RELATIONSHIP BETWEEN INBREEDING COEFFICIENT AND CLONAL SELECTION IN A POTATO CULTIVAR DEVELOPMENT PROGRAM

F. Loiselle[1], G.C.C. Tai[2], B.R. Christie[3], and T.R. Tarn[2]

Abstract

It is often assumed that the inbreeding status of progenies influences artificial selection. A study of the influence of the inbreeding coefficient of potato genotypes on the selection intensity in a potato cultivar development program was conducted. The inbreeding coefficient for the genotypes of 105 crosses investigated ranged from 0 to 0.11 and averaged 0.022. No significant relationship was found between the inbreeding coefficient and the proportion of genotypes saved at the single-hill, four-hill, ten-hill and hundred-hill stage of selection. The inbreeding coefficient was of little use in predicting *a priori* the selection pattern of a cross in a multitrait type of breeding program.

Compendio

Se asume con frecuencia que la condición de endocría de las progenies influencia la selección artificial. Se condujo un estudio de la influencia del coeficiente de endocría de genotipos de papa sobre la intensidad de selección en un programa de desarrollo de cultivares de papa. El coeficiente de endocría para los genotipos de 105 cruzamientos investigados varió de 0 a 0,11 y promedió 0,022. No se encontró una relación significativa entre el coeficiente de endocrío y la producón de genotipos retenidos durante las etapas de selección con una, cuatro, diez y cien matas. El coeficiente de endocría fue de escaso valor para predicir *a priori* el modelo de selección de unb cruzamiento en un programa de mejoramiento del tipo de características múñtiples.

---

[1] Graduate Student, Department of Crop Science, University of Guelph, Guelph, Ontario, Canada, N1G 2W1. Present address: Station Épuiseau - Pioneer Génétique, 41290 Oucques, France.

[2] Research Scientist, Agriculture Canada Research Station, P.O. Box 20280, Fredericton, New Brunswick, Canada, E3B 4Z7.

[3] Professor, Department of Crop Science, University of Guelph, Guelph, Ontario, Canada, N1G 2W1. Present address: Research Scientist, Agriculture Canada Research Station, P.O. Box 1210, Charlottetown, Prince Edward Island, Canada, C1A 7M8.

Accepted for publication June 30, 1989.

ADDITIONAL KEY WORDS: *Solanum tuberosum* (L.), coancestry, parentage, multiple traits, depression, heterosis, vigor, software.

Introduction

The inbreeding coefficient is sometimes used in breeding programs to estimate genetic similarity or hybrid vigor where its reduced cost is an advantage over agronomic and molecular marker measures of similarity (13). The inbreeding coefficient (F) was first defined by Wright (16) as the correlation between uniting gametes. Malécot (8) further defined the term as the probability for two alleles at a single locus to be identical by descent. Various mathematical estimates of coancestry have been used to estimate genetic similarity, heterozygosity, heterosis or its corollary, inbreeding depression.

For polyploid, clonally propagated crops, it has been claimed that high inbreeding coefficients in the progenies should be avoided (9, 18) and that a large gene pool should be used (4). Linear or curvilinear responses have been observed between vigor related traits and inbreeding coefficients (1, 2, 3, 7, 10). Since inbreeding depression supposedly influences artificial selection (3), an accurate prediction of inbreeding depression with the use of F could have important practical applications in planning crosses in potato breeding programs.

Selection practiced in cultivar development is based on many characteristics. The purpose of this study was to determine if this multitrait selection, at four clonal generations in a potato cultivar development program, was influenced by the inbreeding coefficient of the genotypes.

Materials and Methods

A wide range of potato genotypes were grown and selected at the Benton Ridge Potato Breeding Substation of the Agriculture Canada Research Station, Fredericton, New Brunswick, between 1975 and 1988. Genotypes were successively planted in single-hill (SH), four-hill (FH), ten-hill (TH) and hundred-hill (HH) single row plots and selected for various agronomic traits (appearance, quality, yield, maturity etc.) (14). The number of genotypes planted and selected were recorded every year and entered in a computerized selection data base (15). Entries were chosen from this data base so that genotypes from each of the full-sib families were planted in at least two different years. This reduced biases caused by the influence of combinations of genotypes, years and selectors. The number of single hills planted per cross ranged from 214 to 5570 with an average of 1604. The proportion of genotypes selected was recorded for each of the four stages (SH, FH, TH and HH) and for the four-year selection period (SH-HH). Among the parents used in these crosses, 19 were named cultivars, 39 were advanced clones from the Agriculture Canada Research Station, Fredericton, breeding program and 12 were advanced clones from other breeding programs.

The inbreeding coefficients (F) were calculated with an "APL" program, developed by the senior author for an autotetraploid mode of inheritance.

The pedigree data base program at the Fredericton Research Station served as the source of data for calculating inbreeding coefficients. The computer program runs on a personal computer with custom data entry, can handle many generations of information and can be used to calculate inbreeding and parentage (relationship, coancestry) coefficients for autotetraploid species (This program will be supplied by the authors upon receipt of an empty 5¼" diskette).

The formula for the calculation of F is adapted from Wright (17) and is the following:

$$F_X = 1/6(F_Y + F_Z + 4\,R_{YZ})$$

where: F_X is the inbreeding coefficient of the genotypes of the full-sib family; F_Y and F_Z are the inbreeding coefficients of the parents.

and

$$R_{YZ} = \{(1/4)^{n1 + n2 + 1}[1+3F_A]\}.$$

where R_{YZ} is the relationship coefficient between the parents obtained by summation of the preceding formula over the paths of relationship for all common ancestors (F_A). The terms n1 and n2 are the number of generations separating parents Y and Z from the common ancestor. Up to seven generations of pedigree data were used for calculation of the coefficients.

The coefficient of simple determination (r^2) was computed between F and the proportion of genotypes selected over all four breeding stages (SH-HH). The coefficient of multiple determination (R^2) was computed between F and the proportion of genotypes selected at the SH, FH, TH and HH stages. A cluster analysis called FASTCLUST (12) was performed on the proportions of genotypes selected at the four stages of selection to assist in grouping the crosses into five patterns of selection (clusters). Inbreeding coefficients were averaged for each cluster. A canonical discriminant analysis called CANDISC (12) was also performed, based on the groups separated previously, to identify discrimination factors among clusters.

Results and Discussion

Correlations (Table 1) indicate no significant relationships between inbreeding coefficients and the proportion of genotypes selected at any of the four stages. There were no significant correlations between the number of selections within full-sib families at one stage and the number at another stage, excepted between SH and HH. Tai *et al.* (15) obtained similar results. This can be due to several factors. One is the large influence of non-heritable variation of potato clones in visual selection of early breeding generations (14). Another is the changing emphasis on different traits as the four-year selection process progresses, which results in no significant correlations between selections at succeeding stages (15). Breeder's preference can also introduce biases (11).

TABLE 1. — *Mean and standard deviation for the inbreeding coefficient (F) and for the proportion of genotypes selected at the single-hill (SH), four-hill (FH), ten-hill (TH), and hundred-hill (HH) stages, and correlations between them.*

Variable	Mean	Standard deviation	Correlations F	SH	FH	TH	HH
F	0.022	0.023	1.00				
SH	0.160	0.051	0.07	1.00			
FH	0.176	0.065	-0.10	0.04	1.00		
TH	0.228	0.107	0.12	-0.07	0.04	1.00	
HH	0.403	0.246	-0.07	0.20*	0.09	0.06	1.00

*Significant at the 0.05 level of significance with 103 degrees of freedom.

When simple and multiple determination coefficients were computed, again, no relationships were significant between the inbreeding coefficient of genotypes and the number selected from the full-sib families. This was true for both the global proportion of selection (selected hundred hills divided by planted single hills) ($r^2 = 0.004$) and the combined individual proportions of selection (SH, FH, TH, HH) ($R^2 = 0.039$).

With cluster analysis five clusters were separated containing 6, 19, 56, 2, and 22 crosses in them. Canonical discriminant analysis showed that in decreasing order of importance the hundred-hill, ten-hill, four-hill and single-hill stages discriminated the most among the clusters formed. The average inbreeding coefficients obtained for each of the clusters were 0.010, 0.021, 0.023, 0.017, 0.025 and the standard deviations were 0.015, 0.020, 0.020, 0.024 and 0.032, respectively. The relatively large size of the standard deviation of F values for each cluster indicates that no pattern of selection was associated with a distinct inbreeding coefficient.

These results suggest that valid predictions of the proportion of genotypes that will be selected from a cross cannot be made from calculated inbreeding coefficients. This finding relates specifically to the parental combinations and types of selection conducted by the Potato Breeding Group of the Agriculture Canada Research Station, Fredericton. However, most major potato cultivar development programs are conducted in a manner similar to this Canadian program. Unless drastically different procedures are used, it is felt that the use of the inbreeding coefficient will have limited application for this specific purpose.

There are several possible explanations for the lack of relationships between inbreeding coefficients and proportion of genotypes selected. Ancestors used to calculate inbreeding coefficients were themselves strongly selected, which creates a bias in estimation of inbreeding coefficients (6). There is no biometrical way to estimate this bias but it is possible that the inbreeding coefficient may be overestimated by not taking into account selection pressure towards heterozygous and vigorous genotypes used as parents. On the other hand, the assumption that the oldest ancestors are unrelated probably underestimates the inbreeding coefficient values.

Secondly, the level of inbreeding of the crosses in this Canadian breeding program (an average of 0.022) is probably not high enough to play an important role. The distribution of F values are strongly skewed toward very low values of inbreeding (Figure 1). The genotypes of only a few crosses had F values in the 0.10 to 0.12 range. Glendinning (5) also reported low levels of relationships in European material. Few of the recently released cultivars in Europe possessed relationship coefficients higher than 0.125 (full sibs), if one assumed no relationship between the old ancestors. In general, when a positive relationship between inbreeding coefficients and the performance of genotypes has been found, the inbreeding levels reported were of a greater magnitude than the ones calculated here (6). In sweet potato, an autohexaploid crop, Yoshida (18) reported that inbreeding depressions were not detected when F values were less than about 0.15.

A third reason why negligible relationships have been observed between F values and the proportion of genotypes selected could be the multitrait type of selection used in potato. It can be postulated that plant vigor occupies only a small portion of the decisional weight. Tai and Young (14) pointed out that selection in the first clonal generation primarily retains

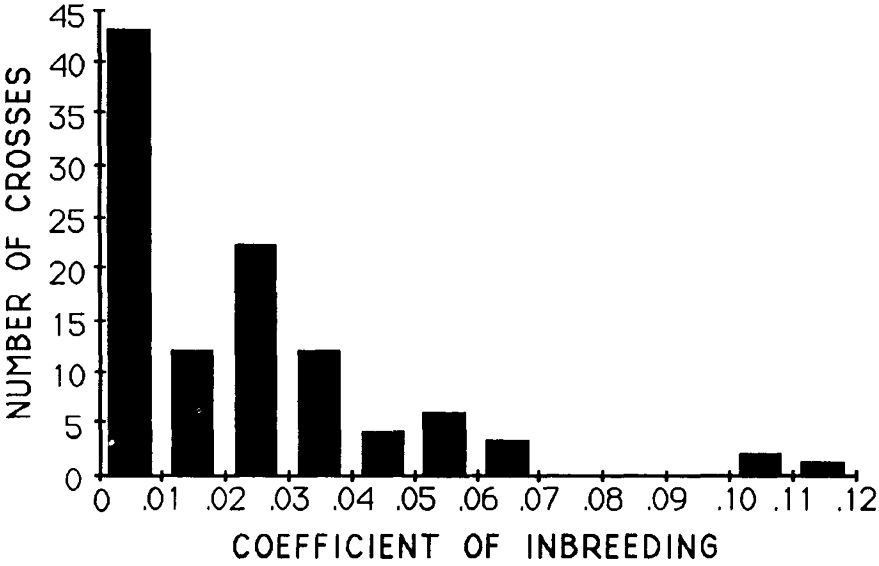

FIG. 1. Distribution of the inbreeding coefficient for the number of crosses studied.

genotypes of a "commercial" type. The selection emphasis is placed on good tuber size and a high marketable yield and not on late maturing, vigorous plants. Therefore, it is unlikely inbreeding coefficients would be a good indicator of commercial value of a cross.

Based on the low levels of coancestry found in this study, we suggest no special effort be put on calculation of F values to screen *a priori* for high retention percentage of genotypes within full-sib families. Nevertheless, in a study conducted recently on potato (manuscript in preparation), F values in the 0.10-0.15 range were shown to be associated with lower yields. Thus, the absence of relationship between F values and hybrid vigor should not be completely overlooked in a potato breeding program.

Acknowledgments

We wish to acknowledge the staff of the potato breeding team of the Agriculture Canada Research Station, Fredericton, for the long term selection data. We also wish to thank Morris M. MacDonald for the implementation of the inbreeding coefficient calculation program. This work was supported by a graduate scholarship awarded by the Natural Science and Engineering Research Council of Canada to the senior author.

Literature Cited

1. Busbice, T.H. and C.P. Wilsie. 1966. Inbreeding depression and heterosis in autotetraploids with application to *Medicago sativa* L. Euphytica 15:52-67.
2. Gallais, A. 1977. An experimental check of quantitative genetics on an autotetraploid plant, *Medicago sativa* L., with special reference to the identity by descent relationship. *In:* E. Pollack, O. Kempthorne and T.B. Bailey, Jr. Proc Inter Conf Quant Genet, Iowa State University Press, Ames. pp. 519-540.
3. Gallais, A. 1984. An analysis of heterosis vs. inbreeding effects with an autotetraploid cross-fertilized plant: *Medicago sativa* L. Genetics 106:123-137.
4. Glendinning, D.R. 1979. The potato gene-pool and benefits deriving from its supplemenation. *In:* A.C. Zeven & A.M. van Harten, Proc Conf Broad Genet Base Crops (1978). Pudoc, Wageningen. pp. 187-194.
5. Glendinning, D.R. 1987. Gene pool of modern potato varieties. *In:* G.J. Jellis and D.E. Richardson. The production of new potato varieties: technological advances. Cambridge University Press, Cambridge. pp. 28-30.
6. Lefort-Buson, M. 1985. Distance génétique et hétérosis. 3. Utilisation des coefficients de consanguinité et de parenté. *In:* M. Lefort-Buson and D. de Vienne. Les distances génétiques - Estimations et applications. I.N.R.A. Paris. pp. 131-141.
7. Lefort-Buson, M., Y. Dattée, B. Guillot-Lemoine. 1986. Heterosis and genetic distance in rapeseed (*Brassica napus* L.): use of kinship coefficient. Genome 29:11-18.
8. Malécot, G. 1948. Les mathématiques de l'hérédité. Masson et Cie. Paris. 63 p.
9. Mendoza, H.A. and F.L. Haynes. 1974. Genetic relationship among potato cultivars grown in the United States. Hortscience 9:328-330.
10. Michaud, R. and T.H. Busbice. 1977. Selection for seed set in noninbred and partly inbred populations of alfalfa. Can J Plant Sci 57:873-881.

11. Pfeffer Ch., K.-H. Möller, M. Scholz and H.-G. Zschüttig. 1988. Die Zuverlässigkeit der visuellen Selektion in der ersten Klongeneration von Kartoffeln. Potato Research 31:17-23.
12. SAS Institute Inc. 1985. SAS user's guide: statistics, Version 5 Edition. Cary, NC. SAS Institute Inc. 956 p.
13. Sidhu, A.S. and M.L. Pandita. 1980. Genetic divergence for yield and its components in potato (*Solanum tuberosum* L.). Genet Agr 34:235-244.
14. Tai, G.C.C. and D.A. Young. 1984. Early generation selection for important agronomic characteristics in a potato breeding population. Am Potato J 61:419-434.
15. Tai, G.C.C., P.Y. Jui and D.A. Young. 1986. Evaluation of parents based on long-term selection records. Z. Pflanzenzüchtg. 96:39-46.
16. Wright, S. 1922. Coefficients of inbreeding and relationship. Amer Nat 56:330-338.
17. Wright, S. 1951. The genetical structure of populations. Eugenics 15:323-354.
18. Yoshida, T. 1986. Inbreeding coefficient and yield in sweet potato (*Ipomoea batatas* (L.) LAM.) Japan J Breed 36:409-415.