador (P₃) X Mammoth (P₅) and Ambassador (P₃) X Little Marvel (P₆). This strongly suggests that these F₁ hybrids could successfully used in raising high-yielding varieties.

Table 1: Mean performance of parental pea genotypes and F₁ hybrids over reciprocals for yield and its related characters.

Genotype* Or Hybrid	Yield/plant		Pod characters			
	No. pods	Pods weight (gm)	Seeds wt./pod (gm)	No. seeds/pod	Pod length (cm)	Pod diameters (cm)
P ₁	50.0	74.4	0.83	4.3	6.1	1.13
P ₂	5.7	25.0	1.41	6.2	8.0	1.60
P ₃	26.3	83.9	0.80	5.7	6.8	1.17
P ₄	8.0	63.7	3.21	10.1	10.3	1.37
P ₅	33.0	136.7	1.62	5.6	9.3	1.93
P ₆	22.7	63.6	0.96	4.5	6.5	1.20
F ₁ (P ₁ XP ₂)	5.7	25.5	1.86	5.4	7.9	1.53
F ₁ (P ₁ XP ₃)	93.2	231.8	1.37	5.5	6.4	1.10
F ₁ (P ₁ XP ₄)	36.2	137.0	2.10	5.9	8.1	1.32
F ₁ (P ₁ XP ₅)	43.7	162.6	1.35	6.3	7.6	1.28
F ₁ (P ₁ XP ₆)	27.3	72.02	1.15	5.7	6.5	1.30
F ₁ (P ₂ XP ₃)	139.0	515.6	1.98	7.1	8.1	1.23
F ₁ (P ₂ XP ₄)	17.0	106.6	2.10	8.0	8.7	1.47
F ₁ (P ₂ XP ₅)	24.0	132.1	1.38	5.9	8.1	1.50
F ₁ (P ₂ XP ₆)	38.0	125.1	2.46	5.0	7.6	1.37
F ₁ (P ₃ XP ₄)	19.0	104.3	2.49	6.5	8.2	1.30
F ₁ (P ₃ XP ₅)	93.2	349.3	2.51	6.6	8.3	1.40
F ₁ (P ₃ XP ₆)	92.3	290.9	1.15	5.2	7.2	1.32
F ₁ (P ₄ XP ₅)	27.8	153.0	3.16	8.0	10.8	1.53
F ₁ (P ₄ XP ₆)	21.8	91.1	2.13	7.4	10.1	1.23
F ₁ (P ₅ XP ₆)	65.0	220.7	1.68	6.1	8.1	1.50

* P₁ = Arica, P₂ = Hunter, P₃ = Ambassador, P₄ = Master, P₅ = Mammoth and P₆ = Little Marvel.

II – Analysis of Variance:

The variances of thirty-six pea genotypes representing parents, F₁'s and their reciprocals, were highly significant for the six characters studied. The uniformity of W_r-V_r, as revealed by the non-significant t² values for two out of the six characters studied indicates the validity of the hypothesis of diallel analysis. Meanwhile, the analysis of variance of W_r-V_r showed significant array effects for number pods/plant, pod weight/plant, number of seeds per pod and pod diameter indicating, thereby, the failure of one or more of the assumptions for the diallel analysis (Table 2). For both number of seeds per pod and pod length, the regression line differs significantly from a slope from b=0, but not from the slope of b=1, which indicates that the gene action for both characters are additive without any genic interaction. Meanwhile, the regression line does not significantly differ from a slope of b=1 and from a slope of b=0 with considerable magnitude of the value from b=0 revealing the presence of epistasis in seeds weight per pod with the prominent effect of additive gene action. Meanwhile, the presence of non-additive gene action was also demonstrated for number of pods per plant, pods weight per plant and pod diameter, since the regression coefficients significantly differ from a slope of b=1.

Table 2: Mean squares and t^2 values of uniformity test of Wr-Vr for six quantitative characters in pea.

Character	Yield/plant		Pod characters			
	No. pods	Pods weight (gm)	Seeds wt./pod (gm)	No. seeds/pod	Pod length (cm)	Pod diameters (cm)
Mean squares	4723.83**	52380.35**	2.08**	6.02**	6.16**	0.133**
t^2 of Wr-Vr	161.742**	101.621**	0.321	2.76*	0.18	7.0441**
(b=0)/S _b	-0.385	-0.347	2.774	6.444**	4.72*	0.5811
(1-b)/S _b	26.026**	20.76**	0.125	-1.153	0.83	5.4467*

*, ** Significant at 5% and 1 % levels, respectively.

III- Components of Genetic Variance and Gene Action:

The estimates of all the six components of variation, viz, D, F, H1, H2, h2 and E and their standard errors, presented in Table (3), indicate that the additive (D) components were highly significant for seeds weight per pod, number of seeds per pod, pod length and pod diameter. This clearly suggests that these characters are mainly determined by genes with additive effects. The insignificant values of (D) for number of pods per plant and pods weight per plant were considerable in magnitude, indicating that these characters are largely determined by genes with dominant effects and to some extent by genes with additive effects.

Table 3: Components of genetic variance for six quantitative characters in pea.

Components of genetic variance	Yield/plant		Pod characters			
	No. pods	Pods weight (gm)	Seeds wt./pod (gm)	No. seeds/pod	Pod length (cm)	Pod diameter (cm)
D	268.6 +56.4	1214 +10143.0	4.16 +0.08**	4.39 +0.21**	2.87 +0.18**	0.081 +0.005**
F	-7.7 +1798.8	-662.67 +2475.9	6.98 +0.20**	2.52 +0.51**	0.103 +0.42	0.066 +0.013**
H1	4486.9 +1869.0*	5219.3 +25742.7*	4.19 +0.21**	2.12 +0.53**	1.205 +0.43**	0.049 +0.014**
H2	3452.7 +1669.8*	41147.5 +22998.9	0.80 +0.09**	1.68 +0.47**	1.214 +0.39**	0.037 +0.012**
h2	10639.8 +1123.8**	189388.8 +15479.5**	3.43 +0.13**	0.90 +0.10**	1.073 +0.26**	0.027 +0.008**
E	2.6 +278.6	113.6 +3836.98	0.01 +0.03	0.05 +0.08	0.013 +0.67	0.002 +0.021

*, **, Significant at 5% and 1% levels of probability, respectively.

The dominance components of genetic variance (H1) were highly significant for seeds weight per pod, number of seeds per pod, pod length and pod diameter. Meanwhile these characters had highly significant D values indicating that both dominant and additive gene effects are controlling the expression of these characters.

Although, the magnitude and significance of D and H1 estimates indicated the importance of both additive and dominance gene effects in the inheritance of all studied character, the relative magnitudes of both types of gene action varied from character to another. Generally, dominance variance

effects were found to be more important in number of pods and pods weight per plant in these material.

Results, in Table (3), showed that higher estimates of H1 and H2 were associated with epistatic interactions. The low magnitudes of additive genetic variance might reflect the role of intense selection pressure applied on the materials used in this study which might have resulted in the fixation of genes controlling these characters at many loci. Such intense selection may be expected to substantially reduce additive genetic variance (Dudley and Lambert, 1969).

The overall dominance effects of heterozygous loci (h^2) were highly significant for all characters, indicating that dominance is unidirectional and that many positive genes are involved in controlling most of these characters. The importance of additive and non-additive gene effects for most of these characters has been reported by a number of workers; Kumar and Agrawal, (1981); Dubey and Lai, (1983); Venkateswarlu and Singh, (1983); Singh *et al.*, (1987); Mointra *et al.*, (1988); Singh and Singh (1989, 1990a and 1990b), Mahgoub *et al.*, (1992); Ahmed and Ismail, (1999) for number of pods per plant.

The F values were positive and highly significant for seeds weight per pod, number of seeds per pod and pod diameter, indicating the predominance of recessive alleles in the material under study. Meanwhile, the mean estimates of covariance of additive and dominance effect over the arrays (F) were insignificant for number of pods and pods weight per plant and pod length, suggesting that there could be an equality of the relative frequencies of positive and negative alleles in the parents (Table 3).

Data, in Table (4), showed that the average degree of dominance over all loci $(H1/D)^{1/2}$ were indicated that overdominance for number of pods and pod weight per plant and complete dominance for seeds weight per pod. Meanwhile, for number of seeds per pod, pod length and pod diameter results clearly suggest that partial dominance is controlling the allelic interaction in loci of dominance gene effects for these characters. The parameter "H2/4H1" which measures the proportion of positive genes X proportion of negative genes over all arrays "ui vi" was found to be the highest (0.236) for pod length and the lowest (0.047) for seeds weight per pod. This clearly suggests the presence of some sort of asymmetry at loci showing dominance for almost at the characters studied ($u \neq v$).

Table 4: Proportions of genetic components and narrow-sense (ns) heritability estimates for six quantitative characters in pea.

Parameter	Yield/plant		Pod characters			
	No. pods	Pods weight (gm)	Seeds wt./pod (gm)	No. seeds/pod	Pod length (cm)	Pod diameters (cm)
$(H1/D)^{1/2}$	3.585	6.557	1.004	0.694	0.669	0.782
$(H2/4H1)$	0.192	0.197	0.047	0.199	0.236	0.18497
$(4DH1)^{1/2}+F$						
$(4DH1)^{1/2}-F$	0.997	0.92	11.161	2.412	1.055	3.148
$h^2/H2$	3.082	4.603	4.313	0.537	0.884	0.7395
$h^2(ns)$	0.996	0.983	0.98	0.955	0.991	0.891

The values $(4DH1)^{1/2} + F/(4DH1)^{1/2} - F$, which reflect the proportion and dominant and recessive genes, were less than one for number of pods and weight of pods per plant (Table 4). These estimates were associated with negative values of F (Table 3) indicating that recessive genes were higher in frequency than dominant ones in the parents for the four characters.

Estimates of number of gene groups controlling the characters and exhibits dominance (h^2/H^2) showed that pods weight per plant, seeds weight per pod and number of pods per plant are controlled by about five, four and three dominant gene groups, respectively.

The narrow-sense heritability estimates presented in Table 4 showed that the most heritable characters having significantly high values for all studied characters. High heritability estimates were also obtained by Partap *et al.*, (1992) and Ahmed *et al.*, (1998). These results indicated that the selection programmes in segregated generations of a high performance hybrids like $F_1(P_2 \times P_3)$; Hunter X Ambassador, and $F_1(P_3 \times P_5)$; Ambassador X Mammoth, $F_1(P_3 \times P_6)$; Ambassador X Little Marvel, and $F_1(P_1 \times P_3)$; Arica X Ambassador, would be of great value in raising promising high-yielding new varieties.

The correlation coefficient between the parental order of dominance ($W_r + V_r$) and parental measurements (Y_r) were significant and positive for number of seeds per pod and pod diameter indicating that the parents containing the most dominant genes which has the lowest $W_r + V_r$ values are characterized with the lowest Y_r values hereafter, it suggests that dominant factors are responsible for determining the low expression for these characters (Table 5).

The r^2 values could suggest the existence of regression of Y_r on $W_r + V_r$ for number seeds per pod and pod diameter (0.70 and 0.62, respectively). This showed that P_4 (Master) is the completely recessive parent and P_1 (Little Marvel) is completely dominant for number of seeds per pod (Table 5).

IV. The Graphical Analysis and the Relationship between Standardized Parental Measurements and Order of Dominance:

An over-estimation of the degree of dominance was observed for pods weight/plant and number of pods/plant, seeds weight/pod, and pod diameter. Although, the mean degree of dominance $(H1/D)^{1/2}$ estimates (Table 4) were more than their correspondent regression lines in their graphical representation in Figure (1) which indicated the existence of partial dominance or at most complete dominance. This over-estimation of the level of dominance in these three cases reflected the presence of correlated gene distribution of the dispersion type. Moreover, this indicated the presence of non-randomness of genes controlling each of the three characters among the parents (Hill, 1964). However, absence of non-allelic interaction for number of seeds/pod and pod length was demonstrated as the regression of W_r on V_r is significantly closer to unity, revealing that the system of additive dominance gene action is adequate without any complication of epistasis.

Table 5: Parental order of dominance (Wr + Vr) and parental measurements (Yr) and their correlation coefficients in six yield characters in pea.

Characters	P ₁	P ₂	P ₃	P ₄	P ₅	P ₆	r(Wr+Vr), Yr r ² (Wr+Vr),Yr
No.Pods/plant							
Wr+Vr	1074.47	2625.11	2325.41	238.88	830.74	879.17	-0.188
Yr	50	5.67	26.33	8.0	33.0	22.67	0.035
Pod.Wt./plant							
Wr+Vr	7315.78	35341.46	24564.19	1722.40	7142.46	10165.69	-0.517
Yr	74.4	25.03	83.96	63.73	136.67	63.55	0.267
Pod seeds Wt.(gm)							
Wr+Vr	0.555	0.17	1.031	0.64	0.976	0.728	-0.122
Yr	0.83	1.41	0.80	3.21	1.62	0.96	0.015
No seeds/Pod.							
Wr+Vr	1.065	3.323	1.374	4.873	2.193	2.771	0.839**
Yr	4.3	6.2	5.7	10.1	5.6	4.5	0.704
Pod length (cm)							
Wr+Vr	2.10	0.62	1.84	2.81	3.25	3.97	0.101
Yr	6.07	8.03	6.80	10.33	9.33	6.53	0.0102
Pod diameter(cm)							
Wr+Vr	0.049	0.037	0.036	0.045	0.11	0.04	0.784*
Yr	1.13	1.60	1.17	1.37	1.93	1.20	0.615

*, ** Significant at 5% and 1% levels of probability, respectively.

P₁ = Arica, P₂ = Hunter, P₃ = Ambassador, P₄ = Master, P₅ = Mammoth and P₆ = Little Marvel.

The insignificant negative correlation coefficients (Table 5); -0.517, -0.517 and -0.122, for number of pods/plant, pod weight/plant and seeds weight/pod, respectively, indicated that there is only a tendency for the values of P₁ and P₅ for number of pods/plant, P₅ for pod weight/plant and P₄ for seeds weight/pod to be associated with dominance. Moreover, association was observed between low values in P₂ in both number of pods/plant and pods weight/plant and in P₃ for seeds weight/pod, with recessiveness (Fig.2). In this concern, Hayman (1954) stated that the parental measurement (Yr) is closely correlated with the number of dominant homozygotes and the values (Wr+Vr) is correlated with the number of recessive homozygotes.

The insignificant positive correlation coefficients between Wr + Vr and Yr suggest a tendency for the higher values of pod length in P₄ and P₅ to be associated with recessiveness (Fig.2).

The significant positive correlation coefficients between Wr + Vr and Yr values, for number of seeds/pod and pod diameter (Table 5) indicate that high number of seeds/pod in P₄ is found to be closely associated with recessiveness and low values of this character are associated with dominance in P₃, P₁ and P₅, in descending order (Fig. 2). Also, the high values of pod diameter in P₅ are closely associated with the presence of most recessive genes in this parent.

REFERENCES

- Ahmed, M.A. (1999): Genetic studies on some quantitative characters in crosses of pea (*Pisum sativum* L.). Zagazig J. Agric. Res., 26(5): 1269-1279.
- Ahmed M.A., A.H. Amer and El.S.M.S. El-Sharkawy (1998): Genetic behaviour of plant height, dry yield and some attributable characters in some crosses of pea (*Pisum sativum* L.) Zagazig J. Agric. Res. 25(6): 1039-1049.
- Ahmed, M.A. and T.A. Ismail (1999): Gene action in pea and esterase isozyme activity and its association to heterosis. Zagazig J. Agric. Res. 26(5): 1281-1292.
- Dudley J.W. and R.J. Lambert (1969): Genetic variability after 65 generations of selection in Illinois high oil, low-oil, high protein and low protein strains of *Zea mays* L. Crop Sci., 9:179-181.
- Dubey R.S. and S. Lai (1983): Combining ability in peas. Indian J. Genet., 43: 314-317.
- Hayman, B.I. (1954): Theory and analysis of diallel crosses. Genet, 39:789-809.
- Hill, J. (1964): Effects of correlated gene distribution in the analysis of diallel crosses. Hered. 19(1): 27-46.
- Kumar H. and R.K. Agrawal (1981): Combing ability analysis of certain productive traits in pea (*Pisum sativum* L.) Z. Pflanzenzuechtg., 84: 133-138.
- Mahgoub, E.M.; M.A. Ahmed; S.S. Soliman and A.S. Mandour (1992): Diallel analysis of earliness and some yield components in pea. Zagazig J. Agric. Res. 19, (6): 2463-2471.
- Mather, K. and J.L. Jinks (1971): Biometrical Genetics. Chapman and Hall Ltd, London.
- Mointra, P.K.; S.P. Singh and A.K. Mehta (1988): Combining ability in pea (*Pisum sativum* L.). Indian J. Agric. Sci., 58:479-480.
- Partap, P.S.; G.L. Bhatia and S.K. Arora (1992): Studies on genetic variability and heritability for yield and component characters in pea (*Pisum sativum* L.). Crop. Research (Hisar), 5(3): 505-511.
- Singh, K.N.; U. Singh Santoshi and H.G. Singh (1987): Genetic analysis of yield components and protein content in pea: the analysis of general and specific combining ability. Indian J. Genet. 47. 115-117.
- Singh, M.N. and R.B. Singh (1989): Genetic analysis of yield traits in pea. Crop Improv. 16:62-67.
- Singh, M.N. and R.B. Singh (1990a): Estimation of additive, dominance and digenic episatic interaction effects for certain yield characters in pea, Indian J. Genet. 50:348-353.
- Singh, M.N. and R.B. Singh (1990b): Combining ability analysis over environments in diallel crosses of pea. Indian J. Genet. 50:359-363.
- Venkateswarlu S. and R.B. Singh (1983): Combining ability over environments in pea. Indian J. Genet. 43:185-187.

تقييم الاختلافات الوراثية وطبيعة الفعل الجيني فى البسلة

1 - صفات المحصول

سوزان عباس سويدان

معهد بحوث المحاصيل البستانية، مركز البحوث الزراعية، القاهرة، جمهورية مصر العربية

تم استخدام الاختلافات الموجودة فى ستة وثلاثون تركيبا وراثيا فى البسلة والممثلة بصنفين محليين وأربعة أصناف أجنبية وخمسة عشرة هجيناً ناتجاً منها وهجتها العكسية وذلك لتقييم أداء المحصول والصفات المشاركة فيه فى تلك التركيب الوراثية وطبيعة الفعل الجيني الذى يحكم هذا الأداء أثناء الموسمين 1998/97، 1999/98 وذلك فى محطة بحوث البساتين بالقصاصين.

يوضح كل من متوسط أداء صفات المحصول ولفعل الجيني أن هجن الجيل الأول عالية الإنتاج Ambassador X Mammoth, Hunter X Ambassador يمكن استخدامها بنجاح للحصول على أصناف بسلة مبشرة عالية الإنتاج.

وعلى أية حال فقد وجد أن التأثيرات الجينية المضيقة دون أدنى تفاعل جيني كانت أكثر أهمية فى التحكم فى كل من عدد البذور فى القرن وطول القرن، بينما اثبتت النتائج أن الفعل الجيني الغير مضيق يظهر فى صفات عدد القرون فى النبات ووزن البذور فى القرن. بينما وجد أن التأثيرات الجينية السائدة تلعب دوراً رئيسياً فى التحكم فى صفات عدد القرون فى النبات ووزن القرون فى النبات.

وقد لوحظت توزيعات جينية غير عشوائية من النوع التشتت على مستوى التركيب الوراثية الأبوية وذلك بالنسبة للجينات التى تحكم كل من عدد ووزن القرون فى النبات ووزن البذور فى القرن وقطر القرن. وقد وجد أن الجينات المتنحية تكون مرتبطة بالقيم العالية لصفات قطر القرن وعدد البذور فى القرن فى الأباء Mammoth و Master على الترتيب ومرتبطة مع صفة طول القرن فى كلا الأبوين، وفيما يخص صفة عدد البذور فى القرن يعتبر الصنف Master هو الأب الذى يشتمل على كل الجينات المتنحية والأب Arica يشتمل على كل الجينات السائدة.

