

Erratum to: Hybrid maize breeding with doubled haploids: V. Selection strategies for testcross performance with variable sizes of crosses and S_1 families

Thilo Wegenast · H. Friedrich Utz ·
C. Friedrich H. Longin · Hans Peter Maurer ·
Baldev S. Dhillon · Albrecht E. Melchinger

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In the original version of the article, an error was detected in the simulation of breeding scheme S_1 TC-DHTC. This error led to an overestimation of the selection gain ($\Delta \hat{G}^*$) and the probability of selecting superior genotypes ($\hat{P}(q)^*$) in this breeding scheme. The corrected results for all selection strategies of breeding scheme S_1 TC-DHTC in Tables 2 and 3, as well as Fig. 1 are presented in the following pages.

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T. Wegenast · H. F. Utz · B. S. Dhillon · A. E. Melchinger (✉)
Institute of Plant Breeding, Seed Science,
and Population Genetics, University of Hohenheim,
70593 Stuttgart, Germany
e-mail: melchinger@uni-hohenheim.de

T. Wegenast
e-mail: wegenast@uni-hohenheim.de

C. F. H. Longin
Limagrain Verneuil Holding,
BP 58 Route de Lavardac, 47600 Nérac, France

H. P. Maurer
State Plant Breeding Institute,
University of Hohenheim, 70593 Stuttgart, Germany

Table 2 Optimum allocation of test resources maximizing the optimization criteria (OC), selection gain ($\Delta\hat{G}^*$) and the probability of selecting superior genotypes ($\hat{P}(0.1\%)^*$), in two-stage selection with evaluation of testcross progenies of (1) DH lines at both stages (DHTC) and (2) S_1 families at first stage and DH lines of S_1 families at second stage (S_1 TC-DHTC)

Breeding scheme/selection strategy	Optimum allocation				OC	SD _{OC}	$\bar{\Theta}$
	N_1^* ^a	N_2^* ^b	L_1^*	L_2^*			
Optimization criterion $\Delta\hat{G}^*$							
DHTC–1	5,538 = 3 × 1,846	392 = 2 × 196	2	14	3.322	0.385	0.500
DHTC–2a	5,812 = 4 × 1,453	320	2	15	3.384	0.324	0.311
DHTC–2b	6,152	330	2	12	3.335	0.340	0.324
DHTC–2c	4,704	203	3	14	3.347	0.326	0.323
S_1 TC-DHTC–1	816 = 4 × 204	646 = 2 × 1 × 323	12	14	3.581	0.516	0.750
S_1 TC-DHTC–2a	800 = 5 × 160	660 = 3 × 1 × 220	12	14	3.610	0.485	0.663
S_1 TC-DHTC–2b	824 = 4 × 206	753	10	14	3.624	0.484	0.581
S_1 TC-DHTC–2c	725 = 5 × 145	781	11	14	3.612	0.494	0.584
Optimization criterion $\hat{P}(0.1\%)^*$							
DHTC–1	5,655 = 3 × 1,885	400 = 2 × 200	2	13	0.631	0.295	0.500
DHTC–2a	5,644 = 4 × 1,411	348	2	15	0.671	0.252	0.316
DHTC–2b	6,204	320	2	12	0.640	0.258	0.322
DHTC–2c	4,640	220	3	14	0.651	0.258	0.322
S_1 TC-DHTC–1	820 = 4 × 205	680 = 2 × 1 × 340	13	12	0.771	0.295	0.750
S_1 TC-DHTC–2a	775 = 5 × 155	735 = 3 × 1 × 245	11	14	0.773	0.265	0.566
S_1 TC-DHTC–2b	1,057 = 7 × 151	712	9	13	0.779	0.258	0.541
S_1 TC-DHTC–2c	828 = 6 × 138	804	11	12	0.775	0.262	0.576

Assumptions: a budget of 20,000 testcross plot equivalents, variance component ratios VC2, and a correlation $\rho_P = 0.71$ between the mean performance of the parental lines and the mean genotypic value of the testcross performance of their progeny

N_j^* = optimum number of test candidates in stage j , L_j^* = optimum number of test locations in stage j , SD = the standard deviation, and $\bar{\Theta}$ = the average coefficient of coancestry among the selected DH lines

^a DHTC–1 and 2a: number of crosses × DH lines within crosses, DHTC–2b and 2c: the number of DH lines within crosses depended on the rank of the cross; S_1 TC-DHTC: number of crosses × S_1 families within crosses

^b DHTC–1: number of crosses × DH lines within crosses, DHTC–2: number of DH lines; S_1 TC-DHTC–1 and 2a: number of crosses × S_1 families within crosses × DH lines within S_1 families; S_1 TC-DHTC–2b and 2c: the number of S_1 families within crosses and DH lines within S_1 families depended on the rank of the cross and the S_1 family

Table 3 Optimum allocation of test resources maximizing the optimization criteria (OC), selection gain ($\Delta\hat{G}^*$) and the probability of selecting superior genotypes ($\hat{P}(0.1\%)^*$), in two-stage selection with evaluation of testcross progenies of (1) DH lines at both stages (DHTC–2a) and (2) S_1 families at first stage and DH lines of S_1 families at second stage (S_1 TC-DHTC–2c) and its dependence on the phenotypic correlation ρ_P (between the mean performance of the parents and the mean genotypic value of the testcross performance of their progenies), the variance component ratios (VC), and the budget in terms of testcross plot equivalents

Breeding scheme/selection strategy	Assumptions			Optimum allocation				OC	SD _{OC}	$\bar{\Theta}$
	Budget	VC	ρ_P	N_1^* ^a	N_2^*	L_1^*	L_2^*			
Optimization criterion $\Delta\hat{G}^*$										
DHTC–2a	10,000	2	0.71	2,874 = 3 × 958	191	2	13	3.257	0.316	0.340
DHTC–2a	20,000	2	0.71	5,812 = 4 × 1,453	320	2	15	3.384	0.324	0.311
DHTC–2a	40,000	2	0.71	9,325 = 5 × 1,865	427	3	14	3.491	0.322	0.296
DHTC–2a	20,000	1	0.71	9,556 = 4 × 2,389	390	1	13	3.662	0.309	0.318
DHTC–2a	20,000	3	0.71	3,564 = 2 × 1,782	232	4	14	3.089	0.317	0.399
DHTC–2a	20,000	2	0.50	6,069 = 7 × 867	297	2	14	3.070	0.369	0.268

Table 3 continued

Breeding scheme/selection strategy	Assumptions			Optimum allocation				OC	SD _{OC}	$\bar{\Theta}$
	Budget	VC	ρ_P	N_1^* ^a	N_2^*	L_1^*	L_2^*			
S ₁ TC-DHTC-2c	10,000	2	0.71	267 = 3 × 89	686	9	10	3.434	0.505	0.592
S ₁ TC-DHTC-2c	20,000	2	0.71	725 = 5 × 145	781	11	14	3.639	0.494	0.584
S ₁ TC-DHTC-2c	40,000	2	0.71	848 = 4 × 212	2,391	10	12	3.751	0.484	0.561
S ₁ TC-DHTC-2c	20,000	1	0.71	888 = 4 × 222	980	10	11	3.991	0.498	0.601
S ₁ TC-DHTC-2c	20,000	3	0.71	522 = 3 × 174	856	13	14	3.224	0.476	0.605
S ₁ TC-DHTC-2c	20,000	2	0.50	794 = 12 × 66	720	11	14	3.376	0.524	0.551
Optimization criterion (OC) $\hat{P}(0.1\%)^*$										
DHTC-2a	10,000	2	0.71	3,153 = 3 × 1,051	149	2	12	0.595	0.273	0.338
DHTC-2a	20,000	2	0.71	5,644 = 4 × 1,411	348	2	15	0.671	0.252	0.316
DHTC-2a	40,000	2	0.71	9,375 = 5 × 1,875	447	3	13	0.730	0.225	0.296
DHTC-2a	20,000	1	0.71	9,728 = 4 × 2,432	371	1	13	0.833	0.197	0.315
DHTC-2a	20,000	3	0.71	3,222 = 2 × 1,611	342	4	14	0.500	0.284	0.397
DHTC-2a	20,000	2	0.50	6,216 = 7 × 888	293	2	13	0.479	0.271	0.271
S ₁ TC-DHTC-2c	10,000	2	0.71	267 = 3 × 89	686	9	10	0.683	0.321	0.566
S ₁ TC-DHTC-2c	20,000	2	0.71	775 = 5 × 155	735	11	14	0.778	0.265	0.566
S ₁ TC-DHTC-2c	40,000	2	0.71	852 = 4 × 213	2,388	10	12	0.829	0.242	0.559
S ₁ TC-DHTC-2c	20,000	1	0.71	1,115 = 5 × 223	868	9	10	0.924	0.152	0.599
S ₁ TC-DHTC-2c	20,000	3	0.71	477 = 3 × 159	896	13	14	0.570	0.321	0.610
S ₁ TC-DHTC-2c	20,000	2	0.50	737 = 11 × 67	820	11	13	0.648	0.316	0.552

N_j^* = optimum number of test candidates in stage j , L_j^* = optimum number of test locations in stage j , SD = the standard deviation, and $\bar{\Theta}$ = the average coefficient of coancestry among the selected DH lines

^a DHTC-2a: number of crosses × DH lines within crosses; S₁TC-DHTC-2c: number of crosses × S₁ families within crosses

Fig. 1 Selection gain ($\Delta\hat{G}$) and the probability of selecting superior genotypes ($\hat{P}(0.1\%)$) as a function of the number of crosses in the first stage (N_{1c}) for selection strategies 1 (open square), 2a (open circle), 2b (open triangle), and 2c (open diamond) in breeding scheme DHTC (solid symbols) and S₁TC-DHTC (hollow symbols)

