Short Communication   **Open Access**

Inbreeding and yield of synthetic varieties derived from single and double cross hybrids

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Abstract

Maize (*Zea mays* L) seed saving among producers in low-income and lesser in developed countries is often practiced. In México, advanced generations of maize hybrids and even mixtures of single-cross (SCs) and double-cross hybrids (DCs) are grown. These populations are expected to perform similar to the synthetic varieties (SVs) that could be derived from the lines involved in the derivation of the hybrids that, presumably, are good combiners. The derivation of SVs from hybrids seems attractive because would be easier because of the reduced number of potential parents. The frequencies of the genes of the SCs, however, may differ from those of the DCs, may affect the inbreeding coefficient, and thereby the genotypic mean. To address these and related issues, this study was conducted to derive formulae to calculate the inbreeding coefficient (IC) and to predict the genotypic mean (GM) of SVs derived from a mixture of s SCs and d DCs, each represented by m individuals. Formulae for its IC ($FSyn_{SC,DC}$) and GM ($\overline{Y}Syn_{SC,DC}$) were derived. For hybrid parents derived from fully inbred and unrelated lines, $FSyn_{SC,DC} = [2ms+d(m+1)]/[4m(s+d)^2]$ and, independently of the type of lines, $\overline{Y}Syn_{SC,DC} = \overline{Y}_{PS}/(s+d)+\overline{Y}_{PC}(s+d-1)/(s+d)$, where $\overline{Y}_{PS}$ is the genotypic mean of the s + d populations that result from randomly mating the m individuals of each parent, and $\overline{Y}_{PC}$ is the mean of all crosses between the s + d parents. From eight lines, three sets of parents (each set involved all eight lines) were considered: 1) four SCs (4SC), 2) two SCs and one DC (2SC+DC), and 3) two DCs (2DC). The SV produced by 4SC shows the lowest IC, although for large m (m > 10) the IC of the SV produced by 2DC is about equal. The largest IC, and thereby the smallest GM, is associated to 2SC+DC because the coancestry between individuals and gene frequencies in SCs are twice those of DCs. What is more noticeable, however, is that 2DC produces the cheapest way of deriving and predicting a SV since only three entries are required (two parents and their cross) and with large m the IC is about the minimum.

Keywords: *Zea mays* L, yield prediction, inbreeding coefficient, synthetic variety

Introduction

Maize (*Zea mays* L) synthetics are low-cost and stable varieties. They are particularly important for situations where the use of hybrid seed and related inputs are too expensive. Although this is particularly true in developing countries, in the USA and Canada open-pollinated varieties are also grown successfully for forage yield production (Bertoia, 2001). Furthermore, in Mexico the use of advanced generations of single- and double-cross hybrids is observed despite the yield decrease normally observed due to inbreeding depression (Villanueva et al, 1994). Sahagún and Villanueva (1997) have suggested the use of several single-cross hybrids (SCs) as parents of synthetic varieties (SVs), and Sahagún and Villanueva (2007) studied the prediction of performance of SVs derived from double-cross hybrids (DCs). From the breeding standpoint, this approach seems to be promising since the lines involved in a hybrid must have undergone selection for combining ability. In addition, relative to the classical case where the parents of a SV are lines, predicting performance where the parents are several hybrids of the same type might be easier since a lower number of potential parents should be considered; inbreeding depression of such varieties must be lower than the inbreeding observed in an advanced generation of one single hybrid and thereby the synthetic performance might be better.

In reality, however, besides advanced generations of individual hybrids, mixtures of hybrids may also be encountered in the field of resource-low maize producers in Mexico. The resulting populations are expected to perform similar to the conventional synthetic varieties that could have been derived from the lines that are the parents of the hybrids, and have prompted the study of SVs derived from mixtures of hybrids. The SVs derived from several SC hybrids do not differ from their corresponding conventional SVs (Sahagún and Villanueva, 1997). In addition, formulae for the inbreeding coefficient and yield prediction have been derived for SVs whose parents are several DCs (Sahagún-Castellanos et al, 2005; Márquez-Sánchez, 2008). Studies for synthetics derived from a mixture of SC and DC hybrids ($Syn_{SC,DC}$), however, have not yet been made. And they seem to be appropriate since the unbalanced participation of the lines that occurs when double and single crosses are

parents may affect the genotypic mean and inbreeding coefficient. It is also expected that the magnitude of the effects depend on the relative numbers of SC and DC parents. To assess the truthfulness of these expectations, this research was conducted to derive formulae for the inbreeding coefficient and for yield prediction of the varieties whose parents are *d* double – cross and *s* single – cross hybrids.

Methods and Theory

The parents of the synthetic variety under study were *s* single crosses (SCs) and *d* double crosses (DCs), each represented by *m* plants. At the individual level, let *Api1Api2* be the genotype of the *p-th* plant of parent *i* (*p = 1, 2, …, m; i = 1, 2, …, s, s + 1, s + 2, …, s + d*). It will be considered that if *i ≤ s* (*i ≥ s + 1*) the parent is a SC (DC) hybrid. Thus the synthetic variety derived from these *s + d* parents (*Syn$_{SC,DC}$*) must be the population formed by randomly mating these *m(s + d)* individuals (Busbice, 1970). Since their gametic array is

$$\left[2m(s+d)\right]^{-1} \sum_{p=1}^{m}\sum_{i=1}^{s+d}\sum_{k=1}^{2} A_{pik},$$

and the reproduction is by random mating, according to Kempthorne (1957) the genotypic array of such synthetic variety (*GASyn$_{SC,DC}$*) must be:

$$GASyn_{SC,DC} = \frac{1}{\left[2m(s+d)\right]^2}\sum_{p=1}^{m}\sum_{q=1}^{m}\sum_{i=1}^{s+d}\sum_{j=1}^{s+d}\sum_{k=1}^{2}\sum_{l=1}^{2} A_{pik}A_{qjl} \ (1)$$

Inbreeding Coefficient

Sahagún-Castellanos (1994) showed how the genotypic array of a SV can be decomposed into relevant components to study its inbreeding coefficient. From Equation 1, considering that there is no difference between a direct cross and its reciprocal the components that can be considered are, for example:

$$\sum_{p=1}^{m}\sum_{q=1}^{m}\sum_{i=1}^{s}\sum_{j=1}^{s}\sum_{k=1}^{2}\sum_{l=1}^{2} A_{pik}A_{qjl} \ (2)$$

$$\sum_{p=1}^{m}\sum_{q=1}^{m}\sum_{i=s+1}^{s+d}\sum_{j=s+1}^{s+d}\sum_{k=1}^{2}\sum_{l=1}^{2} A_{pik}A_{qjl} \ (3)$$

$$2\sum_{p=1}^{m}\sum_{q=1}^{m}\sum_{i=1}^{s}\sum_{j=s+1}^{d}\sum_{k=1}^{2}\sum_{l=1}^{2} A_{pik}A_{qjl} \ (4)$$

Expressions 2 and 3 are formed by the genotypes of the SVs whose parents are *s* SC hybrids (*Syn$_{SC}$*) and *d* DC hybrids (*Syn$_{DC}$*), respectively; and Expression 4 contains only the genotypes generated by all *2sd* crosses (assuming that direct and reciprocals do not differ) between a single cross and a double cross. Thus, according to this illustration, the inbreeding coefficient of the synthetic variety (*FSyn$_{SC,DC}$*) can be expressed in terms of the inbreeding coefficients of the two synthetic varieties and the coancestry between the two types of hybrids. To derive a formula for *FSyn$_{SC,DC}$*, the probability (P) that the genes of the genotypes in the genotypic array are identical by de-

scent was used. Based on Equation 1, the basic expression for Fsyn$_{SC,DC}$ is

$$Fsyn_{SC,DC} = \left[2m(s+d)\right]^{-2}\sum_{p=1}^{m}\sum_{q=1}^{m}\sum_{i=1}^{s+d}\sum_{j=1}^{s+d}\sum_{k=1}^{2}\sum_{l=1}^{2} P(A_{pik} \equiv A_{qjl}) \ (5)$$

The total sum in Equation 5 can also be decomposed into three components, two related with the inbreeding coefficients of the synthetics formed by the *s* single crosses (*FSyn$_{SC}$*) and by the d double crosses (*FSyn$_{DC}$*); and the third term is related with the coancestry between SC and DC hybrids ($\Gamma_{SC,DC}$). Thus Equation 5 becomes expressible as:

$$FSyn_{SC,DC} = \left[2m(s+d)\right]^{-2}\left\{ \sum_{p=1}^{m}\sum_{q=1}^{m}\sum_{i=1}^{s}\sum_{j=1}^{s}\sum_{k=1}^{2}\sum_{l=1}^{2} P(A_{pik} \equiv A_{qjl}) \right.$$

$$+\sum_{p=1}^{m}\sum_{q=1}^{m}\sum_{i=s+1}^{s+d}\sum_{j=s+1}^{s+d}\sum_{k=1}^{2}\sum_{l=1}^{2} P(A_{pik} \equiv A_{qjl})$$

$$\left. +2\sum_{p=1}^{m}\sum_{q=1}^{m}\sum_{i=1}^{s}\sum_{j=s+1}^{s+d}\sum_{k=1}^{2}\sum_{l=1}^{2} P(A_{pik} \equiv A_{qjl}) \right\} \ (6)$$

Considering the average inbreeding coefficient of each of the three components of Equation 6, and that, for example,

$$FSyn_{SC} = \left[2ms\right]^{-2}\sum_{p=1}^{m}\sum_{q=1}^{m}\sum_{i=1}^{s}\sum_{j=1}^{s}\sum_{k=1}^{2}\sum_{l=1}^{2} P(A_{pik} \equiv A_{qjl})$$

Equation 6 is expressible as

$$FSyn_{SC,DC} = \frac{s^2}{(s+d)^2}FSyn_{SC}$$

$$+\frac{d^2}{(s+d)^2}FSyn_{DC} + \frac{2sd}{(s+d)^2}\Gamma_{SC,DC} \ (7)$$

To obtain numerical values for *FSyn$_{SC,DC}$* (Equation 7), the inbreeding coefficients of the lines and their coancestries are required.

Synthetic Performance Prediction

To predict the genotypic mean of the generation *t* of a synthetic variety ($\overline{Y}_t$) whose inbreeding coefficient is *F$_t$*, Busbice (1970) proposed the equation

$$\overline{Y}_t = A + (1 - F_t)B,$$

where A and B were defined, respectively, as "the average yield of the conceptual (or real) homozygous parents in the ancestry of the synthetic" and "the yield resulting from heterozygosis when it is maximum (*F = 0*)". This author considered the equations for synthetic-0 (the population formed by the parents) and synthetic-1 (the population formed by all crosses among parents) whose inbreeding coefficients are *F$_0$*

and F_1, respectively, to find a solution for A and B, which is possible whenever $F_0 \neq F_1$. But if the $s + d$ hybrids were derived from fully inbred and unrelated parents, $F_0 = 0$: and if the synthetic-1 were formed by the crosses among parents, $F_1 = 0$, and with only this information it is not possible to predict according Busbice's (1970) prediction procedure. However, since this formula implies a linear relationship between the genotypic mean and the inbreeding coefficient of a SV, it gives an idea of the relative magnitudes of the genotypic means of several SVs on the basis of their inbreeding coefficients.

Sahagún-Castellanos et al (2005) made a decomposition of the total of the genotypic values of a synthetic to express its genotypic mean in terms of identifiable genotypic means that can be estimated from experimental data. According to this procedure, if the genotypic value of $A_{pik}A_{qjl}$ is represented by $Y_{pik,qjl}$, the genotypic mean of the synthetic variety under study ($\overline{Y}Syn_{SC,DC}$), according to Equation 5, is expressed as:

$$\overline{Y}Syn_{SC,DC} = \left[2m(s+d)\right]^{-2} \sum_{p=1}^{m} \sum_{q=1}^{m} \sum_{i=1}^{s+d} \sum_{j=1}^{s+d} \sum_{k=1}^{2} \sum_{l=1}^{2} Y_{pik,qjl} \quad (8)$$

The right-hand side of Equation 8 can be decomposed into components of interest, as it was made for the inbreeding coefficient in Equation 7, for example. With this decomposition, the expression for the genotypic mean is:

$$\overline{Y}Syn_{SC,DC} = \left[s/(s+d)\right]^2 \overline{Y}Syn_{SC} + \left[d/(s+d)\right]^2 \overline{Y}Syn_{DC} + \left[2sd/(d+s)^2\right] \overline{Y}_{SC,DC} \quad (9)$$

Where $\overline{Y}Syn_{SC}$ and $\overline{Y}Syn_{DC}$ are the genotypic means of two SVs derived, one from s SC hybrids, and the other from d DC hybrids, respectively; and $\overline{Y}_{SC,DC}$ is the genotypic mean of all $2sd$ crosses between the s single and the d double crosses. Thus with experimental data to estimate $\overline{Y}Syn_{SC}$ (Sahagún and Villanueva, 1997), $\overline{Y}Syn_{DC}$ (Sahagún-Castellanos et al, 2005), and $\overline{Y}_{SC,DC}$, $\overline{Y}Syn_{SC,DC}$ can be estimated.

To assess the value of the different ways of predicting the performance of a synthetic variety the variance of the estimator of the genotypic mean was calculated. According to this criterion, the quality of an estimator is inversely related to its variance. Wricke and Weber (1986) derived the variance of the experimental mean of a synthetic variety ($\overline{Y}_S$) when this is expressed as

$$\overline{Y}_S = (1/P)\overline{Y}_P + \left[(P-1)/P\right]\overline{Y}_{PC},$$

where $\overline{Y}_P$ is the experimental mean of the P populations that result from the random mating of the m individuals that represent each parent, and $\overline{Y}_{PC}$ is the experimental mean of the $P(P–1)/2$ direct crosses of the P parents. The variance (Var) of this predictor ($\overline{Y}_S$) in terms of one replication and σ^2 (the error variance) is

$$Var(\overline{Y}_S) = \left[(2P-1)/P^3\right]\sigma^2 \quad (10)$$

Results and Discussion

Inbreeding Coefficient

On the basis of Equations 2, 3, and 5, the inbreeding coefficients of the synthetic varieties derived one from s single-cross hybrids ($FSyn_{SC}$) and the other from d double-cross hybrids ($FSyn_{DC}$) can be expressed, at the onset, as:

$$FSyn_{SC} = \left[2ms\right]^{-2} \sum_{p=1}^{m} \sum_{q=1}^{m} \sum_{i=1}^{s} \sum_{j=1}^{s} \sum_{k=1}^{2} \sum_{l=1}^{2} P(A_{pik} \equiv A_{qjl}) \quad (11)$$

and

$$FSyn_{DC} = \left[2md\right]^{-2} \sum_{p=1}^{m} \sum_{q=1}^{m} \sum_{i=s+1}^{s+d} \sum_{j=s+1}^{s+d} \sum_{k=1}^{2} \sum_{l=1}^{2} P(A_{pik} \equiv A_{qjl}) \quad (12)$$

Further, for the average coancestry between two individuals, one from a SC and one from a DC ($\Gamma_{SC,DC}$):

$$\Gamma_{SC,DC} = (2m)^{-2} \bullet$$
$$(sd)^{-1} \sum_{p=1}^{m} \sum_{q=1}^{m} \sum_{i=1}^{s} \sum_{j=s+1}^{s+d} \sum_{k=1}^{2} \sum_{l=1}^{2} P(A_{pik} \equiv A_{qjl}) \quad (13)$$

With respect to $FSyn_{SC}$, a particular further decomposition gives:

$$FSyn_{SC} = (2ms)^{-2} \left[\sum_{p=1}^{m} \sum_{i=1}^{s} \sum_{k=1}^{2} P(A_{pik} \equiv A_{pik}) \right.$$
$$+2\sum_{p=1}^{m} \sum_{i=1}^{s} P(A_{pi1} \equiv A_{pi2})$$
$$+\sum_{p \neq}^{m} \sum_{q}^{m} \sum_{i=1}^{s} \sum_{k=1}^{2} \sum_{l=1}^{2} P(A_{pik} \equiv A_{qil})$$
$$+\left. \sum_{p=1}^{m} \sum_{q=1}^{m} \sum_{i \neq}^{s} \sum_{j}^{s} \sum_{k=1}^{2} \sum_{l=1}^{2} P(A_{pik} \equiv A_{qjl}) \right] \quad (14)$$

The four terms in Equation 14 are for the probability of identity by descent (PID) of the two genes of a genotype produced by randomly mating the m individuals that represent each of the SCs. The first and second terms are for selfpollinations ($p = q, i = j$), and the third and fourth are for crosses between individuals from the same ($i = j, p \neq q$) and from different ($i \neq j$) parent, respectively. It will be first considered that the inbreeding coefficient of the lines used to derive the SCs and DCs is F_L and that they are unrelated. Thus the probabilities of identity by descent (PIDs) of the four terms of Equation 14 are 1, 0, $(1 + F_L)/4$, and 0, respectively, and $FSyn_{SC}$ becomes expressable as:

$$FSyn_{SC} = (2ms)^{-2} \left\{ 2ms + 0 + 4m(m-1)s\left[(1+F_L)/4\right]+0 \right\}$$

$$= \frac{1}{2s}\left[\frac{1+F_L}{2} + \frac{1-F_L}{2m}\right]. \quad (15)$$

Similarly, since for the SV derived from d DCs, the co-ancestry between different individuals from the same parent is $(1 + F_L)/8$,

$$FSyn_{DC} = (2md)^{-2}\left\{2md + 0 + 4m(m-1)d\left[(1+F_L)/8\right]+0\right\}$$

$$= \frac{md(1/2)}{(md)^2} + \frac{dm(m-1)\left[(1+F_L)/8\right]}{(md)^2}$$

This result of $FSyn_{DC}$ suggests another approach to derive the formula for $FSyn_{DC}$: The intermating of the d DCs each represented by m plants produces $(md)^2$ matings where the PID of each of the md self-pollinations and each of the $dm(m-1)$ crosses between two plants of the same DC are 1/2 and $(1 + F_L)/8$, respectively. And these numbers produce the result for $FSyn_{DC}$ under discussion that reduces to

$$\frac{m+1}{4md}\left[\frac{3+m(1+F_L)-F_L}{2(m+1)}\right] \quad (16)$$

Since all lines are unrelated, $\Gamma_{SC,DC} = 0$, and thus according to Equations 7, 15, and 16,

$$FSyn_{SC,DC} =$$

$$\frac{s^2}{(s+d)^2}\frac{1}{2s}\left[\frac{1+F_L}{2}+\frac{1-F_L}{2m}\right]+$$

$$\frac{d^2}{(s+d)^2}\frac{m+1}{4md}\left[\frac{3+m(1+F_L)-F_L}{2(m+1)}\right] \quad (17)$$

As expected, $FSyn_{SC,DC}$ (Equation 17) is reduced to $FSyn_{SC}$ (Equation 15) when $d = 0$, and to $FSyn_{DC}$ (Equation 16) when $s = 0$. In general, regarding the inbreeding coefficient of the parental lines of a synthetic the more intensively studied case is for $F_L=1$. In this case Equation 15 reduces to $FSyn_{SC} = 1/(2s)$. This equation shows independence of $FSyn_{SC}$ relative to m. This is because the average contributions to $FSyn_{SC}$ from individuals produced by selfpollinations and by crosses between individuals from the same single-cross hybrid are always equal (the probability of identity by descent is 1/2 in both cases). This is not so, however, in a synthetic variety derived from only d double crosses where, as already considered, the probabilities of identity by descent (PIDs) of an individual generated by selfpollination (1/2) and by crosses between individuals from the same double cross (1/4) differ, and the relative frequencies of these two events also differ and the magnitude of the difference depends on m.

When $F_L = 1$, $FSyn_{DC}$ (Equation 16) reduces to $(m+1)/(4md)$, which implies that, for example, for $d = 1$ and $s = 0$, the inbreeding is a number of the interval (0.25, 0.50); close to 0.25 when m is large, and

0.5 when $m = 1$. In reality, m is more likely large, and the inbreeding coefficient would be closer to 0.25, whereas for a synthetic variety derived from one single-cross hybrid, independently of the size of m, this coefficient is 0.5, which might be too large in terms of the decrease in grain yield that it might cause, in maize for example (Villanueva et al, 1994; Carena, 2005).

Synthetic varieties derived from 2, 4, and 6 single-cross hybrids derived from fully inbred and unrelated lines, have inbreeding coefficients of 0.25, 0.125, and 0.083 ($F_L = 1$, Equation 15), respectively. But, if the parents were 1, 2, and 3 double crosses, the numbers of required individuals would be m, $2m$, and $3m$ instead of $2m$, $4m$, and $6m$, respectively; and the inbreeding coefficients would be, for a large m, just a little larger than 0.25, 0.125, and 0.083, respectively ($F_L = 1$, Equation 16). Thus these inbreeding coefficients and numbers of individuals required suggest that when the DCs and SCs are available, the best choice of parents to derive a synthetic variety should be double crosses rather than single-cross hybrids. This is because for two SVs that involve the same lines, relative to SCs the use of DCs implies a 50% decrease of the number of parents, and thereby a decrease in cost and labor. It should be noted that these numbers of parents are realistic for maize, whose optimum number in terms of lines is from 4 to 6, according to Kinman and Sprague (1945), from 8 to 12 according to Márquez-Sánchez (1977), and from 5 to 8 according to Kutka and Smith (2007).

There is a result that seems to be contradictory. If one considers one SV derived from $2s$ SCs and one from s DCs formed directly with the same $2s$ SCs, one might think that both SVs would be identical. This is not so, however; according with Equations 15 and 16, for $F_L = 1$, $FSyn_{DC} − FSyn_{SC} = 1/(4md)$. This difference is more important as m and d are smaller. For example, when $m = 1$, and $d = 1$, $FSyn_{DC} = 0.5$, whereas for $m = 1$, $d = 0$, and $s = 2$, $FSyn_{SC} = 0.25$. The explanation of these results is that whereas in a SV derived from $2s$ SCs the frequencies of the genes contributed by $4s$ parental lines are balanced, in the SV derived from these the s DCs derived from the same lines this balance might not be found, especially when m is small. In the extreme, when $m = 1$, $d =1$, and $s = 0$, only two out of the four genes of the DC are present in the SV.

Inbreeding and Prediction

To identify the best synthetic varieties that can be derived from the $s + d$ hybrids, the genotypic mean of every one of the $2^{s+d} − 1$ possible varieties that can be derived, including those having a single parent, should be predicted when this number is too large.

Equation 9 provides a procedure for predicting the genotypic mean of a synthetic variety based on a decomposition of the total of the genotypic values into components whose genotypic means can be estimated. Another relevant decomposition of the total

of the genotypic values of Equation 8 is:

$$\overline{Y}Syn_{SC,DC} = \left[2m(s+d)\right]^{-2}\left[\sum_{p=1}^{m}\sum_{q=1}^{m}\sum_{i=1}^{s+d}\sum_{k=1}^{2}\sum_{l=1}^{2}Y_{pik,qil}\right.$$

$$\left.+\sum_{p=1}^{m}\sum_{q=1}^{m}\sum_{i\neq}^{s+d}\sum_{j}^{s+d}\sum_{k=1}^{2}\sum_{l=1}^{2}Y_{pik,qjl}\right] \quad (18)$$

Each of the two terms in Equation 18 is the total of the genotypic values of one set of populations: 1) the $s + d$ populations that result when the m individuals that represent each parent are randomly mated in isolation (RMI populations), and 2) the $(s + d)(s + d – 1)$ crosses among the $s + d$ parental hybrids. If the genotypic means of these two sets of populations are represented by $\overline{Y}_{PS}$ and $\overline{Y}_{PC}$, respectively, from Equation 18, the resulting equation for the genotypic mean is:

$$\overline{Y}Syn_{SC,DC} =$$
$$\left[1/(s+d)\right]\overline{Y}_{PS}+\left[(s+d-1)/(s+d)\right]\overline{Y}_{PC} \quad (19)$$

Equation 19 is a case of the prediction formula derived by Wright (1981).

To estimate each of the $2^{s+d} – 1$ genotypic means of the possible synthetic varieties according to Equation 19, the field evaluation of each of the $s + d$ RMI populations and the $(s + d)(s + d – 1)$ crosses between the $s + d$ parents should be made. But, if the reciprocal crosses were not considered necessary, the phenotypic mean of the $(s + d)(s + d – 1) / 2$ direct crosses should be used to make predictions.

On the context of prediction, as already observed, the genotypic mean ($\overline{Y}Syn_{SC,DC}$) and the inbreeding coefficient of a $Syn_{SC,DC}$ ($FSyn_{SC,DC}$) can be expressed as the same linear combination of the genotypic means and inbreeding coefficients of the components produced by a decomposition of the genotypic array of the $Syn_{SC,DC}$, respectively. An example of this result is given by Equations 7 ($FSyn_{SC,DC}$) and 9 ($\overline{Y}Syn_{SC,DC}$). Further, $\overline{Y}Syn_{SC,DC}$ can be expressed as this linear combination of genotypic means which in turn are expressed in terms of the inbreeding coefficients of the involved components (Busbice, 1970). For example, according to Equations 7 and 9 for the genotypic mean of the $Syn_{SC,DC}$ and Busbice's (1970) prediction equation,

$$\overline{Y}Syn_{SC,DC} =$$
$$\left[s/(s+d)\right]^{2}\left\{A+(1-FSyn_{SC})B\right\}+$$
$$\left[d/(s+d)\right]^{2}\left\{A+(1-FSyn_{DC})B\right\}+$$
$$\left[2sd/(d+s)^{2}\right]\left\{A+(1-\Gamma_{SC,DC})B\right\} \quad (20)$$

In particular, when the initial lines are fully inbred (F_L = 1) and unrelated, according with Equations 15, 16, and 20,

$$\overline{Y}Syn_{SC,DC}=\left[s/(s+d)\right]^{2}\left\{A+(1-1/2s)B\right\}+$$

$$\left[d/(s+d)\right]^{2}\left\{A+(1-(m+1)/(4md))B\right\}+$$
$$\left[2sd/(s+d)^{2}\right]\left\{A+B\right\} \quad (21)$$

Since A and B are unknown, however, Equation 21 is not of applied value. In addition, it should also be noted that prediction Equations 9 and 19 do not include the generation number of the synthetic. In a crop species such as maize, the random mating of the parents (m is large) produces a fairly large population whose genotypic array is expected to be the same after each generation of random mating. And thus, the genotypic mean and the inbreeding coefficient should be practically stable as well.

Selection of Type of Parents

To study the effect of the choice of type of parental hybrids, let us consider three synthetic varieties whose parents are three sets of hybrids derived from the same eight equally inbred and unrelated lines: 1) four single crosses (4SC), 2) two single crosses and one double cross (2SC+DC), and 3) two double crosses (2DC). According to Table 1, for fully inbred lines the largest and smallest inbreeding coefficients were produced by 2DC and 4SC, respectively, when the number of individuals per parent (m) was 5 or less. For $m \geq 10$ the largest and smallest inbreeding coefficients are produced by 2SC+DC, and 4SC, respectively, and for large m the inbreeding coefficient of 2SC+DC was the largest (0.139) and those produced by 2D and 4SC were practically the same (0.1250). A pattern similar to the one just described for fully inbred lines was observed in the inbreeding coefficients (ICs) of the SVs derived from lines whose ICs were 0.000 and 0.500 (Table 1). And, as expected, the ICs of the SVs were directly related with the ICs of the lines.

The largest inbreeding coefficient for large m was observed in the synthetic variety produced by 2SC+DC for two reasons: 1) the frequencies of the two genes in a locus of a single cross are larger than those in a double cross (while the m individuals of a double cross carry genes from four lines, only are two genes carried by the m individuals of a single cross); and 2) the coancestry between individuals within a single cross doubles the one of the double cross.

Relative to precision, for the prediction of the genotypic means of the synthetics derived from: 1) 4SC, 2) 2SC+DC, and 3) 2DC made according to Equation 19 (Wright, 1981), the variances (Equation 10) of the three predictors are $(0.1094)\sigma^{2}$, $(0.1852)\sigma^{2}$, and $(0.375)\sigma^{2}$, respectively. These calculations, however, are based on one replication of different numbers of entries. For a comparison of the three variances on the basis of an equal number of plots, the entries for predicting performance of the two synthetics derived one from 2SC+DC and 2DC must be evaluated in 10/6 and 10/3 replicates per replicate of the 10 entries necessary to predict the genotypic mean of the synthetic derived from 4SC (4 parents and their 6 di-

Table 1 - Inbreeding coefficients of three synthetic varieties (SVs), each derived from a particular set of hybrids: 1) four single crosses (4SC), two single crosses and one double cross (2SC + DC), and two double crosses (2DC). Each set was derived from the same eight lines at each of three levels of inbreeding (0.00, 0.50, and 1.00). Each parent was represented by m individuals.

SV	m										
	1	2	3	4	5	10	20	50	100	200	500
						1.000					
4SC	0.125	0.125	0.125	0.125	0.125	0.125	0.125	0.125	0.125	0.125	0.125
2SC+DC	0.167	0.153	0.148	0.146	0.144	0.142	0.140	0.139	0.139	0.139	0.139
2DC	0.500	0.188	0.167	0.156	0.150	0.138	0.131	0.128	0.126	0.126	0.125
						0.500					
4SC	0.125	0.101	0.104	0.102	0.100	0.097	0.095	0.094	0.094	0.094	0.094
2SC+DC	0.134	0.119	0.114	0.111	0.110	0.107	0.106	0.105	0.104	0.104	0.104
2DC	0.192	0.143	0.127	0.119	0.114	0.108	0.099	0.096	0.095	0.094	0.094
						0.000					
4SC	0.125	0.094	0.083	0.078	0.075	0.069	0.066	0.064	0.063	0.063	0.063
2SC+DC	0.167	0.149	0.102	0.094	0.089	0.079	0.074	0.071	0.070	0.070	0.070
2DC	0.250	0.156	0.125	0.109	0.100	0.081	0.072	0.066	0.064	0.063	0.063

rect crosses). For these three cases the variances of the estimators would be $(0.1094)\sigma^2$, $(0.1111)\sigma^2$, and $(0.1125)\sigma^2$, respectively. These results, which are an example of a generality, show that the largest and smallest precisions are obtained using 4SC and 2DC as parents, respectively.

It is remarkable, however, that when all SCs and DCs are available, the cheapest way of forming and thus predicting the genotypic mean of a synthetic variety should be based on 2DC because only three entries are required (the two parents and their cross); in addition, its inbreeding coefficient is practically equal to 4SC's.

Conclusions

For each of several decompositions of the genotypic array of the synthetic variety (SV) derived from s single crosses (SCs) and d double crosses (DCs), formulas for the inbreeding coefficient ($FSyn_{SC,DC}$) and for the genotypic mean ($\overline{Y}Syn_{SC,DC}$) were derived. It was observed that $FSyn_{SC,DC}$ and $\overline{Y}Syn_{SC,DC}$ depends on the relative values of s and d, with the SVs derived from a mixture of SCs and DCs. In particular, for hybrids derived from a fixed set of $2s + 4d$ fully inbred and unrelated initial lines, $FSyn_{SC,DC} = [2ms + d(m + 1)]/[4m(s + d)^2]$. In this case, the largest inbreeding coefficients are those from SVs whose parents are a mixture of SC and DC hybrids, whereas the lowest inbreeding coefficient, and hence the largest genotypic mean, was for the SVs derived from either SCs or DCs.

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