



Analysis of responses of novel double mutant (*sh2sh2/su1su1*) sweet corn hybrids for kernel sweetness under different sowing- and harvest-time

BRIJESH K MEHTA¹, FIROZ HOSSAIN², VIGNESH MUTHUSAMY³, RAJKUMAR U ZUNJARE⁴,
JAVAJI C SEKHAR⁵ and HARI S GUPTA⁶

ICAR-Indian Agricultural Research Institute, New Delhi 110 012

Received: 06 April 2017; Accepted: 12 July 2017

ABSTRACT

Sweet corn used as vegetable and component of various snack items, has emerged as one of the popular choices across the world. Identification of suitable sowing- and harvest-time for achieving high-kernel sweetness and yield is of paramount importance for successful commercialization of sweet corn hybrids. In the present study, 11 novel double mutant sweet corn (*sh2sh2/su1su1*) hybrids along with traditional *sh2sh2*-based checks were evaluated at three sowing- and harvest-dates. Kernel brix across double mutant sweet corn hybrids ranged from 17.6-26.6% (Mean: 21.0%) and was comparatively higher than *sh2sh2*-based checks (19.3%). Sowing- and harvest- time had significant influence on brix accounting 19.4% and 8.5% of the total variation, respectively. Genotype × sowing time, genotype × harvest time and genotype × sowing time × harvest time interactions contributed 11.4%, 10.3% and 15.2% of the total variation for brix, respectively. Average brix across harvest dates attained highest value in third sowing and 24-days after pollination recorded the highest brix across sowing dates. Few hybrids also displayed stable brix across sowing- and harvest- time. Significant influence of sowing time on both cob- and fodder- yield was also observed, and third sowing was identified as the most favourable environment for both the traits. Kernel sweetness did not show any correlation with cob- and fodder- yield. The information generated here hold significant promise in the improvement of sweet corn. This is the first ever report of responses of *sh2sh2/su1su1*-based hybrids to different sowing- and harvest- time for kernel sweetness and yield.

Key words: Brix, Double mutant, Harvest time, *Shrunken2*, *Sugary1*, Sowing time

Sweet corn consumed as immature kernel has become a popular choice, and holds significant share in both domestic- and international- market worldwide (Lertrat and Pulam 2007, Hossain *et al.* 2013). The demand of sweet corn has increased tremendously in the last few years primarily due to urbanization, increased consumption and availability of organized food processing industries. Besides, after the harvest of sweet corn cobs, green plants serve as a source of large quantities of fodder/forage to the cattle (Bian *et al.* 2015).

Maize kernel is composed of 70-75% starch and its biosynthesis is regulated by a series of genes, viz. *Brittle2* (*Bt2*), *Shrunken2* (*Sh2*), *Waxy1* (*Wx1*), *Dull1* (*Du1*), *Sugary1* (*Su1*) and *Amylose extender1* (*Ae1*) (Coe *et al.* 1988, Whitt *et al.* 2002). Mutation in any one of the genes has drastic

effect on carbohydrate metabolism, in which starch content in the endosperm reduces with a concomitant increase in kernel sweetness with the availability of more sugar residues. Among the various available mutants, *su1* and *sh2* have been extensively used for development of sweet corn cultivars (Hossain *et al.* 2013). Mutant version of *Sh2* aids in the formation of glucose, while enzyme coded by *su1* produces different proportion of amylose and amylopectin (Fisher and Boyer 1983). Sugary varieties (*su1su1*) at the milky ripening stage contain nearly three times more sweetness compared to normal maize. It possesses kernels that are creamy in texture and attractive in appearance and flavour (Feng *et al.* 2008). However, after harvest, the sugar level decline much faster in the *su1* types (Garwood *et al.* 1976). On the other hand, the *sh2*-based sweet corn types popularly called ‘super sweet’ or ‘extra sweet corn’ possess sweetness that is six-fold higher than the ordinary maize (Feng *et al.* 2008, Khanduri *et al.* 2011). The depletion of sugar level is much slower in *sh2*-type even without refrigeration, thus varieties have extended shelf life, and are better suited for prolonged storage. Sweet corn cultivar with *sh2sh2/su1su1* as one of the parents while the other parent being *sh2sh2* or *su1su1* has been explored primarily for imparting higher sweetness in the kernel (Lertrat and Pulum 2007).

¹PhD Scholar (brijeshmehtaiari@gmail.com), ²Senior Scientist (fh_gpb@yahoo.com), ³Scientist (pmvignesh@yahoo.co.in), ⁴Scientist (raj_gpb@yahoo.com), ⁶Former Director and Vice-chancellor (hsgupta.53@gmail.com), ICAR-Indian Agricultural Research Institute New Delhi 110012; ⁵Principal Scientist (jcswncc@rediffmail.com), Winter Nursery Centre, ICAR-Indian Institute of Maize Research, Hyderabad.

In view of the growing importance of sweet corn and to accelerate the pace of progress of sweet corn cultivar development, it is therefore, important to develop promising sweet corn hybrids with high kernel sweetness and *per se* productivity (Ko *et al.* 2016, Mehta *et al.* 2017). Only few centres in selected countries possess organized sweet corn breeding programmes, and hybrids are predominantly in the genetic background of either *sh2sh2* or *su1su1*. We developed a set of novel sweet corn hybrids with both the parents being *sh2sh2/su1su1* and evaluation of these novel sweet corn hybrid combinations for kernel sweetness and yield therefore assumes great significance.

Starch biosynthesis in kernels is dependent upon several factors that also include environmental factors besides governed by a multiplicity of conserved enzymatic activities encoded by a series of genes (Hannah and James 2008). Identification of suitable environmental conditions thus is of paramount importance for successful commercialization of sweet corn hybrids developed by manipulation of mutant allele of the key genes. So far very few studies have been undertaken on effects of either sowing- or harvest- time on kernel sweetness, cob- and fodder- yield in maize. To best of our knowledge, no study on simultaneous effects of both sowing- and harvest- time and their interactions on kernel sweetness among a set of sweet corn hybrids have been carried out. Further, the limited studies that were conducted dealt only with *sh2sh2*- and/or *su1su1*- hybrids, and no report on the effects of these environmental factors on novel combination of hybrids (*sh2sh2/su1su1*) is available. With this consideration, a novel set of double mutant sweet corn hybrids were evaluated to understand the effects of sowing- and harvest- time on kernel sweetness, study the effects of sowing time on fodder- and cob- yield, and identify superior hybrids with enhanced kernel sweetness and high productivity.

MATERIALS AND METHODS

A set of double mutant inbreds (*sh2sh2/su1su1*) developed earlier by crossing *sh2sh2*- and *su1su1*-inbreds under the 'Specialty Corn Breeding Programme' at ICAR-Indian Agricultural Research Institute, New Delhi, were crossed to generate 11 F₁s during *rabi* (post-rainy season) 2013-14 at Winter Nursery Centre, ICAR-Indian Institute of Maize Research (IIMR), Hyderabad, India. These single cross experimental hybrids (MGUSCH-22 to -32) along with four checks [three *sh2sh2*-based hybrids (ASKH-1, ASKH-2 and Sugar-75) and one *sh2sh2*-composite (Madhuri)] were evaluated under three sowing dates (14th July, 04th August and 25th August) at ICAR-IARI Experimental Farm, New Delhi (28°08' N, 77°12' E, 229 MSL) during *kharif* (rainy season) 2014. The first, second and third date of sowing, hence after are referred to as S-I, S-II and S-III, respectively. ASKH-1 and ASKH-2 are the promising experimental hybrids earlier developed at ICAR-IARI, New Delhi. Madhuri is a public sector bred composite, while Sugar-75 is a hybrid developed by Syngenta India Limited.

Sweet corn genotypes were evaluated in a randomized

complete block design (RCBD) with two replications per entry, having two rows per replication. Plant-to-plant spacing of 20 cm and row-to-row spacing of 75 cm were maintained. Standard agronomic practices were followed for raising the crop. In each plot of 3 m length, a uniform plant stand of 30 plants were maintained by thinning. Nine to ten plants in each of the genotypes per replication were self-pollinated to avoid any xenia effect caused due to fertilization by foreign pollen. Three self-pollinated ears from each genotype were harvested at 20-, 24-, and 28-days after pollination (DAP) for estimation of kernel sweetness. Digital refractometer/brix meter (Atago, Japan) was used to measure brix which corresponds directly to percent sucrose (Reid *et al.* 2016).

The green cobs from open pollinated plants were harvested at 28-DAP for measuring the cob yield. Weight of three randomly selected green cobs was taken, and after removal of the husks, weight of the cob (without husk) was noted from each entry. Husk percentage was used to calculate cob yield (dehusked) from green cob yield. Cob yield per plot (from open pollinated cobs) was calculated considering plant stand of 30/plot. Cob yield was further transformed to tonnes/hectare (t/ha) using the following formula: cob yield (t/ha) = [cob yield (kg/plot) × 10000 m²]/[4.5 m² × 1000]. Weight of the plants/plot was measured as fodder yield at 28-DAP. Fodder yield (kg/plot) was converted to t/ha similar to the calculation of cob yield. Analysis of variance (ANOVA) and critical difference (CD) were computed using Windostat 8.0. Pearson's simple correlation coefficients among cob-, fodder- yield and brix at 20-, 24- and 28- DAP, were calculated based on the means achieved across sowing dates using MS-Office-Excel 2007.

RESULTS AND DISCUSSION

ANOVA revealed significant variation among genotypes for kernel sweetness measured by brix (Table 1). Significant variation for brix is due to the diverse nature of *sh2sh2/su1su1*-based inbreds used in the study (Mehta *et al.* 2017). QTL/modifier genes in the starch biosynthesis pathway may influence kernel sweetness (Qi *et al.* 2009, Whitt *et al.* 2002) in the *sh2sh2/su1su1* genetic background. Wide genetic

Table 1 Combined ANOVA for kernel brix among sweet corn genotypes

Sources of variation	df	MS
Sowing time	2	106.21**
Harvest time	2	46.44**
Genotype	14	22.32**
Replication	1	0.08
Genotype × Sowing time	28	4.45**
Genotype × Harvest time	28	4.03**
Genotype × Sowing time × Harvest time	60	2.78**
Error	134	0.55
Total	269	4.07

** Significance at 1%; df: degrees of freedom; MS: mean squares

variation for kernel sugar among sweet corn hybrids has been reported earlier by Khanduri *et al.* (2010, 2011) and Solomon *et al.* (2012a, b). Further, sowing time accounted 19.4% of the total variation for brix, while the same for harvest time was 8.5%. Brix value also exhibited genotype \times sowing time, genotype \times harvest time and genotype \times sowing time \times harvest time interactions, accounting 11.4%, 10.3% and 15.2% of the total variation, respectively.

Kernel sweetness was measured using refractometer/brix meter, and it has been effectively utilized as a rapid method to determine sugar concentration in sweet corn kernel by various researchers (Randle *et al.* 1984, Zhu *et al.* 1992, Kardoso *et al.* 2002, Khanduri *et al.* 2010, 2011). Genotypes contributed 28.5% of the total variance of the kernel sweetness, while remaining 71.5% of the variation is due to other contributing factors. Sowing time accounted one fifth of the total variation of kernel sweetness.

Brix among double mutant hybrids at 20-DAP varied from 17.7-21.0% in S-I, while it was 19.1-24.1% and 20.2-24.8% in S-II and S-III, respectively (Table 3). The average brix of these experimental hybrids in S-I was 19.4%, and the same was 21.4% in S-II and 22.1% in S-III. Among the experimental hybrids, MGUSCH-23 recorded the highest brix (21.0%) in S-I. MGUSCH-27 (24.1%), MGUSCH-30 (23.4%) and MGUSCH-32 (23.2%) were the promising hybrid combinations for kernel sweetness in S-II. For S-III, MGUSCH-24 (24.8%) was the best experimental hybrid, followed by MGUSCH-23 (23.9%). Across environments, MGUSCH-23 (22.3%) was identified as the best combination. The average brix at 20-DAP among *sh2sh2*-based checks was lower (18.8%, 19.2% and 19.9% in S-I, S-II and S-III, respectively) than the mean of the experimental hybrids in all three sowing dates (Table 3). Across sowing dates, ASKH-1 emerged as the best hybrid with 20.1% brix, followed by Madhuri (19.8%), ASKH-2 (19.4%) and Sugar-75 (17.8%).

Average brix at 24-DAP in S-I was 20.9%, while it was 22.0% and 22.9% in S-II and S-III, respectively (Table 3). The range for brix was 17.9-23.6% in S-I, while S-II recorded a variation of 19.7-24.1%. In case of S-III, it was found to be 19.5-26.6% brix. Experimental hybrid, MGUSCH-27 recorded the highest brix (23.6%) in S-I. Other promising hybrid was MGUSCH-24 with a brix value of 23.1%. In S-II, promising combinations include MGUSCH-30

(24.1%), MGUSCH-22 (24.0%), MGUSCH-25 (23.8%) and MGUSCH-27 (23.3%). In case of S-III, MGUSCH-22 recorded the highest brix (26.6%), followed by MGUSCH-27 (25.7%) and MGUSCH-25 (24.5%). Across environments, MGUSCH-27 (24.2%) and MGUSCH-22 (24.0%) were identified as the best combination. Mean brix at 24-DAP among the checks were lower (18.4%, 18.5% and 21.3% in S-I, S-II and S-III, respectively) than the mean of the double mutant combinations, and all the four checks recorded almost similar brix (19.2-19.7%) (Table 3).

At 28-DAP, the average brix among the new hybrids was 19.3% in S-I, while it was 19.9% and 21.0% in S-II and S-III, respectively (Table 3). The range for the same was 17.6-21.9% in S-I, while S-II and S-III recorded a variation of 18.5-22.1% and 19.0-22.5%, respectively. Among the experimental hybrids, MGUSCH-26 achieved the highest brix (21.9%) in S-I. MGUSCH-22 (22.1%) was the best genotype in S-II, while MGUSCH-22 (22.5%), MGUSCH-32 (22.2%) and MGUSCH-30 (22.0%) were the other promising genotypes in S-III. Across sowing time, MGUSCH-22 was identified as the best genotype with 21.3% brix. The mean brix among checks was lower in S-I (18.2%) and S-II (18.0%) than the average of the experimental hybrids, however it was at par in S-III (21.1%). Madhuri among the checks recorded the highest brix (20.3%), followed by ASKH-2 (19.5%), ASKH-1 (18.5%) and Sugar-75 (17.9%).

The mean brix was highest in S-III, and was significantly superior to brix obtained in S-I and S-II (Fig 1). 87% of the genotypes attained peak at S-III, while 13% possessed highest brix in S-II. No hybrid could achieve highest brix in S-I. This indicates sowing on 4th August (third sowing) was favourable for kernel sweetness over earlier planting dates. Rogers *et al.* (2000) also reported higher tenderness of sweet corn cob in late sown than early sowing of sweet corn. The study also reported the significance of genotype \times sowing time interaction accounting one tenth of the total variation. Farsiani *et al.* (2011) evaluated SC403, a single cross sweet corn hybrid at four different planting dates, and reported the significance of genotype \times sowing time interactions for kernel sucrose concentration.

The highest brix across harvest time was achieved in S-III (21.7%), and was significantly superior than S-II (20.5%) and S-I (19.5%). Across sowing time, brix attained

Table 2 Combined ANOVA for cob- and fodder- yield among sweet corn genotypes

Source of variation	df	MS	
		Cob yield	Fodder yield
Sowing time	2	15.22**	98.36**
Genotype	14	14.06**	45.50**
Genotype \times Sowing time	28	1.23	9.38
Error	45	1.14	6.19
Total	89		

**Significance at 1%; df: degrees of freedom; MS: mean squares

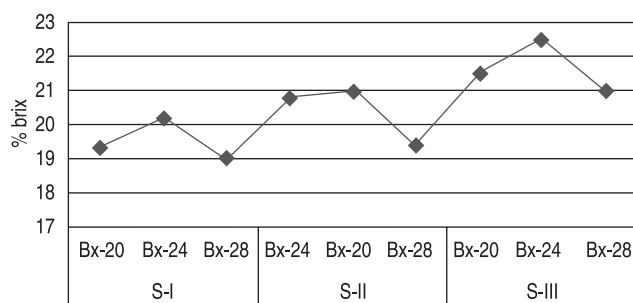


Fig 1 Line diagram depicting the kernel sweetness among the sweet corn hybrids across sowing and harvest-time

Table 3 Mean performance of *sh2sh2/su1su1*-based sweet corn hybrids, their comparison with *sh2sh2*-based genotypes for brix, cob- and fodder- yield

Hybrid	S-I					S-II					S-III				
	Bx-20 (%)	Bx-24 (%)	Bx-28 (%)	Cob yield (t/ha)	Fodder yield (t/ha)	Bx-20 (%)	Bx-24 (%)	Bx-28 (%)	Cob yield (t/ha)	Fodder yield (t/ha)	Bx-20 (%)	Bx-24 (%)	Bx-28 (%)	Cob yield (t/ha)	Fodder yield (t/ha)
<i>sh2sh2/su1su1</i> -based hybrids															
MGUSCH-22	18.6	21.4	19.4	8.3	17.1	20.2	24.0	22.1	7.7	17.0	21.6	26.6	22.5	9.4	23.4
MGUSCH-23	21.0	22.7	20.1	8.0	21.9	22.0	20.1	19.5	9.6	16.5	23.9	23.0	20.2	10.6	24.5
MGUSCH-24	20.7	23.1	20.1	8.3	21.4	21.0	21.4	21.3	9.3	17.1	24.8	22.9	21.7	8.0	20.2
MGUSCH-25	19.7	19.9	18.1	8.6	18.4	20.8	23.8	21.3	9.6	17.8	21.4	24.5	20.8	11.7	18.4
MGUSCH-26	18.3	19.7	21.9	10.5	25.8	20.9	20.6	19.1	10.7	20.8	21.8	20.1	19.0	12.1	24.7
MGUSCH-27	19.0	23.6	18.7	10.5	29.9	24.1	23.3	20.4	10.1	23.4	22.9	25.7	21.2	11.3	30.4
MGUSCH-28	17.7	21.4	17.8	8.9	20.4	21.4	20.3	18.5	7.0	20.8	20.9	19.5	19.1	9.6	23.3
MGUSCH-29	20.6	17.9	18.5	7.6	22.5	19.6	22.0	18.6	8.6	18.3	22.6	23.3	21.2	9.6	25.6
MGUSCH-30	18.6	19.4	17.6	8.7	24.7	23.4	24.1	20.2	9.9	18.6	21.6	22.3	22.0	9.9	22.2
MGUSCH-31	20.0	19.1	20.0	6.8	23.4	19.1	19.7	18.5	8.1	21.9	20.2	21.4	20.8	8.8	18.3
MGUSCH-32	19.6	21.2	19.8	9.7	19.2	23.2	22.3	19.9	9.7	16.3	21.2	22.3	22.2	9.5	17.9
<i>sh2sh2</i> -based checks															
Madhuri	18.8	18.5	21.2	6.0	17.9	19.2	19.3	18.8	5.2	14.2	21.6	21.5	21.1	6.9	17.5
Sugar-75	17.0	17.4	16.2	10.1	22.1	18.4	19.2	17.5	11.4	20.7	17.9	21.1	20.0	11.9	20.0
ASKH-1	19.5	18.1	16.7	13.0	22.9	20.6	17.7	17.5	10.4	18.4	20.2	21.7	21.3	13.3	17.3
ASKH-2	20.0	19.5	18.6	9.6	22.5	18.5	17.9	18.0	9.7	17.2	19.7	20.9	21.9	11.5	17.1
Mean	19.3	20.2	19.0	9.0	22.0	20.8	21.0	19.4	9.1	18.6	21.5	22.5	21.0	10.3	21.4
CD (P=0.05)	1.19	1.42	1.52	1.83	5.44	2.15	1.62	1.04	1.98	4.48	1.16	1.75	1.93	2.92	6.31
CD (P=0.01)	1.65	1.97	2.11	2.54	7.55	2.99	2.24	1.45	2.75	6.22	1.62	2.43	2.68	4.05	8.75

S-I: first date of sowing; S-II: second date of sowing; S-III: third date of sowing; Bx-20: brix at 20 days after pollination; Bx-24: brix at 24 days after pollination; Bx-28: brix at 28 days after pollination

peak at 24-DAP (21.2%) and was significantly higher than brix attained at 20-DAP (20.5%) and 28-DAP (19.8%). Across sowing- and harvest- time, MGUSCH-27 recorded the highest brix (22.1%), followed by MGUSCH-24 (21.9%), MGUSCH-22 (21.8%), MGUSCH-23 (21.4%), MGUSCH-32 (21.3%), MGUSCH-25 (21.1%), MGUSCH-30 (21.0%), MGUSCH-29 (20.5%) and MGUSCH-26 (20.2%). Check genotypes with *sh2sh2* genetic constitution possessed 18.3-20.0% brix across sowing- and harvest- time.

Harvest time displayed significant effects on kernel sweetness as well, though the magnitude was of lower extent compared to sowing time. In general, brix at 24-DAP recorded the highest value compared to 20- and 28-DAP. However, 67% of the genotypes had peak in kernel sweetness at 24-DAP, while 20% of the hybrids recorded highest brix at 20-DAP, and only 3% of the genotype possessed the highest brix at 28-DAP. Khanduri *et al.* (2011) also observed different sweet corn genotypes possessing peaks at different DAP, with majority of them recorded highest brix value at 20-DAP. Szymanek *et al.* (2015) analyzed sugar concentration among *su1su1*- and *sh2sh2*-based sweet corn genotypes at four days interval during 20-32 DAP, and observed gradual decrease in kernel sweetness from first

to third pickings. The study also reported the presence of significant genotype \times harvest time interaction for brix, contributing more than the variance caused due to harvest time alone. The effects of interactions were prominent in many of the hybrid combinations. Khanduri *et al.* (2011) also observed similar trend of interaction of brix values with different harvest dates.

Significant influence of genotype \times sowing time \times harvest time interactions were also observed for kernel sweetness, and was more than the genotype \times sowing time and genotype \times harvest time interactions. This indicates, that genotype also interacted simultaneously with both sowing- and harvest-date. Khanduri *et al.* (2011) also reported the occurrence of similar response while experimenting with a set of sweet corn hybrids. Despite the existence of genotype \times sowing time, genotype \times harvest time, genotype \times sowing time \times harvest time interactions, some hybrids displayed stability across sowing- and/or harvest- time. MGUSCH-31 at 20-DAP, MGUSCH-26 and MGUSCH-32 at 24-DAP, and MGUSCH-23 and MGUSCH-24 at 28-DAP were the most stable hybrids across sowing time. These hybrids thus hold promise for their cultivation across a wide window ranging from 14th July to 25th August.

Across harvest time, MGUSCH-25 and MGUSCH-31 in S-I, MGUSCH-24, MGUSCH-26 and MGUSCH-31 in S-II, and MGUSCH-28, MGUSCH-29, MGUSCH-30, MGUSCH-31 and MGUSCH-32 in S-III possessed brix that were highly stable. Harvest for these hybrids under a specific sowing time can be undertaken at any time during 20-28 DAP. This characteristic feature provides opportunity to the farmers to have much larger window for harvest compared to hybrids that attains peak at specific date. Considering both sowing- and harvest-time, MGUSCH-31 was the most stable genotype, followed by MGUSCH-26 that displayed moderate stability for kernel sweetness. These hybrids therefore hold significant promise for cultivation at diverse sowing- and harvest-time.

Across sowing- and harvest-time, the average brix of *sh2sh2/su1su1* genotypes was 21.0%, while the same was 19.3% among the checks, and nine of the eleven hybrids possessed comparatively more average brix than the highest value of the checks. This suggested that hybrids with double mutant combinations tend to have more sweetness over *sh2sh2*-type sweet corn genotypes (Lertrat and Pulam 2007). The recessive *sh2* blocks starch biosynthesis at the initial stages, while *su1* functions at the later stages of the pathway. Since starch biosynthesis is simultaneously affected at both the stages (Whitt *et al.* 2002), the kernels tend to possess more sweetness. However, background genome/modifier genes also play vital role in kernel sweetness. For example, though all the experimental hybrids possessed *sh2sh2/su1su1*-genetic constitution, brix showed wide variation (19.5-26.6% at 24-DAP in S-III), thereby suggesting the influence of modifier loci. Besides modifier loci, environmental factors also played important role in determining the brix. Double mutant hybrids though potentially possess the capability of having higher sweetness than *sh2sh2*-genotypes, the extent of sweetness is a factor of interactions of *sh2* and *su1* with modifier loci/background genome and environmental factors.

ANOVA also revealed significant variation for cob- and fodder- yield across sowing time (Table 2). The contribution of sowing time for cob yield was 9.7% of the total sum of square, while it was 14.3% for fodder yield. Though genotype \times sowing time interaction was non-significant, but it accounted 11.0% and 19.1% of the total variation for cob- and fodder-yield, respectively. Variation for cob- and fodder-yield among sweet corn hybrids, was also observed by Khanduri *et al.* (2010, 2011), Rosa (2014) and Solomon *et al.* (2012a, b). Across sowing time and genotypes, highest cob yield was achieved in S-III (10.3 tonnes/ha), which was significantly lower than S-II (9.10 tonnes/ha) and S-I (9.00 tonnes/ha). Cob yield across *sh2sh2/su1su1*-based sweet corn genotypes varied from 6.8-10.5 tonnes/ha in S-I. The same was 7.0-10.7 tonnes/ha and 8.0-12.1 tonnes/ha in S-II and S-III, respectively (Table 3). MGUSCH-26 and MGUSCH-27 were identified as the most promising hybrids in S-I with highest yield of 10.5 tonnes/ha. Both the hybrids (MGUSCH-26: 10.7 tonnes/ha, MGUSCH-27: 10.1 tonnes/ha) were also promising in S-II as well. In

S-III, MGUSCH-26 recorded the highest cob yield of 12.1 tonnes/ha, followed by MGUSCH-25 (11.7 tonnes/ha), MGUSCH-27 (11.3 tonnes/ha) and MGUSCH-23 (10.6 tonnes/ha). MGUSCH-26 (11.1 tonnes/ha) and MGUSCH-27 (10.6 tonnes/ha) were identified as the most promising hybrid combinations across environments. Among the checks evaluated across environments, ASKH-1 had the highest cob yield (12.2 tonnes/ha), while the same for Sugar-75, ASKH-2 and Madhuri was 11.1 tonnes/ha, 10.2 tonnes/ha and 6.0 tonnes/ha, respectively.

The study also reported significant impact of sowing time on cob yield, with third date of sowing being the most favourable, followed by second date of sowing. Recently, Rosa (2014) also reported the mean total and marketable yield of sweet corn ear increased proportionally with delay in planting dates. Khan *et al.* (2010) and Farsiani *et al.* (2011) also reported higher ear yield in sweet corn genotypes during later dates of planting as compared earlier dates. However, the contribution of sowing date for cob yield was also much less as compared to brix. Genotype \times sowing time interactions contributed more than the sowing time to cause variation in cob yield, and it was apparent in many hybrids. Farsiani *et al.* (2011) and Khan *et al.* (2010) reported the presence of genotype \times sowing time interactions for grain yield. Despite this interaction, MGUSCH-32 and MGUSCH-27 had stable cob yield across sowing dates.

Fodder yield among the novel hybrids ranged from 17.1-29.9 tonnes/ha in S-I, while the same was 16.3-23.4 tonnes/ha and 17.9-30.4 tonnes/ha in S-II and S-III, respectively. MGUSCH-27 recorded highest fodder yield across all environments (S-I: 29.9 tonnes/ha; S-II: 23.4 tonnes/ha; S-III: 30.4 tonnes/ha). Across sowing time and all genotypes, similar fodder yield was achieved in S-I (22.0 tonnes/ha) and S-III (21.4 tonnes/ha), which were significantly higher than the yield received in S-II (18.6 tonnes/ha). Among checks, Sugar-75 recorded the highest fodder yield of 20.9 tonnes/ha across environments. ASKH-1, ASKH-2 and Madhuri had 19.5 tonnes/ha, 18.9 tonnes/ha and 16.5 tonnes/ha of average fodder yield, respectively.

Sowing time also had significant impact on fodder yield, but was of higher magnitude as compared to cob yield. First and third sowing produced comparable fodder yield, while second sowing recorded the least. Sowing \times genotype interaction for fodder yield was also of significance, and contributed higher than that of cob yield. However, Farsiani *et al.* (2011) did not record any significant influence of sowing time and genotype \times sowing time interaction for fodder yield. In the present study, several hybrids viz. MGUSCH-23, MGUSCH-24, MGUSCH-25, MGUSCH-28 and MGUSCH-32 produced reasonably stable fodder yield in all three sowing dates. Based on kernel sweetness, stability of brix, cob- and fodder- yield, MGUSCH-27 was identified as the best sweet corn hybrid.

Based on the mean data across sowing time, brix at 20-DAP was found to be positively correlated with brix attained at 24-DAP ($r=0.67$) and 28-DAP ($r=0.57$) (Table not shown). Brix at 24-DAP was also found to have significant positive

correlation with brix attained at 28-DAP ($r=0.68$). This is due to the fact that almost same set of genes regulate the starch biosynthesis pathway at different dates of harvest. Cob- and fodder-yield exhibited no significant association with brix values obtained at different DAP. This indicates that it is possible to develop sweet corn hybrids with high cob yield and sweetness (Solomon *et al.* 2012b, Saleh *et al.* 2002; Khanduri *et al.* 2010). Cob yield did not show any association with fodder yield, thereby indicating that high yielding sweet corn hybrids with high fodder yield can be developed. Sweet corn hybrids with higher fodder production provides additional income to the farmers as fodder can be sold in the market, besides required for maintaining their own cattle in the household (Bian *et al.* 2015). The information generated here hold significant promise in the improvement of novel sweet corn hybrids, and this is the first ever report of responses of *sh2sh2/su1su1*-based hybrids to different sowing- and harvest-date.

ACKNOWLEDGEMENT

The financial support from ICAR-Indian Agricultural Research Institute, New Delhi is gratefully acknowledged.

REFERENCES

- Bian Y, Gu X, Sun D, Wang Y, Yin Z, Deng D, Wang Y and Li G. 2015. Mapping dynamic QTL of stalk sugar content at different growth stages in maize. *Euphytica* **205**: 85–94.
- Coe E H, Neuffer M G and Hoisington D A. 1988. *The Genetics of Corn. Corn and Corn Improvement*, pp 81–258. Sprague G F and Dudley J W (Eds). American Soc Agron, Madison, WI.
- FAOSTAT (2014) <http://faostat.fao.org>
- Farsiani A, Ghobadi M E and Honarmand S J. 2011. The effect of water deficit and sowing date on yield components and seed sugar contents of sweet corn (*Zea mays* L.). *African Journal of Agricultural Research* **6**: 5769–74.
- Feng Z L, Liu J, Fu F L and Li W C. 2008. Molecular mechanism of sweet and waxy in maize. *International Journal of Plant and Genetics* **2**: 93–100.
- Fisher M B and Boyer C. 1983. Immunological characterization of maize starch branching enzymes. *Plant Physiology* **72**: 813–6.
- Garwood D L, Mc-Ardle F J, Vander-slice S F and Shannon J C. 1976. Postharvest carbohydrate transformations and processed quality of high sugar maize genotypes. *Journal of American Society of Horticultural Science* **101**: 400–4.
- Hannah L C and James M G. 2008. The complexities of starch biosynthesis in cereal endosperms. *Current Opinion on Biotechnology* **19**: 160–5.
- Hossain F, Nepolean T, Vishwakarma A K, Pandey N, Prasanna B M and Gupta H S. 2013. Mapping and validation of microsatellite markers linked to *sugary1* and *shrunk2* genes in maize. *Journal of Plant Biochemistry and Biotechnology* DOI 10.1007/s13562-013-0245-3.
- Kardoso E T, Sereno M and Barbosa N J F. 2002. Heritability estimates for quality and ear traits in sweet corn. *Crop Breeding and Applied Biotechnology* **2**: 493–8.
- Khan Z H, Khalil S K, Khan M Y, Israr M and Basir A. 2010. Database: Selecting optimum planting date for sweet corn in Peshawar, Pakistan. *Sarhad Journal of Agriculture* **27**: 342–7.
- Khanduri A, Hossain F, Lakhera P C and Prasanna B M. 2011. Effect of harvest time on kernel sugar concentration in sweet corn. *Indian Journal of Genetics* **71**: 231–4.
- Khanduri A, Prasanna B M, Hossain F and Lakhera P C. 2010. Genetic analysis and association studies of yield components and kernel sugar concentration in sweet corn. *Indian Journal of Genetics* **70**: 257–63.
- Ko W R, Sa K J, Roy N S, Choi H J and Lee J K. 2016. Analysis of the genetic diversity of super sweet corn inbred lines using SSR and SSAP markers. *Genetics and Molecular Research* **15**: gmr.15017392.
- Letrat K and Pulum T. 2007. Breeding for increased sweetness in sweet corn. *International Journal of Plant Breeding* **1**: 27–30.
- Mehta B, Hossain F, Muthusamy V, Baveja A, Zunjare R, Jha S K and Gupta H S. 2017. Microsatellite-based genetic diversity analyses of *sugary1*-, *shrunk2*- and double mutant- sweet corn inbreds for their utilization in breeding programme. *Physiology Molecular Biology of Plants* DOI 10.1007/s12298-017-0431-1.
- Qi X, Zhao Y, Jiang L, Cui, Wang Y and Liu B. 2009. QTL analysis of kernel soluble sugar content in super sweet corn. *African Journal of Biotechnology* **8**: 6913–7.
- Randle W M, Davis D W and Groth J V. 1984. The effects of corn leaf rust on maturity and quality of fresh market ears of sweet corn. *Journal of American Society for Horticultural Science* **109**: 648–54.
- Reid L M, Zhu X, Jindal K K, Kebede A Z, Wu J and Morrison M J. 2016. Increasing stalk sucrose in sugar corn (*Zea mays* L.): genetic analysis and preliminary breeding. *Euphytica* **209**: 449–60.
- Rogers B T, Stone P J, Shaw S R and Sorensen I B. 2000. Effect of sowing time on sweet corn yield and quality. *Agronomy* **30**: 55–61.
- Rosa R. 2014. Response of sweet corn cultivated in eastern Poland to different sowing dates and covering with non-woven pp. Part I: Corn yield. *Acta Sci Pol Agricultura* **13**: 93–112.
- Saleh G B, Abdullah D and Anuar A R. 2002. Performance, heterosis and heritability in selected tropical maize single, double and three-way cross hybrids. *Journal of Agricultural Science* **138**: 21–8.
- Solomon K F, Martin I and Zeppa A. 2012b. Genetic effects and genetic relationship among *shrunk2* (*sh2*) sweet corn lines and F_1 hybrids. *Euphytica* **185**: 385–94.
- Solomon K F, Zeppa A and Mulugeta S D. 2012a. Combining ability, genetic diversity and heterosis in relation to F_1 performance of tropically adapted *shrunk2* (*sh2*) sweet corn lines. *Plant Breeding* **131**: 430–6.
- Szymanek M, Tanasa W and Kassarb F H. 2015. Kernel carbohydrates concentration in *sugary-1*, *sugary* enhanced and *shrunk2* sweet corn kernels. *Agricultural and Agricultural Science Procedia* **7**: 260–4.
- Whitt S R, Wilson L M, Tenailon M I, Gaut B S and Buckler E S. 2002. Genetic diversity and selection in the maize starch pathway. *Proceedings of National Academy of Science USA* **99**: 12959–62.
- Zhu S, Mount J R and Collins J L. 1992. Sugar and soluble solid changes in refrigerated sweet corn (*Zea mays* L.). *Journal of food science* **57**: 454–7.