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Assessment of inbreeding depression tolerance of local maize germplasm

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Abstract
We carried out an experiment to study the inbreeding depression tolerance of maize germplasm. The field experiment was conducted at Assam Agricultural University during *rabi* season of 2019-2020. Six germplasm and their corresponding S_1 lines and one check hybrid were evaluated at randomized block design with two replications. Analysis of variance revealed that all the entries differed significantly for all the traits except moisture content. The entries namely, ARW1, ARY5, ARR1 and ASKAW1 which showed the minimum level of inbreeding depression from studies on inbreeding depression, can be used as components for developing high yielding and inbreeding tolerant composite variety in future.

Keywords: Inbreeding, maize, germplasm, northeast, S_1 lines

Introduction
Inbreeding depression refers to decrease in vigour and fertility due to either inbreeding in a highly heterozygous cross pollinated populations or mating of related individuals or both. The continuous selfing of a highly heterozygous cross pollinated population leads to homozygosity at different loci with associated loss of vigour and fertility. Inbreeding depression is usually predominant in cross pollinated crops. Selfing can potentially be used for the development of inbred lines. The superior inbred lines with desirable combining ability are used in maize for the development of single cross, double cross, three-way crosses and synthetic varieties. For derivation of superior inbreds, the source population should have high *per se* performance in desirable direction and low inbreeding depression (ID) with respect to grain yield and other important traits. It is, therefore, important to collect and evaluate various maize germplasm and test them for tolerance to ID for different traits.
In a hybrid maize breeding programme, inbred lines are developed by exercising inbreeding in a potential heterozygous population such as broad base gene pool, germplasm complex, open pollinated variety (OPV), synthetic, composite and F_2 populations derived from a heterotic single cross hybrid or a double cross hybrid. Such inbred lines are evaluated for mean performance as well as combining ability for grain yield and other component traits. Recycling procedures in maize breeding have been found encouraging in improvement of inbred lines and such lines are important in popularizing and commercializing of the single cross hybrid technology worldwide. For derivation of superior inbreds the source population should have high per se performance in desirable direction and low inbreeding depression (ID) with respect to grain yield and other important traits. It is, therefore, important to collect and evaluate various maize germplasm and to test them for tolerance to ID for different traits. Identification of maize germplasm such as landraces, hybrids and composites for tolerance to inbreeding will open up possibilities for development of a germplasm pool with capacity of low ID. Genes from some of these germplasm may also be introgressed into an already existing and established gene pool. In the present investigation, some of the local germplasm of maize were selfed to produce corresponding S_1 progenies and to test the extent of ID in the latter with respect to various traits.

Materials and Method
The present study was carried out at Assam Agricultural University, Jorhat. Six germplasm were selected based on different kernel colours and grain yield. Sufficient number of plants was randomly selected from each germplasm and they were hand pollinated in the breeding nursery during *rabi* 2018-19.

The experimental material for the present investigation for estimating tolerance to inbreeding during *rabi* 2019-20 comprised of the six germplasm (S_0 populations), their corresponding six S_1 progenies and one check. The experiment was laid out at randomized block design with two replications. Each row length consisted of 4 meter with row to row and plant to plant spacing of 60 and 20 cm respectively. Observations were recorded for twenty three quantitative traits. The mean data for each of the morphological traits were subjected to analysis of variance. Percentage inbreeding depression was calculated by using the following formula (Kempthorne, 1957) [4].

$$\text{Percent inbreeding depression (ID)} = \frac{\overline{F_1} - \overline{F_2}}{\overline{F_1}} \times 100$$

Table 1: List of germplasm included in the present study

Sl. No.	Germplasm	Colour
1	ARW1	White
2	ASKAW1	White
3	ARY2	Yellow
4	ARR1	Red
5	MNB2	Black
6	ARY5	Yellow
7	VMH-53	VPKAS (ICAR), Almora, UK

Table 2: ANOVA for the quantitative traits during *rabi* 2019-2020

Source	DF	D50%PS	D50%S	D75%DH	DM	PH	EH	TL	B/T	EL	KR/E	K/R	ED	ELL	ELW	L/P	LL	LW	LA	100KW	KL	KW	MC	GY/P
Replication	1	15.39	28.04	7.54	12.46	1274	361.85	34.62	15.08	8.77	0.1	3.25	0.26	26	2.7	6.9	18.61	0.01	600	8.08	0.001	0.001	1.29	7.53
Treatment	12	235.12**	243.47**	234.51**	218.72**	1312.78**	1125.53**	23.12**	8.39**	5.78**	4.96**	45.99**	0.20**	154.29**	1.27**	5.45**	165.64**	1.22**	7886.37**	20.91**	0.06**	0.11**	5.14	419.35**
Error	12	3.05	2.95	2.54	4.05	76.67	16.64	5.95	2.62	1.07	0.69	2.88	0.02	4.08	0.17	1.66	2.19	0.19	534	0.77	0.001	0.001	4.15	7.03
CV (%)		2.03	1.88	1.08	1.26	4.78	4.82	9.82	14.42	8.10	6.28	7.14	3.92	2.91	5.28	11.43	2.1	5.73	6.03	3.52	8.24	9.41	8.10	4.53

*, **Significant at 5% and 1% level, respectively

D50%PS= Days to 50% pollen shed
D50%S = Days to 50% silking
D75%DH= Days to 75% dryhusk
DM = Days to maturity
PH= Plant height
EH= Ear height
TL= Tassel length
B/T= Branches per tassel
L/P= Leaves per plant
EL = Ear length
LL= Leaf length
LW =Leaf width
LA = Leaf Area
ED = Ear diameter
KR/E = Kernel rows per ear
K/R = Kernels per rows
ELL= Ear leaf length
ELW = Ear leaf width plant
100KW= 100 Kernel weight
KL = Kernel length
KW = Kernel width
MC = Moisture Content
GY/P=Grain yield per

Table 3: Inbreeding depression in S_1 progenies for various quantitative traits

	D50%PS	D50%S	D 75%DH	DM	PH	EH	TL	B/T	EL	KR/E	K/R
ARW1	0.0	2.0	-1.0	-1.0	18.0	13.0**	3.0	1.2	-2.8*	0.0	-5.0*
MNB2	-2.0	-4.0*	-4.0*	-2.0	3.0	-15.0**	4.0	1.4	-4.2**	0.0	-9.0**
ASKAW1	0.0	-1.0	4.0*	2.0	15.0	-50.0**	1.0	3.0	-1.3	0.0	0.0
ARY5	0.0	0.0	0.0	0.0	37.0	7.0	7.0**	1.2	1.2	-1.0	2.0
ARR1	-2.0	-3.0	-1.0	-2.0	14.0**	30.0**	6.0**	0.2	1.1	1.0	3.0
ARY2	-6.0**	-5.0*	-5.0**	-5.0*	12.0	31.0**	4.0	0.4	2.5*	-1.0	9.0**

	ED	ELL	ELW	L/P	LL	LW	LA	100KW	KL	KW	GY/P
ARW1	0.2	-3.0	-0.6	2.0	10.0**	0.3	75.0**	1.0	0.0	0.0	1.0
MNB2	-0.5**	-10.0**	1.5**	2.0	3.0	0.3	34.0	2.0*	0.1	0.1*	30.0
ASKAW1	0.2	6.0*	0.9	-1.0	-16.0**	0.5	-74.0**	4.0**	0.1	0.0	24.0**
ARY5	0.2	4.0	-1.2*	1.0	-1.0	1.0*	36.0	2.0*	0.1	0.1	12.0**
ARR1	0.2	8.0**	-0.1	2.0	0.0	-0.2	-9.0	2.0*	0.1	0.1	17.0**
ARY2	-0.4*	14.0**	2.5**	-2.0	2.0	1.5**	98.0**	2.0*	0.1	0.1	9.0**

*, **Significant at 5% and 1% level, respectively

D50%PS= Days to 50% pollen shed
D50%S = Days to 50% silking
D75%DH= Days to 75% dryhusk
DM = Days to maturity
PH= Plant height
EH= Ear height weight
TL= Tassel length
B/T= Branches per tassel
L/P= Leaves per plant
EL = Ear length plant
LL= Leaf length
LW =Leaf width
LA = Leaf Area
ED = Ear diameter
KR/E = Kernel rows per ear
K/R = Kernels per rows
ELL= Ear leaf length
ELW = Ear leaf width per
100KW= 100 Kernel
KL = Kernel length
KW = Kernel width
GY/P=Grain yield

Table 4: Mean performance of maize germplasm and their corresponding S_1 progenies for the quantitative traits for *rabi* 2019-20

S_0 (Germplasm)	D50%PS	D50%S	D 75% DH	DM	PH	EH	TL	B/T	EL	KR/E	K/R	ED	ELL	ELW	L/P	LL	LW	LA	100KW	KL	KW	GY/P
ARW1	100	106	161	173	210	116	25	8.3	10.3	13	20	3.9	75	7.2	14	84	7.1	452	23	0.4	0.35	54
MNB2	96	101	157	169	188	94	25	12.6	10	14	18	3.7	71	8.6	14	77	8.8	507	24	0.74	0.72	80
ASKAW1	74	79	142	153	189	59	22	12.4	10.5	15	23	3.8	64	8	10	55	8	328	24	0.37	0.28	72
ARY5	72	77	132	145	193	73	33	14.1	13.6	10	20	4.3	63	7.1	10	58	7.9	341	32	0.6	0.9	50
ARR1	92	96	154	164	211	103	29	10.5	13.6	14	27	3.7	78	8.6	12	68	6.9	354	26	0.72	0.64	75
ARY2	81	87	141	152	193	93	27	13	16.1	14	36	3.7	81	9.4	10	73	7.6	419	26	0.36	0.38	54

S_1 (Progenies)																						
ARW1	100	104	162	174	192	103	22	7.1	13.1	13	25	3.7	78	7.8	12	74	6.8	377	22	0.43	0.33	53
MNB2	98	105	161	171	185	109	21	11.2	14.2	14	27	4.2	81	7.1	12	74	8.5	473	22	0.65	0.59	50
ASKAW1	74	80	138	151	174	109	21	9.4	11.8	15	23	3.6	58	7.1	11	71	7.5	402	20	0.28	0.26	48
ARY5	72	77	132	145	156	66	26	12.9	12.4	11	18	4.1	59	8.3	9	59	6.9	305	30	0.53	0.81	38
ARR1	94	99	155	166	197	73	23	10.3	12.5	13	24	3.5	70	8.7	10	68	7.1	363	24	0.65	0.57	58
ARY2	87	92	146	157	181	62	23	12.6	13.6	15	27	4.1	67	6.9	12	71	6.1	321	24	0.3	0.33	45
VMH53 (Check)	84	87	142	154	113	40	26	11.4	13	13	22	4.5	57	7.4	10	55	8.3	342	27	0.75	0.86	85
C.D.(5%)	4	4	4	4	19	9	5	4	2.3	1.8	3.7	0.3	4	0.9	2.8	3	0.9	51	1.9	0.09	0.11	6

D 50% PS= Days to 50% pollen shed
D 50% S = Days to 50% silking
D 75% DH= Days to 75% dryhusk
DM = Days to maturity
PH= Plant height
EH= Ear height
TL= Tassel length
B/T= Branches per tassel
L/P= Leaves per plant
EL = Ear length
LL= Leaf length
LW =Leaf width
LA = Leaf Area
ED = Ear diameter 100
KR/E = Kernel rows per ear
K/R = Kernels per rows
ELL= Ear leaf length
ELW = Ear leaf width
KW= 100 Kernel weight
KL = Kernel length
KW = Kernel width
GY/P=Grain yield per plant

Result and Discussion

The analysis of variance (ANOVA) was performed for twenty three quantitative traits in the experiment conducted during *rabi*, 2019-20. The ANOVA revealed significant to highly significant mean square for the entries for all the traits except moisture content. Results were presented in table 2.

The mean data for different S_0 and S_1 entries were used to estimate ID for various characters (Table 3). The data observed revealed non-significant ID in the following S_1 progenies for the traits shown alongside (Table 4): ARW1 for D50% PS, D50%S, D75%DH, DM, PH, TL, B/T, KR/E, ED, ELL, ELW, L/P, LW, 100KW, KL, KW and GY/P; MNB2 for D50%PS,DM, PH,TL, B/T,KR/E, L/P, LL, LW, LA,KL and GY/P ; ASKAW1 for D50%PS, D50%S, DM, PH, TL, B/T, EL, KR/E, K/R, ED, ELW, L/P, LW, KL and KW ; ARY5 for D50%PS, D50%S, D75%DH, PH, EH, B/T,EL, KR/E, K/R, ED, ELL, L/P,LL, LA, KL and KW ARR1 for D50%PS, D50%S, D75%DH, DM, B/T,EL, KR/E, K/R, ED, ELW, L/P,LL, LW, LA, KL and KW, and ARY2 for PH, TL, B/T, KR/E, L/P, LL,KL and KW. High inbreeding depression for yield in maize crop was reported by Singh and Khalidi, 2001 [7], Simon *et al*. 2004 [6], Aramendiz *et al*. 2006 [3] and Andreoli *et al*. 2006 [2]. Ahmad *et al* (2011) [1] reported that the average value of inbreeding depression for the traits namely, number of ears per row (2.5), kernel rows per ear (2.11), ear length (1.80), ear-diameter (0.2) and 100 grain weight (3.89). Raj, G.S *et al.* (2020) reported that significant values of inbreeding depression for cob height (-9.02% to 19.40%), cob length (0.22% to 10.32%) and grain yield (1.63% to 23.63%).

All the six germplasm showed significant to highly significant inbreeding depression for few or many of the eighteen quantitative traits mentioned below.

Days to 50% pollen shed

Among the entries, ARY2 showed significant ID with the value -6 days (d). This germplasm took fewer numbers of days to 50% pollen shed reflecting earliness upon inbreeding.

Days to 50% silk

Among the entries, MNB2 (-4 d) and ARY2 (-5 d) showed significant ID. These two S_1 progenies showed more number of days to 50% silk as compared to the corresponding parental population.

Days to 75% dry husk

Among the entries, MNB2 (-4 d), ASKAW1 (4 d) and ARY2 (-5 d) showed significant to highly significant ID**.** The S_1 progeny of MNB2 and ARY2 showed more number of days to 75% dry husk as compared to the corresponding parental population. The S_1 progeny of ASKAW1 showed earliness with respect to this trait.

Days to maturity

Among the entries, ARY2 (-5 d) showed significant ID**.** The S_1 progeny of ARY2 showed more number of days to maturity as compared to the corresponding parental population.

Plant height

Among the entries, ARR1 (14 cm) showed significant ID**.** The S_1 progeny of ARR1 showed minimum plant height as compared to the corresponding parental population.

Ear height

All the entries except ARY5 (7 cm) showed highly significant ID ranging from MNB2 (-15) to ARY2 (31). The S_1 progeny of all the entries except ARY5 showed lower ear height than the original population.

Tassel length

Among the entries, both ARY5 (7 cm) and ARR1 (6 cm) showed highly significant ID. The S_1 progeny of ARY5 and ARR1 showed lower length of tassel than the original population.

Ear length

Among the entries, ARW1 (-2.8 cm), MNB2 (-4.2 cm) and ARY2 (2.5 cm) showed significant to highly significant ID. The S_1 progenies of ARW1 and MNB2 showed longer ear length than original population. However, S_1 progeny of ARY2 showed shorter ear length than original population.

Kernels per row

Among the entries, ARW1 (-5), MNB2 (-9) and ARY2 (9) showed significant to highly significant ID. The S_1 progenies of ARW1 and MNB2 showed more kernels per row than original population. However, S_1 progeny of ARY2 showed less kernels per row than original population.

Ear diameter

Among the entries, MNB2 (-5 cm) and ARY2 (-0.4 cm) showed highly significant ID. The S_1 progenies of MNB2 and ARY2 showed more ear diameter than original population.

Ear leaf length

Among the entries, MNB2 (-10 cm), ASKAW1 (6 cm), ARY2 (14 cm), and ARR1 (8 cm) showed highly significant ID. The S_1 progeny of ASKAW1, ARY2 and ARR1 showed lower ear leaf length than their corresponding parental population. However, S_1 progeny MNB2 showed more ear leaf length than parental population.

Ear leaf width

Among the entries, MNB2 (1.5 cm), ARY5 (-1.2 cm), and ARY2 (2.5 cm) showed significant to highly significant ID. The S_1 progeny of MNB2 and ARY2 showed lower ear leaf width than their corresponding parental population. However, S_1 progeny ARY5 showed more ear leaf width than parental population.

Leaf Length

Among the entries, ARW1 (10 cm) and ASKAW1 (-16 cm) showed highly significant ID. The S_1 progeny of ARW1 showed lower leaf length than their corresponding parental population. However, S_1 progeny ASKAW1 showed more leaf length than parental population.

Leaf width

Among the entries, ARY5 (1 cm) and ARY2 (1.5 cm) showed highly significant ID. The S_1 progeny of ARY5 and ARY2 showed lower leaf width than their corresponding parental population.

Leaf area

Among the entries, ARW1 (75 cm^2) and ASKAW1 (-74 cm^2) showed highly significant ID. The S_1 progeny of ARW1 showed lower leaf area than their corresponding parental population. However, S_1 progeny ASKAW1 showed more leaf area than parental population.

100 kernel weight

Among the entries, MNB2 (2 g), ASKAW1 (4 g), ARY5 (2 g), ARR1 (2 g) and ARY2 (2 g) showed significant to highly significant ID. The S_1 progeny of MNB2, ASKAW1, ARY5, ARY2 and ARR1 showed lower 100 kernel weight than their corresponding parental population.

Theoretically, maize is a random mating population with equilibrium of genes and genotype frequencies and no inbreeding depression. But in practice, the population size of landrace maintained by the farmers is small and ID occurs. In hilly areas of the north east India, the farmers are poor and they don't have sufficient land. Maize is cultivated primarily in *jhum* with other crops. Small farmers maintain smaller plot of land with fewer plants of maize landrace as the same plot of land also accommodate other crops of *jhum* system. Recurrence of such practice year after year might have caused significant ID in the population at a relatively faster rate resulting in elimination of very lethal, sub lethal and sub vital genes over the years. This has caused genetic drift in such population resulting in fixation of several genes. Selfing of such landraces might cause non-significant ID for certain genes or traits as the landraces have already got partially immunized against further inbreeding. In the present investigation, small population size, long term ID and genetic drift in the test population may be the possible causes for reduced or negligible ID in the population.

Conclusion

The present study generated useful information on inbreeding tolerance of local maize germplasm. Presence of sufficient variability was exhibited among the local germplasm through highly significant differences for all the traits except moisture content. The entries namely, ARW1, ARY5, ARR1 and ASKAW1 showed non-significant estimates of ID for as many as fifteen traits including days to 50% pollen shed, days to 50% silk, days to maturity, branches per tassel, kernel rows per ear, ear diameter, leaves per plant, kernel length and kernel width. These germplasm can be used as components for developing high yielding and inbreeding tolerant composite variety in future.

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