Inbreeding in modified ear-to-row selection in maize

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Abstract

The corrected calculation of inbreeding in mass selection was shown in a previous paper; inbreeding in modified ear-to-row selection was calculated in that paper with the uncorrected equation. In the present paper, inbreeding is calculated for the modified ear-to-row selection method using the corrected equation. Establishing a detasseling plot is the second phase of the aforementioned method. Inbreeding values were quite small; inbreeding was about 6% in selection cycle 100. The reason behind widespread use of modified ear-to-row selection may be smaller inbreeding values.

Keywords: *Zea mays* L, inbreeding, modified ear-to-row selection

Introduction

Inbreeding is a problem through selection cycles in maize improvement. Large population sizes are used to avoid increases in inbreeding. Another alternative is the use of families with smaller inbreeding, such as the half-sib families, which are used in modified ear-to-row selection. As inbreeding causes reduction on selection gain, it is useful to know its value at least for the most used selection methods. A detasseling plot of modified ear-to-row selection consists of families planted, one per row, together with male rows, which actually is basically a mass selection plot, since families are pollinated by a random sample of pollen from all families.

Review of literature

Modified ear-to-row selection was designed by Paterniani (1967). This method consists of two phases; in the first phase, half-sib families are evaluated in several locations; in the second phase, the same half-sib families are seeded in an experimental plot; families are detasseled and a balanced composite of their seed is sown in additional rows to be used as male rows. The best families from the evaluation at several locations are then placed in the detasseling plot, and the best plants from the best families are chosen in order to generate half-sib families for the next selection cycle.

Márquez-Sánchez (2011) corrected the equation of inbreeding for mass selection previously calculated by Márquez-Sánchez (1998), whose equation for any selection cycle (t) was:

$F(MS,98)_t = (1/2nm)[(1+2m(n–1)F_{t-1} + 2(m-1)F_{t-2} + F_{t-3}]$

where n is the number of families and m is the number of plants per family.

Materials and Methods

A detasseling plot in modified ear-to-row selection is essentially the same as that used for mass selection, since the former is a plot under free pollination.

Figure 1 shows a diagram of the detasseling plot, with n families and m plants per family. The total number of crossings, including selfings, is n^2m^2. Figure 2 shows one family with m2 plants; the left-to-right diagonal represents m selfings (11, 22, 33, mm); the rest are plants resulting in a number of half-sibs of m(m – 1) from crossings. Outside the diagonal there are unrelated families with n(n – 1) crosses among them.

When considering the whole detasseling plot (HS-D), the number of selfings is nm, the number of crosses within the same family is nm(nm – 1), and the number of crossings among plants of unrelated families is $nm^2(n – 1)$. The common factor nm is used to obtain the respective codified numbers: 1, m – 1 and m(n – 1) whose sum is nm. Coancestries in each

	1 m	2 m	3 m	n m
1 m	11 m^2	12 m^2	13 m^2	1n m^2
2 m	21 m^2	22 m^2	23 m^2	2n m^2
3 m	31 m^2	32 m^2	33 m^2	3n m^2
n m	n1 m^2	n2 m^2	n3 m^2	nn m^2

Figure 1 - A diagram of a half-sib families detasseling plot on obtaining a synthetic with n families and m plants per family.

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	1	2	3	m
1	11	12	13	1m
2	21	22	23	2m
3	31	32	33	3m
m	m1	m2	m3	mm

Figure 2 - A half-sib family with m^2 plants.

group need to be considered, since in the next cycle they will be the corresponding inbreeding coefficients. The pertinent information is given in Table 1.

Results and Discussion

Average inbreeding in the detasseling plot is equal to the sum of the products: codified number x inbreeding, divided by nm.

$F(HS\text{-}D)_1 = [(1 + F_0)/2 + (1 + 6\,F_0 + F_{-1})/8 + m(n-1)\,F_1]/nm$

$= (1/nm)\,[(1 + F_0)/2 + (m - 1)(1 + 6F_0 + F_{-1})/8 + m(n\text{-}1)\,F_1]/8$

$= (1/8nm)[4 + 4F_0 + m + 6m\,F_0 + m\,F_{-1} - 1 - 6\,F_0 - F_{-1} + 8m(n - 1)F_1]$

$= (1/8nm)[(m + 3) + (4 + 6m - 6)F_0 + (m - 1)F_{-1} + 8m(n - 1)F_1]$

$= (1/8nm)[(m + 3) + 8m(n - 1)F_1 + (6m - 2)F_0 + (m - 1)F_{-1}]$ [1]

Equation [1] is equal to the corrected formula of inbreeding in mass selection.

Usually the HS-D is made with n = 200 and m = 20, resulting in 4,000 plants. But, as said before, male rows are added; if there is a 2♀/1♂ ratio, the whole plot will end up with (200 x 20) + (100 x 20) 4,000 ♀ + 2,000 ♂ = 6,000 plants; yet the effective inbreeding (F) number ($Ne_{(F)}$) has to be calculated as follows (Falconer, 1964):

$Ne_{(F)} = (4N_f \times N_m)/(N_f + N_m)$

$= (4 \times 4{,}000 \times 2{,}000)/(4{,}000 + 2{,}000)$

$= 5{,}333.33$

where N_f and N_m are the respective numbers of female and male plants.

The ratio Q = n/m = 200/20 = 10 and the product nm = 5333.33 form a system of two equations from which n´ and m´ can be obtained; thus, n´ = 230.94 and m´ = 23.094, with a Q´= n´/m´ ratio that is approximately equal to 10.

However, as there is selection in the detalessing plot, numbers of families and of plants per family should be adjusted through the variance effective number as follows (Crossa and Venkovsky, 1997):

Table 1 - Crossings, actual number of crossings, codified number, and inbreeding in a detasseling plot of half sibs.

Crossings	Actual number	Codified number	Inbreeding
Selfing	nm	1	$(1/2)\,(1 + F_0)$
Among HS within same family	nm(m – 1)	m – 1	$(1/8)(1 + 6F_0 + F\text{-}1)$
Among HS of unrelated families	$n(n - 1)m^2$	m(n – 1)	F_1

total = n^2m^2, total codified number = nm

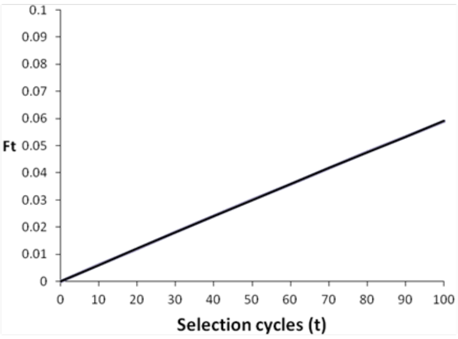

Figure 3 - Inbreeding (Ft) during 100 cycles of modified ear-to-row selection.

The variance effective number is $N_{e(v)(HS)} = N(4s/(4 - s)]$, where N = 5,333.33, s = 230.94/5,333.33 = 0.0433; thus: $N_{e(v)(HS)} = 5{,}333.33(0.1732/3.9567) = 233.46$. Numbers n and m should be adjusted using the auxiliary Q = (number of families)/(number of plants per family) = 200/20 = 10, as follows.

$n^* = [233.46 \times 10]^{1/2} = 48.3176$

$m^* = [233.46/10]^{1/2} = 4.8317$

thus, $n^*m^* = 48.3176 \times 4.8317 \approx 233.46$, and $Q^* = n^*/m^* = 48.3176/4.8317 \approx 10$, therefore

$F(HS\text{-}D)_t = (1/8n^*m^*)[(m^* + 3) + 8m^*(n^* - 1)F_{t-1} + (6m^* - 2)\,F_{t-2} + (m^* - 1)F_{t-3}]$

By extrapolation, Equation [2] provides the inbreeding for the t selection cycle:

$F(HS\text{-}D)_t = (1/1867.65)(7.83 + 1828.99\,F_{t-1} + 26.99\,F_{t-2} + 3.83\,F_{t-3})$ [2]

Figure 3 shows the graph of inbreeding coefficients from Equation [2] for 100 selection cycles, with an approximate value of 6% at cycle 100. Using the uncorrected formula for mass selection, Márquez-Sánchez (1998) found an inbreeding value of 5.1% for selection cycle 100.

In practice, the reduced inbreeding value may be the reason why modified ear-to-row selection is a widely used method. In Hallauer et al (2010) selection gain in modified ear-to-row selection has been as high as 9% per cycle in one year; in mass selection the response varies from 2 to 4% per year, and, by selecting full-sib families, the response is about 6% in two years.

Conclusions

The theoretical values of inbreeding in this research are very low. In selection cycle 100, inbreeding was about 6%. Such low values of inbreeding may be the cause of the wide use of ear-to-row selection by maize breeders.

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