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REVIEW PAPER

Analysis of maize populations for developing quality protein maize

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Abstract: Maize, being a staple food crop in a large segment of the human population, is the most suitable crop for nutritional enhancement. Quality protein maize (QPM) is a nutritionally improved commodity possessing enhanced levels of limiting amino acids such as lysine and tryptophan. In order to identify promising germplasm for developing high-yielding QPM genotypes a meta-study comprising twenty maize populations containing 441 genotypes was conducted. The experimental lines were analysed for protein quality (protein and tryptophan), and physical parameters including hundred kernel weight (HKW) and specific gravity. Twelve populations showed desirable tryptophan content (≥0.51%). Ten populations showed high values (≥22) for HKW. The population S91SIWQ showed the highest value (1.289) for specific gravity. A moderately negative to strongly negative correlation has been observed between protein and tryptophan. Although a negative correlation has been observed between HKW and tryptophan content, however on the basis of data generated, three populations namely P69, S87, and S-99TLWQ-HGB were found to be the potential populations for the development of the hard kernel, high yielding QPM cultivars.

Keywords: Lysine · Maize · Protein · Tryptophan

Introduction

Cereals are the only source of nutrition for a large segment of human populations worldwide. Wheat, rice, and maize are the major cereals in Southeast Asia and Sub-Saharan Africa. Maize is known as the "Queen of cereals" due to its high yield potential and wider utilization for diverse purposes (Sethi *et al.,* 2021). It is supposed to be originated about seven thousand years ago in Central Mexico from a wild grass called teosinte. In India, it was introduced during the 17th century by the Portuguese. It is cultivated in many countries due to its wider adaptability to varied agro-climatic conditions and soil types. Generally, cereals have low protein content and as a result the populations solely dependent on cereals for deriving all of their nutritional requirements usually suffer from protein-energy malnutrition (Temba *et al.,* 2016). Although maize contributes around 15% to the global protein consumption, however, its protein quality is poor due to a higher concentration of zeins which leads to reduced levels of essential amino acids particularly lysine and tryptophan in maize kernel (Prasanna *et al.,* 2001). Zein proteins are involved in the formation of the regular protein-starch matrix which provides vitreous and hard endosperm to maize kernel. Based on their functions, zein proteins are further divided into four classes as α, β, γ and δ zeins (Wu and Messing, 2014). Zeins do not contain any lysine, with the exception of δ-zeins which contains one lysine codon (Wu *et al.,* 2012). However, many natural mutants of maize have been identified which are associated with enhanced protein quality and better kernel appearance. In 1920, a naturally-occurring mutant, *opaque-2* was identified that is associated with higher levels of essential amino acids in the maize kernel (Vasal, 2000). Since then, many more mutants like *floury-2, Mucronate, Defective*

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Endosperm 30, etc. have been identified but *opaque-2* was found to be the most suitable and thus extensively used for the development of quality protein maize. The increase in protein quality resulted from an increase in the proportion of non-zein proteins concomitant with a decrease in the proportion of zein proteins in the *opaque-2* endosperm (Jia *et al.,* 2013).

Zein proteins of maize also assume clinical significance due to their interaction with the human immune system in some patients with celiac disease. Although maize is generally considered an alternative to wheat, for such patients, however in some cases, zein proteins from maize may elicit an immune response (Cabrera-Chavez *et al.,* 2012). Hence, a reduction in the concentration of zein proteins may result in nutritionally improved maize suitable for a broader range of populations affected with nutritional disorders and celiac disease, etc.

Although the *opaque-2* gene is associated with higher lysine and tryptophan content, however, its pleiotropic effects such as soft and chalky kernel and susceptibility to insect and pest infestation, are responsible for its un-popularization (Lodha *et al.,* 2014). The intensive research interventions carried out to improve the kernel texture in *opaque-2* maize resulted in the development of present-day quality protein maize (QPM) which is characterized by a hard and vitreous kernel enriched with lysine and tryptophan content (Chaudhary, 2017). The vitreousness and hardness in the *opaque-2* kernel have been attributed to endosperm modifiers, which modify the kernel from soft and chalky to hard and vitreous. The mechanism, by which the endosperm modifiers change the grain structure from chalky to vitreous in modified *opaque-2*, is not clearly understood. The modified *opaque-2* maize with hard endosperm is known as quality protein maize (QPM). Thus, the term QPM now refers to maize homozygous for the o2 allele, with increased lysine and tryptophan content but without the negative secondary effects of a soft and chalky endosperm (Scott *et al.,* 2004). The QPM essentially has about twice the levels of lysine and tryptophan than normal maize and also increased levels of histidine, arginine, aspartic acid, and glycine, but a reduced level of leucine (Lodha *et al.,* 2014). However, a delicate interplay is needed to be maintained between kernel modification and the protein quality threshold during the development of QPM genotypes. Complete modification of the kernel usually reduces its lysine and tryptophan below the threshold concentration required for the maize to be termed as QPM. The QPM development, therefore, requires continuous monitoring of both protein quality and physical parameters such as hundred kernel weight and specific gravity. Further, the increasing production of maize also wants parallel improvements in its post-harvest management and therefore attention must be given to improve physical quality parameters that ensure better milling performance. Milling also determines flaking characteristics, which influence the quality of breakfast foods produced from maize.

Therefore, a need arises to evaluate a large set of maize germplasm comprising wider natural variability for protein quality characteristics and physical parameters. Keeping in view a meta-study was conducted on 441 maize genotypes belonging to twenty maize populations for protein and tryptophan content, hundred kernel weight, and specific gravity in order to identify the most suitable populations required to develop high-yielding QPM cultivars.

Materials and methods

Plant material

A set of twenty maize populations consisting of 441 genotypes received from Winter Nursery Center, Hyderabad of the Indian Institute of Maize Research was analysed for the present study. Detailed information on the experimental material is presented in Table 1. The genotypes were grown during the rainy season of 2014 in paired rows of 2 meters each. A sufficient number of ears was selfed to maintain the genetic purity of the material. The selfed ears were harvested and a sufficient quantity of kernels was shelled from the middle of the ear in order to maintain uniformity of kernel shape and size. The samples were dried in sun and processed for further analysis.

Sample screening

Seeds from selfed ears of three different replications were pooled and treated as a single accession in order to minimize the effect of biological variation of gene expression between ears. The samples were screened on lightbox to analyse the degree of opaqueness which varies from 0% to 100% with subsequent modification scores ranging from 1 to 5 i.e., 1: 0%, 2: 25%, 3: 50%, 4: 75%

Table 1. Nomenclature and correlation data of the experimental populations

S.No.	Name of population	Number of lines with protein percentage > 11 %	Number of lines with tryptophan percentage > 0.7 %	Correlation between protein and tryptophan	Correlation between tryptophan and Specific Gravity	Population size
1.	97P65	7 (1)	0	0.429	0.026	15
2.	CML 161-65	3	8	0.285	0.003	12
3.	CompMod (BC0)	0	0	0.053	0.118	14
4.	G33QC20	5	0	0.415	0.010	13
5.	P61C1	4	2	0.225	0.046	39
6.	P65C6	1	0	0.034	0.005	24
7.	P66C0	16 (4)	0	0.585	0.116	42
8.	P67C1	1	0	0.020	0.023	17
9.	P69	1	1	0.246	0.086	23
10.	S00TLYQ	2	3	0.302	0.175	23
11.	S01SIWQ	7 (3)	1	0.204	0.095	43
12.	S01SIYQ	11 (1)	0	0.426	0.017	19
13.	S87	0	0	0.234	0.353	14
14.	S91SIWQ	18 (9)	0	0.213	0.026	32
15.	S99SIYQ	0	0	0.137	0.013	10
16.	S99TLWQ-1	2	1	0.002	0.065	14
17.	S99TLWQ-HGA	0	0	0.000	0.000	14
18.	S99TLWQ-HGAB	0	3	0.001	0.187	34
19.	S99TLWQ-HGB	2	0	0.715	0.184	11
20.	S991SIWQ-ET	0	0	0.000	0.003	28

(Correlation is represented as R^2. The number in parenthesis indicates the number of lines with a protein percentage of > 12%)

and 5: 100% opaqueness. Kernel with modification score 4, and 5 are considered *opaque-2* mutants, whereas gradation 2, and 3 is assigned to QPM. Score 1 can be considered both for QPM and normal genotypes.

Estimation of hundred kernel weight and specific gravity

Hundred kernel weight was estimated by measuring the weight of 100 maize kernels, whereas, specific gravity was analysed by measuring the rise in water volume with the addition of 10 maize kernels. For this purpose, 5 ml of water was taken in a measuring cylinder (10 ml capacity). The rise in volume was noted after the addition of 10 kernels and divided by a hundred kernel weights giving the value of specific gravity.

Sample processing

As already mentioned, equal numbers of maize kernels from 3 different ears were pooled and treated as one sample. A minimum of three technical replicates were used for each experiment. To extract the endosperm, the kernels were soaked in water to make them soft. The germ and pericarp were then easily extracted using forceps. The endosperm was dried at low temperature in a hot air oven followed by grounding and then defatting for 36 hours using petroleum ether (40–60°C). The endosperm was dried at low temperature in a hot air oven followed by grounding in wiley mill grinder samples were stored at –20°C for further processing.

Estimation of protein quality

Protein quality is expressed as the concentration of tryptophan in the endosperm protein. Protein content was estimated by the micro-Kjeldahl method (AOAC, 1965), whereas Tryptophan content was estimated by the papain hydrolysis method given by Hernandez and Bates (1969) and expressed as per cent tryptophan in endosperm protein. Single-step papain hydrolysis is utilized for protein solubilisation by incubating maize samples with papain solution at 65ºC overnight. Freshly prepared reagent C was used for colour generation composed of $FeCl_3.6H_2O$ (high purity) in glacial acetic acid and 30 N sulphuric acids. The iron ions oxidize acetic acid to glyoxylic acid in the presence of sulphuric acid. The indole ring of free tryptophan as well as that bound in soluble proteins reacts with glyoxylic acid to produce the violet-purple compound. The intensity of the violet-purple colour is measured at 545 nm. Tryptophan content was calculated with respect to the endosperm protein for each sample.

Results and discussion

As mentioned, the experimental populations were evaluated for protein, tryptophan, hundred kernel weight, and specific gravity in order to identify hard endosperm *opaque*-2 lines required for breeding high-yielding QPM genotypes. Quality improvement of cereals is considered an important factor towards eradicating malnutrition prevailing in the underprivileged sections of society worldwide (Guite *et al.*, 2014). The protein content is an important quality parameter to assess the nutritional quality of any cereal as it is a cost-effective way of protein intake. The protein content of the experimental lines is presented in Figure 1. Out of the twenty populations tested, seven populations viz. CML 161-65, 97P65, G33QC20, P65C6, P66CO, SO1TLYQ, and SO1SIWQ exhibited more than 9.8% of protein, the mean value averaged over all populations. The population S91SIWQ was found to possess the highest number of genotypes exhibiting more than 12% of protein. The same population also showed the highest average value for protein (11%). Two other populations *viz.*, P66C0 and S01SIWQ contain two genotypes each with more than 12% of protein. The above populations, therefore, can be utilized for breeding high-protein maize cultivars. Protein content has been shown to be associated with dry milling characteristics as a high correlation coefficient was reported to exist between protein content and dry-milling yields of maize (Yuan and Flores, 1996). Protein content was also found to be positively correlated with the yield of flaking grits in white maize (Yuan and Flores, 1996). Maize protein also finds applications in foodstuffs for people affected by enteropathic ailments such as celiac disease. High-protein cereals are also considered to be important for healthcare

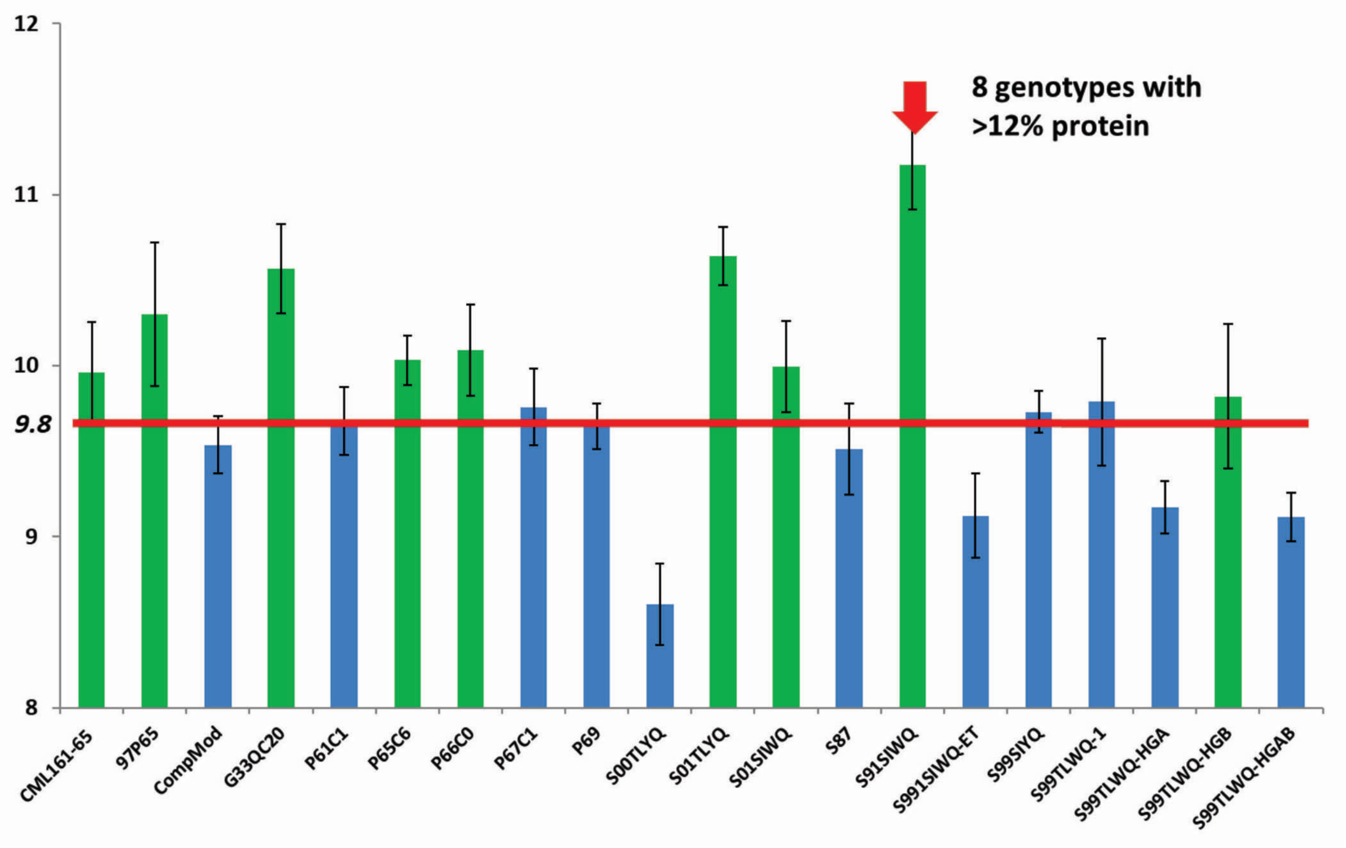

Figure 1. Protein (%) profile of the experimental populations

in patients with chronic kidney disease (Daly *et al.*, 2003). The high-protein-containing maize populations and genotypes identified in the present study can also be utilized for developing specialized maize cultivars required to produce functional foods to serve the needs of consumers with special requirements for a protein diet.

Tryptophan is one of the nine essential amino acids and a precursor for the biosynthesis of neurotransmitters (serotonin and tryptamine), vitamin (nicotinic acid), and melatonin hormone (Heine *et al.*, 1995). The tryptophan concentration of the experimental populations is presented in Figure 2. The mean value of tryptophan was found to be 0.50±0.06%. In normal maize, tryptophan content ranges from 0.2–0.6%, whereas it ranges from 0.5–1.1% in *o2o2* maize (Vivek *et al.,* 2008). Hence, 0.51% was considered as the mean value of tryptophan to analyse diversity for protein quality in the experimental populations. Twelve population viz. CML161-69, G33QC20, P61C1, P65C6, P69, SOOTLYQ, SO1TLYQ, S87, S991SIWQ-ET, S99SIYQ, S99TLWQ-1, S99TLWQ-HGAB exhibited concentration higher than the mean value of tryptophan. Population S99TLWQ-HGAB contains three, whereas the populations P61C1 and P69 contain two genotypes each having tryptophan values of more than 0.7%. It was also observed that populations CML 161-165, G33QC20, and S99SIYQ have high amounts of both proteins as well as tryptophan. Hence, these lines can be used for breeding high-protein QPM cultivars. The higher tryptophan concentrations (≥0.6%) observed in sweet corn populations (S00TLYQ, S87, and S99SIYQ) might be the result of the shrivelled grain size usually observed in sweet corn kernels.

A highly positive correlation has been reported to exist between tryptophan and lysine content in maize endosperm and an increase in the percentage of tryptophan is accompanied by a concomitant increase in lysine (Vivek *et al.*, 2008). Due to ease of its quantification, tryptophan content is usually analysed in order to quantify the protein quality in maize. The amount of tryptophan and lysine was found to be double in QPM as compared to normal maize (Vivek *et al.*, 2008). The health benefits of QPM consumption are well-documented. QPM has been instrumental in fulfilling the protein needs in low-resource settings of the world (Nuss *et al.*, 2011).

Hundred kernel weight (HKW) is an important trait in selecting promising lines for the development of hard

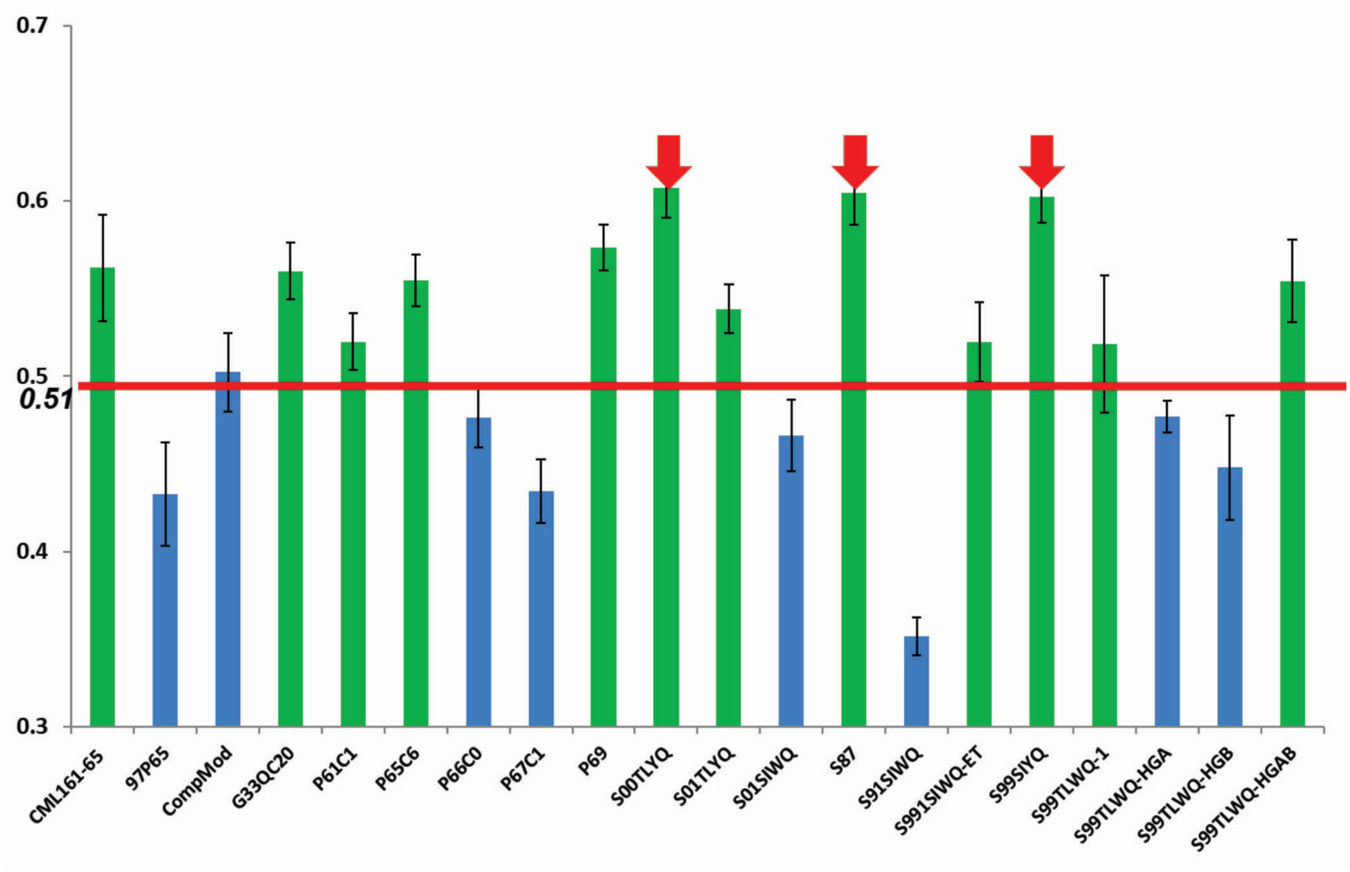

Figure 2. Tryptophan content (%) of the experimental populations

kernel QPM genotypes. The distribution of HKW amongst 20 experimental populations is presented in Figure 3. The mean value of HKW was found to be 22.0±4. Ten populations were found to possess HKW higher than the mean value. Population S91SIWQ exhibited the highest values for HKW (29.52), whereas G33QC20 exhibited the lowest (18.3) HKW. Hundred kernel weight is an important parameter contributing toward higher grain yield. It is associated with kernel number, a trait which is further correlated with ear length, ear row number, and kernel number per row (Chen *et al.*, 2016). Much work is currently being done to elucidate putative QTLs for this trait. Kernel weight also determines seed size for optimal crop density and is also used for calibrating seed drills and for estimating shattering losses during harvest. HKW has also been found to positively influence the test weight of maize, a parameter important to the yield of large flaking grits (Paulsen and Hill, 1985).

Specific gravity is also an important quality trait as along with porosity, it determines kernel hardness, susceptibility to breakage, rate of drying, and propensity to disease development (Chang, 1987). The mean value of specific gravity in the experimental populations was found to be 1.2±0.5 (Figure 4). Eight populations showed specific gravity higher than (1.2). The population S91SIWQ showed the highest value (1.289), whereas S87 exhibited the lowest (1.129). Maize grains are reported to have a high porosity of around 12–13%. (Chang, 1987). The nutritional composition of the kernel including starch, amylose/amylopectin ratio, protein, and oil, and its packaging, influences kernel density (Paulsen *et al.,* 2003). While hard kernel maize is desired for the production of dry milled products like flour and grits, soft kernels find applications in feed, ethanol, and glucose/fructose production as less steeping time is required for maize having soft kernels. Kernel hardness, therefore, needs to be optimized as per the end-use application.

HKW and specific gravity are important traits in developing QPM genotypes as QPM is defined as the maize homozygous for the o2 allele with increased lysine and tryptophan content along with hard and vitreous endosperm. The high tryptophan *opaque-2* genotypes developed during the 70’s and 80’s remained unpopular due to soft and opaque kernel which leads to lower yields and susceptibility to insects and pest infestation. The development of hard kernel genotypes becomes a necessity in order to harness the

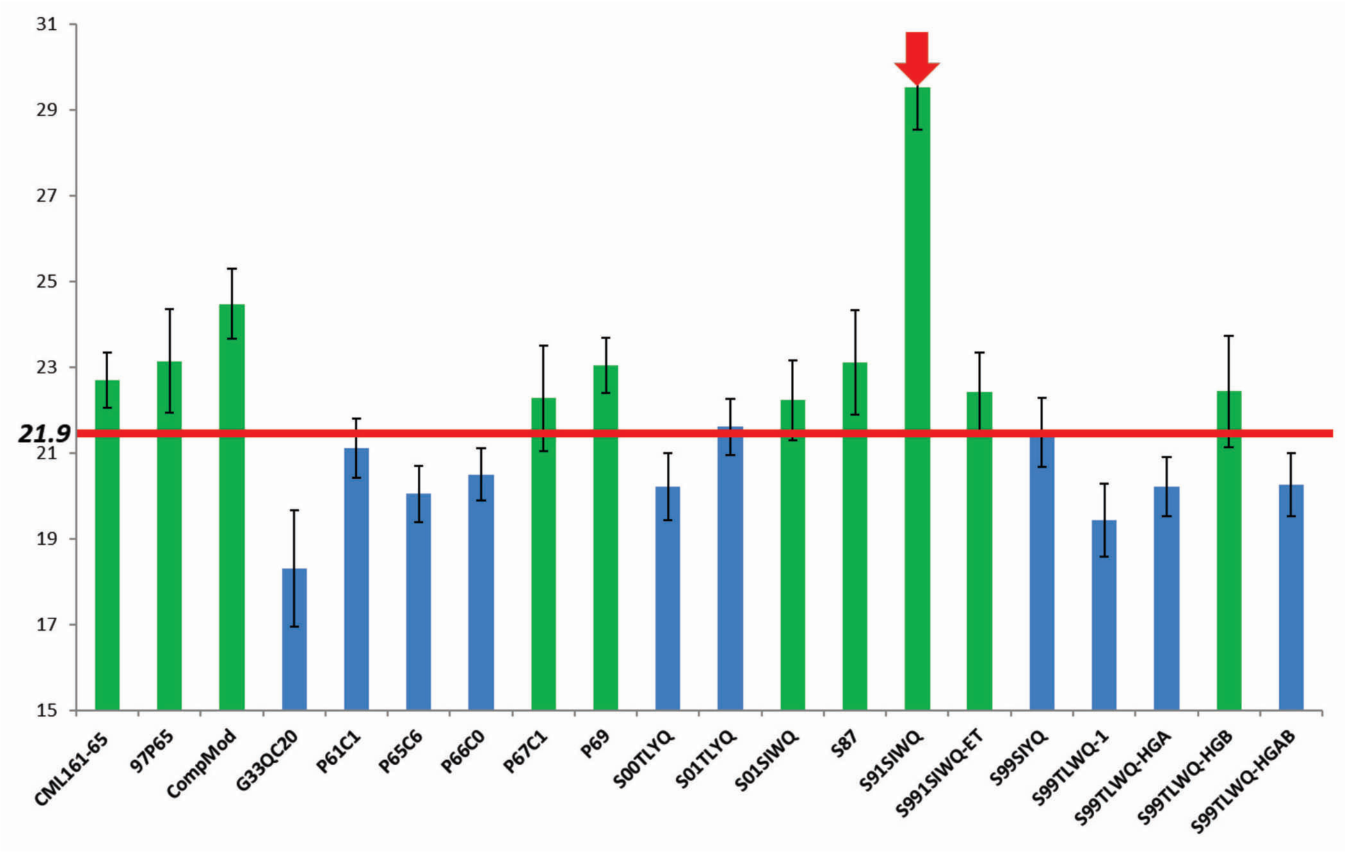

Figure 3. Hundred kernel weight of the experimental populations

benefits of nutritionally improved *opaque-2* maize. Since specific gravity is directly associated with the kernel hardness, therefore, the estimation of lysine and tryptophan along with 100 kernel weight and specific gravity measurement is a must for developing hard kernel high yielding QPM cultivars. Recently, fine-mapping of a QTL region *qGW4.05* has revealed a candidate gene responsible for the HKW trait (Cheng *et al.,* 2016). The molecular information can further be utilized to improve the character of elite maize lines.

From the results, it is observed that populations CML 161-165, P69, and S01TLYQ have a high content of protein, tryptophan, and HKW traits. S91SIWQ contains higher amounts of protein along with high HKW and specific gravity. None of the experimental populations showed high values for all four traits. However, it is observed that populations *viz*., CompMod and S991SIWQ-ET may be used to breed high-yielding QPM cultivars as they possess high value for HKW and specific gravity along with higher amounts of tryptophan. It is also found that tryptophan content showed a moderately negative correlation with specific gravity. This is expected since a lesser amount of prolamin fraction of proteins in *opaque-2* maize results in soft and opaque kernels owing to the incomplete starch-protein matrix. The kernel hardness and specific gravity are, therefore, important traits in developing hard endosperm QPM genotypes.

The data on the correlation between various traits are presented in Tables 1 and 2. Although no strong correlation has been observed among any of the parameters, however, the population-wise data analysis revealed that five out of the twenty populations showed a moderate to strong negative correlation between tryptophan and protein contents. Hence, it can be concluded that the negative correlation usually observed between protein and tryptophan is not universal and presumable depending on gene action. Interestingly, in one population S99TLWQ-HGB, a strong positive correlation is found between protein and tryptophan contents. This population can be assessed for gene action and the development of new germplasm/breeding lines. Although a negative correlation has been observed between HKW and tryptophan content, however, on the basis of data the populations P69, S87 and S-99TLWQ-HGB can be utilized for the development of the hard kernel, high-yielding QPM cultivars.

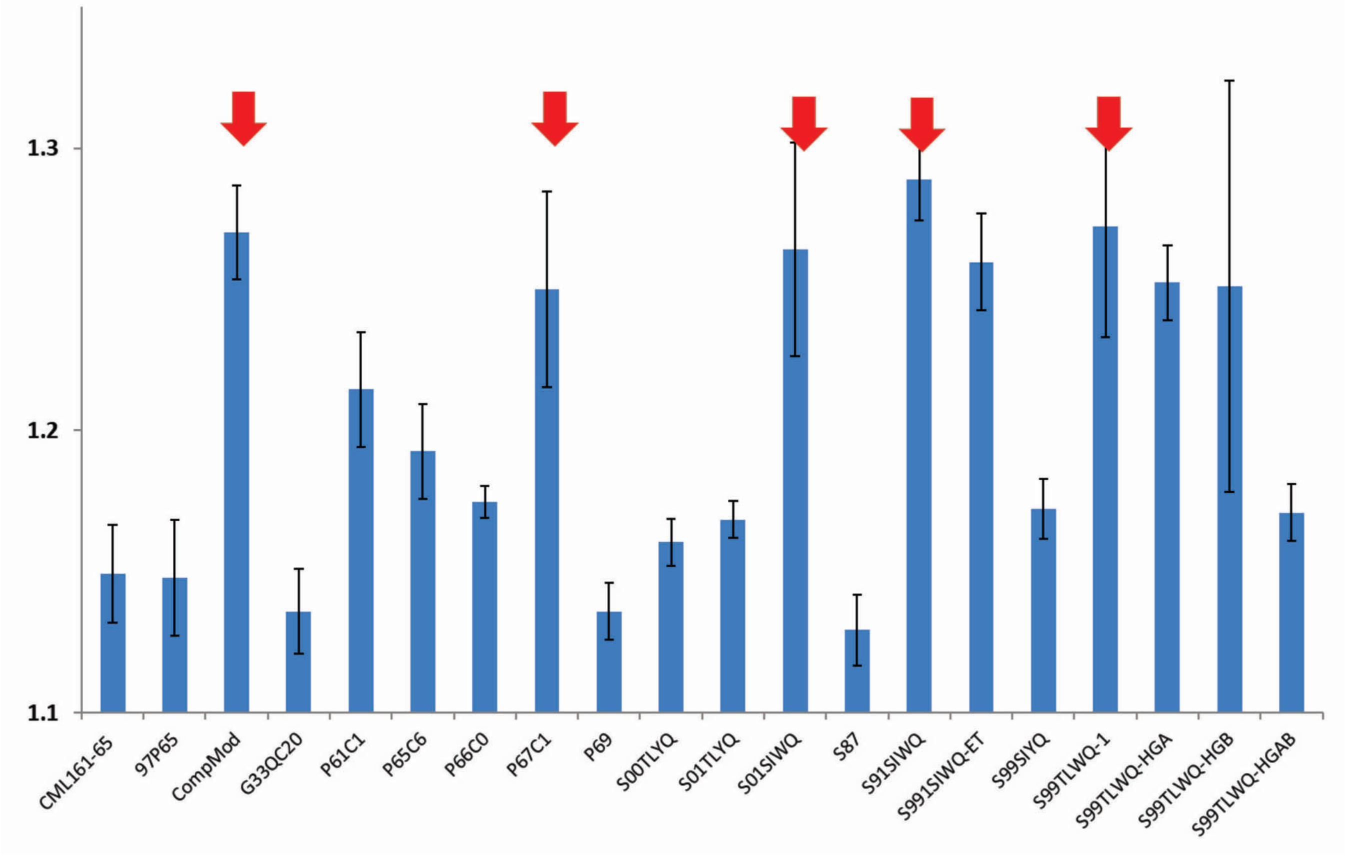

Figure 4. The specific gravity of the experimental populations

Table 2. Populations showing a moderate to strong correlation between protein and tryptophan contents

S.No.	Name of the population	Pearson correlation coefficient (R)	Coefficient of determination (R^2)	Nature of correlation	Significance level
1.	97P65	- 0.6654	0.429	Moderate negative	0.05
2.	G33QC20	- 0.6442	0.415	Moderate negative	0.05
3.	P66C0	- 0.765	0.585	Strong negative	0.01
3.	S01SIYQ	- 0.653	0.426	Strong negative	0.01
4.	S99TLWQ-HGB	0.8457	0.715	Strong positive	0.01

Conclusion

The present study immensely helped to identify potent maize populations required for breeding high-yielding hard kernel QPM genotypes. The data on correlations amongst different quality parameters in maize might be helpful for designing the future breeding program for the development of nutritionally improved maize. Opaqueness, related to tryptophan content, results in higher porosity due to the enlargement of starch granules and reduction in the size of protein bodies. The increased porosity may be expected to result in a decrease in specific gravity. However, analysis in the present study does not reveal any correlation between specific gravity and tryptophan content, demonstrating that other mechanisms may be in place apart from the reduction in the size of protein bodies. The present study clearly elucidated some potential populations (CML 161-165, P69, S01TLYQ, S91SIWQ) with desired physical parameters like hundred kernel weight and specific gravity along with protein and tryptophan which can effectively be utilized in the development of high-yielding, hard kernel QPM genotypes.

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References

AOAC. (1975). Association of Official Agricultural Chemists, official methods of analysis, Washington, D.C.

Cabrera-Chavez, F., Iametti, S., Miriani, M., de la Barca, A. M., Mamone, G. & Bonomi, F. (2012). Maize prolamins resistant to peptic-tryptic digestion maintain immune-recognition by IgA from some celiac disease patients. *Plant Foods for Human Nutrition*, **67**: 24–30.

Chang, C. S. (1987). Measuring density and porosity of grain kernels using gas pycnometer. *Cereal Chemistry*, **65**: 13–15.

Chaudhary, D. P., Kumar, S. & Singh, S. (2014). Maize: Nutrition dynamics and novel uses. Springer India.

Chen, J., Zhang, L., Liu, S., Li, Z., Huang, R., Li & Ding, J. (2016). The genetic basis of natural variation in kernel size and related traits using a four-way cross population in maize. *PLoS ONE*, **11**: 1–12.

Chen, L., Li, Y. X., Li, C., Wu, X., Qin, W., Li, X., Jiao, F., Zhang, X., Zhang, D., Shi, Y., Song, Y., Li, Y. & Wang, T. (2016). Fine-mapping of qGW4.05, a major QTL for kernel weight and size in maize. *BMC Plant Biology*, **16**: 81–94.

Daly, A., Franz, M. & Holzmeister, L. A. (2003). Exchange lists for meal planning. *American Diabetes Association, Alexandria*, **9**: 10–15.

Guite, N., Ghosh, S. & Brahmachari, A. (2014). Addressing issues of malnutrition in children through public nutrition using local resources of agriculture and land use: Evidence from the field based evaluation study in Uttar Pradesh. *Indian Journal of Community Health*, **26**: 237–244.

Heine, W., Radke, M. & Wutzke, K. D. (1995). The significance of tryptophan in human nutrition. *Amino Acids*, **3**: 91–205.

Hernandez, H. & Bates, L. S. (1969). A modified method for rapid tryptophan analysis of maize. Research Bulletin 19th edn, pp. 1–42. International Maize and Wheat improvement centre, Mexico.

Jia, M., Wu, H., Clay, K. L., Jung, R., Larkins, B. A. & Gibbon, B. C. (2013). Identification and characterization of lysine-rich proteins and starch biosynthesis genes. In the opaque2 mutant by transcriptional and proteomic analysis. *BMC Plant Biology*, **13**: 60–69.

Nuss, E. T. & Tanumihardjo, S. A. (2011). Quality protein maize for Africa. Closing the protein inadequacy gap in vulnerable populations. *Advances in Nutrition*, **3**: 217–224.

Paulsen, M. R., Watson, S. A. & Singh, M. (2003). Measurement and maintenance of corn quality. *Corn: Chemical Technology*, **2**: 159–220.

Prasanna, B. M., Vasal, S. K., Kassahun, B. & Singh, N. N. (2001). Quality protein maize. *Current Science*, **81**: 1308–1319.

Rosenzweig, C., Tubiello, F. N., Goldberg, R., Mills, E. & Bloomfield, J. (2002). Increased crop damage in the US from excess precipitation under climate change. *Global Environmental Change*, **12**(3): 197–202.

Scott, M. P., Bhatnagar, S. & Betran, J. (2004). Tryptophan and methionine levels in quality protein maize breeding germplasm. *Maydica*, **49**: 303–311.

Sethi, M., Singh, A., Kaur, H., Kumar, R., Rakshit, S. & Chaudhary, D. P. (2021). Expression profile of protein fractions in the developing kernel of normal, opaque-2 and quality protein maize. *Scientific Reports,* **11**: 2469.

Temba, M. C., Njobeh, P. B., Adebo, O. A., Olugbile, A. O. & Kayitesi E. (2016). The role of compositing cereals with legumes to alleviate protein energy malnutrition in Africa. *International Journal of Food Science and Technology,* **51**(3): 543–554.

Vasal, S. K. (2000). The quality protein maize story. *Food and Nutrition,* **21**: 445–450.

Vivek, B. S., Krivanek, A. F., Palacios-Rojas, N., Twumasi-Afriyie, S. & Diallo, A. O. (2008). Breeding Quality Protein Maize (QPM): Protocols for developing QPM cultivars. Mexico, CIMMYT.

Wu, Y. & Messing, J. (2014). Proteome balancing of the maize seed for higher nutritional value. *Frontiers in Plant Science,* **5**: 240–254.

Wu, Y., Wang, W. & Messing. J. (2012). Balancing of sulphur storage in maize seed. *BMC Plant Biology,* **12**: 77–87.

Yuan, J. & Flores, R. A. (1996). Laboratory dry-milling performance of white corn: effect of physical and chemical corn characteristics. *Cereal Chemistry,* **73**: 574–578.

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REVIEW PAPER

Nutritional and medicinal importance of maize in human health

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Abstract: Maize (*Zea mays* L.) has worldwide importance due to its nutritional and medicinal value. It is an excellent source of carbohydrates, dietary fibers, polyunsaturated fatty acids, vitamins, minerals, and natural antioxidants which play significant roles in different physiological processes for maintaining good health and preventing chronic diseases in humans. Decoction of the maize silk, roots, leaves, and cob are used for bladder problems, nausea, vomiting, and stomach complaints. Resistant starch from maize reduces the risk of cecal cancer and atherosclerosis. Its consumption in the diet is beneficial in the reduction of chronic-degenerative diseases such as cancer, diabetes, obesity, and cardiovascular and metabolic problems. The rate of genetic gain for further improvement in nutrient content in maize is being accelerated with the rapid advances made in understanding the genetic control of many macro-and micro-nutrients in maize grains with the increased availability and accessibility of new technologies, especially in developing countries of the world.

Keywords: Diseases · Food · Health · Maize · Nutrition · Phytochemicals

Introduction

Globally, Maize (*Zea mays* L.) is known as the 'Queen of Cereals' because of its highest genetic yield potential among all the cereals. *Zea* is an ancient Greek word that means 'sustaining life' and *mays* is a word from the Taino language meaning 'life-giver' (Milind and Isha, 2013). Various other synonyms like corn, *zea*, *makka*, *makai*, *makkacholam*, *makkaya*, *makkajanna*, bhutta, *majs*, *mais*, *anaaj*, *jagung*, *barajovar*, etc. are used to recognize this plant in different regions of the world. Botanically, it belongs to Kingdom-Plantae, Subkingdom-Tracheobionta, Superdivision-Spermatophyta, Division-Magnoliophyta, Class- Liliopside (Monocotyledon), Order-Poales, Family-Poaceae (Gramineae), Subfamily- Panicoideae, Tribe-Andropogoneae Genus- *Zea*, and species- *mays*. The *mays spp.* divided into eight groups on the basis of the nature of the endosperm of kernels i.e. popcorn (*Z. mays* var. *everta*), dent corn (*Z. mays var. indentata*), sweet corn (*Z. mays var. saccharata*), flint corn (*Z. mays var. indurate*), flour corn (*Z. mays var. amylacea*), baby corn (*Z. mays var. huehuetenangensis*), pod corn (*Z. mays tunicate*), waxy corn (*Z. mays ceratin*) (Iltis and Doebley, 1980).

Maize is native to South America but extensively cultivated in various other countries throughout the world for food and fodder. The global consumption pattern of maize is: feed-61%, food-17%, and industry-22%. Currently, nearly 1147.7 million MT of maize is being produced together by over 170 countries from an area of 193.7 million ha with average productivity of 5.75 t/ha (FAOSTAT, 2020). The United States of America is the largest producer of maize accounting for nearly 40% of the total world's maize production. The other major maize-producing countries are China, Brazil, Argentina, Indonesia, France, South Africa, Mexico, India, Canada, Australia,

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New Zealand, Pakistan, Nigeria, Japan, Malaysia, Thailand, Taiwan, Philippines, Colombia, Singapore, Netherlands, Romania, Uruguay, Czech Republic, Egypt, Zimbabwe, and Kenya. India produced 31.51 million tonnes in an area of 9.86 million hectares during 2020–21 (DES, 2021). In India, the major maize-growing states, *viz*., Karnataka, Madhya Pradesh, Maharashtra, Tamil Nadu, West Bengal, Rajasthan, Bihar, Andhra Pradesh, Uttar Pradesh, Telangana, Gujarat, Punjab and Odisha, jointly account for over 95% of the national maize production. The acreage, production and productivity of different states of India is presented in Figures 1, 2 & 3 which are based on the data of DES, 2021. Together with rice and wheat, maize provides at least 30% of the dietary calories of over 4.5 billion people in 94 countries and by 2050, maize demand in developing countries will double.

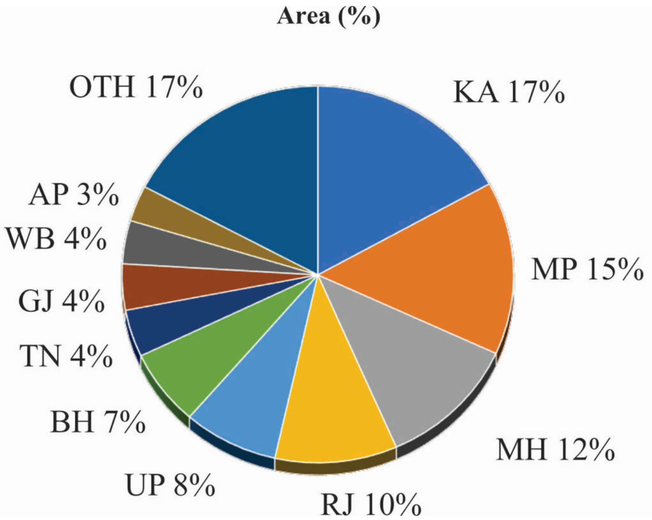

Figure 1. Percentage area under maize in different states of India

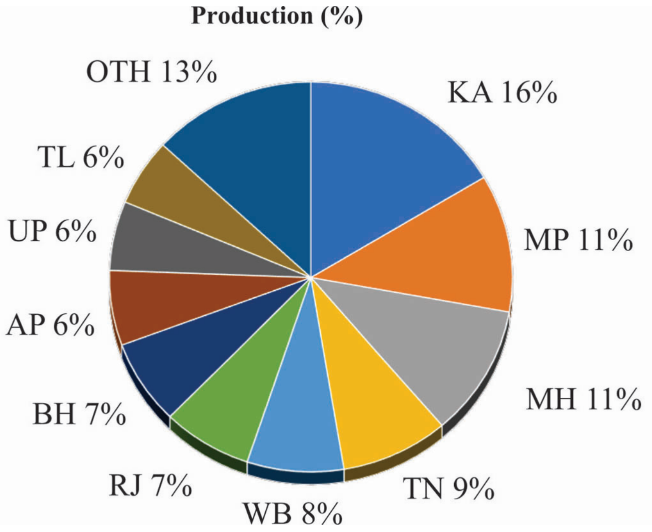

Figure 2. Contribution (%) of different states in maize production in India

In the 21st century, the challenge is not only to produce enough to feed the growing world population, but also providing to all nutritionally balanced diets for good health. Thus, this review aims to discuss the nutritional and medicinal importance of maize in disease prevention and maintaining good health through the intake of it in the diet.

Nutraceutical properties of maize

Maize has a high nutritional value in the human diet as it is an excellent source of vitamins, minerals, protein, carbohydrates, dietary fibers, polyunsaturated fatty acids, and natural antioxidants with a nutraceutical function. Thus, maize has been acknowledged as a functional food. Maize contains near about 65% carbohydrate, 12% fiber, 9% protein, and 4% lipid (Longvah *et al.* 2017). Due to the presence of a high amount of carbohydrates. The complex carbohydrates in maize are digested at a slow rate by the stomach, so provide a good balance of energy levels. It contains all the nine essential amino acids and five conditionally essential amino acids that are required for a human body to perform various functions (Table 1). Maize is also enriched with vitamins and minerals (Tables 2 & 3) which are very essential for different physiological processes in the human body. However, its chemical constituents vary due to differences in genotypes, and environmental factors such as weather and climate, types of soil, agronomical practices, and also depend on the type of corn such as yellow, white, and purple corn. The resistant starch in maize is a type of non-digestible fiber, as it is highly resistant to the activity of digestive enzymes. In maize, the resistant starch seems to be directly related to the percentage of amylose content. In normal corn, the presence of 34% of amylose is related to 0.8% of resistant starch, while in high-amylose corn starch, the recorded presence of 83% amylose results in 39% resistant starch (Jin *et al.*, 2016; Jongfeng and Jay-Lin, 2016). However, the resistant starch can be metabolized by the microbiota of the large intestine through the fermentation process (Higgins, 2004). Both the starch and the resistant starch contained in maize kernels have relevance due to their possible function as regulators of body weight, thus a possible natural alternative for the treatment of obesity and hemorrhoids. (Keenan *et al*., 2006).

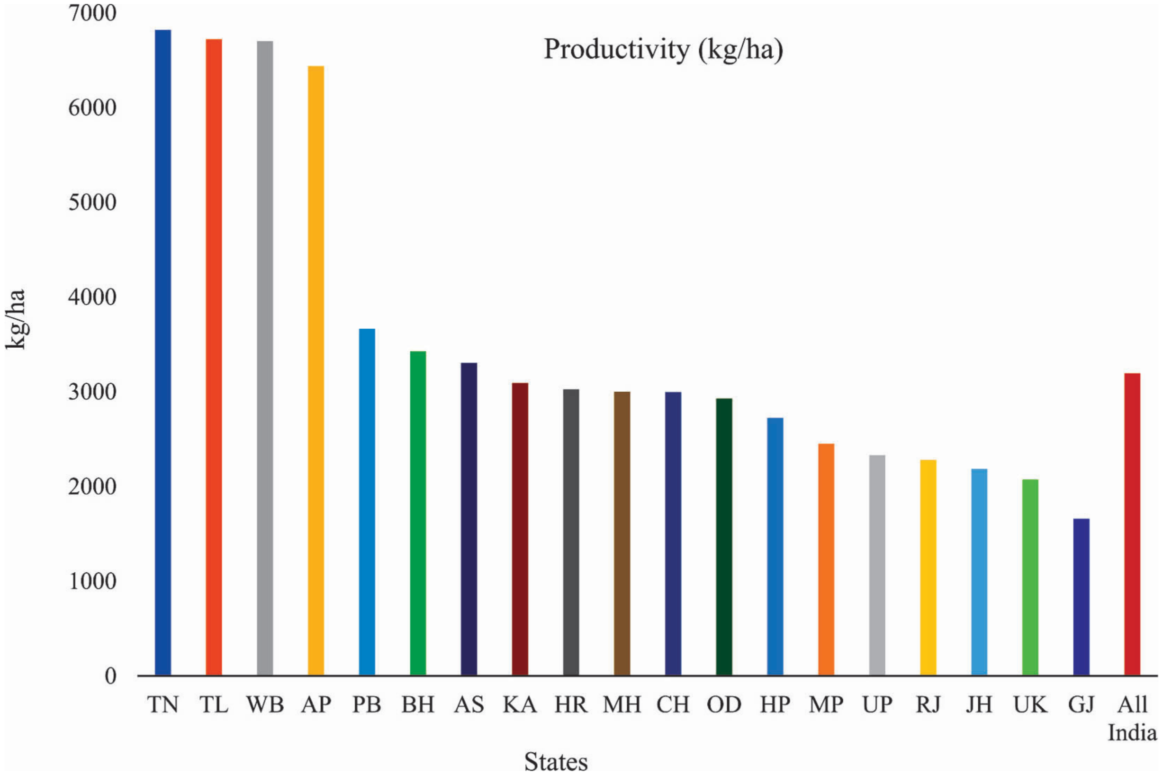

Figure 3. Productivity of maize in different states of India
TN- Tamil Nadu, TL- Telangana, WB- West Bengal, AP- Andhra Pradesh, PB- Punjab, BH- Bihar, AS- Assam, KA- Karnataka, HR-Haryana, MH- Maharashtra, CH- Chhattisgarh, OD- Odisha, HP- Himachal Pradesh, MP- Madhya Pradesh, UP- Uttar Pradesh, RJ-Rajasthan, JH- Jharkhand, UK- Uttarakhand, GJ- Gujrat, OTH- Other

In the endosperm of corn kernels, protein is the second most abundant component having 8–10% of the total weight after the starch (Hannah *et. al*., 1993). The kernel proteins have been classified into four groups in relation to their solubility i.e. albumins (water-soluble proteins), globulins (proteins soluble in saline solutions), prolamins or zeins (proteins soluble in alcoholic solutions), and glutelins (unable to be solubilized in water/saline/ alcoholic. The albumins and globulins are located mainly in the germ, while the prolamins and glutelins can be found predominantly in the endosperm. In relation to their concentration, proteins are distributed unevenly in the maize kernel, where, 40% of the proteins are concentrated in zeins, followed by the glutelins (30%), whereas, globulins and albumins together constitute less than 5%. Of these, approximately 60% of the proteins are concentrated in the endosperm and are prolamins, with á-zein being the most abundant, reaching up to 75% of the total prolamins (Momany *et al*., 2006). Maize proteins are hydrolyzed by the activity of gastrointestinal enzymes such as pepsin, trypsin, and chymotrypsin. Studies have shown that the bioactive peptides in maize have many beneficial effects on health, mainly as antihypertensive, anticholesterolemic, antioxidant, anti-inflammatory, anticarcinogenic, antimicrobial, and others, due to their immunomodulatory properties.

The corn kernel oil, popularly known as corn oil is a concentrated source of energy that provides essential fatty acids, vitamin E, and a rich source of polyunsaturated fatty acids (PUFA), which help in regulating blood cholesterol and lower elevated blood pressure (Dupont *et al*., 1990). Animal and human studies showed that at least 97% of the oil is digested and absorbed (Chen *et al*., 1987). Carrillo *et al*. (2017) reported that corn oil shows a good content of omega 6 and 9 fatty acids (FA), where, omega 6 contributes 52.7% of the FA content. It is comprised of 40–68% of linoleic acid, 20–32% of oleic acid, and 8–14% of saturated fatty acids, mainly palmitic acid. Moreover, corn oil is a good source of tocopherols with ã-tocopherol (Moreau, 2011). Corn oil was also shown to reduce elevated blood pressure. Corn oil diets have shown blood pressure lowering of about 12% in men and 5% in women with pre-existing hypertension (Iacono and Dougherty, 1993).

Table 1. Essential amino acid profile of maize (dry)

Amino acids	**Nutritive value***
Essential amino acids	
Histidine	2.70 ± 0.21
Isoleucine	3.67 ± 0.22
Leucine	12.24 ± 0.57
Lysine	2.64 ± 0.18
Methionine	2.10 ± 0.17
Phenylalanine	5.14 ± 0.29
Threonine	3.23 ± 0.29
Tryptophan	0.57 ± 0.12
Valine	5.41 ± 0.71
Conditionally essential amino acids	
Arginine	4.20 ± 0.24
Cysteine	1.55 ± 0.14
Tyrosine	3.71 ± 0.18
Glycine	3.27 ± 0.15
Proline	7.88 ± 0.71

*All the values are presented as per 100 g of edible portion. (Longvah *et al*., 2017)

Table 2. Vitamin content in maize (dry)

Vitamins	**Scientific name**	**Nutritive value***
Vitamin-A	Retinol	59.2± 17.1 µg
Vitamin-B1	Thiamine	0.33 ± 0.032 mg
Vitamin-B2	Riboflavin	0.09 ± 0.009 mg
Vitamin-B3	Niacin	2.69 ± 0.06 mg
Vitamin-B5	Pantothenic Acid	0.34 ± 0.03 mg
Vitamin-B6	Pyridoxine	0.34 ± 0.017 mg
Vitamin- B7	Biotin	0.49 ± 0.05 µg
Vitamin-B9	Folic Acid	25.8 ± 1.44 µg
Vitamin-C	Ascorbic acid	4.26 ± 0.55 mg
Vitamin-D	Ergocalciferol	33.6 ± 2.82 µg
Vitamin-E	α-Tocopherol	0.36 ± 0.03 mg
Vitamin-K	Phylloquinones	2.50 ± 0.76 µg

*All the values are presented as per 100 g of edible portion (Longvah *et al*., 2017)

Medicinal importance of maize in human health

From ancient times, maize has been used to pacify *kapha*, *pitta*, anorexia, general debilities, emaciation, and hemorrhoids (Kumar and Jhariya, 2013). A kapha diet consisting of barley, maize, millet rye, and buckwheat is favored superior over a diet of oats, rice, and wheat in balancing and managing *kapha dosha*. In recent years, its consumption has been linked to the reduction of chronic-degenerative diseases such as cancer, diabetes, obesity, cardiovascular and metabolic problems, neurodegenerative problems, etc.

Table 3. Mineral content of maize

Minerals	**Nutritive value***
Phosphorus (P)	299.6 ± 57.8
Potassium (K)	324.8 ± 33.9
Calcium (Ca)	48.3 ± 12.3
Magnesium (Mg)	107.9 ± 9.4
Sodium (Na)	59.2 ± 4.1
Iron (Fe)	4.8 ± 1.9
Copper (Cu)	1.3 ± 0.2
Manganese (Mn)	1.0 ± 0.2
Zinc (Zn)	4.6 ± 1.2

*All the values are presented as per 100 g of edible portion (Bressani *et al*., 1989)

Table 4. Major phytochemical compounds in maize

Compounds	**Concentration (mg/100 g)**	**References**
(1) Carotenoids		
(a) Carotene	2.20	Watson and Ramstad (1987)
b) Xanthophylls		
(i) Lutein	1.50	Moros *et al*. (2002)
(ii) Zeaxanthin	0.57	
(2) Phenolic compounds		
(a) Ferulic acid (FA)	174	Zhao *et al*. (2005)
(b) Anthocyanins	141.7	Salinas-Moreno *et al*. (1999)
(3) Phytosterols		
(a) Sitosterol	9.91	Locatelli and Berardo (2014)
(b) Stigmasterol	1.52	
(c) Campesterol	3.40	

The phytochemicals in maize grains demonstrate a significant beneficial contribution to reducing the risk of many diseases due to their potent antioxidant activities (Liu, 2007; Madhujith and Shahidi, 2007). Major phytochemical compounds in maize and their concentration are given in Table 4. Maize grains, especially the yellow variety contain large quantities of carotenoid pigments and have a vital significance in the diet of human beings. These carotenoid pigments are also beneficial in preventing cancer (Michaud *et al*., 2000). Alpha (α) and beta (β) carotene possess provitamin-A activity. A high concentration of β-carotene has been observed to act as a pro-antioxidant and induces apoptosis of colon cancer cells, leukemia cells, melanoma cancer cells, and gastric cancer cells, thus rendering a potent chemopreventive effect (Palozza *et al.*, 2001, 2003; Jang *et. al.*, 2009). Xanthophylls i.e. lutein and zeaxanthin protect humans against phototoxic damage and are useful for healthy vision and play a role in age-related macular degeneration and age-related cataract formation. The lutein supplements in the diet for a specific period showed a significant enhancement in macular pigment optical density and notable protection of the macula from light damage (Landrum *et. al.*, 1997). Lutein also acts as cancer chemopreventive/suppressing agent (Moreno *et al.,* 2007). Lutein supplementation in a food dose-dependent manner increases tumor latency and inhibits mammary tumor growth, enhances lymphocyte proliferation, lowers the incidence of the palpable tumor, and significantly protects cells against oxidant-induced damages (Chew *et al.*, 1996). Ferulic acid (FA) found in maize has potent antioxidant properties and protects the cell membranes against oxidation. The various benefits of FA derived from maize include anticancer, anti-inflammatory, reducing bone loss, anti-diabetic, and hepatoprotective effects (Kawabata *et al.*, 2000; Ou *et al.*, 2003; Rukkumani *et al.*, 2004). Anthocyanins in maize have been well known for their health-promoting benefits such as anti-carcinogenic, anti-atherogenic, lipid-lowering, anti-diabetic, anti-hypertensive, anti-microbial, and anti-inflammatory properties. Due to their potent antioxidant properties, they are able to decrease capillary permeability and fragility, immune system stimulation, and inhibit platelet aggregation (Ghosh and Konishi, 2007, Shindo *et al.*, 2007). Hagiwara *et al.* (2001) have been carried out to demonstrate the anti-neoplastic effects of maize anthocyanins, finding that it prevents carcinogenesis due to exposure to 2-amino-1-methyl-6-phenylimidazo pyridine (a free radical belonging to the nitrosamines group). Long *et al.* (2013) demonstrated the chemopreventive properties of purple corn in the *in-vitro* models of prostate cancer. Urias-Lugo *et al.* (2015) reported on the anti-cancer properties of the phenolic and anthocyanins compounds in maize and they are useful in breast, liver, colon, and prostate cancer. Maysin can be used for the treatment of prostate cancer in humans who are resistant to chemotherapy. The non-amylaceous peptide polysaccharide of corn was isolated and characterized, and after a series of tests, it showed anticancer properties by blocking metastasis mediated by galectin-3 (Jayaram *et al*., 2015). It has also been shown that the bioactive peptides of maize exert antitumor activity through the key mechanisms such as (a) the induction of apoptosis mediated through specific proteases or caspases; the strategies to overcome tumor resistance to apoptotic pathways include the activation of pro-apoptotic receptors, the restoration of the *p53* activity, the modulation of caspases, and the inhibition of the proteasome; (b) by blocking the intermediate generation of tumors by regulating cellular mechanisms associated with cell proliferation and survival, or biosynthetic pathways that control cell growth; and (c) regulation of immune system functions, increasing the expression of antigens associated with the tumor (antigenicity) in cancer cells, activating the tumor cells for them to release warning signals that stimulate the immune response (immunogenicity), or increasing the predisposition of the tumor cells to be recognized and neutralized by the immune system by means of autophagy and apoptosis (Díaz-Gómez *et al*., 2017). Resistant starch in maize, also called as high-amylose maize helps in altering microbial populations and enhance fecal output. It increases fermentation and short-chain fatty acid production in the large intestine and reduces symptoms of diarrhea, which altogether reduce the risk of cecal cancer (Wang *et al.,* 2002; Murphy *et al.,* 2008).

Diabetes, the most severe chronic metabolic disease with a great impact on the health of the world population is one of the fastest growing global health emergencies of the 21st century and has reached alarming levels. According to the International Diabetes Federation, approximately 537 million adults (20–79 years) have been reported with diabetes worldwide during the year 2021 and is expected to increase to 643 million by 2030 and 783 million by 2045. More than 1.2 million children and adolescents (0–19 years) are living with type-1 diabetes. One in six live births is affected by diabetes during pregnancy. Almost one in every two adults living with diabetes is undiagnosed. Diabetes already caused near about 6.7 million deaths (IDF, 2021). Several studies have shown that the consumption of maize improves insulin sensitivity along with a reduction of glucose concentration and a change in blood lipid profile due to the consumption of resistant starch in humans (Keenan *et al*., 2015; Zhou *et al*., 2015). Its consumption influences cholesterol metabolism and lowers body fat storage, therefore, reducing the risk of atherosclerosis, hyperlipidemia, diabetes, and obesity (Higgins, 2004). Resistant starch has also been suggested to be potentially beneficial for improving insulin sensitivity in both animal and human subjects (Johnston *et al.*, 2010). Diabetic nephropathy is one of the main complications of diabetes and is mainly caused by chronic renal failure, which is growing in prevalence. The consumption of feruloylated oligosaccharides from maize bran has been shown to be effective in the regulation of serum insulin levels (Huang *et al.*, 2018). In addition, the maize extract rich in anthocyanins have been used as a therapeutic agent focused on the regulation of the abnormal angiogenesis that occurs in diabetic nephropathy, which can lead to renal failure. This is mediated by the decrease in receptor-2 activity for vascular endothelial growth factor after consumption of purple corn, tested in diabetic mice (Kang *et al.*, 2013). Huang *et al.* (2015) reported that purple corn extract can have anti-diabetic effects through the protection of the β cells of the pancreas, favoring the secretion of insulin and the activation of the AMPK pathway in diabetic mice i.e. increased phosphorylation by AmpC-activated kinase protein (AmpK), decreases the activity of phosphoenolpyruvate carboxykinase (PEPCK), decreases the transcriptional activity of genes for glucose 6-phosphatase in the liver, and increases the expression of the glucose transporter 4 (GLUT4) in skeletal muscle.

The polyphenols in maize, particularly flavonoids, can also modulate the neuronal signaling cascade activated by aging, acting on the ERK/CREB pathway involved in synaptic plasticity and long-term potentiation, improving learning and memory capacity in humans (Han *et al.*, 2007). In the ear and seeds of maize, cyanidin-3-glucoside, pelargonidin-3-glucoside, peonidin-3-glucoside, and its malonated counterparts can be found. Many biological activities have been attributed to these phytochemicals, so it is considered that maize and its byproducts that contain them have an intrinsic capacity to prevent cognitive deterioration and memory decline and are useful in the management of Alzheimer's disease (Choi *et al.*, 2012). Maize is believed to have potential anti-HIV activity due to the presence of the *Galanthus nivalis* agglutinin (GNA) lectin. The GNA-lectins are special proteins that can bind to carbohydrates or carbohydrate receptors found on cell membranes. In some micro-organisms including the HIV virus, the binding of lectins onto sugars is believed to inhibit the activity of the virus (Shah *et al.*, 2016).

Present and future prospective

The kernels of yellow maize cultivars commonly grown by farmers contain less than 2 µg/g of provitamin A (PVA) which is insufficient to meet the recommended daily requirement in a diet. To increase the concentrations of PVA carotenoids in maize considerable efforts have been made by researchers through modern breeding technologies (Pixley *et al.*, 2013; Andersson *et al.*, 2017; Giuliano, 2017; Menkir *et al.*, 2017). The biofortified yellow maize rich in beta-carotene might be recommended as an efficient food source to combat Vitamin A deficiency (VAD) in those countries where VAD is a public health problem. Biofortification of maize kernels with high Zn has been undertaken at CIMMYT and IITA for more bioavailability of Zn (Bänziger and Long, 2000; Ortiz-Monasterio *et al.*, 2007; Menkir *et al.*, 2008; Hindu *et al.*, 2018), The phytic acid in maize adversely affects the Zn content. Due to a lack of Phytase enzyme, the phytic acid is not digested in the gut of humans, poultry, and swine and is expelled directly to the environment through excreta, posing a serious pollution concern due to the continuous expulsion of high phosphorus load into the nearby water bodies (Jorquera *et al.*, 2008). Hence, bringing down the phytate in maize might be an important strategy for Zn biofortification.

Lysine and tryptophan are two essential amino acids and these are deficits in maize grain thus, posing the problem of lysine and tryptophan deficiency human diseases like cognitive disorder, kwashiorkor disease, reduced appetite, impaired skeleton development, delayed growth, and aberrant behavior are associated with. These amino acids are also important for curing pellagra disease. Researchers have identified several mutants in maize especially *opaque-2* which are responsible for higher lysine and tryptophan contents. Concerted efforts of researchers spanning over the period of four decades to develop quality protein maize (QPM) which is nutritionally superior maize with high lysine and tryptophan. The *opaque-2* genetic system, endosperm modifier genetic system, and associated gene systems-based approaches are followed in maize for the improvement of quality protein (Maqbool *et al.*, 2021). Recently, researchers reported promising result in the development of edible Rabies vaccines in maize, which is safer, cheaper, effective, and does not need to be refrigerated (Loza-Rubio *et al.*, 2008; Das *et al.*, 2021).

The anaphylaxis symptoms i.e. sudden drop in blood pressure, difficulty in breathing, tightness in the chest, dizziness, and unconsciousness developed in some persons due to the presence of allergic compounds (9 kd protein and 16 kd protein) in maize. Again, if someone eats corn in large quantities, then it can cause bloating & flatulence due to the presence of a high percentage of starch. Although the milling of the maize kernel into flour and subsequent cooking may increase the accessibility of maize food, further research is needed to develop suitable varieties to solve these problems.

Conclusion

Maize is one of the best nutritive foods for the human diet due to its excellent source of carbohydrates, fiber, protein, vitamins, minerals, and antioxidants such as different types of polyphenols. Thus, based on its health benefits, it is suggested to make it part of our daily diet. The rapid advances that have been made in understanding the genetic control of many macro-and micro-nutrients in maize grains, coupled with the availability of new technologies will accelerate the rate of genetic gain for further improvement in nutrient content in maize. In a developing country like India, the maize crop has great potential to eradicate poverty as well as malnutrition. Modern breeding and biotechnology approaches, Interdisciplinary research, and more effective integration and collaboration of national and international research efforts can enhance the nutritional status as well as productivity of maize.

References

Andersson, M. S., Saltzman, A., Virk, P. S. & Pfeiffer, W. H. (2017). Progress update: crop development of biofortified staple food crops under Harvestplus. *African Journal of Food, Agriculture, Nutrition and Development*, **17**: 11905–11935.

Bänziger, M. & Long, J. (2000). The potential for increasing the iron and zinc density of maize through plant-breeding. *Food and Nutrition Bulletin* **21**: 397–400.

Bressani, R., Breuner, M. & Ortiz, M. A. (1989). Contenido de fibra ácido- y néutro-detergente y de minerales menores en maíz y su tortilla. *Arch. Lat. American Nutrition,* 39: 382–391.

Carrillo, W., Carpio, C., Morales, D., Vilcacundo E, Alvarez, M. & Silva, M. (2017). Content of fatty acid in corn (*Zea Mays* L.) Oil. *Asian Journal of Pharmaceutical and Clinical Research*, **10**(8): 150–153.

Chen, I. S., Hotta, S. S., Ikeda, I., Cassidy, M. M., Sheppard, A. J. & Vahouny, G. V. (1987). Digestion, absorption and effects on cholesterol absorption of menhaden oil, fish oil concentrate and corn oil by rats. *Journal of Nutrition*, **117**: 1676–1680.

Chew, B. P., Wong, M. W. & Wong, T. S. (1996). Effects of lutein from marigold extract on immunity and growth of mammary tumors in mice. *Journal of Anticancer Research,* **16**: 3689–3694.

Choi, D. Y., Lee, Y. J., Hong, J. T. & Lee, H. J. (2012). Antioxidant properties of natural polyphenols and their therapeutic potentials for Alzheimer's disease. *Brain Research Bulletin*, **87**(2–3): 144–153.

Das, T. R., Samantarai, R. K. & Panda, P. K. (2021). Prospects of plant based edible vaccines in combating COVID-19 and other viral pandemics: A review. *e-planet*, **19**(1): 1–18.

DES. (2021). Agricultural Statistics at a glance-2021, Directorate of Economics and Statistics, DA&FW, Ministry of Agriculture and Farmers Welfare, Government of India. pp. 38–80.

Díaz-Gómez, J. L., Castorena-Torres, F., Preciado-Ortiz, R. E. & García-Lara, S. (2017). Anti-cancer activity of maize bioactive peptides. *Frontiers in Chemistry*, **5**: 44.

Dupont, J., White, P. J., Carpenter, M. P., Schaefer, E. J., Meydani, S. N., Elson, C. E. & Gorbach, S. L. (1990). Food uses and health effects of corn oil. *Journal of the American College of Nutrition*, **9**: 438–470.

FAOSTAT. (2020). https://www.fao.org./faostat/en/#data/QCL.

Ghosh, D. & Konishi, T. (2007). Anthocyanins and anthocyanin rich extracts: Role in diabetes and eye function. *Asia Pacific Journal of Clinical Nutrition,* **16**: 200–208.

Giuliano, G. (2017). Provitamin A biofortification of crop plants: a gold rush with many miners. *Current. Opinion. in Biotechnology*, **44**: 169–180.

Hagiwara, A., Miyashita, K., Nakanishi, T., Sano, M., Tamano, S., Kadota, T. & Shirai, T. (2001). Pronounced inhibition by a natural anthocyanin, purple corn color, of 2-amino-1-methyl-6-phenylimidazo[4,5-b]pyridine (PhIP)-associated colorectal carcinogenesis in male F344 rats pretreated with 1,2-dimethylhydrazine. *Cancer Letters,* **171**: 17–25.

Han, X., Shen, T. & Lou, H. (2007) Dietary polyphenols and their biological significance. *International Journal of Molecular Sciences*, **8**(9): 950–988.

Hannah, L. C., Giroux, M. & Boyer, C. (1993). Biotechnological modification of carbohydrates for sweet corn and maize improvement. *Scientia Horticulturae*, **55**(1): 177–197.

Higgins, J. A. (2004). Resistant starch: Metabolic effects and potential health benefits. *Journal of AOAC International,* **87**: 761–768.

Hindu, V., Palacios-Rojas, N., Babu, R., Suwarno, W. B., Rashid, Z., Usha, R., *et al.* (2018). Identification and validation of genomic regions influencing kernel zinc and iron in maize. *Theoretical and Applied Genetics*, **131**: 1443–1457.

Huang, B., Wang, Z., Park, J. H., Ryu, O. H., Choi, M. K., Lee, J. Y., Kang, Y. H. & Lim, S. S. (2015). Anti-diabetic effect of purple corn extraction. *Nutrition Research and Practice*, **9**(1): 22–29.

Iacono, J. M. & Dougherty, G. E. (1993). Effects of polyunsaturated fats on blood pressure. *Annual Review of Nutrition*, **13**: 243–260.

IDF. (2021). IDF diabetes atlas, 10th edition, International Diabetes Federation. Belgium. pp. 1–63.

Iltis, H. H. & Doebley, J. F. (1980). Taxonomy of *Zea* (Gramineae). II. Subspecific categories in the *Zea mays* complex and a generic synopsis. *American Journal of Botany*, **67**: 994–1004.

Jang, S. H., Lim, J. W. & Kim, H. (2009). Mechanism of β-carotene-induced apoptosis of gastric cancer cells: Involvement of ataxia-telangiectasia-mutated. *Annals of the New York Academy of Sciences*, **1171**: 156–162.

Jayaram, S., Kapoor, S. & Dharmesh, S. M. (2015). Pectic polysaccharide from corn (*Zea mays* L.) effectively inhibited multi-step mediated cancer cell growth and metastasis. *Chemico-Biological Interactions*, **235**: 63–75.

Jin, D., Xiao-lan, L., Xi-qun, Z., Xiao-Jie, W. & Jun-fang, H. (2016). Preparation of antioxidative corn protein hydrolysates, purification and evaluation of three novel corn antioxidant peptides. *Food Chemistry*, **204**: 427–436.

Johnston, K. L., Thomas, E. L., Bell, J. D., Frost, G. S. & Robertson, M. D. (2010). Resistant starch improves insulin sensitivity in metabolic syndrome. *Diabetic Medicine*, **27**: 391–397.

Jongfeng, A. & Jay-Lin, J. (2016). Macronutrients in corn and human nutrition. *Comprehensive Reviews in Food Science and Food Safety*, **15**(3): 581–598.

Jorquera, M., Martinez, O. Z., Maruyama, F., Marschner, P. & de la Luz Mora, M. (2008). Current and future biotechnological applications of bacterial phytases and phytase-producing bacteria. *Microbes Environment*, **23**: 182–191.

Kang, M. K., Lim, S. S., Lee, J. Y, Yeo, K. M. & Kang, Y. H. (2013). Anthocyanin-rich purple corn extract inhibits diabetes-associated glomerular angiogenesis. *PLoS One*, **8**(11): e79823.

Kawabata, K., Yamamoto, T., Hara, A., Shimizu, M., Yamada, Y., Matsunaga, K. & Mori, H. (2000). Modifying effects of ferulic acid on azoxymethane-induced colon carcinogenesis in F344 rats. *Cancer Letters*, **157**: 15–21.

Keenan, M. J., Zhou, J., Hegsted, M., Pelkman, C., Durham, H. A., Coulon, D. B. & Martin, R. J. (2015). Role of resistant starch in improving gut health, adiposity, and insulin resistance. *Advances in Nutrition*, **6**: 198–205.

Keenan, M. J., Zhou, J., Mc Cutcheon, K. L., Raggio, A. M., Bateman, H. G., Todd, E., Jones, C. K., Tulley, R. T., Melton, S., Martin, R. J. & Hegsted, M. (2006). Effects of resistant starch, a non-digestible fermentable fiber, on reducing body fat. *Obesity* (Silver Spring), **14**: 1523–1534.

Kumar, D. & Jhariya, A. N. (2013) Nutritional, medicinal and economical importance of corn: A mini review. *Research Journal of Pharmaceutical Sciences*, **2**(7): 7–8.

Landrum, J. T., Bone, R. A. & Kilburn, M. D. (1997). The macular pigment: A possible role in protection from age-related macular degeneration. *Journal of Advanced Pharmacology*, **38**: 537–556.

Liu, R. H. (2007). Whole grain phytochemicals and health. *Journal of Cereal Science*, **46**: 207–219.

Locatelli, S., & Berardo, N. (2014). Chemical composition and phytosterols profile of degermed maize products derived from wet and dry milling. Consiglio per la Ricercae la sperimentazione in Agricoltura, Unità di Ricerca per la Maiscoltura (CRA-MAC), via Stezzano 24, 24126 Bergamo, Italy. *Maydica*, **59**: 261–266.

Long, N., Suzuki, S., Sato, S., Naiki-Ito, A., Sakatani, K., Shirai, T. & Takahashi, S. (2013). Purple corn color inhibition of prostate carcinogenesis by targeting cell growth pathways. *Cancer Science*, **104**: 298–303.

Longvah, T., Ananthan, R., Bhaskarachary, K. & Venkaiah, K. (2017). Indian Food Composition Tables. India: National Institute of Nutrition, Indian Council of Medical Research, Department of Health Research, Ministry of Health & Family Welfare, Government of India. pp. 3–171.

Loza-Rubio, E., Rojas, A. E., Gómez, N. L., Olivera, F. M. T. J. & Gómez-Lim, M. 2008. Development of an edible rabies vaccine in maize using the Vnukovo strain. *Developmental Biology* (Karger), **131**: 477–482.

Madhujith, T. & Shahidi, F. (2007). Antioxidative and antiproliferative properties of selected barley cultivars and their potential of inhibition of copper induced LDL cholesterol oxidation. *Journal of Agricultural and Food Chemistry*, **55**: 5018–5024.

Maqbool, M. A., Issa, A. R. B. & Khokhar, E. S. (2021). Quality protein maize (QPM): Importance, genetics, timeline of different events, breeding strategies and varietal adoption. *Plant Breeding*, **140**: 375–399.

Menkir, A., Liu, W., White, W. S., Mazlya-Dixon, B. & Rocheford, T. (2008). Carotenoid diversity in tropical-adapted yellow maize inbred lines. *Food Chemistry*, **109**: 521–529. doi: 10.1016/j.foodchem.2008.01.002

Menkir, A., Maziya-Dixon, B., Mengesha, W., Rocheford, T. & Alamu, E. O. (2017). Accruing genetic gain in pro-vitamin A enrichment from harnessing diverse maize germplasm. *Euphytica*, **213**: 105.

Michaud, D. S., Feskanich, D., Rimm, E. B., Colditz, G. A., Speizer, F. E., Willett, W. C. & Giovannucci, E. (2000). Intake of specific carotenoids and risk of lung cancer in 2 prospective US cohorts. *American Journal of Clinical Nutrition*, **72**: 990–997.

Milind, P. & Isha, D. (2013). *Zea maize*: A modern craze. *International Research Journal of Pharmacy*, **4**(6): 39–43.

Momany, F. A., Sessa, D. J., Lawton, J. W., Selling, G. W., Hamaker S. A., & Willett, J. L. (2006). Structural characterization of a-Zein. *Journal of Agricultural and Food Chemistry*, **54**: 543–547.

Moreau, R. A. (2011). Corn oil. Vegetable Oils in Food Technology: Composition, Properties and Uses, Second Edition. pp. 273–289.

Moreno, F. S., Toledo, L. P., de Conti, A., Heidor, Jr. R., Jordão, A., Vannucchi, H. & Ong, T. P. (2007). Lutein presents suppressing but not blocking chemopreventive activity during diethyl nitrosamine-induced hepatocarcinogenesis and this involves inhibition of DNA damage. *Chemico- Biological Interactions*, **168**: 221–228.

Moros, E. E., Darnoko, D., Cheryan, M., Perkins, E. G. & Jerrell, J. (2002). Analysis of Xanthophylls in corn by HPLC. *Journal of Agricultural and Food Chemistry*, **50**: 5787–5790.

Murphy, M. M., Douglass, J. S. & Birkett, A. (2008). Resistant starch intakes in the United States. *Journal of the American Dietetic Association*, **108**: 67–78.

Ortiz-Monasterio, J. I., Palacios-Rojas, N., Meng, E., Pixley, K., Trethowan, R. & Pena, R. J. (2007). Enhancing the mineral and vitamin content of wheat and maize through plant breeding. *Journal of. Cereal Science,* **46**: 293–307. doi: 10.1016/j.jcs.2007.06.005

Ou, L., Kong, L. Y., Zhang, X. M. & Niwa, M. (2003). Oxidation of ferulic acid by *Momordica charantia* peroxidase and related anti-inflammation activity changes. *Biological and Pharmaceutical Bulletin,* **26**: 1511–1516.

Palozza, P., Calviello, G., Serini, S., Maggiano, N., Lanza, P., Ranelletti, F. O. & Bartoli, G. M. (2001). β–carotene at high concentrations induces apoptosis by enhancing oxyradical production in human adenocarcinoma cells. *Free Radical Biology and Medicine,* **30**: 1000–1007.

Palozza, P., Serini, S., Torsello, A., Di Nicuolo, F., Maggiano, N., Ranelletti, F. O. & Calviello, G. (2003). Mechanism of activation of caspase cascade during β-carotene-induced apoptosis in human tumor cells. *Nutrition and Cancer,* **47**: 76–87.

Pixley, K., Palacios, N. R., Babu, R., Mutale, R., Surles, R. & Simpungwe, E. (2013). Biofortification of maize with provitamin A carotenoids. In: Carotenoids in Human Health. Ed. S. A. Tanumihardo (New York: Springer Science and Business Media), pp 271–292.

Rukkumani, R., Aruna, K., Varma, P. S. & Menon, V. P. (2004). Influence of ferulic acid on circulatory prooxidant prooxidant-antioxidant status during alcohol and PUFA induced toxicity. *Journal of Physiology and Pharmacology,* **55**: 551–561.

Salinas-Moreno, Y., Soto-Hernández, M., Martínez-Bustos, F., González-Hernández, V. & Ortega-Paczka, R. (1999). Análisis de antocianinas en maíces de grano azul y rojo provenientes de cuatro razas [Analysis of anthocyanins in four races from blue and Red grain maize]. *Revista Fitotecnia Mexicana,* **22**: 161–174.

Shah, T. R., Prasad, K. & Kumar, P. (2016). Maize–A potential source of human nutrition and health: A review. *Cogent Food & Agriculture*, **2**(1): 1–9.

Shindo, M., Kasai, T., Abe, A. & Kondo, Y. (2007). Effects of dietary administration of plant-derived anthocyanin-rich colors to spontaneously hypertensive rats. *Journal of Nutritional Science and Vitaminology,* **53**: 90–93.

Urias-Lugo, D. A., Heredia, J. B., Muy-Rangel, M. D., Valdez-Torres, J. B., Serna-Sald'ivar, S. O. & Guti'errez-Uribe, J. A. (2015). Anthocyanins and phenolic acids of hybrid and native blue maize (*Zea mays* L.) extracts and their antiproliferative activity in mammary (MCF7), liver (HepG2), colon (Caco2 and HT29) and prostate (PC3) cancer cells. *Plant Foods for Human Nutrition*, **70**(2): 193–199.

Wang, X., Brown, I. L., Khaled, D., Mahoney, M. C., Evans, A. J. & Conway, P. L. (2002). Manipulation of colonic bacteria and volatile fatty acid production by dietary high amylase maize (amylo maize) starch granules. *Journal of Applied Microbiology,* **93**: 390–397.

Watson, S. A. & Ramstad, P. E. (1987). *Corn: Chemistry and technology* (1st ed.). St. Paul, MN: American Association of Cereal Chemists. pp. 453–455.

Zhao, Z., Egashira, Y. & Sanada, H. (2005). Phenolic antioxidants richly contained in corn bran are slightly bioavailable in rats. *Journal of Agricultural and Food Chemistry,* **53**: 5030–5035.

Zhou, Z., Wang, F., Ren, X., Wang, Y. & Blanchard, C. (2015). Resistant starch manipulated hyperglycemia/hyperlipidemia and related genes expression in diabetic rats. *International Journal of Biological Macromolecules,* **75**: 316–321.

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RESEARCH PAPER

Weed management in maize with new generation herbicides under vertisols of Rajasthan

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Abstract: A field experiment was conducted at Research Farm of Agricultural Research Station, Ummedganj, Kota (Agriculture University, Kota), Rajasthan, India during *Kharif* 2017 and 2018, with the objective to find out effective post-emergence new generation herbicides for controlling weeds as season long and increasing the productivity of maize under vertisols of Rajasthan. The treatments comprised of T_1: Weedy check, T_2: Hand weeding twice (20 & 40 DAS), T_3: Atrazine 50% WP @ 0.5 kg a.i./ha (PE), T_4: Bentazone 48% SL @ 1.2 kg a.i./ha (15-20 DAS), T_5: Tembotrione 42% SC @ 120.75 g a.i./ha (15-20 DAS), T_6: Tembotrione 42% SC @ 150.95 g a.i./ha (15-20 DAS), T_7: Topramezone 33.6% SC @ 25.2 g a.i./ha (15-20 DAS), T_8: Topramezone 33.6% SC @ 31.5 g a.i./ha (15-20 DAS), T_9: Tembotrione 42% SC @ 120.75 g a.i./ha +Atrazine 50 WP @ 0.5 kg a.i./ha (15-20 DAS) and T_{10}: Topramezone 33.6% SC @ 25.2 g a.i./ha + Atrazine 50 WP @ 0.5 kg a.i./ha (15-20 DAS). Results showed that the application of Topramezone 31.5 g a.i./ha at 15-20 DAS recorded significantly minimum weed density, weed dry weight and maximum weed control efficiency at 30 & 60 DAS being at par with Tembotrione 150.95 g a.i./ha followed by Topramezone 25.2 g a.i./ha and Tembotrione 120.75 g a.i./ha, which were at par with hand weeding twice at 20 & 40 DAS over rest of the treatments. Maximum yield attributes viz., no. of cobs/ plant, no. of grains/cob, 100-grain weight and grain yield was recorded with the Topramezone 31.5 g /ha at 15-20 DAS and being on par with Tembotrione 150.95 g a.i./ha, Topramezone 25.2 g a.i./ha, Tembotrione 120.75 g a.i./ha and hand weeding twice at 20 & 40 DAS over rest of the weed management practices. Post emergence application of Topramezone 31.5 g a.i./ha at 15-20 DAS also fetched significantly higher net returns (Rs. 66503/ha) and B:C ratio to the tune of 207.39 & 158.33 per cent, respectively over weedy check and being on par with Tembotrione 150.95 g a.i./ha, Topramezone 25.2 g a.i./ha, Tembotrione 120.75 g a.i./ha, Tembotrione 120.75 g a.i./ha + Atrazine 0.5 kg a.i./ha, Topramezone 25.2 g a.i./ha + Atrazine 0.5 kg a.i./ha and hand weeding twice at 20 & 40 DAS.

Keywords: Economics · Maize · New generation herbicide · Weed control efficiency · Weed management

Introduction

Maize (*Zea mays* L.) is one of the important cereal crop of the world, known as "Queen of cereals" due to its great importance in human and animal diet. It is very efficient utilizer of solar energy and has immense potential for higher yield. It is known for its wider adaptability and multipurpose uses as food, fodder and industrial products (Murdia *et al*., 2016). It is also an important source of vitamins and minerals like Ca, P, S and small amounts of Na. Its flour is considered to be a good diet for heart patients due to its low gluten (protein) content (Rasool and Khan, 2016). The productivity of maize in India is relatively very low compared to developed countries of world mainly due to lack of timely weed control. The major yield reducing factors for maize cultivation in India are weeds (Gharde *et al*., 2018) and about 100 weed

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species in 66 genera and 24 plant families are known to be problematic for maize in the country. Most of the presently available herbicides provide only a narrow spectrum weed control (Patel *et al.*, 2006). Weed control practices in maize resulted in 65 to 90% higher yield than unweeded (Barla *et al.*, 2016). Topramezone and Tembotrione are the new selective, post-emergence herbicides introduced for use in maize that inhibit hydroxy-phenyl pyruvate dioxygenase (4-HPPD) enzyme and the biosynthesis of plastoquinone (Swetha *et al.*, 2015). There is need for some alternate post-emergence herbicide like Tembotrione which can provide broad spectrum weed control in *kharif* maize without affecting the growth and yield of crop (Williams *et al.*, 2011; Yadav *et al.*, 2017). Thus, weed management with new generation broad spectrum herbicides are needed. Therefore, this study was conducted to evaluate the weed control efficiency of new generation herbicides in *kharif* maize under vertisols of Rajasthan.

Materials and methods

A field experiment was conducted on weed management in maize with new generation herbicides during *Kharif* 2017 and 2018 at Agricultural Research Station, Ummedganj, Kota, Rajasthan with the objective to find out effective post emergence new generation herbicide for controlling weeds as season long and increasing the productivity of maize. The region falls under the Agro Climatic Zone V of Rajasthan *i.e.* Humid South-Eastern Plain zone.

The mean weekly meteorological observations recorded during the crop period are presented in Figure 1. The mean daily maximum and minimum temperature during the growing season fluctuated between 30.0 to 43.2°C and 15.3 to 29.0°C, respectively in the year 2017. The corresponding values for the year 2018 were between 28.3 to 43.4°C and 18.9 to 29.1°C, respectively. The total rainfall received was 487 and 524 mm and total rainy days were 25 and 29 days respectively, during the growing season of the year 2017 and 2018.

The soil of the experimental field was clay loam with slightly alkaline pH (7.65), having medium available nitrogen (395.0 kg/ha), available phosphorus (22.5 kg/ha) and high available potassium (360.0 kg/ha) content. The experiment was laid out in randomized block design with three replications. The experimental site was mainly infested with grassy and broad leaf weeds *viz.*, *Echinochloa colona*, *Cyperus rotundus*, *Cynodon Dectylon*, *Commelina benghalensis*, *Trianthema monogyana* and *Digera arvensis etc.* It was observed that maize crop was majorly infested with grassy weeds followed by broad leaf weeds during growing season. The treatments comprised of T_1: Weedy check, T_2: Hand weeding twice (20 & 40 DAS), T_3: Atrazine 50% WP @ 0.5 kg a.i./ha (PE), T_4: Bentazone 48% SL @ 1.2 kg a.i./ha (15-20 DAS), T_5: Tembotrione 42% SC @ 120.75 g a.i./ha (15-20 DAS), T_6: Tembotrione 42% SC @ 150.95

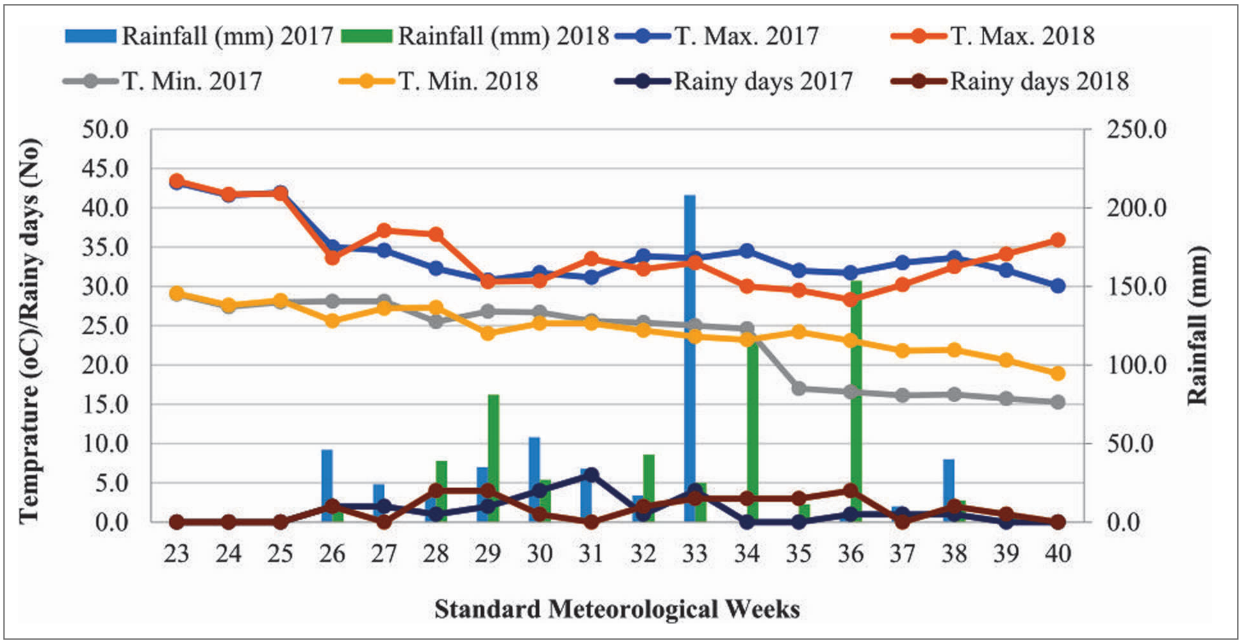

Figure 1. Weekly meteorological observatory data during experimental years (2017 & 2018)

g a.i./ha (15-20 DAS), T_7: Topramezone 33.6% SC @ 25.2 g a.i./ha (15-20 DAS), T_8: Topramezone 33.6% SC @ 31.5 g a.i./ha (15-20 DAS), T_9: Tembotrione 42% SC @ 120.75 g a.i./ha +Atrazine 50 WP @ 0.5 kg a.i./ha (15-20 DAS) and T_{10}: Topramezone 33.6% SC @ 25.2 g a.i./ha + Atrazine 50 WP @ 0.5 kg a.i./ha (15-20 DAS). The crop was grown and managed with the recommended package of practices for the zone. All the herbicides were applied uniformly in the experimental plots with the help of knapsack sprayer. The maize variety "Hybrid Kaveri Seeds (218+)" was sown at a spacing of 60×25 cm^2 between rows and plants. All the recommended agronomic and plant protection measures were adopted to raise the crop. Observation recorded on weed density (Nos/m^2), weed dry weight (g/m^2) at 30 & 60 DAS, these were subjected to square root transformation to normalize their distribution, yield attributes (number of cobs $plant^{-1}$, number of grains cob^{-1}, 100-grain weight (g) and grain yield (kg/ha). The efficiency of weed management treatments was assessed by weed control efficiency (%) calculated as:

$$\text{WCE (\%)} = \frac{WD_C - WD_t}{WD_C} \times 100$$

Where, WCE is weed control efficiency, WD_C is the weed dry matter in control plot and WD_t is the weed dry matter in the respective treatment.

The economics was calculated on the basis of prevailing market prices of input and produce.

Results and discussion

The data on pooled basis depicted in Table 1, revealed that the significantly minimum weed density and weed dry weight was observed with the application of Topramezone 31.5 g a.i./ha at 15-20 DAS, however it was at par with Tembotrione 150.95 g a.i./ha over rest of the treatments. The next best treatment was Topramezone 25.2 g a.i./ha being on par with Tembotrione 120.75 g a.i./ha, which were at par with hand weeding twice at 20 & 40 DAS. Maximum weed density was found in weedy check which was significantly higher over rest of the treatments. These findings were in close conformity with the Stephenson *et al.* (2015), Rana *et al.* (2017), Sundari *et al.* (2019) and Kantwa *et al.* (2020).

The data in Table 1 also revealed that the maximum per cent weed control efficiency (92.87 and 86.01) was recorded under the treatment of Topramezone 31.5 g a.i./ha, being at par with Tembotrione 150.95 g a.i./ha (90.67 and 83.88) followed by Topramezone 25.2 g a.i./ha (90.38 and 79.05) and Tembotrione 120.75 g a.i./ha (87.92 and 77.40) which were at par with hand weeding twice at 20 & 40 DAS (88.11 and 82.40) at 30 & 60 DAS, respectively over rest of the treatments. This might be due to post-emergence application of Topramezone and

Table 1. Effect of different herbicides on weed density, weed dry weight and weed control efficiency (WCE) in maize (Pooled mean of 2 years)

Treatments	Weed density (Nos/m^2)		Weed dry weight (g/m^2)		WCE (%)	
	30 DAS	60 DAS	30 DAS	60 DAS	30 DAS	60 DAS
Weedy check	13.80 (190.00)*	15.43 (237.83)	6.52 (43.01)	8.06 (64.74)	0.00	0.00
Hand weeding twice (20 & 40 DAS)	3.97 (15.50)	5.82 (33.67)	2.24 (4.86)	3.40 (11.36)	88.11	82.40
Atrazine 50% WP @ 0.5 kg ai/ha (PE)	7.81 (60.33)	11.35 (128.17)	4.07 (16.28)	6.28 (39.04)	59.89	38.36
Bentazone 48% SL @ 1.2 kg ai/ha (15-20 DAS)	9.31 (85.83)	12.84 (163.67)	5.00 (24.60)	7.07 (49.35)	37.83	22.12
Tembotrione 42 % SC @ 120.75 g ai/ha (15-20 DAS)	3.74 (13.67)	6.75 (45.00)	2.24 (4.82)	3.82 (14.26)	87.92	77.40
Tembotrione 42 % SC @ 150.95 g ai/ha (15-20 DAS)	3.26 (10.33)	5.73 (32.50)	1.95 (3.63)	3.24 (10.21)	90.67	83.88
Topramezone 33.6 % SC @ 25.2 g ai/ha (15-20 DAS)	3.39 (11.17)	6.16 (37.33)	2.01 (3.88)	3.69 (13.28)	90.38	79.05
Topramezone 33.6 % SC @ 31.5 g ai/ha (15-20 DAS)	2.91 (8.17)	5.08 (25.50)	1.73 (2.83)	3.02 (8.93)	92.87	86.01
Tembotrione 42 % SC @ 120.75 g ai/ha +Atrazine 50 WP @ 0.5 kg a.i./ha (15-20 DAS)	3.96 (15.33)	6.50 (41.67)	2.22 (4.72)	3.74 (13.62)	88.13	78.21
Topramezone 33.6 % SC @ 25.2 g ai/ha + Atrazine 50 WP @ 0.5 kg a.i./ha (15-20 DAS)	3.23 (10.17)	5.98 (35.33)	1.92 (3.50)	3.61 (12.69)	91.10	79.70
SEm±	0.13	0.19	0.09	0.10	1.49	1.65
CD (P=0.05)	0.38	0.55	0.26	0.30	4.27	4.74

*$\sqrt{x+0.05}$ Transformed values and data in parenthesis are original values

Tembotrione controlled majority of weeds. The results are in close agreement with the findings of Swetha *et al*. (2015), Damalas *et al*. (2018) and Kantwa *et al*. (2020).

A perusal of data presented in Table 2 reveals that all weed management practices significantly affected the yield attributes and grain yield of maize over weedy check. Maximum yield attributes *viz*., no. of cobs/plant, no. of grains/cob, 100-grain weight and grain yield was recorded with the Topramezone 31.5 g a.i./ha at 15-20 DAS and being on par with Tembotrione 150.95 g ai/ha, Topramezone 25.2 g a.i./ha, Tembotrione 120.75 g a.i./ha and twice hand weeding twice at 20 & 40 DAS over rest of the weed management practices. The better expression of yield attributes in herbicide treated plots might be due to minimum crop-weed competition during critical phases of crop growth chemically exerts an important regulation function on complex processes of yield formation, due to better availability of growth inputs *viz*., water, space and nutrients. These findings are close conformity with the Teame *et al*. (2017), Patel *et al*. (2018) and Kantwa *et al*. (2020).

Results further shown in Table 3 reported that post-emergence application of Topramezone 31.5 g a.i./ha at 15-20 DAS fetched significantly higher net returns (Rs. 66503/ha) and B:C ratio (2.48) to the tune of 207.39 and 158.33 per cent, respectively over weedy check and while

Table 2. Effect of different herbicides on yield attributes and yield of maize (Pooled mean of 2 years)

Treatments	No. of cobs /plant	No. of grains /cob	100-grain weight (g)	Grain yield (kg/ha)
Weedy check	0.93	254.83	30.88	2830
Hand weeding twice (20 & 40 DAS)	1.15	434.50	32.79	5736
Atrazine 50% WP @ 0.5 kg ai/ha (PE)	1.00	352.33	31.96	4645
Bentazone 48% SL @ 1.2 kg ai/ha (15-20 DAS)	1.00	342.67	31.93	4494
Tembotrione 42 % SC @ 120.75 g ai/ha (15-20 DAS)	1.12	429.67	32.85	5701
Tembotrione 42 % SC @ 150.95 g ai/ha (15-20 DAS)	1.15	452.67	32.75	5884
Topramezone 33.6 % SC @ 25.2 g ai/ha (15-20 DAS)	1.13	438.00	32.89	5764
Topramezone 33.6 % SC @ 31.5 g ai/ha (15-20 DAS)	1.17	463.00	32.94	5990
Tembotrione 42 % SC @ 120.75 g ai/ha +Atrazine 50 WP @ 0.5 kg a.i./ha (15-20 DAS)	1.08	398.83	32.37	5382
Topramezone 33.6 % SC @ 25.2 g ai/ha + Atrazine 50 WP @ 0.5 kg a.i./ha (15-20 DAS)	1.09	406.67	32.47	5417
SEm±	0.02	11.59	0.13	170
CD (P=0.05)	0.05	33.22	0.37	487

Table 3. Effect of different herbicides on economics of maize (Pooled mean of 2 years)

Treatments	Cost of cultivation (Rs/ha)	Net returns (Rs/ha)	B:C Ratio
Weedy check	22562	21636	0.96
Hand weeding twice (20 & 40 DAS)	30602	58752	1.92
Atrazine 50% WP @ 0.5 kg ai/ha (PE)	22962	49298	2.15
Bentazone 48% SL @ 1.2 kg ai/ha (15-20 DAS)	24122	45743	1.90
Tembotrione 42 % SC @ 120.75 g ai/ha (15-20 DAS)	26422	62383	2.36
Tembotrione 42 % SC @ 150.95 g ai/ha (15-20 DAS)	27387	64166	2.34
Topramezone 33.6 % SC @ 25.2 g ai/ha (15-20 DAS)	25712	64090	2.49
Topramezone 33.6 % SC @ 31.5 g ai/ha (15-20 DAS)	26762	66503	2.48
Tembotrione 42 % SC @ 120.75 g ai/ha +Atrazine 50 WP @ 0.5 kg a.i./ha (15-20 DAS)	27072	64422	2.38
Topramezone 33.6 % SC @ 25.2 g ai/ha + Atrazine 50 WP @ 0.5 kg a.i./ha (15-20 DAS)	26362	65721	2.49
SEm±	-	2759	0.11
CD (P=0.05)	-	7912	0.30

Figure 2. (a) Weedy Check, (b) Tembotrione 42% SC 120.75 g a.i./ha, (c)Topramezone 33.6% SC 25.2 g a.i./ha

being at par with Tembotrione 150.95 g a.i./ha, Topramezone 25.2 g a.i./ha, Tembotrione 120.75 g a.i./ha, Tembotrione 120.75 g a.i./ha + Atrazine 0.5 kg a.i./ha, Topramezone 25.2 g a.i./ha + Atrazine 0.5 kg a.i./ha and hand weeding twice at 20 & 40 DAS. This might be due to the higher grain yield of maize under these treatments. The results are in close conformity with the findings of Kantwa *et al*. (2020).

Conclusion

Post-emergence application of new generation herbicides *viz.*, Topramezone 25.2 g a.i./ha or Tembotrione 120.75 g a.i./ha at 15-20 DAS found effective for controlling season long weeds, higher yield and returns in *kharif* maize under vertisols of south-eastern Rajasthan.

References

Barla, S., Upasani, R. R., Puran, A. N. & Thakur, R. (2016). Weed management in maize. *Indian Journal of Weed Science,* **48**(1): 67–69.

Damalas, C. A., Gitsopoulos, T. K., Koutroubas, S. D., Alexoudis, C. & Georgoulas, I. (2018). Weed control and selectivity in maize (*Zea mays* L.) with Tembotrione mixtures. *International Journal of Pest Management,* **64**(1): 11–18.

Gharde, Y., Singh, P. K., Dubey, R. P. & Gupta P. K. (2018). Assessment of yield and economic losses in agriculture due to weeds in India. *Crop Protection,* **107**: 12–18.

Kantwa, S., Jadon, C. K., Tetarwal, J. P., Ram, B., Kantwa, S. R. & Yadav, R. K. (2020). Effect of weed management practices on weed dynamics, yield attributes and yield of maize. *International Journal of Bio-resource and Stress Management.* **11**(5): 488-493.

Murdia, L. K., Wadhwani, R., Wadhawan, N., Bajpai, P. & Shekhawat, S. (2016). Maize utilization in India: an overview. *American Journal of Food and Nutrition,* **4**(6): 169–176.

Patel, B. D., Chaudhari, D. D., Patel, V. J., Patel, H. K. & Mishra, A. (2018). Weed dynamics and production potential of *kharif* maize (*Zea mays* L.) as influenced by new generation herbicides. *Crop Research,* **53**(5&6): 209–214.

Patel, V. J., Upadhyay, P. N., Patel, B. & Patel, B. D. (2006). Evaluation of herbicide mixtures for weed control in maize (*Zea mays* L.) under middle Gujarat conditions. *The Journal of Agricultural Science,* **2**(1): 81–86.

Rana, S. S., Badiyala, D., Sharma, N., Kumar, R. & Pathania, P. (2017). Impact of Tembotrione on weed growth, yield and economics of maize (*Zea mays* L.) under mid hill conditions of Himachal Pradesh. *Pesticide Research Journal,* **29**(1): 27–34.

Rasool, S. & Khan, M. H. (2016). Growth and yield of maize (*Zea mays* L.) as influenced by integrated weed management under temperate conditions of North Western Himalayas. *American Journal of Experimental Agriculture,* **14**(1): 1–9.

Sundari, A., Kalaisudarson, S., Srinivasaperumal, A. P. & Gowtham, S. S. R. (2019). Response of irrigated maize to new herbicides. *Plant Archives,* **19**(2): 2465–2468.

Swetha, K., Madhavi, M., Pratibha, G. & Ramprakash, T. (2015). Weed management with new generations herbicides in maize. *Indian Journal of Weed Science,* **47**(4): 432-433.

Teame, G., Tsegay, A. & Abrha, B. (2017). Effect of organic mulching on soil moisture, yield and yield contributing components of sesame (*Sesamum indicum* L.) *International Journal of Agronomy*. https://doi. org/10.1155/2017/4767509.

Williams, M. M., Boydston, R. A., Peachey, R. E. & Robinson, D. (2011). Significance of Atrazine as a tank-mix partner with Tembotrione. *Weed Technology,* **25**(3): 299–302.

Yadav, T. K., Choudhary, R. S., Jat, G., Singh, D. & Sharma, N. (2017). Effect of weed management practices on yield attributes, yield and economics of maize (*Zea mays* L.). *Chemical Science Review and Letters,* **6**(23): 1452-1456.

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RESEARCH PAPER

Soil physico-chemical properties and nutrient balance as influenced by integrated weed and nutrient management in a transitional plain zone of Luni basin of Rajasthan

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Abstract: An experiment was conducted during *Kharif* 2019 and 2020 at Instructional Farm, College of Agriculture, Sumerpur (Rajasthan) to study the impact of integrated methods of weed management and organic nutrient sources on the nutrient balance sheet after harvest of maize (*Zea mays* L.). The experiment comprised 6 weed management and 5 nutrient management practices in a split-plot design with three replications. The treatments stale seedbed + hoeing once at 20 DAS + application of 5 t/ha straw mulch at 30 DAS and weed-free check maintained up to 60 DAS of maize was found significantly effective in increasing the crop productivity but improved the above properties non significantly over rest of treatments. The soil chemical properties *viz*., pH, EC, and available nutrients *viz*., N, P_2O_5, K_2O, Zn, and Fe in soil did not influence significantly by various weed management treatments after harvesting of maize except for organic carbon content. The nutrient balance was negative but the minimum was in weed-free check and stale seedbed + hoeing at 20 DAS + straw mulch at 30 DAS. Among the organic nutrient management treatments, 75% RDN through vermicompost in two splits + seed treatments with *beejamurt* + two sprays of *jeevamurt* did not affect the soil physio-chemical properties *viz*., pH & EC and available nutrients (Fe and Zn) in the soil after harvest of maize was remained unaffected while the available NPK and organic carbon of soil was influenced significantly during the study period. The treatment of 100% RDN through FYM gave the mean maximum values of these parameters while the lowest was recorded in the treatment of 75% RDN through vermicompost + seed treatment with *beejamurt* + two sprays of *jeevamurt* (at 500 l/ha at sowing and 30 DAS). The balance sheet indicated that the minimum net loss of nitrogen was in 100% RDN through vermicompost while minimum net loss of phosphorus and potassium gain were recorded at 100% RDN through FYM at the end of the experiment. The mean soil available nitrogen, phosphorus, and organic carbon were also significantly increased in this treatment.

Keywords: *Beejamurt* · FYM · *Jeevamurt* · Physical soil properties · Stale seedbed · Straw mulch · Vermicompost · Yield

Introduction

Organic farming is being practiced in 187 countries on a 72.3 M ha area showing a 1.6% increase over 2018. In India, the cultivable area under organic certification is only 2.30 M ha, which is around 1.6% of the net cultivated area of the country besides having the maximum number of registered organic producers (13.33 million) during 2019 (FIBL and IFOAM, 2021). Rajasthan has the highest area (4.82 lakh hectares) in organic farming after Madhya Pradesh. The maize occupied a consistent area (8.75 lakh ha) in Rajasthan where it is grown during *Kharif* as rainfed and irrigated during the *Rabi* season with a production of 11.35 lakh tonnes (Vital Agriculture Statistics, 2019–20). The decreasing or stagnating in seed yields has been attributed to imbalances of nutrients and multiple-nutrient

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deficiencies which created a serious threat to the long-term sustainability of crop production (Karunakaran and Behera, 2013). Developing and implementing tillage, mulching, organic nutrients and organic concoction strategies to maintain the quality of soil is of utmost need to enhance the performance and sustainability of an agro-ecosystem. The benefits of using tillage, mulching, organic nutrients, and organic concoction in maintaining soil quality have been increasingly recognized (Shukla *et al*., 2011).

The mineralization through soil microorganisms maintains the long-term sustainability of agricultural eco-systems and are important factors in nutrient cycling. The physico-chemical properties of the soil are greatly altered by organic nutrient management practices and by maintaining mulches on the soil surface. Some researchers have shown that the incorporation of organic manures increased soil-microbial activity and densities of bacteria (Pawar *et al.,* 2012). The most of research indicated increased microbial diversity in soils from organic farming systems compared to conventional farming systems (Shannon *et al.,* 2006). Since information on the effect of organic weed and nutrient management practices on maize is very scanty as it is an exhaustive crop, the present experiment was undertaken to study their effects on nutrient uptake and soil chemical properties in western Rajasthan.

Materials and methods

Geographically, the experimental site is situated in the western part of Rajasthan at 25°09' N latitude and 73°04' E longitude with at an elevation of 297.7 m above mean sea level. The region has a typical semi-arid and sub-tropical climate characterized by mild winter and moderate to high summers, associated with mild relative humidity, especially during the months of July to September. The total rainfall received during the crop season of *Kharif* 2019 and 2020 was 636.9 mm and 473.5 mm, respectively. The experiment was conducted in a split-plot design where six weed management and five organic nutrient management treatments were replicated thrice. The gross sub-plot size was 18 m^2 while the main plot size was 90 m^2. The maize crop was cultivated as per recommended package of practices and supplied 90 kg N, 60 kg P_2O_5 and 60 kg K_2O/ha using the recently notified maize cultivar Pratap Hybrid Maize 3 at the seed rate of 25 kg/ha. The layout of the experimental site was prepared well in advance to incorporate the recommended quantity of well rotten FYM and vermicompost in respective sub-plots as per treatment (Table 1), spread and mixed properly and irrigation was provided to prepare a stale seedbed. The black polythene of 25 microns was spread and punctured at the prescribed distance at the time of the sowing of maize. The intercultural practices were performed as per treatments at 20 and 40 DAS while the straw was spreaded at the rate of 5 t/ha at 30 DAS. The fermented organic products i.e. *jeevamurt* (Aulakh *et al*., 2013) and *beejamurt* (Shyamsunder and Menon, 2021) were locally prepared and applied @ 500 l/ha as per treatment at the time of sowing and 30 DAS. The details of the experimental units are as follows:

A. Weed management through tillage and mulch

W_1 - Stale seedbed (SS) + two hoeing at 20 & 40 DAS,

W_2 - SS + hoeing with power weeder at 20 DAS + hoeing once manually at 40 DAS,

W_3 - SS + hoeing once manually at 20 DAS + straw mulch (5 t/ha) at 30 DAS,

W_4 - SS + black plastic mulch at sowing (25 microns),

W_5 - Weed free check (up to 60 DAS) and

W_6 - Weedy check

B. Nutrient management through organics sources and concoction

N_1 - 100% recommended dose of nitrogen (RDN) through FYM,

N_2 - 75% RDN through FYM + seed treatment with *beejamrut* + two sprays of *jeevamrut* @ 500 l/ha at sowing and 30 DAS,

N_3 - 100% RDN through vermicompost,

N_4 - 75% RDN through vermicompost as basal + seed treatment with *beejamrut* + two sprays of *jeevamrut* @ 500 l/ha at sowing and 30 DAS and

N_5 - 75% RDN through vermicompost (75% as basal + 25% as a top dress at 30 DAS) + seed treatment with *beejamrut* + two sprays of *jeevamrut* @ 500 l/ha at sowing and 30 DAS.

Soil samples were taken from each experimental unit up to 30 cm depth and were dried, ground to pass through a 2 mm sieve, and analyzed for pH, EC, organic carbon (%), available nitrogen, phosphorus, potassium, zinc, and

Table 1. The average composition of organic inputs used for experimental purpose

Particulars	Vermicompost	FYM	Method employed
Available N (%)	1.53	0.48	Modified Kjeldahl method (Jackson, 1973)
Available P_2O_5 (%)	0.43	0.23	Vanadomolybdate yellow color method (Jackson, 1973)
Available K_2O (%)	2.09	0.51	Wet oxidation method (Jackson, 1973)

Table 2. Initial chemical properties of the soil

Soil parameters	2019–20	References
Soil pH (1:2.5 soil: water suspension)	7.92	Glass electrode pH meter (Richards, 1968)
EC (dS/m at 25° C)	0.43	Conductivity bridge meter (Richards, 1968)
Organic carbon (%)	0.26	Rapid titration method (Walkley and Black, 1934)
Organic matter (%)	0.45	By factor (1.724)
Available nitrogen (kg/ha)	198.7	Alkaline permanganate method (Subbiah and Asija, 1956)
Available P_2O_5 (kg/ha)	26.6	Olsen's method (Olsen *et al.*, 1954)
Available K_2O (kg/ha)	260.0	Flame photometer (Richards,1968)
Available Zn (ppm)	0.42	DTPA-extract with AAS (Lindsay and Norvell, 1978)
Available Fe (ppm)	4.10	DTPA-extract with AAS (Lindsay and Norvell, 1978)

iron before and after maize harvest during both years as per methods mentioned in Table 2.

Results and discussion

Effect on soil chemical properties

Two years' mean data on various soil chemical properties i.e. pH, EC, and organic carbon content in the soil after harvest of maize under different weed management and organic nutrient management practices are presented in Table 3. The various weed management and organic nutrient management treatments applied to maize were found to non-significantly affected the value of pH and EC of soils after harvest of maize in individual as well as in pooled analysis however significantly the available organic carbon status of the soil. The significantly higher organic carbon was found with the application of straw mulch and was at par to stale seedbed + hoeing twice at 20 & 40 DAS and statistically superior over the rest of the treatments while 100% RDN through FYM (0.28%) as against the minimum in 75% RDN through vermicompost as basal application + organic concoction [75% RDN VC (2 splits) + STM + JM (T)] (0.26%) and was also statistically at par to rest of all other treatment. Organic manures improved the physico-chemical properties of soil and results in better utilization and movement of nutrients towards crop (Onte *et al.,* 2019).

Available nutrient status

The data presented in Table 3 reflected that weed management treatments applied to maize failed to affect the soil available N, P, and K status significantly after the harvest of the crop. However, different organic nutrition applied to maize significantly affected the available nutrients in the soil. The available N, P, and K were 3.5, 15.4, and 2.9% higher than 100% RDN through FYM as against a minimum of 75% RDN through vermicompost as basal application organic concoction [75% RDN VC + ST BM + JM (T)].

The various weed management and nutrient management treatments failed to exert any significant effect on the available Zn and Fe status of soil after the harvest of maize (Table 3). This might be ascribed to the fact that the recommended dose of organic manures applied to soil maintained nutrient supply and fertility of the soil due to slow mineralization of organic manures particularly FYM resulting in significant differences in post-harvest soil properties. Organic concoction performed better for improving the biochemical properties of soil by enhancing microorganism population through increased root exudates, and biomass and ultimately provides carbon and energy to the soil microbes resulting in the proliferation of microbial population and increased nutrients in soil pool (Singh *et al*., 2019). The organic concoction plays an important role through its regulatory

Table 3. Effect of organic weed and organic nutrient management practices on soil properties after maize harvest (pooled data of two years)

Treatment	pH	EC (dS/m)	Organic carbon (%)	Available nutrients N (kg/ha)	P_2O_5 (kg/ha)	K_2O (kg/ha)	Fe (ppm)	Zn (ppm)
*Weed management**								
SS + HT at 20 & 40 DAS	7.92	0.43	0.28	190.8	24.5	295.6	4.10	0.42
SS + H with power weeder at 20 DAS + HO at 40 DAS	7.82	0.43	0.27	190.8	24.6	296.5	4.04	0.43
SS + Hoeing once at 20 DAS + Straw mulch at 30 DAS	7.80	0.43	0.29	193.8	25.0	296.2	4.05	0.43
SS + Plastic mulch at sowing	7.73	0.42	0.27	194.1	24.6	295.9	4.02	0.42
Weedy check	7.66	0.42	0.26	189.3	24.2	295.4	3.96	0.41
Weed free check up to 60 DAS	7.74	0.42	0.27	195.0	25.1	297.2	3.95	0.43
SEm (±)	0.06	0.01	0.00	2.32	0.25	1.3	0.04	0.01
CD (P=0.05)	NS	NS	0.01	NS	NS	NS	NS	NS
*Nutrient management***								
100% RDN FYM	7.82	0.43	0.28	194.6	26.4	301.1	3.96	0.42
75% RDN FYM + ST BM + JM (T)	7.81	0.42	0.27	193.7	25.1	298.7	4.02	0.42
100% RDN VC	7.72	0.42	0.27	193.7	24.4	295.5	4.01	0.43
75% RDN VC + ST BM + JM (T)	7.71	0.42	0.27	188.1	22.9	292.5	4.05	0.42
75% RDN VC (2 splits) + ST .M + JM (T)	7.82	0.42	0.26	190.9	24.4	292.8	4.05	0.43
SEm (±)	0.04	0.00	0.00	1.33	0.16	1.06	0.03	0.01
CD (P=0.05)	NS	NS	0.01	3.74	0.45	2.97	NS	NS

*Stale seed bed (SS), two hoeing (HT), Days after sowing (DAS), hoeing once (HO),
** Recommended dose of nitrogen (RDN), Seed treatment with *beejamrut* (ST) and two spray of *jeevamrut* @ 500 l/ha at sowing and 30 DAS JM (T), FYM (Farm yard manure, Vermicompost (VC), 2 splits (75% as basal + 25% as a top dress at 30 DAS).

and bio-stimulatory effect on plant growth and development besides supplying a small amount of nutrients at critical growth stages as a foliar spray (Kumar *et al.*, 2005).

Nutrient balance sheet

The balance sheet of various nutrients in soils are presented in Tables 4–6. The results showed that the net nitrogen and phosphorus balance in soil remained negative in all weed management as well as in organic nutrition treatments during both years. Though, the net nitrogen and phosphorus loss were lowest under treatment weed-free check after completion of the experiment i.e., *Kharif* 2020 (-0.50 and -2.70 kg/ha, respectively) followed by stale seedbed + hoeing once at 20 DAS + straw mulch at 30 DAS as against maximum in weedy check -6.40 and -3.30 kg/ha, respectively). Among the nutrient management treatments, the maximum net losses of nitrogen were occurred in the treatment of 75% RDN through vermicompost as basal application + organic concoction [75% RDN VC + ST BM + JM (T)] (-7.70 and -4.70 kg/ha, respectively) as against the minimum losses was in 100% RDN through FYM (-1.77 and -1.13 kg/ha, respectively). Unlike to nitrogen and phosphorus, the actual potassium balance in soil was positive in weed management through mulching and tillage during both years. Though, the actual potassium balance (gain) in soil was highest under treatment weed-free check up to 60 DAS (16.15 kg/ha) followed by stale seedbed + hoeing once at 20 DAS + straw mulch at 30 DAS as against the minimum net gain in weedy check (13.81 kg/ha). The minimum net gain of potassium was recorded in the treatment of 75% RDN through vermicompost as basal application organic concoction [75% RDN VC + ST BM + JM (T)] (11.49 kg/ha) while the treatment of 100% RDN through FYM recorded a maximum gain (20.02 kg/ha). The application of vermicompost and FYM recorded more growth and yield attributes might be due to the expected higher nutrient balance with organic sources. Similar results were reported by Meena *et al.* (2011). The organic matter used as mulch and organic manures as a nutrient source restore humus status of the soil ecosystem to hold its fertility and productivity resulting into a net gain of

Table 4. Effect of different treatments on nitrogen (kg/ha) balance after harvest of maize

Treatment	Initial status (A)		Added (B)	Uptake by weeds (C)		Uptake by crop (D)		Expected balance (E) E=A+B-C-D		Actual balance (F)		Apparent gain (G) G= F–E		Net gain (H) H=F–A	
	2019	2020		2019	2020	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020
Weed management															
SS + HT at 20 &40 DAS	198.7	197.3	76.5	5.7	5.0	92.0	96.0	188.9	182.8	189.6	192.1	0.7	9.3	-9.1	-5.2
SS + H with power weeder at 20 DAS + HO at 40 DAS	198.7	197.3	76.5	6.1	5.4	89.7	94.3	191.6	184.9	189.8	191.9	-1.8	7.0	-8.9	-5.4
SS + Hoeing once at 20 DAS + Straw mulch at 30 DAS	198.7	197.3	76.5	4.4	3.6	94.9	100.2	184.7	177.2	192.1	195.4	7.4	18.2	-6.6	-1.9
SS + Plastic mulch at sowing	198.7	197.3	76.5	0.0	0.0	91.7	95.1	183.5	178.7	192.9	195.4	9.4	16.7	-5.8	-2.0
Weedy check	198.7	197.3	76.5	38.8	37.2	66.1	70.5	247.9	240.5	187.7	191.0	-60.2	-49.5	-11.0	-6.4
Weed-free check up to 60 DAS	198.7	197.3	76.5	3.8	3.1	98.7	103.2	180.3	173.7	193.3	196.8	13.0	23.1	-5.4	-0.5
Nutrient management															
100% RDN FYM	198.7	197.3	90.0	12.4	11.4	81.9	85.7	219.1	213.1	193.6	195.5	25.5	17.5	-5.1	-1.8
75% RDN FYM + ST BM + JM (T)	198.7	197.3	67.5	11.8	10.9	85.2	90.4	192.8	185.3	192.2	195.1	0.6	-9.8	-6.5	-2.2
100% RDN VC	198.7	197.3	90.0	12.0	11.1	88.8	93.5	211.9	204.9	192.4	195.9	19.5	8.9	-6.3	-1.4
75% RDN VC + ST BM + JM (T)	198.7	197.3	67.5	11.5	10.6	91.5	95.7	186.2	179.7	186.7	189.6	-0.5	-9.8	-12.0	-7.7
75% RDN VC (2 splits) + ST B.M + JM (T)	198.7	197.3	67.5	11.1	10.2	96.8	100.8	180.5	174.2	189.5	192.4	-9.0	-18.1	-9.2	-4.9

Table 5. Effect of different treatments on phosphorus (P_2O_5 kg/ha) balance after harvest of maize

Treatment	Initial status (A)		Added (B)	Uptake by weeds (C)		Uptake by crop (D)		Expected balance (E) E=A+B-C-D		Actual balance (F)		Apparent gain (G) G= F–E		Net gain (H) H=F–A	
	2019	2020		2019	2020	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020
Weed management															
SS + HT at 20 & 40 DAS	26.6	27.8	27.6	1.3	1.1	17.1	18.5	38.4	38	24.1	24.8	-14.3	-13.2	-2.5	-3.0
SS + H with power weeder at 20 DAS + HO at 40 DAS	26.6	27.8	27.6	1.4	1.2	16.5	18.1	39.1	38.5	24.3	24.8	-14.8	-13.7	-2.3	-3.0
SS + Hoeing once at 20 DAS + Straw mulch at 30 DAS	26.6	27.8	27.6	1.0	0.9	17.9	19.5	37.3	36.8	24.9	25.0	-12.4	-11.8	-1.7	-2.8
SS + Plastic mulch at sowing	26.6	27.8	27.6	0.0	0.0	17.1	18.2	37.1	37.2	24.3	24.9	-12.8	-12.3	-2.3	-3.0
Weedy check	26.6	27.8	27.6	9.8	9.2	12.4	13.4	51.6	51.2	23.6	24.8	-28	-26.4	-3.0	-3.0
Weed-free check up to 60 DAS	26.6	27.8	27.6	0.8	0.6	18.6	20.1	36.4	35.9	25.0	25.1	-11.4	-10.8	-1.6	-2.7
Nutrient management															
100% RDN FYM	26.6	27.8	43.0	3.0	2.7	15.2	16.6	57.5	57.0	26.2	26.7	31.3	30.3	-0.4	-1.1
75% RDN FYM + ST BM + JM (T)	26.6	27.8	32.3	2.8	2.6	15.9	17.4	45.9	45.3	24.8	25.3	21.1	20.0	-1.8	-2.5
100% RDN VC	26.6	27.8	25.0	3.0	2.7	16.7	18.0	37.9	37.5	24.2	24.7	13.8	12.8	-2.4	-3.1
75% RDN VC + ST BM + JM (T)	26.6	27.8	18.8	2.7	2.5	17.2	18.5	31.0	30.6	22.6	23.1	8.3	7.5	-4.0	-4.7
75% RDN VC (2 splits) + ST B.M + JM (T)	26.6	27.8	18.8	2.7	2.4	18.1	19.4	29.9	29.6	24.1	24.6	5.8	5.0	-2.5	-3.2

Table 6. Effect of different treatments on potassium (K_2O kg/ha) balance after harvest of maize

Treatment	Initial status (A)		Added (B)	Uptake by weeds (C)		Uptake by crop (D)		Expected balance (E) E=A+B-C-D		Actual balance (F)		Apparent gain (G) G= F–E		Net gain (H) H=F–A	
	2019	2020		2019	2020	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020
Weed management															
SS+ HT at 20 & 40 DAS	260.0	283.0	95.1	5.29	4.63	91.2	95.9	269.2	286.8	293.7	297.6	24.5	10.8	33.7	14.6
SS + H with power weeder at 20 DAS + HO at 40 DAS	260.0	283.0	95.1	5.74	5.08	89.9	95.3	270.9	287.9	295.0	297.9	24.1	10.0	35.0	14.9
SS + Hoeing once at 20 DAS + Straw mulch at 30 DAS	260.0	283.0	95.1	4.4	3.8	90.8	96.1	268.7	285.8	293.8	298.7	25.1	12.9	33.8	15.7
SS + Plastic mulch at sowing	260.0	283.0	95.1	0	0	88.7	93.7	266.4	284.4	294.0	297.9	27.6	13.5	34.0	14.9
Weedy check	260.0	283.0	95.1	42.7	41.1	73.9	78.7	323.9	340.5	293.9	296.8	-30.0	-43.7	33.9	13.8
Weed-free check up to 60 DAS	260.0	283.0	95.1	3.29	2.67	93.8	98.6	264.6	282.2	295.2	299.2	30.6	17.0	35.2	16.2
Nutrient management															
100% RDN FYM	260.0	283.0	96.0	13.02	12.18	81.8	87.4	287.2	303.8	299.1	303.0	-11.9	0.7	39.1	20.0
75% RDN FYM + ST BM + JM (T)	260.0	283.0	72.0	12.11	11.28	86.2	91.9	258.0	274.4	296.8	300.7	-38.8	-26.3	36.8	17.7
100% RDN VC	260.0	283.0	123.0	12.91	12.06	88.7	93.5	307.2	324.5	294.0	297.0	13.2	27.6	34.0	14.0
75% RDN VC + ST BM + JM (T)	260.0	283.0	92.3	11.77	10.97	90.0	94.9	274.1	291.4	290.6	294.5	-16.5	-3.1	30.6	11.5
75% RDN VC (2 splits) + ST B.M + JM (T)	260.0	283.0	92.3	11.61	10.8	93.5	97.5	270.4	288.6	290.8	294.7	-20.4	-6.1	30.8	11.7

nutrients as compared to the rest of the treatments. These organics also maintain the nutrients for a longer period and realize higher nutrient status in the soil after the harvest of the crop. The residual soil nutrient status was maintained with organic nutrient management practices because they enable greater uptake of nutrients by crop, the balance with slow mineralization from the organic sources, which maintained or enhanced the soil nutrient status (Jeyaselvin Inbaraj, 1995). With judicious application of organic matter, the leaching and fixation of nutrients could be reduced and moreover sustain soil fertility and yield.

Conclusion

The organic weed management through tillage and mulching significantly increased the yield as against their respective checks. The crop feed through organic nutrients along with fermented organic products was found beneficial in terms of increasing yield besides improving soil status. The application of organic mulch and FYM helped to maintain the health of the soil as compared to the rest of the treatments either applied as weed management or nutrient management.

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References

Aulakh, C. S., Singh, H., Walia, S. S., Phutela, R. P. & Singh, G. (2013). Evaluation of microbial culture (*Jeevamrit*) preparation and its effect on productivity of field crops. *Indian Journal of Agronomy*, **58**(2): 182–186.

FiBL & IFOAM. (2021). The World of Organic Agriculture, pp. 23-24.

Jackson, M. L. (1973). *Soil Chemical Analysis*. Prentice Hall of India Pvt. Ltd., New Delhi, pp. 263–393.

Jeyaselvin Inbaraj. (1995). Nutrient management in rice cotton sequential cropping system. M.Sc. (Ag.) Thesis, TNAU, Coimbatore.

Karunakaran, V. & Behera, U. K. (2013). Effect of tillage, residue management and crop establishment techniques on energetics, water use efficiency and economics in soybean (*Glycine max*) -wheat (*Triticum aestivum)* cropping system. *Indian Journal of Agronomy*, **58**(1): 42–47.

Kumar, A., Guatam, R. C., Singh, R. & Rana, K. S. (2005). Growth, yield and economics of maize (*Zea mays*) -wheat (*Triticum aestivum*) cropping sequence as influenced by integrated nutrient management. *Indian Journal of Agricultural Sciences,* **75**(11): 709–711.

Lindsay, W. L. & Norvell, W. A. (1978). Development of a DTPA soil test for zinc, iron, manganese and copper. *Soil Science Society of America Journal,* **42**: 421–428.

Meena, K. N., Kumar, A., Rana, D. S. & Meena M. C. (2011). Productivity and nutrient uptake of maize (*Zea mays*)-wheat (*Triticum aestivum*) cropping system under different bio-sources and nitrogen levels. *Indian Journal of Agronomy,* **56**(3): 182-188

Olsen, S. R., Cole, C. V., Watenabe, D. S. & Dean, L. A. (1954). Estimation of available phosphorus in soils by extraction with sodium bicarbonate. *USDA Circular*, pp. 939.

Onte, S., Singh, M., Kumar, S. & Pyati, P. S. (2019). Impact of organic nutrient management on crop quality, yield and soil health: A Review. *International Journal of Current Microbiology and Applied Sciences,* **8**(5): 394-402

Pawar, V. R., Tambe, A. D., Raut, S. A. & Udmale, K. B. (2012). Response of sweet corn (*Zea mays* var. *Saccharata*) cv. SUGAR 75 to different organic sources. *Advance Research Journal of Crop Improvement,* **3**(2): 122–125.

Richards, L. A. (1968). Diagnosis and improvement of saline and alkaline soils. USDA Handbook No. 60, Oxford and IBH Pub. Co., New Delhi.

Shannon, U., Sen, A. M. & Johnson, D. B. (2006). A comparative study of the microbiology of soils managed under organic and conventional regimes. *Soil Use and Management,* **18**(s1): 274 –283

Shukla, L. & Tyagi, S. P. (2009). Effect of integrated application of organic manures on soil parameters and growth of mungbean (*Vigna radiata*). *Indian Journal of Agricultural Sciences,* **79**(3): 174–177.

Shyamsunder, B. & Menon, S. (2021). Study of traditional organic preparation *beejamrita* for seed treatment. *International Journal of Modern Agriculture,* **10**(2): 1823–1828.

Singh, P., Agrawal, V. P. & Singh, Y. V. (2019). Effect of potassium and FYM on growth parameters, yield and mineral composition of wheat (*Triticum aestivum* L.) in alluvial soil. *Journal of Pharmacognosy and Phytochemistry,* **8**(3): 24–27

Subbiah, B. V. & Asija, G. L. (1956). A rapid procedure for the estimation of the available nitrogen in soils. *Current Science,* **25**: 259-260.

Vital Agricultural Statistics. (2020). Department of Agriculture, Government of Rajasthan. www.agriculture.rajasthan.gov.in.

Walkley, A. & Black, CI. A. (19471934). An examination of different methods for determining soil organic matter and proposed modifications of the chromic acid titration method. *Soil Science,* **37**: 29–38.

Maize Journal (April 2022) 11(1): 31-35

RESEARCH PAPER

Efficient and large-scale field screening procedure for maydis leaf blight

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Abstract: *Bipolaris maydis* (Y. Nisik. & C. Miyake) Shoemaker is a necrotrophic fungal pathogen that causes maydis leaf blight (MLB) also known as Southern corn leaf blight (SCLB) mainly infects maize leaves. Lesions are initially small and diamond-shaped, and then become elongated as they mature. Under severe disease pressure, lesions may coalesce, blighting the entire leaf. This disease is found in almost all maize-growing regions of the world including India and significantly affects maize productivity. In the present study, an efficient and large-scale field screening procedure was developed to identify resistant maize genotypes. The plants were inoculated at the 5–6 leaf stage by placing around 10–20 sorghum grains prior infested with the fungus into the whorl of each maize plant. Primary inoculum is eventually dispersed by environmental factors, causing multiple cycles of infection that assure a high uniform disease pressure over the entire field. The intensity of the disease was recorded as disease scoring on a scale of 1–9 at the pre-flowering, tasseling and silking stage.

Keywords: *Bipolaris maydis* · Field screening · Fungal diseases · Maize · Maydis leaf blight

Introduction

Maize (*Zea mays* L.) is one of the most versatile emerging crops having wider adaptability under varied agro-climatic conditions. Globally, maize is known as the queen of cereals because it has the highest genetic yield potential among cereals. In India, maize is the third most important food crop after rice and wheat. MLB is a major disease in the states of Jammu & Kashmir, Himachal Pradesh, Sikkim, Meghalaya, Punjab, Haryana, Rajasthan, Delhi, Uttar Pradesh, Bihar, Madhya Pradesh, Gujrat, Maharashtra, Andhra Pradesh, Telangana, Karnataka and Tamil Nadu having warm humid temperate to the tropical climate in the cropping period.

The causal agent *Bipolaris maydisis* is a member of the ascomycetes, the sac fungi which produces a toxin that attacks the mitochondria and destroys the plants' ability to capture energy from metabolism. Three races of *B. maydis* have been described. Race 'O' is considered the most common and indigenous throughout most areas where SCLB occurs. This infects the leaf blade tissue only, and forms small, tan, and parallel-side lesions with buff or brown borders (Agrios, 1997). On the other hand, race T, the cause of the 1970 SCLB epidemic in North America, is specifically virulent on Texas male sterile cytoplasm (cmsT) maize due to its ability to produce a polypeptide toxin (T toxin) to which cmsT maize is sensitive (Levings and Siedow, 1992). It attacks all above-ground parts of the maize plant. B. maydis releases either asexual conidia or sexual ascospores to infect maize plants. The asexual cycle is known to occur in nature and is of primary concern. Upon favourable conditions, conidia (the primary inoculum) are released from lesions of an infected corn plant and carried to plants in close proximity via wind or rain. Once conidia have landed on the leaf or sheath of a healthy plant, they will germinate on the tissue

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by way of polar germ tubes. The germ tubes either penetrate through the leaf or enter through a natural opening such as the stomata. This procedure for the mass screening of maize genotypes for MLB resistance was based on a methodology developed by Carson *et al*. (2004) and Sermons and Balint-Kurti (2018) with some modifications.

Materials and methods

Genotypes

Ten maize genotypes, LM 5, LM 11, LM 13, LM 14, LM 15, LM 16, CM 139, CM 140, CM 143 and CM 144 were sown in the *Kharif* season under a randomized complete block design arrangement. Two seeds per hill were placed by hand and later thinned 15 days after sowing to a single healthy plant per hill. Each row contained a total of 20 plants and each plot was consisted of ten rows. Spacing was 70 cm between and 20 cm within the rows covering a plot area of 14 m^2 with a population density of 50,000 plants/ha. Each plot was replicated thrice in the experimental field of Punjab Agricultural University, Ludhiana.

Reagents and Instruments

Pure fungal culture of *B. maydis*, KOH, HCL, glass beaker, conical flask / Erlenmeyer flask, spatula, measuring cylinder, pH meter, weighing balance, distilled water, butter paper, magnetic stirrer and pellet, pipettes and tips, petri plates and/or test tubes, hot plate, ddH_2O, ready to use potato dextrose agar media or raw potatoes, agar and dextrose, streptomycin or chloramphenicol, sorghum grain, ethanol, tween-20, aluminium foil, cotton plug, laminar air flow, incubator, autoclave and hot air oven, muslin cloth, conical flasks, autoclave bags.

Preparation of media

The fungal strain was cultured on a full strength of PD media that were prepared by autoclaving conical flask containing 10 g PDA powder in 500 ml double distilled water (ddW). After autoclaving, the molten PDA media could cool to about and 0.1% streptomycin was added to eliminate bacterial contaminant. To each glass Petri dish, 18 to 20 ml molten PDA media was poured and allowed to cool. The sorghum grain media was prepared by soaking 100 g clean sorghum grains for 24 hours in ddW. After draining off excess water from the flasks, a pinch of sucrose added to the moistened grains and then autoclaved at 121^{o}C (15 psi) for 30 min. Sorghum grain flasks were kept at 4^{o}C till further use.

Culture inoculation

Maintenance and inoculation of the fungal pathogen of *B. maydis* were done according to the methodology developed by Carson *et al*. (2004). PDA plates were inoculated (inside a laminar flow hood) by placing 1 cm round cork from the 25 days old fungal colony and dabbing it over the surface of a fresh PDA plate. After inoculation, plates were sealed with the parafilm and placed into an incubator at 25±1 °C, under 12 hours light/dark cycle. Culture at a growing stage, was cut into the smaller used to inoculate previously autoclaved sorghum grain conical flasks under laminar air flow conditions and was kept in an incubator at 30±1 ^{o}C. Fungal growth was

Figure 1. Culture growth of *B. Maydis* on PDA media plate (left) and sorghum grains covered with the fungal growth (right)

observed 3–4 days after inoculation and allowed to continue for 14 days (Figure 1). This grain inoculum was collected in a plastic container covered with a plastic bag by a sterile spatula. The inoculum was allowed to dry either by using a fan or by simply placing it under the shed for 1–2 hours.

Inoculation of maize plants

Maize plants at the 5–6 leaf stage was inoculated by *B. maydis* in the evening by dropping about ten to twenty grains of inoculum directly into the whorl. After two weeks of inoculation, the secondary inoculum was spread all over the plots creating a high, uniform disease pressure. Humidity or light irrigation is required in order to produce secondary inoculum for dispersion and successful germination of fungal spores. Upon germination, it gives rise to conidiophores which, upon favorable conditions, can either further infect the original host plant (kernels, husks, stalks, leaves) or release conidia to infect other nearby plants thus completing the disease cycle (Figure 2). For inoculum to grow and proliferate, moisture was maintained by irrigation the next day after inoculation. Initial SLB symptoms were appeared within one week and they spread over all field within the next week.

Disease scoring

Disease scoring was done at the pre-flowering stage (approximately three weeks after inoculation) tasseling and silking stage by observing the ear leaf and the leaf above, then rating the symptoms on a 1 to 9 scale where the maximum score of nine indicates complete death of the plant and the minimum score of one indicates healthy plants without disease symptoms (Kump *et al*., 2011) (Table 1).

Data analysis

For the disease scoring analysis, data sets were subjected to factorial ANOVA (Analysis of variance) in accordance with the RCBD experimental design using SPSS version

Figure 2. Disease cycle of *B. maydis*

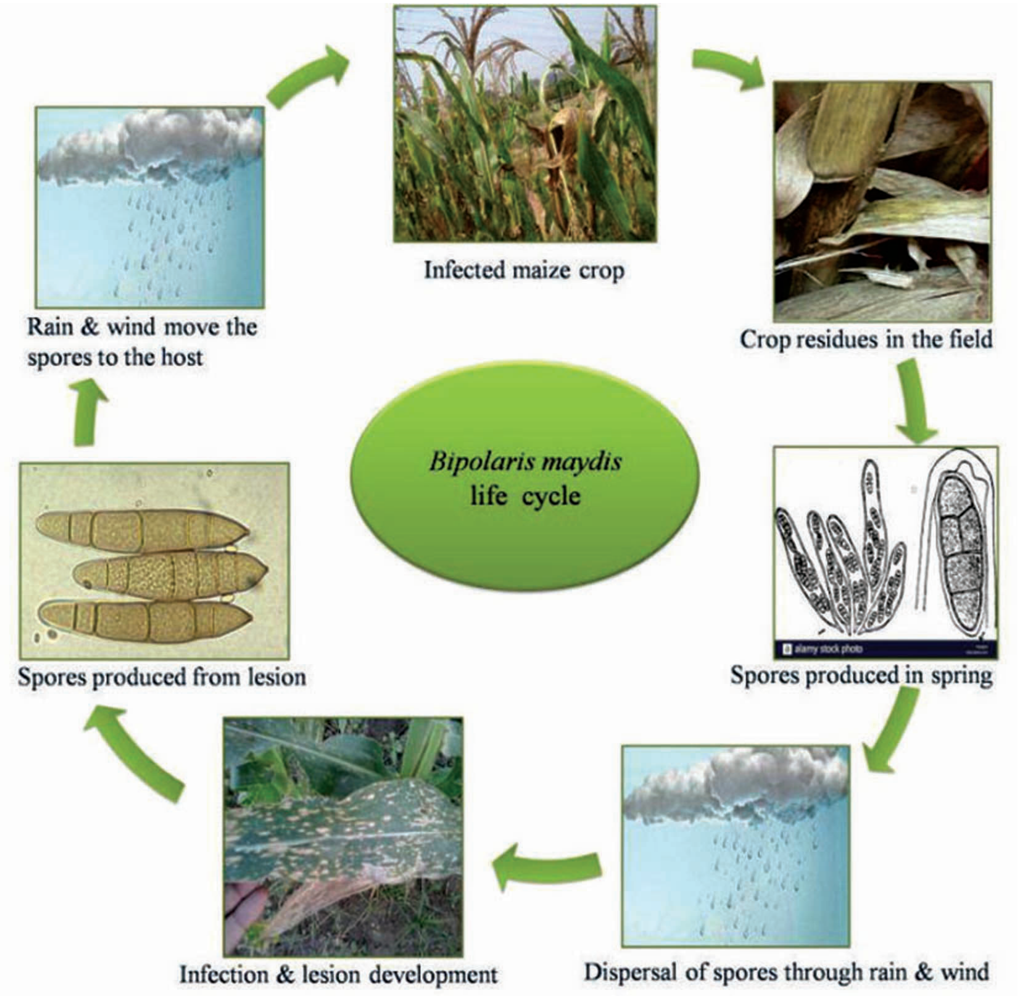


Table 1. SCLB disease rating scale (1–9)

Rating scale	Degree of infection
1.0	Nil to very slight infection (<10%). Very slight to slight infection, one or two to few scattered lesions on lower leaves
2.0	Slight infection, a few lesions scattered on two lower leaves (10.1–20%).
3.0	Light infection, a moderate number of lesions scattered on four lower leaves (20.1–30%).
4.0	Light infection, a moderate number of lesions scattered on lower leaves, and a few lesions scattered on middle leaves below the cob (30.1–40%).
5.0	Moderate infection, an abundant number of lesions scattered on lower leaves, moderate number of lesions scattered on middle leaves below the cob (40.1–50%).
6.0	Heavy infection, an abundant number of lesions scattered on lower leaves, moderate infection on middle leaves, and a few lesions on two leaves above the cob (50.1–60%).
7.0	Heavy infection, an abundant number of lesions scattered on lower and middle leaves, and a moderate number of lesions on two to four leaves above the cob (60.1–70%).
8.0	Very heavy infection, lesions abundant scattered on lower and middle leaves and spreading up to the flag leaf (70.1–80%).
9.0	Very heavy infection, lesions abundant scattered on almost all the leaves, plant prematurely dried and killed (>80%).

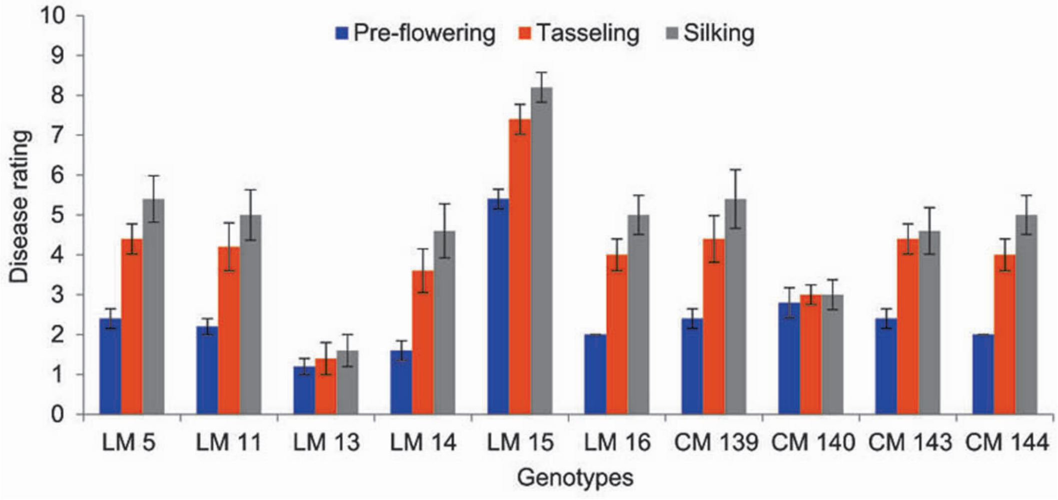
23.0 (IBM, Armonk, NY) in triplicates to evaluate the source of variation and interactions within and between genotypes and disease scoring.

Results and discussion

Here we presented the detailed methodology used for the mass screening of maize genotypes against MLB. The first disease score was recorded at the pre-flowering stage only after the consistent spread of disease through the field mainly due to secondary inoculum. Disease scoring for the screening of genotypes for MLB was reported by Vasmatkar *et al.* (2021), on a rating scale of 1–5. The disease score on a scale of 1–9 was recorded at the pre-flowering, tasseling and silking stage and all the stages of LM 15 showed higher disease scores as compared to other genotypes. However, LM 13 was the least affected genotype, showing the lowest MLB scoring (Figure 3).

The detailed biochemical profiling of these genotypes under MLB infestation was reported by Vasmatkar *et al.* (2019). Symptoms were found to be aggravated at the silking stage in all studied genotypes except CM 140. The highest disease score of 8.2 was observed in LM 15 at silking stage (Figure 4). There was moderate rain three days after the inoculation due to which disease in the field plots was evenly spread thus during the scoring whole plot was showing a similar disease score. We wanted to record the disease score for five times after the inoculation at ten days intervals but due to unusually hot and humid weather decrease plant specifically, LM 15 genotype has started to senesce because of severe necrosis thus it was no longer possible to score disease. Goudar and Harlapur

Figure 3. Disease score rating of different maize genotypes for maydis leaf blight



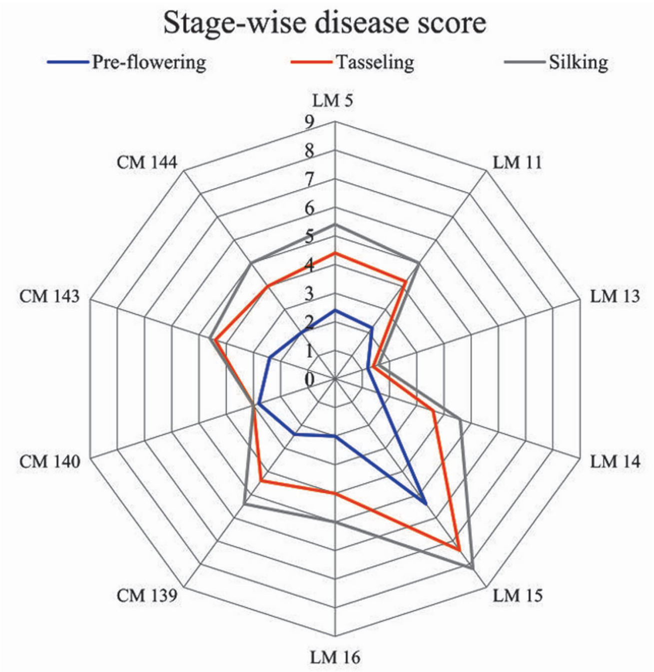


Figure 4. Stage-wise disease score rating of different maize genotypes for maydis leaf blight

(2019) also screened the maize genotypes against MLB. The least disease severity in LM 13 lead to high grain yield which might attribute to its higher resistance whereas in LM 15 highest disease severity and lowest grain yield could be attributed to the susceptibility toward MLB (Vasmatkar *et al.*, 2021).

We observed that, the plants with asynchronous ear development had a significant effect on the disease development and appearance of symptoms. The disease pressure was uniform across the field, various factors such as soil type soil moisture, wind velocity, temperature, and humidity may cause the variation in disease symptoms development at least somewhat in some genotypes. The effect of these factors on disease development needs to be studied further to minimize experimental error.

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References

Agrios, G. N. (1997). Control of plant diseases. In Plant Pathology, 4th Edition, Academic Press, San Diego, pp 200–216.

Carson, M. L., Stuber, C. W. & Senior, M. L. (2004). Identification and mapping of quantitative trait loci conditioning resistance to southern leaf blight of maize caused by *Cochliobolus heterostrophus* race O. *Phytopathology,* **94**(8): 862–867.

Goudar, S. V. & Harlapur, S. I. (2019). Studies on loss assessment of maydis leaf blight (*Bipolaris maydis*. Nisikado) Shoemaker in maize. *International Journal of Chemical Studies,* **7**: 1831–1833.

Kump, K. L., Bradbury, P. J., Wisser, R. J., Buckler, E. S., Belcher, A. R., Oropeza-Rosas, M. A., Zwonitzer, J. C., Kresovich, S., McMullen, M. D., Ware, D., Balint-Kurti, P. J. & Holland, J. B. (2011). Genome-wide association study of quantitative resistance to southern leaf blight in the maize nested association mapping population. *Nature Genetics,* **43**(2): 163–168.

Levings, C. C. S. & Siedow, J. N. (1992) Molecular basis of disease susceptibility in the Texas cytoplasm of maize. *Plant Molecular Biology,* **19**: 135–147.

Sermons, S. M. & Balint Kurti, P. J. (2018). Large scale field inoculation and scoring of maize southern leaf blight and other maize foliar fungal diseases. *Bio-protocol*, 2745.

Vasmatkar, P., Kaur, K. & Pannu, P.P.S. (2021). Field based assessment of yield-related traits and flowering response in *Zea mays* towards Southern corn leaf blight. *Indian Phytopathology*, **74**: 969–979.

Vasmatkar, P., Kaur, K., Pannu, P.P.S., Pannu, Kaur, G. & Kaur, H. (2019). Unraveling the metabolite signatures of maize genotypes showing differential response towards southern corn leaf blight by ^{1}H-NMR and FTIR spectroscopy. *Physiological and Molecular Plant Pathology,* **108**: 101441.

Maize Journal (April 2022) 11(1): 36-40

RESEARCH PAPER

Status of parasitization of fall armyworm, *Spodoptera frugiperda* (J. E. Smith) in Punjab maize ecosystem

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Abstract: Fall armyworm (FAW) is a devastating pest that voraciously feeds on the foliage of maize and has been recognized as a potential threat to the crop. The natural enemies establishment is the key to the integrated pest management (IPM) of FAW in different maize agro-ecosystems. The present study showed the increase in the rate of natural enemies i.e., parasitoids in Punjab maize fields under natural conditions during the rainy season in 2021. The parasitoids of FAW larvae were recorded from 1st week of June 2021 up to the 2nd week of October 2021. The parasitoids observed were *Chelonus formosanus* Sonan and *Temelucha* sp. and the former is more prevalent with per cent parasitism rate ranging from 1.1 to 34.2%, followed by *Temelucha* sp. with parasitism of 0.8–14.7%. *C. formosanus* resulted in a maximum parasitism rate in the 3rd week of July (34.17%) while the minimum rate was observed in the 2nd week of October (1.07%). The per cent parasitism due to *Temelucha* sp. was maximum in 1st week of August (14.67%) whereas the value was minimum in 4th week of June as well as in 3rd week of July 2021. The total parasitism rate of FAW was maximum in the 3rd week of June 2021 (36.84%), and the minimum rate (2.86%) was observed in the 2nd week of October 2021. The maximum and minimum survival rate of parasitoids was recorded in 1st week of August 2021 (76.19%) and 2nd week of October 2021 (37.50%), respectively. The correlation between per cent parasitism and the survival rate of parasitoids was observed to be positively significant.

Keywords: *Chelonus formosanus* · Fall armyworm · Natural enemies · Parasitoids · Parasitism rate · Punjab · *Temelucha* sp.

Introduction

Fall armyworm (FAW), *Spodoptera frugiperda* (J.E. Smith) is a noctuid moth that originates from tropical and sub-tropical America (Agboyi *et al.,* 2020). It is a polyphagous pest, known to be a dominant feeder of maize and other cereals (Montezano *et al.,* 2018). Outside its natural range, a severe outbreak of FAW was reported in Africa in 2016 in maize agroecosystems, since then this pest has been reported in 100 countries across the globe including India (Rwomushana *et al.,* 2018; Baloch *et al.,* 2020). In India, FAW was first reported from Karnataka in 2018 (Sharanbassapa *et al.,* 2019) and subsequently it attacked almost all the maize-growing areas in the country including Punjab where it was reported in 2019. It is estimated that the yield losses in maize due to FAW in sub-Saharan African countries account for about US$13 billion per annum (Tefera *et al.,* 2019).

As a quick line of defense, synthetic insecticides are being used to control this pest (Sisay *et al.,* 2019). But an integrated approach is required for sustainable control of the pest, especially with biological control for managing FAW in the long-term. This invasive pest has been established recently in the Indian conditions, its biotic regulatory factors i.e. the native natural enemy diversity

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of other closely related pest species present in our conditions need to be identified and used for effective biological control. Species such as *Temelucha biguttula* (Munakata), *Temelucha philippinensis* (Ashmed) and *Trathala flavo orbitalis* (Cameron) have been reported from Southern India (Daniel *et al.*, 2020). Whereas under Punjab conditions, two major parasitoids were observed for the first time i.e., *Chelonus formosanus* Sonan (Hymenoptera: Braconidae) and *Campoletis* sp. (Hymenoptera: Ichneumonidae) (Jindal *et al.*, 2021).

Spodoptera sp. is a well-established pest of various host crops in India harbouring a rich source of native natural enemies (Sharanbassapa *et al.*, 2019). These natural enemies can broaden their spectrum of control by parasitizing FAW and controlling its further spread. Keeping these points in mind, the present study has been planned to know the status of the parasitization of FAW in the Punjab (North Indian) maize ecosystem.

Materials and methods

The present studies were carried out at the experimental area of Punjab Agricultural University, Ludhiana, India during the rainy season of 2021. Plants were visually examined regularly for the presence of FAW eggs and larvae. Different larval stages of the pest and 10–20 egg masses were collected randomly on weekly basis. The collected egg masses were placed in Petri dishes with a piece of moistened filter paper while the larvae were individually placed in plastic vials (3 cm × 4.5 cm). These were maintained at standard conditions (temperature of 25±1°C and 70% relative humidity) in Maize Entomology Laboratory, Punjab Agricultural University (PAU), Ludhiana. The holes were made in the lid of vials for the ventilation. The larvae were fed separately, untreated natural food (maize whorls) in plastic vials. The food was changed every 3rd – 4th day or whenever needed. The culture was observed regularly and the emerged parasitoids were preserved in 70 per cent ethanol. The parasitoid emergence was checked by examining the parasitized FAW larvae which were found to be shrinked, and blackish in colour on the parasitoid arrival (Plate 1). The observations on parasitism rate and the survival rate of parasitoids were made and calculated as per Canico *et al.* (2020) as given below:

Plate 1. Emergence of the parasitoid (*Chelonus formosanus*) from FAW larvae

The parasitism rate of each parasitoid species (Pp) was determined by dividing the number of parasitized larvae (Lp) by the number of collected larvae (TL) and converted to per cent values by multiplying with 100 (Equation 1).

$$Pp = \frac{Lp}{TL} \times 100\% \qquad \text{…..(1)}$$

The survival rates of different larval parasitoids (SR) were determined by dividing the number of individuals reaching the adult stage (Pa) by the number of individuals emerging from field collect FAW larvae (Pe) and converted to per cent values (Equation 2).

$$SR = \frac{Pa}{Pe} \times 100\% \qquad \text{…..(2)}$$

Results and discussion

Different stages of FAW were collected from PAU fields during the rainy season of 2021 from 1st week of June to the 4th week of October 2021. The parasitism rate observed was 10.81% during the 1st week of June 2021 which increased up to 36.84% (maximum) by the 3rd week of June 2021 and fluctuated between 25–35% up to August 2021. Then the parasitism rate started decreasing steadily after the 4th week of August up to the 2nd week of October 2021 (Table 1). No parasitoid emergence was recorded from the 3rd week of October 2021 onwards due to the termination of the crop. The per cent parasitism ranged from 2.9–36.8% with an overall

Table 1. The parasitism rate and survival rate of parasitoids on fall armyworm under natural conditions at PAU, Ludhiana, in rainy season maize 2021

Week No.	Week of month	Percentage parasitism	Survival rate of parasitoids (%)
23	1st week of June 2021	10.8	62.5
24	2nd week June 2021	12.0	66.7
25	3rd week June 2021	36.8	68.6
26	4th week June 2021	25.0	70.0
27	1st week of July 2021	26.9	60.0
28	2nd week July 2021	30.3	75.8
29	3rd week July 2021	35.0	66.7
30	4th week July 2021	35.0	53.6
31	1st week August 2021	28.0	76.2
32	2nd week of August 2021	21.7	73.7
33	3rd week of August 2021	25.0	61.8
34	4th week of August 2021	29.4	72.0
35	5th week of August 2021	26.3	71.7
36	1st week of September 2021	23.3	68.6
37	2nd week of September 2021	18.9	55.9
38	3rd week of September 2021	16.9	65.2
39	4th week of September 2021	10.6	48.0
40	1st week of October 2021	10.0	50.0
41	2nd week of October 2021	2.9	37.5

parasitism rate of 22.1%. However, Jindal *et al*. (2021) also recorded the emergence of parasitoids in the Punjab ecosystem on late-season crop in *Kharif* 2020 from the 4th week of October 2020 up to the 1st week of January 2021 in which the total parasitism rate in the study ranged from 10-60%with overall per cent parasitism of 38.3%. The maximum total parasitism (60%) was observed in the 2nd week of December 2020.

Among different parasitoids, *C. formosanus* was found to be the most prevalent parasitoid followed by *Temelucha* sp. during the rainy season 2021. Whereas, during *Kharif* 2020, *Campoletis* sp. was the predominant parasitoid with a weekly parasitism rate of 2.5–46.7% (Jindal *et al.*, 2021). *Chelonus* genus is an egg-larval parasitoids that is the most common and widely distributed parasitoid of FAW in various countries (Prasanna *et al*., 2018; Firake and Behere, 2020; Gupta *et al.*, 2020; Otim *et al*., 2021). The maximum parasitism rate caused by *C. formosanus* was observed in the 3rd week of July (34.2%) followed by the 4th week of July (33.8%) and 3rd week of June (33.7%) respectively (Figure 1). The minimum per cent parasitism caused by *Chelonus* was found in the 2nd week of October (1.07%) which might be due to the maturity of the crop. Similar observations were given

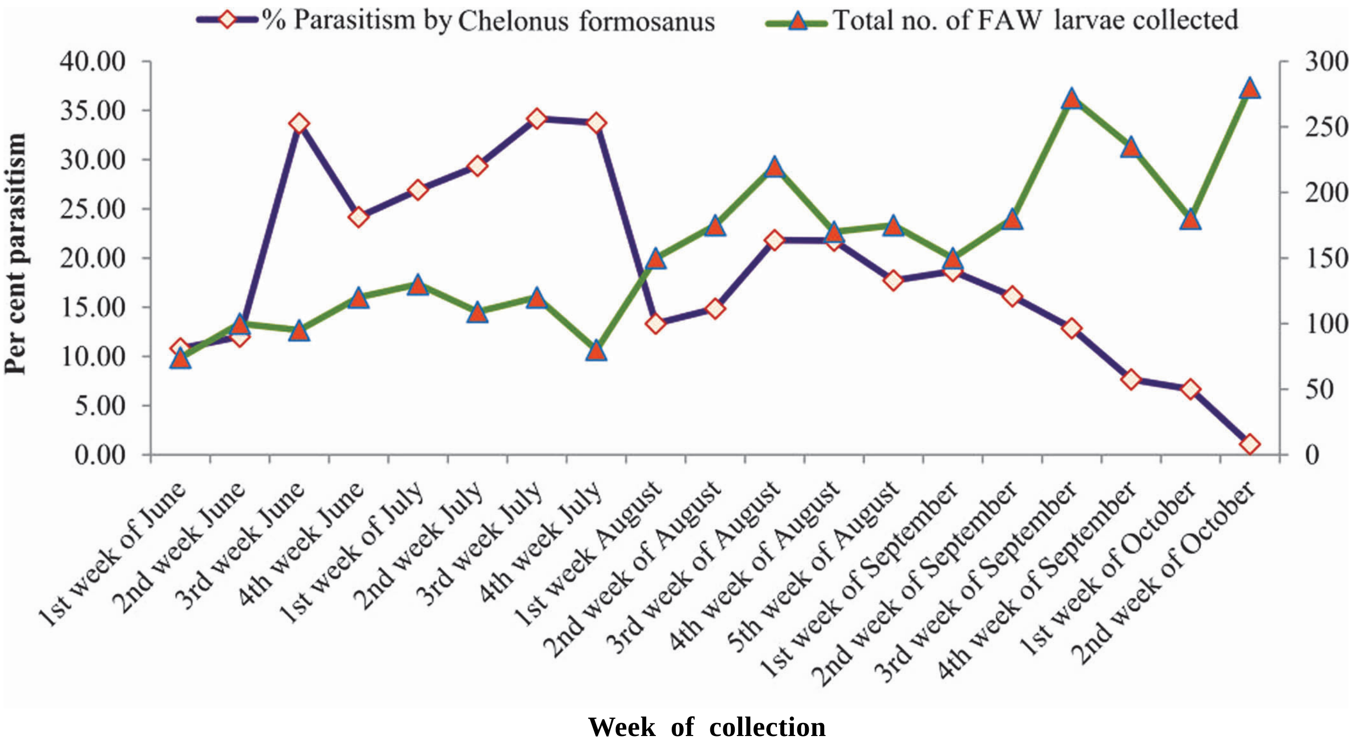

Figure 1. Parasitization of fall armyworm larvae by *Chelonus formosanus* under natural conditions in rainy season 2021 at PAU, Ludhiana

by Agboyi *et al*. (2020) in which *C. bifoveolatus* caused an average parasitism of 18.9%. On the other hand, *Temelucha* spp. is a well-established parasitoid of *Phthorimaea operculella* (potato tuber moth) which is an endo larval parasitoid (Townes, 1971; Ashley *et al.*, 1983; Pair *et al.*, 1986). The per cent parasitism caused by *Temelucha sp*. was recorded as very low ranging from 0.83% to 14.7% (Figure 2). It caused maximum parasitism in 1st week of August (14.7%) followed by the 4th week of August (4.7%). The minimum parasitism rate i.e., 0.83% was observed in the 4th week of June as well as in the 3rd week of July 2021.

In the present study, the maximum survival rate was recorded in the 1st week of August 2021 i.e., 76.2% and the minimum rate (37.5%) were observed in the 2nd week of October 2021. The survival of parasitoids ranged from 37.5–76.2% and the overall survival rate was 62.9% (Table 1). Two more parasitoids also recorded during

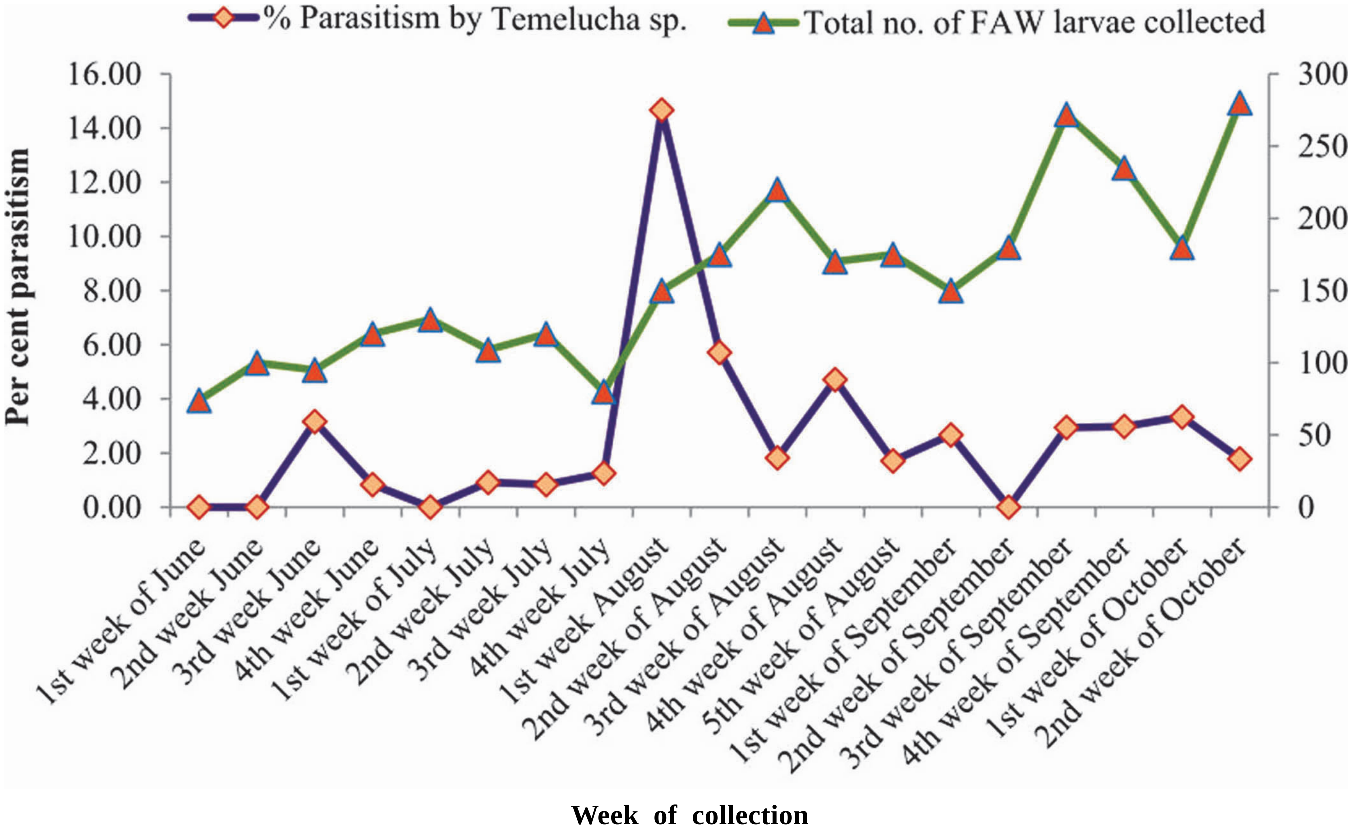

Figure 2. Parasitization of fall armyworm larvae by *Temelucha* sp. under natural conditions in rainy season 2021 at PAU, Ludhiana

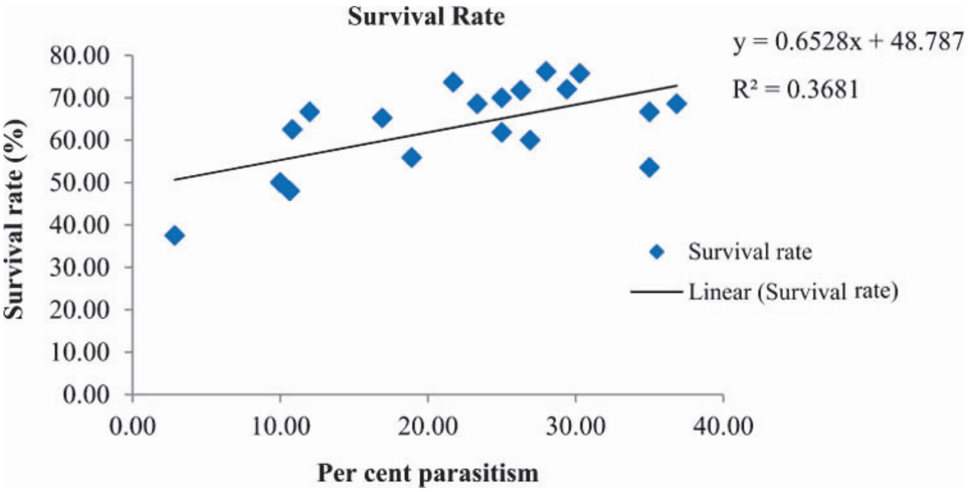

Figure 3. Survival rate of parasitoids in relation to its per cent parasitization on fall armyworm during rainy season 2021 at PAU, Ludhiana. The black line represents the linear model, Y = 0.652x + 48.78, where R^2 = 0.368

Kharif 2021, have been sent to the National Bureau of Agricultural Insect Resources (NBAIR), Bengaluru for their correct identification and description.

A statistically significant correlation (0.607, $^{**}p < 0.01$) was observed between per cent parasitism and the survival rate of parasitoids. The linear regression line between per cent parasitism and survival rate of parasitoids (Y) was $Y = 0.652x + 48.78$ ($Y=bX–a$) (Figure 3). The per cent parasitism shows 36.8% variability in the survival rate of parasitoids ($R^2=0.368$). Therefore, it can be inferred that the survival of parasitoids is dependent on the abundance of the parasitoids in the habitat.

Conclusion

The native natural enemies are establishing as a key factor in IPM of Fall armyworm in different maize agro-ecosystems. Therefore, the emphasis should be given to mass rearing programmes of the prevalent native natural enemies of FAW in specific agro-ecozones. From the present study, it can be suggested that the inoculative release of these natural enemies could be incorporated as a tool in IPM to keep the pest below the threshold levels. Also, the stakeholders i.e., farmers should be made aware of the potential of these natural enemies with more emphasis on conservative biological control programmes and encouraging the use of natural enemies friendly practices.

References

Agboyi, L. K., Goergen, G., Beseh, P., Mensah, S. A., Clottey, V. A., Glikpo, R., Buddie, A., Cafà, G., Offord, L., Day, R. & Rwomushana, I. (2020). Parasitoid complex of fall armyworm, *Spodoptera frugiperda*, in Ghana and Benin. *Insects*, **11**(2): 68.

Ashley, T. R., Barfield, C. S., Waddill, V. H. & Mitchell, E. R. (1983). Parasitization of fall armyworm larvae on volunteer corn, bermudagrass, and paragrass. *Florida Entomologist*, **66**: 267–271.

Baloch, M. N., Fan, J., Haseeb, M. & Zhang, R. (2020). Mapping potential distribution of *Spodoptera frugiperda* (Lepidoptera: Noctuidae) in central Asia. *Insects*, **11**(3): 172.

Caniço, A., Mexia, A. & Santos, L. (2020). First report of native parasitoids of fall armyworm *Spodoptera frugiperda* Smith (Lepidoptera: Noctuidae) in Mozambique. *Insects*, **11**(9): 615.

Daniel, J.A., Ramaraju, K., Sudheer, K. & Vishnu, K. (2020). Ichneumonid fauna associated with rice ecosystems of Tamil Nadu, India. *Journal of Biological Control,* **34**(1): 15–20.

Firake, D. M., & Behere, G. T. (2020). Natural mortality of invasive fall armyworm, *Spodoptera frugiperda* (J. E. Smith) (Lepidoptera: Noctuidae) in maize agroecosystems of northeast India. *Biological Control*, **148**: 104303.

Gupta, A., Lalitha, Y., Varshney, R., Shylesha, A. N. & Van, C. (2020). *Chelonus formosanus* Sonan (Hymenoptera: Braconidae) an egg-larval parasitoid of the invasive pest *Spodoptera frugiperda* (JE Smith) (Lepidoptera: Noctuidae) amenable to laboratory mass production in India. *Journal of Entomology and Zoological Studies*, **8**(1): 1521–1524.

Jindal, J., Sharma, K. P., Shera, P. S. & Cheema, H. K. (2021). Native parasitoids of Fall armyworm *Spodoptera frugiperda* (JE Smith) in maize. *Indian Journal of Entomol*ogy, doi.: 10.5958/IJE.2021.72.

Montezano, D. G., Sosa-Gómez, D. R., Specht, A., Roque-Specht, V. F., Sousa-Silva, J. C., Paula-Moraes, S. D., Peterson, J. A. & Hunt, T. E. (2018). Host plants of *Spodoptera frugiperda* (Lepidoptera: Noctuidae) in the Americas. *African Entomology*, **26**(2): 286–300.

Otim, M. H., Adumo Aropet, S., Opio, M., Kanyesigye, D., Nakelet Opolot, H. & Tek Tay, W. (2021). Parasitoid distribution and parasitism of the fall armyworm *Spodoptera frugiperda* (Lepidoptera: Noctuidae) in different maize producing regions of Uganda. *Insects*, **12**(2): 121.

Pair, S. D., Raulston, J. R., Sparks, A. N. & Martin, P. B. (1986). Fall armyworm (Lepidoptera: Noctuidae) parasitoids: differential spring distribution and incidence on corn and sorghum in the southern United States and northeastern Mexico. *Environmental Entomology*, **15**: 342–348.

Prasanna, B. M., Huesing, J. E., Eddy, R. & Peschke, V. M. (2018). Fall Armyworm in Africa: A Guide for integrated pest management. CDMX: CIMMYT, Mexico.

Rwomushana, I., Bateman, M., Beale, T., Beseh, P., Cameron, K., Chiluba, M., Clottey, V., Davis, T., Day, R., Early, R. & Godwin, J. (2018). Fall armyworm: impacts and implications for Africa. *Fall armyworm: impacts and implications for Africa.* Evidence Note Update. https://www.invasive-species.org/wp-contents/uploads/sites/2/2019/02/FAW-Evidence-Note-October-2018.pdf).

Sharanabasappa, S., Kalleshwaraswamy, C. M., Poorani, J., Maruthi, M. S., Pavithra, H. B. & Diraviam, J. (2019). Natural enemies of *Spodoptera frugiperda* (JE Smith) (Lepidoptera: Noctuidae), a recent invasive pest on maize in South India. *Florida Entomologist,* **102**(3): 619–623.

Sisay, B., Tefera, T., Wakgari, M., Ayalew, G. & Mendesil, E. (2019). The efficacy of selected synthetic insecticides and botanicals against fall armyworm, *Spodoptera frugiperda*, in maize. *Insects*, **10**(2): 45.

Tefera, T., Goftishu, M., Ba, M. N. & Muniappan, R. M. (2019). A guide to biological control of fall armyworm in Africa using egg parasitoids. ipmil.cired.vt.edu/wp-content/uploads/2019/10/A-Guide-to-Biological-Control-of-FAW_Final-updated.pdf.

Townes, H. (1971). The genera of Ichneumonidae, part 4. *Memoirs of the American Entomological Society,* **17**: 1–372.

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RESEARCH PAPER

Novel sources of resistance against foliar diseases identified among the newly derived tropical inbreds of field corn

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Abstract: The investigation was carried out at ICAR-IARI, Regional Research Centre, Dharwad, with the objectives to screen newly developed inbred lines against turcicum leaf blight (TLB), curvularia leaf spot (CLS) and maydis leaf blight (MLB) and common rust (CR) to identify new sources of resistance during *Kharif* 2020 and 2021. The grain yield, and flowering traits were recorded on 45 newly developed inbred lines. The results revealed that none of the inbred is immune to any of the four foliar diseases. However, highly resistant lines are identified against TLB (5 lines *viz*., PDM 4641, PDIM 638, PDIM 639, PDIM 697, PDIM 635), CLS (5 lines *viz*., PDIM 697, LM-14, C-79, CDM-1105, TC-6), MLB (6 lines *viz*., C-79, CDM-1105, PDM-10, C-83, PDM-134, C-2765) and CR (7 lines viz., C-79, CM 202, PDIM 635, PDIM 805, PDIM 697, PML-50, C-67). Among these, PDIM 635 and PDIM 697 displayed resistance against all the four diseases studied, while PDIM 638 and PDIM 639 exhibited resistance against TLB, CLS, and MLB, and C 79 and C 67 showed resistance against CLS, MLB, and CR. Further, there are a few more inbreds that displayed resistance against two of the four diseases studied. The distribution of inbred lines with respect to disease scores showed similar trends for foliar diseases implying the possible linkage of resistance genes against different foliar diseases or multiple disease resistance. Further, the analyses of genetic parameters revealed high PCV, GCV, heritability, and GAM of the traits studied. Based on the results it was suggested to select inbreds for hybrid breeding in the short run and to improve foliar disease resistance through population improvement approaches such as recurrent selection methods.

Keywords: CLS · CR · Inbred · GAM · MLB · TLB

Introduction

Maize (*Zea mays* L.) is an important tropical cereal and staple food crop of the world that originated in Mexico (South America) around 5,000 BC. It is now one of the most widely grown crops around the world in both temperate and tropical regions. It is physiologically more efficient and has the highest genetic yield potential among food grain crops because of its C_4 pathway. It is the most versatile photo-insensitive crop with high adaptability cultivated throughout the year. Globally, maize stands fifth among the cereals in the area, fourth in production, and third in productivity. As per the latest reports by USDA maize has an area of 202 m ha with a production of 1162 m t and with a productivity of 5544 kg/ha (FAOSTAT, 2020). In India, it is the third most important food crop after rice and wheat with an area, production, and productivity of 9.86 m ha, 30.16 m t, and 3058 kg/ha, respectively (FAOSTAT, 2020).

Despite its high yield potential, adaptability and versatility, maize productivity is limited by biotic and

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abiotic factors (Shah, 2016). Approximately, 65 pathogens infect maize, causing substantial yield loss. This necessitates the development of high-yielding and disease-resistant hybrids to meet the country's ever-growing food demands (Barakat *et al.*, 2009). Among the maize diseases, foliar diseases such as turcicum leaf blight (TLB), curvularia leaf spot (CLS) maydis leaf blight (MLB), and common rust (CR), caused by *Exserohilum turcicum*, *Curvularia spp.*, *Bipolaris maydis* and *Puccinia sorghi*, respectively, are important in India. Although these diseases have widespread distribution in cold humid regions with heavy dew conditions and appears in a sizeable form in Karnataka, Maharashtra, Andhra Pradesh, and Himalayan regions with the reduction of grain yield by 28 to 91% (Harlapur *et al.*, 2000). In addition, the incidence of foliar diseases reduces the fodder quality of maize stalks and leaves. The management practices like crop rotation, seed treatment, and the application of fungicides have been recommended (Reddy *et al.*, 2013) to reduce the losses due to foliar diseases. However, host plant resistance (HPR) has been considered the most appropriate and economical strategy due to several advantages, it is environmentally friendly and convenient to adapt at the farmers' level. Hence, resistance breeding in maize has been emerging as an important area of research in recent years due to the recent surge in losses due to disease incidence. Identifying resistant genes and genotypes to foliar diseases and combining them with yield traits has now become an essential objective of maize breeding programs. It is important, therefore, to identify more diverse sources of resistance to foliar diseases, as the increase in the disease severity has the potential of threatening maize grain productivity with a negative influence on food production (Sibiya *et al.*, 2013; Hooda *et al.*, 2017). While breeding for disease resistance, prior knowledge of the genetics of resistance in the population and lines that would be utilized for developing high-yielding resistant varieties is essential.

Keeping these points in mind, the present study was conducted with the 42 new inbred lines developed from diverse sources were screened along with resistant (LM 13 and LM 14) and susceptible check (CM 202) against foliar diseases during two consecutive *Kharif* seasons during 2020 and 2021 with the objective identifying novel sources of resistance and to understand the variability and other genetic parameters in the inbred pool selected.

Materials and methods

The base material for the study consisted of 45 new inbred lines derived from diverse sources. These 45 inbreds were selected based on the disease scores (<6.0) under natural epiphytotics. The list of inbred lines and their pedigree is presented in Table 1.

Table 1. List of inbreads used for the present study during *kharif* 2020 and 2021

S.No.	Inbread line	Pedigree
1	C-79	VL144287 ‖(VL1110435/CML4
2	CM 202	CI21
3	PDIM	(CA34505/CA0
4	PDIM 805	IC 470150
5	PDIM 697	VL175899‖(((CML161xCML45
6	PML-50	P-3501-5-2-K-2-K-2-50
7	C-67	ZL155281‖((Pop61C‖C1QPMTE
8	C-74	VL183808‖(CML451//(ZPop1W
9	PDM-134	(MDRxPC-3xComp 85164
10	JK-1553	IMLSB-2012
11	C-2765	(((CTSO II 072/P3 1 C4S58-
12	C-62	VL18352‖(CLQRCYQ44-
13	C-8	VL18300‖(CLQRCYQ44-
14	DT-2	(DT/LN/EM-46-3-1xCML311-2-
15	BGD-48Y	BGD comp--48(Y)
16	C-14	VL18242‖((CL02450/OFP67//C
17	JK1800	EC 697148
18	C-2760	Pop61 C1 QPMTEYF-40-
19	C-78	Vl18260‖Composite 14-BBB-1-
20	DDM-2313	MWN-2956
21	PDM-10	(O pool x Comp85134 x
22	PML-18 B	RMH-3591-4-1-1-K-1-K-1-18
23	TC-12	Tmap-3-F3-1 Op #-3-1-2-1
24	TC-6	GB-OP sel-2-1-2-1
25	C-12	VL181017‖(CLQRCYQ44-
26	PDM-59	PS-11-2-8-1-1-1-2-1-1-1
27	PML-102_1	KDMH-755-2-1-1-1-1
28	PML-25	KMH-218PLUS-1-1-3-R-1
29	DT-5_1	DTPYC9-F103-5-4-1-2-1-2-1-
30	PDIM 639	(PMH-1 x PMH-3)-4-2-1-2-3-1-1-
31	CDM-1105	(DMSyn-C I) 18-1-8
32	DIM-204 B	Advanta 7074-1-2-1-1-1
33	DIM-316	PHB-14-1-1-3-2-K-2
34	PDM 4641	(Agti 76 X Comp 8527
35	PDM-114-2	(Comp8527xComp
36	C-23	VL19190‖((CML466/CML1
37	C-83	VL18214‖((CL02450Q/OFP

Table 1 contd...

S.No.	Inbread line	Pedigree
38	CML-582	CAL1819-2-1-3-2-3-1
39	D-2282_1	PMH-1-1 Bulk-Bulk-1-2-1-1
40	JK-370	EC699496ÄÄÄÄ
41	BLSB-2 B	MDR pool bpm-2
42	C-25	VL18149||AMDROUT(5x6)
43	PDIM 638	PMH-1 x LM-13-3-2-2-3-2-2-
44	LM-14	CA 00310-xb-xb-xb-1-1-1-1-
45	PML-85	IML307-3-1-1---85

The inbred lines were screened against foliar diseases across two consecutive seasons, *viz.*, *Kharif* 2020 and 2021, and they were also evaluated for yield and flowering traits during *Kharif* 2021. The separate sets of experiments were carried out to screen for different foliar diseases through artificial epiphytotics. The evaluation and screening of inbreds were carried out in randomized complete block designs with two replications with susceptible check CM 202. Each genotype was planted in two rows of 3 m length with a spacing of 60 × 20 cm with two seeds per hill. Finally, one plant per hill was retained and recommended package of practices was followed to raise a healthy crop. The spreader rows (susceptible genotypes) were planted at regular intervals to help create high disease pressure in the experimental plots.

Creation of artificial epiphytotics

After isolating the maize foliar disease pathogen and obtaining the pure culture, the mass multiplication of *E. turciucm*, *B. maydis* and *C. spp.* was done on sterilized sorghum grains. For each pathogen, one hundred grams of sorghum grains were soaked in tap water for 24 hours in a 500 ml conical flask. The excess water was drained off and the material was sterilized twice in the autoclave at 24-hour intervals. To prevent the clumping of the material the flasks were shaken thoroughly. The flasks were inoculated with respective pathogen culture aseptic conditions and incubated at 25±10°C for 20 days. To avoid clumping, the flasks were shaken every alternate day. Within three weeks the mycelial growth and conidia of the fungus were observed on the sorghum grains. A fully colonized sorghum grains culture was used for creating artificial epiphytotic conditions in the field following the whorl method of inoculation. The inoculation of mass multiplied culture was done at 35 and 45 days after sowing and light irrigation was given to create humid conditions to facilitate the growth of the pathogen. Observations were recorded on five randomly selected plants in each replication for disease score, percentage disease index, and characters such as days to 50% tasseling, days to 50% silking, and grain yield (t/ha). The screening was based on the 1-9 scoring method given by IIMR, Ludhiana. Common rust was scored under natural epiphytotic conditions. The data on both disease scores and yield component traits were subjected to statistical analyses using AGRISTAT (V.6.2003) software.

Table 2. Disease scoring scale for turcicum leaf blight disease

Rating scale	Degree of infection	Disease reaction
1	Nil to very slight infection (<10%)	Resistant (Score: < 3.0)
2	Slight infection, a few lesions scattered on two lower leaves (10.1–20%)	
3	Light infection, a moderate number of lesions scattered on four lower leaves (20.1–30%)	
4	Light infection, a moderate number of lesions scattered on lower leaves, a few lesions scattered on middle leaves below the cob (30.1–40%	Moderately resistant (Score: 3.1–5.0)
5	Moderate infection, an abundant number of lesions scattered on lower leaves, a moderate number of lesions scattered on middle leaves below the cob (40.1–50%)	
6	Heavy infection, an abundant number of lesions scattered on lower leaves, moderate infection on middle leaves, and a few lesions on two to four leaves above the cob (50.1–60%)	Moderately susceptible (Score: 5.1–7.0)
7	Heavy infection, an abundant number of lesions scattered on lower leaves, and a moderate number of lesions on two to four leaves above the cob (60.1–70%)	
8	Very heavy infection, lesions abundant scattered on lower and middle leaves and spreading up to the flag leaf (70.1–80%)	Susceptible (Score: > 7.0)
9	Very heavy infection, lesions abundant scattered on almost all the leaves, plant prematurely dried and killed (> 80%)	

Results

Screening of maize inbreds against foliar diseases

The screening of inbred lines for foliar diseases was carried out under artificial epiphytotic conditions. The inoculation of pathogen and planting of spreader rows ensured sufficient inoculum load in test plots as revealed by the highly susceptible reactions of susceptible check CM 202 and spreader rows. The ANOVA for the response of inbred lines against foliar diseases revealed that the mean sum of squares due to genotypes was highly significant during both *Kharif* 2020 and 2021 for all the foliar diseases studied (Table 3). Besides, during *Kharif* 2021, grain yield, days to 50% tasselling, and days to 50% silking were also recorded. The ANOVA for these traits in *Kharif* 2021 also showed a significant mean sum of squares due to genotypes in the newly developed inbred lines.

Response of inbred lines against foliar diseases

The inbred lines exhibited differential responses against foliar diseases, where disease scores varied from 1–9. Most of the genotypes showed disease scores of less than 6 and only a few recorded susceptible reactions. The pooled disease scores along with grain yield and flowering traits of the different inbred lines are given in Table 5.

Among the 42 inbreds screened against different foliar diseases, five inbreds each were highly resistant against TLB and CLS, six against MLB, and seven against common rust. However, more resistant inbreds were observed against MLB. In all four foliar diseases, the moderate resistant category contained more inbreds compared to the resistant category and susceptible category.

Grain yield and maturity behavior of inbreds studied

The inbreds showed a wide range of values for grain yield, days to 50% tasselling, and days to 50% silking. The grain yield ranged from 1.3 (DIM 316) to 5.5 t/ha (PML 102) and 25 inbreds recorded more than 3.0 t/ha (Table 5). For flowering traits, the DFT varied from 50.5 (DT 5–1) to 70.5 (PDIM 635). However, more than 50% of inbreds studied showed days to 50 tasseling in the range 59–65 days, among them 10 inbreds flowered in more than 65 days and four inbreds flowered in less than 54 days.

Genetic variability and genetic parameters under foliar diseases of maize

The analyses were carried out to generate information on genetic variability, heritability, and genetic advance in the traits studied in each season (*Kharif* 2020 and 2021) and are presented in Tables 6 and 7. The results revealed that the pool of inbred lines used for the study recorded high PCV, GCV, heritability(bs), and genetic advance as percent of the mean (GAM) for all the foliar diseases in *Kharif* 2020 and for grain yield, flowering traits and foliar diseases in *Kharif* 2021.

Discussion

The diseases of maize, especially foliar diseases, cause severe losses in India and around the world. The diseases of economic scale vary across growing ecologies and

Table 3. ANOVA for the scores of foliar diseases in maize inbred lines during *Kharif* 2020

Source of variation	df	TLB score (1–9)	CLS score (1–9)	MLB score (1–9)	Rust score (1–9)
Replication	1	0.01	0.01	0.02	0.28
Treatments	24	6.43**	6.14**	4.90**	8.62**
Error	24	0.12	0.28	0.34	1.21

df : Degrees of freedom; DFS : Days to 50% silking; DFT : Days to 50% tasseling

Table 4. ANOVA for the scores of foliar diseases along with grain yield and maturity traits in maize inbred lines during *Kharif* 2021

Source of variation	df	TLB score (1–9)	CLS score (1–9)	MLB score (1–9)	Rust score (1–9)	Grain yield	DFT	DFS
Replication	1	5.88**	1.68	0.18	0.10	0.47**	80.71**	62.40**
Treatments	24	7.35**	4.93 **	4.67**	8.49**	1.99**	44.16**	45.01**
Error	24	0.99	0.88	0.31	1.21	0.07	9.28	9.88

**: significant at 1% probability *: significant at 1% probability df: Degrees of freedom DFT and DFS: Days to 50% tasseling and silking

Table 5. Response maize inbred lines against foliar disease during *Kharif* 2020 and *Kharif* 2021

Inbred line	Grain yield	DFT	DFS	Mean Disease scores [K2020 and 2021 (1–9)]			
				TLB	CLS	MLB	CR
BGD 48Y	4.2	54.5	56.5	7.3	6.0	2.0	3.5
BLSB 2 B	2.4	57.0	59.0	6.8	3.3	5.0	6.5
C 12	2.0	59.0	61.5	7.0	4.0	1.5	4.5
C 14	2.0	64.5	66.5	7.3	2.3	4.0	3.5
C 23	1.9	67.5	70.5	6.8	3.8	1.3	6.0
C 25	3.1	58.0	60.0	6.0	3.8	1.3	6.5
C 2760	3.6	66.5	68.5	5.8	3.8	1.3	4.0
C 2765	2.9	64.0	66.0	5.0	4.5	1.0	3.0
C 62	2.1	61.0	63.0	6.8	4.5	6.0	3.0
C 67	3.6	61.0	63.0	5.3	3.0	1.8	2.0
C 74	2.6	64.5	66.5	7.3	4.3	1.5	2.0
C 78	3.5	61.0	61.0	5.5	2.0	1.8	4.0
C 79	5.0	61.0	63.0	3.8	1.8	1.0	0.0
C 8	3.4	64.0	65.5	4.8	4.8	4.0	3.0
C 83	2.5	57.5	59.5	4.8	3.5	1.0	6.0
CDM 1105	3.6	57.5	59.5	3.8	1.8	1.0	5.5
CM 202	3.1	55.5	58.0	7.5	7	8.5	0
CML 582	4.2	69.0	71.0	3.8	3.3	3.8	6.0
D 2282_1	3.1	60.0	62.0	5.3	4.0	4.0	6.0
DDM 2313	4.3	66.0	67.0	5.5	3.8	2.0	4.0
DIM 204 B	1.6	63.5	65.5	7.0	4.5	1.8	5.5
DIM 316	1.3	66.0	68.0	6.3	4.8	1.3	5.5
DT 2	1.8	54.0	56.0	6.5	4.0	2.0	3.0
DT 5 _1	4.3	50.5	51.0	7.0	4.3	1.3	5.0
JK 1553	3.3	51.5	53.5	6.3	3.3	1.8	2.5
JK 1800	3.4	57.5	59.5	6.5	3.0	1.5	3.5
JK 370	3.1	58.5	61.0	6.8	3.3	1.3	6.0
LM 14	3.2	62.0	64.0	4.3	1.5	2.0	7.0
PDIM 635	4.7	70.5	72.0	2.0	2.3	1.5	0.0
PDIM 638	2.7	67.5	69.0	2.0	2.0	2.8	6.5
PDIM 639	4.3	68.5	70.5	2.0	3.3	2.3	5.0
PDIM 697	2.9	66.0	67.5	2.0	1.3	1.3	1.0
PDIM 805	3.0	57.5	59.0	4.0	6.8	4.5	0.0
PDM 4641	3.7	59.5	61.5	1.8	6.5	3.3	5.5
PDM 10	2.9	57.0	59.0	6.8	2.5	1.0	4.0
PDM 114 2	2.6	59.0	59.0	8.3	4.3	3.3	5.5
PDM 134	3.3	62.5	65.0	5.0	3.8	1.0	2.0
PDM 59	2.6	59.5	62.0	7.3	3.3	1.5	4.5
PML 102 _1	5.5	65.0	67.0	5.8	6.0	1.5	4.5
PML 18 B	2.4	59.0	61.0	6.3	3.5	1.3	4.0
PML 25	5.2	63.0	66.0	6	4	1.5	4.5
PML 50	2.1	59.5	61.5	7.5	4.0	1.5	1.0
PML 85	1.4	63.0	65.0	7.0	2.3	1.5	9.0
TC 12	2.4	53.5	56.5	6.5	2.5	2.0	4.0
TC 6	4.0	62.0	64.5	8.5	1.8	1.8	4.0
Mean	3.0	63.3	65.2	5.7	3.6	2.4	4.1
SEm±	0.2	0.9	0.9	0.3	0.2	0.2	0.3
CD	0.4	2.5	2.5	0.7	0.5	0.6	0.8
CV	8.5	13.9	13.8	3.8	3.0	3.4	4.6

Table 6. Genetic parameters for foliar diseases in *Kharif* 2020

Genetic parameter	TLB	CLS	MLB	Rust
Phenotypic variance	3.28	3.21	2.62	4.91
Genotypic variance	3.15	2.93	2.28	3.70
Environmental variance	0.12	0.28	0.34	1.21
PCV (%)	33.87	43.00	73.55	54.66
GCV (%)	33.22	41.06	68.59	47.46
h^2 (%)	96.19	91.16	86.98	75.39
GAM (%)	67.11	80.75	131.78	84.88

breeding climate smart maize is a major challenge that also requires breeding and deployment of genetic resistance against diseases (Reynolds and Ortiz, 2010). The development and identification of new sources of resistance against important diseases are very crucial and require continuous breeding efforts. The challenge is exacerbated by the changing climates that will affect the diversity and responsiveness of maize diseases as well (Singh *et al.*, 2021). Thus, breeding biotic stress resistance in maize during the era of climate change is the need of the hour. In this direction, ICAR-IARI Regional Research Centre Dharwad has developed new inbred lines from diverse sources. The fixed inbred lines were initially screened against foliar diseases under natural epiphytotics. Dharwad being a hot spot for the diseases like TLB and other foliar diseases, the screening of germplasm against foliar diseases could be accomplished and the genetic resistance sources can be identified under both natural and artificial epiphytotics. In the present study, 45 newly developed inbred lines, which were selected from screening under natural epiphytotics, were subject to artificial epiphytotics. The responses of these inbreds and the salient findings of the study have been discussed below.

Performance and distribution of maize inbreds against foliar diseases and for grain yield

The highly significant mean sum of squares due to genotypes for grain yield, flowering, and foliar diseases suggested the existence of substantial variability among the inbred lines (Table 3). The results indicated the possibility of the selection of desirable genotypes from this pool of inbreds and also the possibility of further improvement by devising appropriate breeding strategies.

The distribution of genotypes with respect to disease scores showed that the majority of the inbreds exhibited resistant to moderately resistant responses against these foliar diseases (Table 8 and Figure 1). This was expected as the inbred lines selected for the screening were initially screened under natural epiphytotics in Dharwad and those with scores of < 6.0 were subject to artificial screening. The disease scores of > 6.0 under artificial epiphytotics from among the inbreds with < 6.0 score implied that the disease pressure and inoculum load were sufficient enough to rule out the disease escape by the inbreds. The extent of disease pressure in the screening plots can also be seen in Figure 2 for TLB, CLS, and MLB. The trend of disease distribution indicated the possible linkage among the two or more resistance genes against different diseases (Figure 1).

In addition, the evaluation of inbred lines for yield and maturity traits, identified 25 productive inbred lines (> 3.0

Table 8. Distribution of inbred lines w.r.t. diseases scores against different foliar diseases

Disease Score	Number of inbreds (Based on average disease scores of K 2020 and 21)			
	TLB	CLS	MLB	Rust
1	0	1	14	2
2	5	9	20	3
3	0	10	3	5
4	5	15	4	10
5	6	5	2	6
6	9	2	1	10
7	16	3	0	4
8	3	0	0	0
9	1	0	1	1

Table 7. Genetic parameters grain yield and foliar diseases during *Kharif* 2021

Genetic parameter	Grain yield	DFT	DFS	TLB	CLS	MLB	Rust
Phenotypic variance	1.0	31.7	32.4	4.2	1.9	2.5	4.9
Genotypic variance	1.0	12.4	12.6	3.2	1.0	2.2	3.6
Environmental variance	0.1	19.3	19.9	1.0	0.9	0.3	1.2
PCV (%)	32.6	9.2	9.1	34.2	44.9	71.1	54.6
GCV (%)	31.5	5.8	5.6	29.9	32.9	66.4	47.3
h^2 (%)	93.3	39.2	38.7	76.2	53.7	87.4	75.0
GAM (%)	62.6	7.5	7.2	53.7	49.6	127.9	84.3

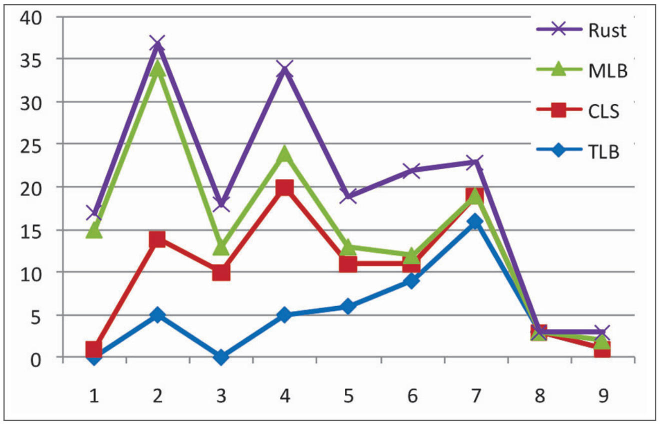
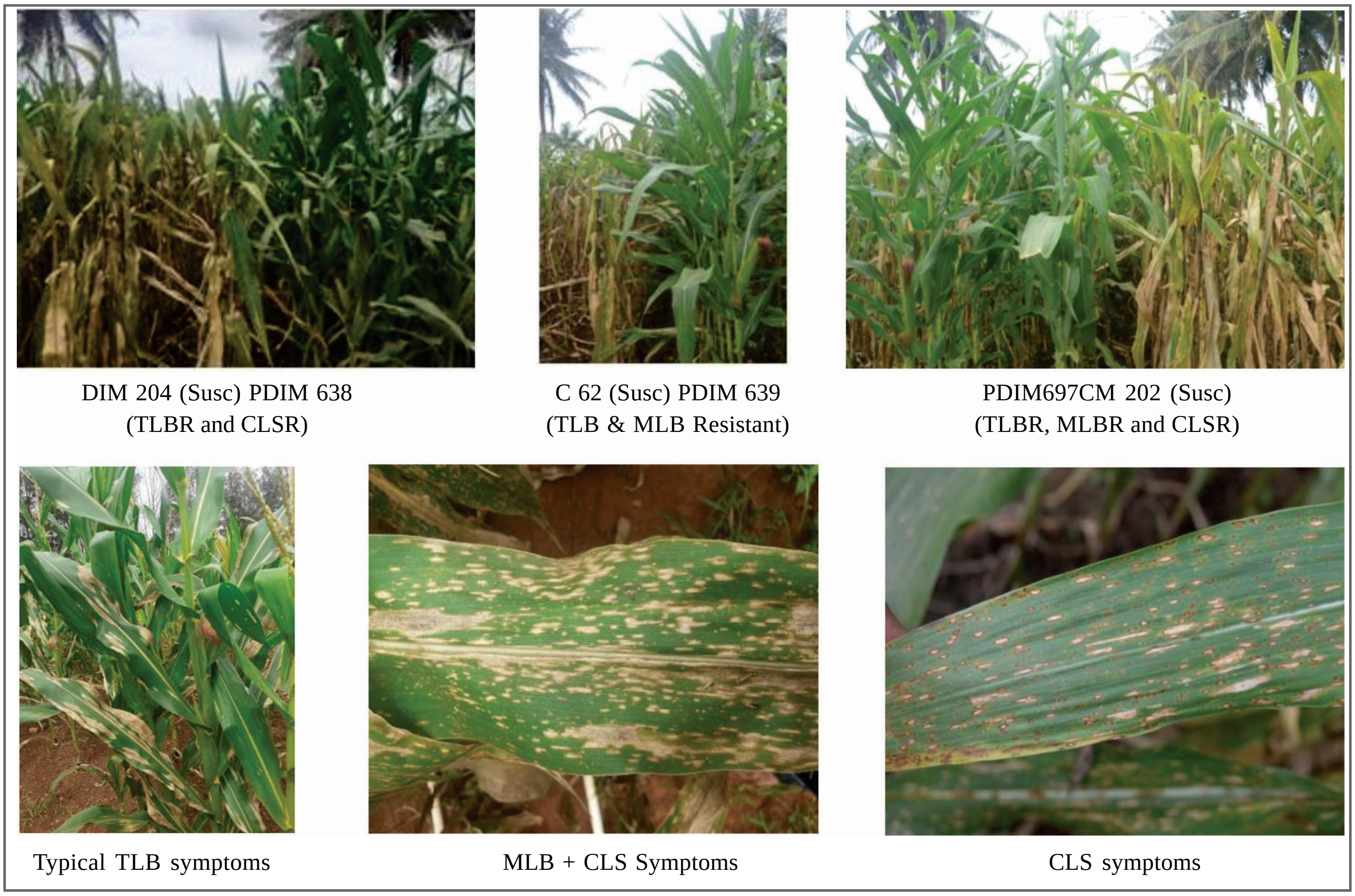


Figure 1. Distribution of inbred lines with respect to disease scores against foliar diseases

t/ha) that fall into different maturity categories. One of the inbred which was most notable is a late inbred line PDIM 635 with a productivity of 4.7 t/ha and resistance against all four diseases studied. The inbred lines C 79 and C 67 had a yield level of 5.0 t/ha and 3.6 t/ha, respectively with resistance against CLS, MLB, and CR. Few more inbreds displayed higher productivity and resistance against more than one foliar disease. For instance, such results have been earlier reported from the studies on different foliar diseases by Craven and Fourie (2011), Ram Dutta *et al*. (2012), Wisser *et al*. (2006), Bindhu *et al*. (2017) and Kuselan *et al*. (2017).

The study identified novel sources of resistance and sources of multiple resistance

The results of the screening against foliar diseases identified novel sources of resistance. The summary of the results is given in Table 9. It identified 5 resistant inbred lines against TLB (PDM 4641, PDIM 638, PDIM 639, PDIM 697, PDIM 635), 14 against CLS (PDIM 697, LM-14, C-79, CDM-1105, TC-6, PDIM 638, C-78, PDIM 635, PML-85, C-14, TC-12, PDM-10, C-67, JK-1800), 35 against MLB and 7 against CR (C-79, CM 202, PDIM 635, PDIM 805, PDIM 697, PML-50, C-67). Among these, PDIM 635 and PDIM 697 displayed resistance against all the four diseases studied, while PDIM 638 and PDIM 639 exhibited resistance against TLB, CLS, and MLB and C 79 and C 67 showed resistance against CLS, MLB, and CR. Further, there are a few more inbreds that displayed



DIM 204 (Susc) PDIM 638
(TLBR and CLSR)

C 62 (Susc) PDIM 639
(TLB & MLB Resistant)

PDIM697CM 202 (Susc)
(TLBR, MLBR and CLSR)

Typical TLB symptoms

MLB + CLS Symptoms

CLS symptoms

Figure 2. The images of susceptible and resistant inbreds against TLB, CLS, and MLB and their typical symptoms

Table 9. Summary of screening of maize inbred against foliar diseases

Foliar disease / Reaction	Inbred lines
Turcicum leaf blight (TLB)	
Resistant	PDM 4641, PDIM 638, PDIM 639, PDIM 697, PDIM 635
Moderate Resistant	C-79, CDM-1105, CML-582, PDIM 805, LM-14, C-8, C-83
Curvularia leaf spot (CLS)	
Resistant	PDIM 697, LM-14, C-79, CDM-1105, TC-6, PDIM 638, C-78, PDIM 635, PML-85, C-14, TC-12, PDM-10, C-67, JK-1800
Moderate Resistant	PDIM 639, CML-582, JK-1553, BLSB-2 B, JK-370, PDM-59, C-83, PML-18 B, PDM-134, DDM-2313, C-2760, C-25, C-23, D-2282_1, PML-25, DT-2, C-12, PML-50, DT-5_1, C-74, PDM-114-2, C-2765, C-62, DIM-204 B, C-8, DIM-316
Maydis leaf blight (MLB)	
Resistant	C-79, CDM-1105, PDM-10, C-83, PDM-134, C-2765, PDIM 697, JK-370, PML-18 B, C-2760, C-25, C-23, DT-5_1, DIM-316, PDIM 635, PML-85, JK-1800, PDM-59, PML-25, C-12, PML-50, C-74, PML-102_1, TC-6, C-78, C-67, JK-1553, DIM-204 B, LM-14, TC-12, DDM-2313, DT-2, BGD-48Y, PDIM 639, PDIM 638
Moderate Resistant	PDM-114-2, PDM 4641, CML-582, C-14, D-2282_1, C-8, PDIM 805
Common Rust (CR)	
Resistant	C-79, CM 202, PDIM 635, PDIM 805, PDIM 697, PML-50, C-67
Moderate Resistant	C-74, PDM-134, JK-1553, C-2765, C-62, C-8, DT-2, BGD-48Y, C-14, JK-1800, C-2760, C-78, DDM-2313, PDM-10, PML-18 B, TC-12, TC-6, C-12, PDM-59, PML-102 _1, PML-25
TLB, CLS, MLB, and CR	The remaining inbreds for each foliar disease were either moderately susceptible or susceptible

resistance against two of the four diseases studied. This multiple disease resistance and its possible genetic linkage were also noted in Figure 1. Such multiple resistances have previously been reported in crop plants including maize. Multiple disease resistance (MDR) loci, are defined as "loci that confer resistance to two or more diseases" (Wiesner-Hanks and Nelson 2016). This multiple disease resistance might be due to the presence of resistance genes against different diseases on the same chromosome or different chromosomes in the genotypes. Previously, colocalization of QTLs for resistance to southern leaf blight, northern leaf blight, and gray leaf spot diseases has been reported in maize (Balint-Kurti *et al*., 2010; Wisser *et al*., 2011; Li *et al*., 2018). It was also reported that a maize caffeoyl-CoA O-methyltransferase encoded by *ZmCCoAOMT2* gene confers quantitative resistance to multiple pathogens (Yang *et al*., 2017).

Further genetic enhancement in foliar disease resistance is possible

The knowledge of heritability and genetic advance of the trait of interest is required to guide the breeder to employ a suitable breeding strategy. Genetic variability together with heritability estimates would give a better idea of the genetic gain expected out of selection (Burton, 1952) and the magnitude of heritable variability is the most important aspect (Panse, 1961). Heritability estimates along with genetic advance are normally more helpful in predicting gain under selection than heritability estimates alone as it is not sufficiently informative about the existence of gene action (additive/non-additive) and the involvement of other factors in the expression of traits (Johnson *et al*., 1955). In the present study, the GCV, PCV, heritability (bs), and GAM were high for all the traits studied indicating the amenability of this pool of inbreds for the selection of desirable genotypes and improvement in these traits through population improvement approaches. As the distribution of inbreds and the earlier reports suggest the possible role of quantitative trait loci in controlling the traits, recurrent selection procedures might be appropriate in breeding for foliar disease resistance and higher yield and that also may result in genetic enhancement of multiple disease resistance.

The results of the present study indicated the possibility of further genetic enhancement in resistance against foliar diseases, grain yield, and flowering traits.

Conclusion

The study could identify resistance sources (inbreds) against all four foliar diseases. Few inbreds displayed multiple disease resistance (MDR) coupled with higher grain yield. The genetic variability noted in the pool of inbreds suggested to go for selection of best resistant inbreds to develop hybrids through heterosis breeding in the immediate future and to breed for lines with higher resistance and grain yield through recurrent selection approaches as the PCV, GCV heritability and GAM in this pool of inbreds is high.

Author's contribution

JSB: Conceptualization of the study and manuscript preparation; GM: Analysis of data and manuscript editing; SB, PS, VK, RS, RT: Disease screening and data recording of foliar diseases; KI: Disease scoring and photography; RNG: Critical inputs and manuscript editing.

Conflicts of interest

Authors declare that there are no conflicts of interest that exist.

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References

Balint-Kurti, P. J., Yang, J., Van Esbroeck, G., Jung, J. & Smith, M. E. (2010). Use of maize advanced intercross line for mapping of QTL for Northern leaf blight resistance and multiple disease resistance. *Crop Science,* **50**: 458–466. https://doi.org/10.2135/cropsci2009.02.0066.

Barakat, M. N., Shafei, A. A. E. & Al-Doss, A. A. (2009). Identification of molecular markers linked to northern corn leaf blight resistance in yellow population of maize. *Genes, Genomes and Genomics,* **16**: 24–29.

Bindhu, K. G., Pandurangegowda, K. T., Lohithaswa, H. C., Madhuri, R. & Mallikarjuna, N. (2017). Genetics of resistance to turcicum leaf blight caused by *Exserohilum turcicum* (Pass.) Leonard and Suggs in maize (*Zea mays* L.). *International Journal of Current Microbiology and Applied Sciences,* **6**(11): 964–969.

Burton, G. W. (1952). Quantitative inheritance in grasses. In: *Proceedings of 6th International Grassland Congress,* **1**: 273–283.

Craven, M. & Fourie, A. P. (2011). Field evaluation of maize inbred lines for resistance to *Exserohilum turcicum. South African Journal of Plant and Soil,* **28**(1): 69–74. doi: 10.1080/02571862.2011.10640015.

Dutta, R., Anita, N., Chandra, S. & Ngachan, S. V. (2012). Sources of resistance to turcicum leaf blight (*Exserohilum turcicum*) of maize for NEH region. *Indian Phytopathology,* **65**(2): 200–202.

FAOSTAT (2020). https://www.fao.org/faostat/en/#data/QCL/visualize.

Harlapur, S. I., Wali, M. C., Anahosur, K. H. & Muralikrishna, S. (2000). A report on survey and surveillance of maize diseases in northern Karnataka. *Karnataka Journal of Agriculture Sciences,* **13**: 750–751.

Hooda, K. S., Khokhar, M. K., Shekhar, M., Karjagi, C. G., Kumar, B., Mallikarjuna, N., Devlash, R. K., Chandrashekara, C. & Yadav, O. P. (2017). Turcicum leaf blight—sustainable management of a re-emerging maize disease. *Journal of Plant Diseases and Protection,* **124**: 101–113.

Johnson, H. W., Robinson, H. F. & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal,* **47**(7): 314–318.

Kuselan, K., Manivannan, N., Ravikesavan, R. & Paranidharan, V. (2017). Combining ability analysis for yield and its component characters in maize (*Zea mays* L.). *Electronic Journal of Plant Breeding,* **8**(2): 591–600.

Li, Y. X., Chen, L., Li, C., Li, P. Bradbury, P. J. & Shi, Y. S. (2018). Increased experimental conditions and marker densities identified more genetic loci associated with southern and northern leaf blight resistance in maize. *Scientific Report,* **8**: 1–12. https://doi.org/10.1038/s41598-018-25304-z

Panse, V. G. & Sukhatme, P. V. (1961). *Statistical Methods for Agric. Workers. 2nd Edition.* ICAR, New Delhi, pp 361.

Reddy, R. V., Sheshagiri, R. A. & Sudarshan, M. R. (2013). Heritability and character association among grain yield and its components in maize (*Zea mays* L.). *Journal of Research ANGRAU,* **40**(2): 45–49.

Reynolds, M. P. & Ortiz, R. (2010). Adapting crops to climate change: a summary. In: Climate change and crop production. (M. P. Reynolds, Ed.), pp. 1–8. CABI, UK.

Shah, T. R., Prasad, K. & Kumar, P. (2016). Maize–A potential source of human nutrition and health: A review. *Cogent Food & Agriculture, part of the Taylor & Francis Group,* **2**(1): 1166995.

Sibiya, J., Tongoona, P. & Derera, J. (2013). Combining ability and GGE biplot analyses for resistance to northern leaf blight in tropical and subtropical elite maize inbred lines. *Euphytica,* **191**(2): 245–257.

Singh, V., Lakshman, D. K., Roberts, D. P., Ismaiel, A., Abhishek, A., Kumar, S. & Hooda, K. S. (2021). Fungal species causing maize leaf blight in different agro-ecologies in India. *Pathogens,* **10**: 1621. https:// doi.org/10.3390/pathogens10121621**.**

Wiesner-Hanks, T. & Nelson, R. (2016). Multiple Disease Resistance in Plants. *Annual Review of Phytopathology,* **54**: 229–252. https://doi.org/10.1146/annurev-phyto-080615-100037.

Wisser, R. J., Balint-Kurti, P. J. & Nelson, R. J. (2006). The genetic architecture of disease resistance in maize: A synthesis of published studies. *Phytopathology,* **96**: 120–129.

Wisser, R. J., Kolkman J. M., Patzoldt M. E., Holland J. B. & Yu, J. (2011). Multivariate analysis of maize disease resistances suggests a pleiotropic genetic basis and implicates a GST gene. *Proceedings. of National. Academy of Sciences,* USA, **108**: 7339–7344. https://doi.org/10.1073/pnas.1011739108.

Yang, Q., He, Y. & Kabahuma, M. (2017). A gene encoding maize caffeoyl-CoA *O*-methyltransferase confers quantitative resistance to multiple pathogens. *Nature Genetics,* **49**: 1364–1372. https://doi.org/10.1038/ng.3919.

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RESEARCH PAPER

Heterosis and combining ability analysis in sweet corn (*Zea mays* L. var *saccharata*) hybrids for various traits

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Abstract: The present study was conducted to estimate heterosis and combining ability effects in sweet corn (*Zea mays* L. var *saccharata*) hybrids and to screen out hybrids having high green cob and fodder yield and high TSS content. About 66 genotypes comprising 45 sweet corn hybrids, 18 parental lines, and 3 standard checks (Priya, Madhuri, and Sugar-75) were evaluated in three different environments (E_1 at Instructional Farm, RCA, Udaipur during *Kharif* 2019, E_2 at ARS, Banswara during *Kharif* 2019 and E_3 at Instructional Farm, RCA, Udaipur during *Rabi* 2019–20) in randomized block design with three replications for twenty diverse traits. Maximum and positively significant heterosis over the best check were shown by the sweet corn hybrid $L_7 \times T_1$ (73.7%) for green cob weight/plant. The highest and positively perceptible economic heterosis for green fodder yield (kg/ha) and total soluble sugar (TSS) content of green grain was observed for the sweet corn hybrids $L_4 \times T_2$ (86.2%) and $L_{11} \times T_1$ (17.9%) respectively. On the basis of specific combining ability effects, among the selected best five hybrids, sweet corn hybrids $L_5 \times T_2$ and $L_6 \times T_3$ were best for green cob yield, green fodder yield, and green cob weight/plant while the hybrid $L_{10} \times T_1$ was best for green cob yield, green cob weight/plant and TSS content of green grain. Combining ability analysis for green cob yield and green cob weight/plant revealed that lines L_2, L_3, L_7, L_8, L_{11}, L_{12}, and L_{13} were good general combiners over the three environments. Sweet corn hybrid $L_5 \times T_2$ was identified to exhibit the highest and positively significant specific combining ability effect for green cob yield (4090.1) over the three environments.

Keywords: Combining ability · Green cob yield · Heterosis · Sweet corn · TSS

Introduction

Sweet corn has high nutritional values, delicate texture, and sweet taste within pericarp and endosperm and is treated as a vegetable. The flavour, texture, and sweetness of sweet corn kernels are due to the presence of some endosperm mutants which alter the starch biosynthesis pathway in the endosperm. The most useful mutations among them, *sh2*, *bt1*, *su1*, and *se*, function either by accumulating sugar at the expense of starch or by changing the types and proportions of different polysaccharides stored in the endosperm (Boyer and Shannon, 1984). The total sugar content in sweet corn at the milky stage ranges from 25–30% as compared to 2–5% of normal corn (Sadaiah *et al*., 2013). The popularity of sweet corn is increasing in the national and international market due to the sweetness and tenderness of its kernels and its appetizing taste, which has in turn resulted in its increased cultivation in the country, ensuring a good return to the farmers. Further, the leftover plants after the harvest of cobs can be used as fresh or dry fodder for the animals. Sweet corn breeding aims to improve quality and appearance as well as cob yield however, the genetic base of the sweet corn breeding programme is relatively narrow and related inbreds often

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are crossed to make hybrids that meet the strict market requirements on quality and appearance (Tracy, 1994). Sweet corn breeders have often focused on improving quality and ear appearance, rather than on enhancing yield (Tracy, 1993). But the emphasis on kernel sweetness along with yield needs to be considered as the major objective of sweet corn improvement. The quality parameters are relatively more important, especially because of the direct consumption of sweet corn as a vegetable and the preference of the consumers. Keeping in view the above facts and the growing demand for sweet corn in the domestic and international market, the development of hybrids exhibiting hybrid vigor using parents with superior combining ability has been taken as an objective of first importance of the research.

Material and methods

Eighteen diverse sweet corn inbred lines, collected from different parts of the country were used as parents (fifteen females and three testers) (Table 1). The crosses were made in line × tester matting design at Instructional Farm, RCA, Udaipur during *Kharif* 2018. Total of 66 genotypes comprising 45 sweet corn hybrids, 18 parental lines, and 3 standard checks (Priya, Madhuri, and Sugar-75) was evaluated in three different environments (E_1 at Instructional Farm, RCA, Udaipur during *Kharif* 2019, E_2 at ARS, Banswara during *Kharif* 2019 and E_3 at Instructional Farm, RCA, Udaipur during *Rabi* 2019-20) in randomized block design with three replications. Recommended agronomic practices were used to raise a healthy crop. Observations were recorded for 20 yields attributing quantitative and qualitative characteristics like days to 50% tasseling, days to 50% silking, plant height, ear height, number of leaves/plant, length of leaf, breadth of leaf, days to green cob harvest, number of ear/plant, ear length, ear girth, number of grain rows/ear, number of grains/row, 100 fresh seed weight, green cob weight/plant, moisture per cent of green grain, green cob yield, green fodder yield, total soluble sugar (TSS) content of green grain and protein content. Ten plants were taken from each row for recording observations from each replication. TSS content was recorded using a hand refractometer.

Estimation was done over the three environments on a pooled basis. Estimates of standard heterosis were calculated according to Virmani *et al*. (1982) and the significance of heterosis was tested using a 't-test'. The analysis of variance for general and specific combining ability effects over the environments and in three individual environments was done for different characters under the study using the line × tester mating design provided by Kempthorne (1957).

Table 1. List of genotypes used

S.No.	Symbol	Pedigree
1.	L_1	SC-7-2-1-2-6-1
2.	L_2	SC-18728
3.	L_3	BAJ-SC-17-6
4.	L_4	BAJ-SC-17-10
5.	L_5	BAJ-SC-17-12
6.	L_6	BAJ-SC-17-9
7.	L_7	BAJ-SC-17-11
8.	L_8	BAJ-SC-17-8
9.	L_9	BAJ-SC-17-4
10.	L_{10}	BAJ-SC-17-2
11.	L_{11}	BAJ-SC-17-1
12.	L_{12}	DMSC-28
13.	L_{13}	Mas Madu (sh2 sh2)
14.	L_{14}	MRCSC-12
15.	L_{15}	SC-33
16.	T_1	SC-35
17.	T_2	SC-32
18.	T_3	DMRSC-1

Result and discussion

The estimation of standard heterosis was done over the best check Sugar-75 over the three environments for all the characters under study. The analysis of data for economic heterosis for green cob yield over the three environments revealed that the sweet corn hybrid $L_7 \times T_1$ exhibited the highest estimates of positively significant standard heterosis against the best check Sugar-75 (71.4%). Maximum and positively significant heterosis over the best check were shown by the sweet corn hybrid $L_7 \times T_1$ (73.7%) for green cob weight/plant. The highest and positively perceptible economic heterosis for green fodder yield (kg/ha) and TSS content of green grain was observed for the sweet corn hybrids $L_4 \times T_2$ (86.2%) and $L_{11} \times T_1$ (17.9%) respectively. For ear length, the maximum estimate of economic heterosis in a positively significant direction was reported for the sweet corn hybrid $L_3 \times T_1$

(40.6%). The sweet corn hybrid $L_1 \times T_3$ (14.5%) exhibited the highest and most positively significant standard heterosis for the number of grain rows/ear. Further, $L_8 \times T_1$ (41.7%) showed a maximum estimate of significant and positive heterosis for the number of grains/rows. The present findings were in close agreement with the earlier findings of Dagla *et al.* (2014) and Kumari *et al.* (2018). None of the sweet corn hybrids were reported to exhibit significant economic heterosis in the required direction for the characters' days to 50% tasseling, plant height, days to green cob harvest, ear girth, and protein content over the three environments against the best check Sugar-75.

The general combining ability effects are considered to be the function of the additive gene effects and additive × additive type of non-allelic interactions. Combining ability analysis for green cob yield and green cob weight/plant revealed that lines L_2, L_3, L_7, L_8, L_{11}, L_{12}, and L_{13} were good general combiners over the three environments. Similarly, for green fodder yield, lines L_1, L_2, L_3, L_4, L_7, L_{11}, L_{12}, and L_{13}, for TSS content of the green grain, lines L_1, L_5, L_7, L_{10}, L_{11}, L_{13}, and L_{14} and for protein content, line L_{12} were identified as superior general combiners over the three environments on the basis of general combining ability analysis. Among the testers, T_1 was identified as a good general combiner for green cob yield, green cob weight/plant, and TSS content of green grain on the basis of general combining ability estimates over the three environments. Similarly, testers T_1 and T_2 were reported as superior combiners for green fodder yield on the basis of general combining ability analysis in pooled environments.

Sweet corn hybrid $L_5 \times T_2$ was identified to exhibit the highest and positively significant specific combining ability effect for green cob yield (4090.1) over the three environments (Table 2). The five best sweet corn crosses which possessed significantly positive specific combining ability effects for green cob yield on pooled basis were $L_5 \times T_2$, $L_{15} \times T_3$, $L_{10} \times T_1$, $L_6 \times T_3$, and $L_9 \times T_1$, among which $L_5 \times T_2$, $L_{10} \times T_1$ and $L_9 \times T_1$ exhibited positively significant standard heterosis over the best check Sugar-75. The sweet corn hybrids $L_5 \times T_2$, $L_{15} \times T_3$ and $L_6 \times T_3$ were crossed between poor general combining ability effects parents, while the hybrids $L_{10} \times T_1$ and $L_9 \times T_1$ were crossed between poor × good and average × good general combining ability effects parents. For green fodder yield, the best five sweet corn hybrids that showed maximum and positively significant specific combining ability effects were $L_4 \times T_2$ followed by $L_{13} \times T_1$, $L_5 \times T_2$, $L_6 \times T_3$ and $L_8 \times T_3$ on the pooled basis (Table 3). The sweet corn hybrids $L_4 \times T_2$ and $L_{13} \times T_1$ were crosses between parents with good general combining ability effects while the hybrids $L_6 \times T_3$ and $L_8 \times T_3$ were crosses between parents with poor general combining ability effects. Hybrid $L_5 \times T_2$ was crossed between the parents with poor × good general combining ability effects. Analysis for green cob weight/plant identified $L_5 \times T_2$, $L_{10} \times T_1$, $L_{15} \times T_3$, $L_6 \times T_3$ and $L_7 \times T_1$ as the top five sweet corn hybrids to exhibit the highest and positively significant specific combining ability effects on a pooled basis. Hybrids $L_5 \times T_2$, $L_{15} \times T_3$ and $L_6 \times T_3$ were produced by crossing both parents with poor general combining ability effects, while $L_{10} \times T_1$ was crossed

Table 2. Five best sweet corn hybrids for green cob yield on the basis of specific combining ability effects over the three environments

S.No.	Sweet corn hybrids/parents	SCA effects	Economic heterosis (%)	Mean green cob yield (kg/ha)
1	$L_5 \times T_2$	4090.05**	35.12**	15,222.2
2	$L_{15} \times T_3$	3584.42**	-19.2**	9,101.1
3	$L_{10} \times T_1$	3551.09**	30.47**	14,695.6
4	$L_6 \times T_3$	3463.68**	1.28	11,407.8
5	$L_9 \times T_1$	1999.60**	38.92**	15,646.7

Table 3. Five best sweet corn hybrids for green fodder yield on the basis of specific combining ability effects over the three environments

S.No.	Sweet corn hybrids/parents	SCA/GCA effects	Economic heterosis (%)	Mean fodder yield (kg/ha)
1	$L_4 \times T_2$	13,377.43**	86.24**	37,163.3
2	$L_{13} \times T_2$	8,799.65**	75.11**	35,061.1
3	$L_5 \times T_2$	8,237.06**	44.16**	28,765.6
4	$L_6 \times T_3$	7,598.84**	-1.11	19,732.2
5	$L_8 \times T_3$	6,938.47**	14.23*	22,794.4

between parents with poor × good general ability combining ability effects. The hybrid $L_7 \times T_1$ was crossed between both parents with good general combining ability effects. Analysis of TSS content of green grain over the three environments identified $L_{14} \times T_2$, $L_{12} \times T_1$, $L_2 \times T_3$, $L_1 \times T_3$ and $L_{10} \times T_3$ as the best five sweet corn hybrids possessing the highest and significantly positive specific combining ability effects. The sweet corn hybrids $L_{14} \times T_2$, $L_1 \times T_3$ and $L_{10} \times T_3$ were crossed between good × poor general combining ability effects parents, $L_{12} \times T_1$ between poor × good general combining ability effects parents while $L_2 \times T_3$ between parents with average × poor combining ability effects. Ola *et al.* (2018); Chinthiya *et al.* (2019); Nanditha *et al.* (2019); Sharma *et al.* (2019) and Tesfaye *et al*. (2019) reported similar results for combining ability analysis on maize.

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Declaration

The authors do not have any conflict of interest.

References

Boyer, C. D. & Shannon, J. C. (1984). The use of endosperm genes for sweet corn improvement. *Plant Breeding Reviews*, **1**: 193–161.

Chinthiya, A., Ganesan, K. N., Ravikesavan, R. & Senthil, N. (2019). Combining ability and association studies on different yield contributing traits for enhanced green cob yield in sweet corn (*Zea mays* L. var *saccharata*). *Electronic Journal of Plant Breeding*, **10**(2): 500–511.

Dagla, M. C., Gadag, R. N., Sharma, O. P. & Kumar, N. (2014). Estimation of heterosis for grain yield and quality traits in sweet corn (*Zea mays* L. var *saccharata*). *Electronic Journal of Plant Breeding*, **5**(4): 775–780.

Kempthorne, O. (1957). An introduction to genetic statistics. New York: John Wiley and Sons, Inc; London: Chapman & Hall, Ltd.

Kumari, R., Singh, A. K. & Suman, S. (2018). Quantitative studies on heterosis and inbreeding depression in maize (*Zea mays* L.). *Journal of Applied and Natural Science*, **10**(1): 64–69.

Nandhitha, G., Ganesan, K. N. & Ravikesavan, R. (2019). Heterosis and combining ability studies in single cross hybrids synthesized with diverse inbred lines of maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, **9**(4): 1503–1511.

Ola, B., Dubey, R. B., Singh, M. & Ameta, K. D. (2018). Combining ability analysis in medium maturing yellow seeded maize (*Zea mays* L.) hybrids. *Journal of Pharmacognosy and Phytochemistry*, **7**(3): 1354–1359.

Sadaiah, K., Reddy, V. N. & Sudheer Kumar, S. (2013). Heterosis and combining ability studies for sugar content in sweet corn (*Zea mays saccharata* L.). *IJSRP*, **3**: 1–5.

Sharma, P., Kamboj, M. C. & Punia, M. S. (2019). Assessment of combining ability effects using quality protein maize donors as testers for yield and yield traits in maize. *Electronic Journal of Plant Breeding*, **10**(4): 3365–3368.

Tesfaye, D., Abakemal, D. & Habte, E. (2019). Combining ability of highland adapted double haploid maize inbred lines using line x tester mating design. *East African Journal of Sciences*, **13**(2): 121–134.

Tracy, W. F. (1994). Sweet corn. In: A. R. Haullauer (ed.) Specialty types of maize. CRC Press, Boca Raton, Fla, pp. 147–187.

Virmani, S. S., Aquino, R. O. & Khush, G. S. (1982). Heterosis breeding in rice (*Oryza sativa* L.). *Theoretical and Applied Genetics*, **63**: 373–380.

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RESEARCH PAPER

Optimization of gamma-ray irradiation dose for induced mutagenesis in field corn (*Zea mays* L.)

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Abstract: The present investigation was carried out to optimize the dose of gamma rays for practical mutation breeding application in field corn. An elite maize inbred line (PML-93) was irradiated with 10 different doses of gamma rays and seedling traits and growth parameters were evaluated by the paper towel and pot method. The observation of seed and seedling growth parameters such as germination percent, mean root length (MRL), mean shoot length (MSL), mean root dry weight (MRDW), mean shoot dry weight (MSDW), vigour index I (V-I), vigour index II (V-II) were recorded. The study revealed significant variations in all the traits under investigation in both the paper towel and the pot method. Out of 10 doses, the dose of 200 Gy was found optimum, it showed a 50 percent growth reduction (GR) in terms of most of the above growth parameters. Further, karyotype analysis showed that the chromosome breakages at one or two places as compared to the control. These aberrations may lead to heritable variation. Hence mutation breeding approach can be undertaken to create variability within this inbred line. The generated variability can be the best source to explore potential mutant line/s for the future breeding program.

Keywords: Gamma radiation · Inbred line · Karyotype · Optimum dose · Variability

Introduction

The mutation is a heritable change that alters the genetic makeup of an individual. It may occur naturally or can be induced. The mutation has been the single most important factor in evolution as the changes in genetic makeup produced are passed on to offspring and hence result in the appearance of new traits (Holme *et al*., 2019). The mutation, in some cases, may also result in reproductive isolation leading to speciation (Ma *et al*., 2021). Induced mutagenesis is being used for widespread application in the biological sciences, primarily for broadening the genetic base of germplasm in plant breeding, and more recently, as a tool for functional genomics (Mba *et al.*, 2010). Mutagens, the agents used to induce mutation, bring about changes in DNA sequences and consequently change the appearance, traits, and characteristics of the treated organism.

Mutagens are broadly classified as physical and chemical mutagens. Further, physical mutagens are classified as classical radiation mutagen, charged particle mutagen, and space radiation mutagen (Ma *et al*., 2021). For seed propagated crops, the use of physical mutagens such as gamma rays were found to be the most appropriate strategy for achieving optimum genetic variation in the germplasm (Du *et al*., 2022). Earlier,

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gamma irradiation has been proved to be more effective and economical compared to other ionizing radiations because of their easy availability and power of penetration, as realized in corn (Al-Salhi *et al*., 2004), chickpea (Hameed *et al*., 2008), wheat (Sünnetcioglu *et al*., 1998), peas (Mashev *et al*., 1995), lentils (Chaudhuri *et al*., 2002), potato (Dale *et al*., 1997), citrus (Ling *et al*., 2008). However, the determination of the appropriate effective dose requires a detailed study of plant growth parameters and their interaction with the mutagens (Shrivastava *et al*., 2021).

Selection of the dose that could produce high mutation rates and may create desired mutant, is the critical and prerequisite step in the mutation breeding approach (Layek *et al*., 2021). The optimum dose might vary with the plant species, variety, *etc*. Hence, standardization of the mutagen dose is the first key step to getting a high mutation rate and assessing of radio sensitivity of the target genotype (Ahloowalia *et al*., 2004). Sidhya and Pandit (2015) recorded dose-dependent retardation in biological parameters *viz*., seed germination, and plant survival, of snake gourd and reported 200 Gy was as the LD50 indicating a less damaging effect at lower doses on the genetic material. Considering the above facts, the induction of mutations to improve kernel size in the inbred line, PML 93, was contemplated. The PML 93 is a conventionally derived inbred line; has excellent general combining ability, and high yield *per se* (3.5 t/ha). It has all the required desirable characteristics to be used as a female parent in the hybrid breeding program (Mukri *et al*., 2021). However, the kernel size of PML 93 falls into the small category, as per the maize DUS descriptor (Das *et al*., 2006), which is becoming a limitation in commercial hybrid seed production and limiting farmers' preference for it. Hence, an experiment was conducted to determine the appropriate dose of acute gamma irradiation producing 50% lethality or 50% growth reduction (considered as LD50 or GR50) in maize inbred line, PML 93 for inducing genetic variability and to correlate it with the growth parameters.

Materials and methods

Mutagen treatment

The inbred lines PML 93 (KDMH-176-5-1-1-B-B), a medium maturing inbred line, used in the active hybrid development program of ICAR-IARI was targeted for mutagenesis. The seeds of the test inbred line were obtained from the two different lots (Lot-I and Lot-II), grown during the post-rainy season, 2020 at two different locations (ICAR-Indian Agricultural Research Institute, New Delhi and ICAR-IARI, Regional Research Centre, Dharwad). These unirradiated seeds were subjected to a germination test by standard paper towel method and Lot II having 100% germination was sent to Bhabha Atomic Research Centre (BARC), Mumbai, India, for irradiating with gamma rays. A sample of 100 seeds each was irradiated with ten different doses of gamma rays *viz*., 50 Gy, 100 Gy, 150 Gy, 200 Gy, 250 Gy, 300 Gy, 400 Gy, 500 Gy, 600 Gy, and 700 Gy at BARC. A set of unirradiated seed samples were taken as a control for comparative analysis. These seed samples were pre-treated with Bavistin (2 g/kg) to prevent fungal infections during germination. The irradiated seed samples along with control were put to germination test using the paper towel method.

Experimental set-up

Paper towel method

A total of 20 seeds each for all 10 doses of gamma rays were grown in two replications under a growth chamber at 30°C for 10 days using a paper towel. One set of unirradiated seeds (PML 93) was taken as control. The seedling growth parameters were recorded 10 days after germination of the control seed. The growth parameters *viz*., percent germination [(number of germinated seeds/ total number of seeds) × 100], seedling length (root and shoot length) in cm, seedling fresh weight, and dry weight (oven-dry weight) in g, vigor index I [(mean root length + mean shoot length)] × percent seed germination) and vigor index II [(mean root dry weight + mean shoot dry weight)] × percent seed germination) were estimated using the data recorded on individual seedlings.

Pot method

The same set of experimental materials with three biological replications was sown in the pot (6-inch diameter) containing solarized soil medium. Here, a total of 30 seeds each for all ten (50 Gy, 100 Gy, 150 Gy, 200 Gy, 250 Gy, 300 Gy, 400 Gy, 500 Gy, 600 Gy, and 700 Gy) dosages of gamma rays were placed in a completely randomized design containing ten seeds per replication, under natural conditions. Pots were irrigated as and when required with potable water. After 10 days, observations on growth parameters as that of the paper towel method were recorded.

Karyotype analysis

An enzyme-based method by Snowdon *et al*. (1997) was used to assess the chromosomal aberrations in the meristematic region of roots. Young growing root tips (1–2 cm) were fixed at the metaphase I stage in Carnoy's solution (cold ethanol: glacial acetic acid (3:1)). To capture the aberrations, first the fixative was rinsed (2 × 10 minutes in double distilled water) and roots were incubated in citrate solution (0.01M, pH 4.5) for 15 minutes. Root tips were treated with enzyme solution containing 5:1 cellulase (Onozuka R-10 cellulase, Yakult Honsha Co. Ltd., Japan) and pectolyase (Y23 pectolyase, Seishin Pharmaceutical Ltd., Japan) prepared in citrate solution (0.01 M, pH 4.5) for 1 hour 5 minutes at 37°C. Treated roots were scrambled on glass slides in Carnoy's solution and covered with a coverslip of the width of about 1 cm and visualized under the light microscope (LEICA DM 750, Germany) at 100 × (100 x/1.25 oil) attached with a high-resolution camera (LEICA DFC 3000 Germany).

The mean value of replications under each experimental setup was used for statistical analysis through SAS 9.3 v(SSCNARS, IASRI, New Delhi).

Results and discussion

Analysis of variance for growth parameters of gamma rays irradiated PML 93 genotype showed significant variation for all the studied parameters *viz*., root length, shoot length, root dry weight, shoot dry weight, vigor index-I, and vigor index-II, both for paper towel and pot method of growth analysis in a dose-dependent manner (Table 1 and 2). This indicated that the different doses used in the experiment have created a significant amount of variability due to cellular damage in PML 93.

Effects of gamma irradiation on germination percentage

The mean percent germination, root length, shoot length, root dry weight, shoot dry weight, vigor index-I, and vigor index-II showed a progressive reduction with the increase in dosage. Seedlings grown in a growth chamber on the paper towel method exhibited 100% germination for control as well as for all the gamma-ray doses except 400 Gy and 700 Gy, which recorded 80% germination (Table 3). The deviation in the germination percentage at 400 Gy and 700 Gy seems to be due to extraneous factors. On the other hand, the germination percentage of seedlings grown in the pot method was 90% in control and 73.3% in 50 Gy. At higher gamma-ray doses, there was a progressive reduction in germination percentage and it got reduced to 50% at 250 Gy. The lowest germination was recorded at 400 Gy (13.3%) and the seed samples irradiated with 500 Gy and above showed no germination implying that these doses are lethal for PML 93 (Table 4).

Table 1. Analysis of variance for growth parameters of PML 93 under different doses of gamma irradiation for paper towel method

Sources of variation	df	MSS					
		Root length	**Shoot length**	**Root dry weight**	**Shoot dry weight**	**Vigour index I**	**Vigour index II**
Replication	1	0.00	0.86	0.00	0.01	6136.58	81.91
Treatment	10	131.22**	55.87**	0.0072**	0.04**	3502154.69**	844.38**
Error	10	2.63	1.71	0.00	0.00	59406.20	24.23

**: Significant at 1% probability.

Table 2. Analysis of variance for growth parameters of PML 93 under different doses of gamma irradiation for pot method

Sources of variation	df	MSS					
		Root length	**Shoot length**	**Root dry weight**	**Shoot dry weight**	**Vigour index I**	**Vigour index II**
Replication	2	3.20	7.41	0.00	0.00	231.01	1.16
Treatment	10	166.73**	268.60**	0.0002**	0.002**	3873.08**	17.11**
Error	20	2.80	1.38	0.00	0.00	72.17	1.06

**: Significant at 1% probability.

Table 3. Effect of Gamma-ray irradiation on maize seedling growth parameters for paper towel method

S.No.	Treatment	Germination (%)	Mean root length (cm)	Mean shoot length(cm)	Mean root dry weight (g)	Mean shoot dry weight (g)	Vigour index I	Vigour index II
1	0 Gy	100.0	26.2	15.85	0.19	0.48	4201.3	67.4
2	50 Gy	100.0	18.7	14.51	0.16	0.38	3318.4	54.1
3	100 Gy	100.0	12.0	11.66	0.14	0.33	2369.4	46.2
4	150 Gy	100.0	11.4	11.62	0.12	0.32	2302.4	44.7
5	200 Gy	100.0	9.7	11.59	0.14	0.31	2131.0	44.6
6	250 Gy	100.0	7.9	11.62	0.12	0.30	1955.0	42.2
7	300 Gy	100.0	4.2	7.64	0.10	0.24	1181.5	33.1
8	400 Gy	80.0	4.6	7.24	0.08	0.16	944.0	19.0
9	500 Gy	100.0	1.5	2.24	0.03	0.08	370.1	10.9
10	600 Gy	100.0	0.14	1.07	0.02	0.07	120.5	8.9
11	700 Gy	80.0	0.04	1.13	0.02	0.04	125.5	4.5
	Mean	96.4	8.8	8.74	0.10	0.25	1729.0	34.1
	SD	8.1	8.1	5.29	0.06	0.14	1323.3	20.6

Table 4. Effect of Gamma-ray irradiation on maize seedling growth parameters for pot method

S.No.	Treatment	Germination (%)	Mean root length (cm)	Mean shoot length(cm)	Mean root dry weight (g)	Mean shoot dry weight (g)	Vigour index I	Vigour index II
1	0 Gy	90.0	16.5	20.9	0.02	0.05	105.9	6.74
2	50 Gy	73.0	15.3	20.3	0.02	0.05	78.2	5.25
3	100 Gy	64.3	15.4	19.5	0.01	0.04	42.4	3.52
4	150 Gy	63.0	12.8	17.2	0.01	0.04	42.7	3.43
5	200 Gy	56.7	12.5	16.9	0.01	0.03	25.6	2.41
6	250 Gy	40.0	2.6	6.4	0.00	0.03	16.6	1.36
7	300 Gy	36.70	0.13	0.73	0.00	0.00	2.8	0.15
8	400 Gy	13.3	0.1	0.67	0.00	0.00	0.0	0.07
9	500 Gy	0.0	0.0	0.0	0.00	0.00	0.0	0.00
10	600 Gy	0.0	0.0	0.0	0.00	0.00	0.0	0.00
11	700 Gy	0.0	0.0	0.0	0.00	0.00	0.0	0.00
	Mean	96.4	39.8	6.9	9.33	0.01	0.02	28.57
	SD	8.1	32.5	7.5	9.46	0.01	0.02	35.93

Effects of gamma irradiation on growth parameters

Among in the seedlings grown in the paper towel method, the mean root length (MRL) of the control was 26.2 cm. The increasing doses of gamma irradiation to seeds showed a progressive decrease in MRL. The MRL decreased from 18.7 cm at 50 Gy to 0.14 cm at 600 Gy and 0.04 cm for 700 Gy. In the pot-grown seedlings, the MRL was 16.52 cm in control, 15.33 Gy for 50 Gy, and the lowest (0.10 cm) at 400 Gy. A 50% reduction in MRL was recorded at 200 Gy. The mean shoot length (MSL) also showed reduction in mean values as a result of gamma irradiation as compared to the 15.85 cm MSL in control for the paper towel method and the reduced MSL were 14.51 cm, 11.66 cm, 11.59 cm, 11.62, 7.64 cm, 7.24 cm, 2.24 cm, 1.07 cm, and 1.03 cm for 50 Gy, 100 Gy, 150 Gy, 200 Gy, 250 Gy, 300 Gy, 500 Gy, 600 Gy, and 700 Gy dose of gamma rays, respectively. The dose of 300 Gy seems to reduce MSL by 50% in the paper towel method. In the pot method, there was not much reduction in MSL from control (20.89 cm) till the dose of 250 Gy 16.94 cm). However, at higher doses, there was a drastic reduction in MSL, which got reduced to 6.42 cm at 300 Gy to 0.77 cm at 400 Gy and to 0.67 cm at 500 Gy (Table 4).

It was observed that the mean root dry weight (MRDW) was 0.02 g for unirradiated seeds and decreased to 0.01 g which is 50% of the control at the dose of 150 Gy in pot germinated seedlings. Though the seeds irradiated with doses of 300 Gy and above showed germination, the MRDW values were negligible or close to zero. Likewise, in the paper towel experiment, a continuous decrease in MRDW values from 0.16 g to 0.02 g from50 Gy to 700 Gy compared to the control (0.19 g) was also observed (Figure 1). A similar trend of decreasing mean shoot dry weight (MSDW) with increasing gamma rays' dosage was noticed that ranged from 0.48 g (unirradiated) to 0.04 g (700 Gy) and 0.05 g (unirradiated) to 0.03 g (200 Gy) under paper towel and pot method of evaluation, respectively

The vigor index (VI) is a determinant of the interaction of multiple factors *i.e.*, seed germination, shoot elongation, and their interaction with environmental conditions. Hence, the information derived by VI was taken to be more reliable than a single trait (Qun *et al.*, 2007). Vigor Index-I was also decreased to 3318.4, 2369.4, 2302.4, 2131.0, 1955.0, 944.0, 370.1, 120.5, and 125.5, respectively with increasing doses of irradiation from 50 Gy to 700 Gy as compared to control value (4201.3) in paper towel method. The same pattern was seen in pot-grown seedlings with values of 105.9 for control, 78.2 for 50 Gy, 42.4 for 100 Gy, 42.7 for 150 Gy, and 25.6 for 200 Gy, 16.6 for 250 Gy, and 2.8 for 300 Gy. The VI-I for doses 400 Gy, 500 Gy, 600 Gy, and 700 Gy were zero. A 50% reduction in the value of VI-I, was observed at the dose 100–150 Gy. Furthermore, VI-II values also decreased continuously as doses increased. The VI-II estimated were 6.74, 5.25, 3.52, 3.43, 2.41, 1.36, and 0.15 for doses of 50 Gy, 100 Gy, 150 Gy, 200 Gy, 250 Gy, 300 Gy, and 400 Gy, respectively with control having a value of 6.74 for pot grown experiment. There was a complete cessation of seedling growth with zero vigor index- II value, beyond 400 Gy of gamma rays (Figure 2). However, the observed VI-II values for different doses of irradiation (50–700 Gy) were 54.1, 46.2, 44.7, 44.6, 42.2, 33.1, 19.0, 10.9, 8.9, and 4.5 with the control value of 67.4 for seedlings grown by paper towel method. In this case, a 50% reduction in VI-II was observed at the dose of 150 Gy.

GR50 doses slightly differed and ranged from 100 Gy to 300 Gy for different growth parameters studied here. To confirm the effect of these concentrations on the genetic component of the maize, karyotype analysis was conducted by taking meristematic root samples from

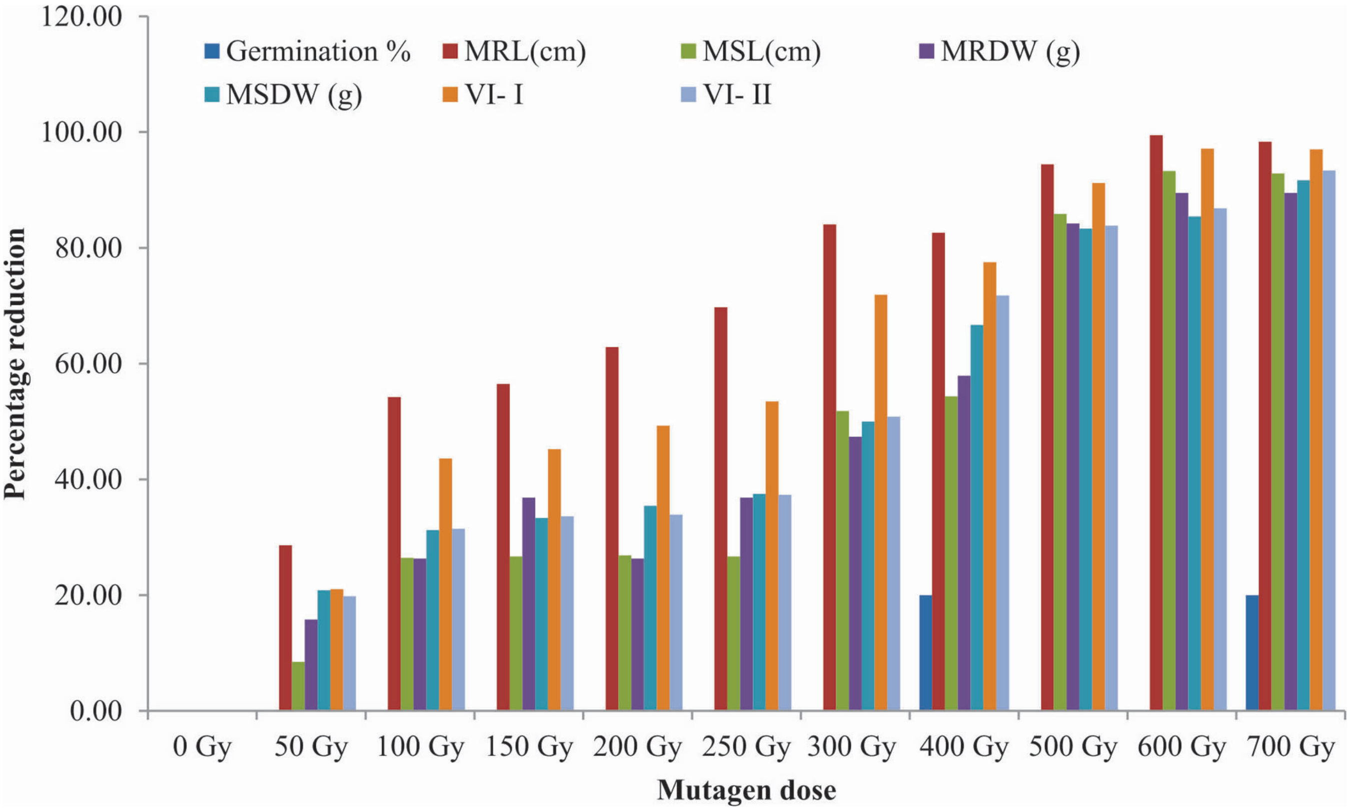

Figure 1. Percent reduction in growth parameters of PML 93, treated with Gamma rays under paper towel method of evaluation

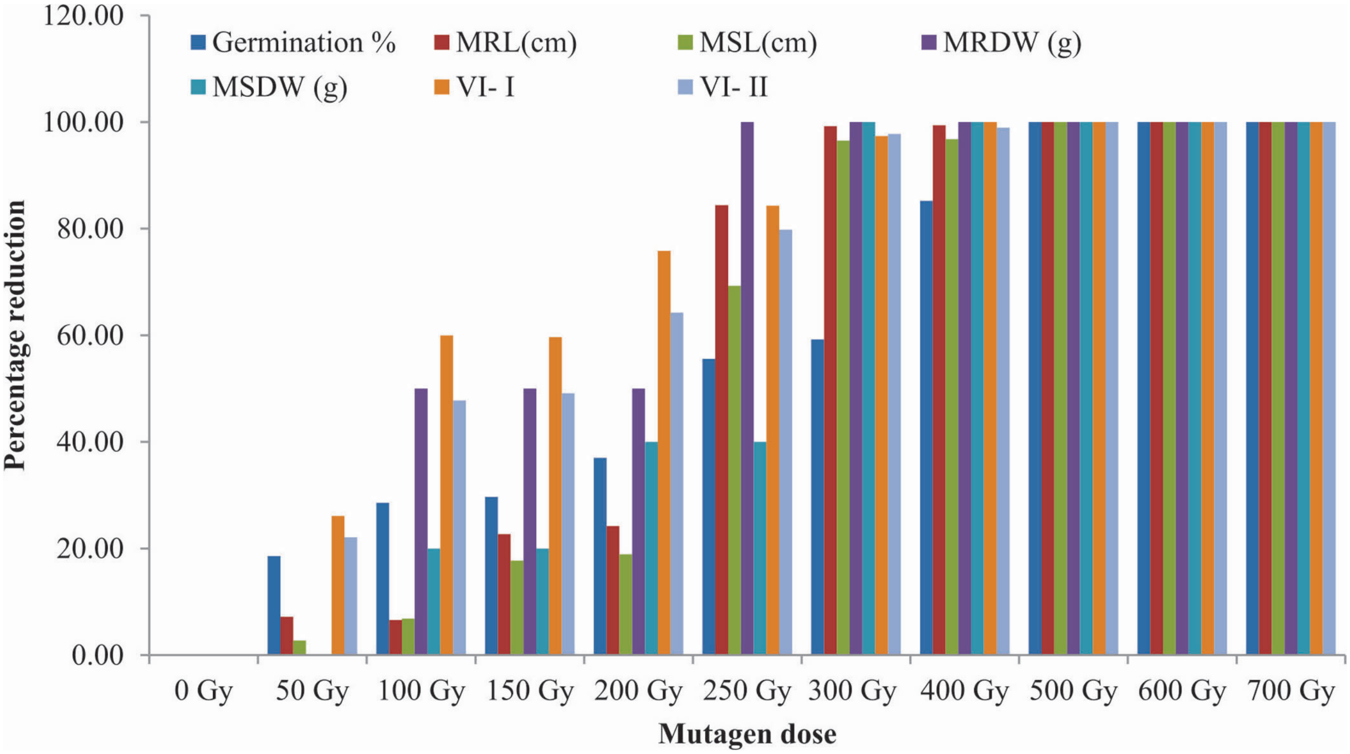

Figure 2. Percent reduction in growth parameters of PML 93, treated with Gamma rays under pot method of evaluation

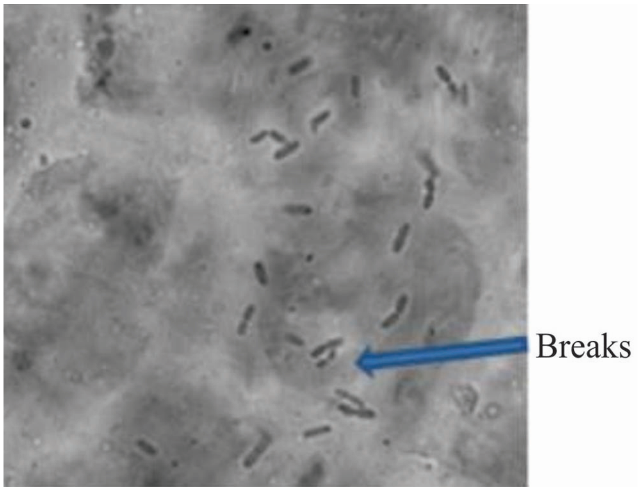

Figure 3. Chromosomal aberrations by the gamma rays at 200 Gy

different doses. It indicated that chromosomal aberration started with minor breakage in the chromosome with the dose of 200 Gy and onwards in gamma irradiation (Figure 3). As the dose increased, aberrations appeared more which justified lethality in maize. A drastic reduction in the establishment of healthy seedlings was observed when doses were increased from 200 Gy (Tables 3 and 4). By considering GR50 doses of all parameters and vigor indices, the 200 Gy can be considered as the actual GR50 dosage for the inbred line PML 93.

Conclusion

Optimization of gamma-ray doses for obtaining high mutation rates that may produce desired mutants is the basic requirement of a mutation breeding program. In the present study, the gamma-ray irradiation of field corn inbred induced significant variations in different growth parameters at 10 different doses ranging from 0 Gy to 700 Gy. Among the 10 doses of Gamma rays employed in the study, a dose of 200 Gy could produce a 50% growth reduction and hence it was decided to use 200 Gy as a GR50 dose to create genetic variability in the inbred line, PML 93. The irradiation of the seeds with gamma rays to generate mutants with desirable traits can be a potential source of novel genes for maize improvement programs.

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References

Ahloowalia, B. S., Maluszynski, M. & Nichterlein, K. (2004). Global impact of mutation-derived varieties. *Euphytica*, **135**(2): 187–204.

Al-Salhi, M., Ghannam, M. M., Al-Ayed, M. S., El-Kameesy, S. U. & Roshdy, S. (2004). Effect of γ-irradiation on the biophysical and morphological properties of corn. *Food/ Nahrung*, **48**(2): 95–98.

Chaudhuri, S. K. (2002). A simple and reliable method to detect gamma irradiated lentil (*Lens culinaris* Medik.) seeds by germination efficiency and seedling growth test. *Radiation Physics and Chemistry*, **64**(2): 131–136.

Dale, M. F. B., Griffiths, D. W., Bain, H. & Goodman, B. A. (1997). The effect of gamma irradiation on glycoalkaloid and chlorophyll synthesis in seven potato cultivars. *Journal of the Science of Food and Agriculture*, **75**(2): 141–147.

Du, Y., Feng, Z., Wang, J., Jin, W., Wang, Z., Guo, T., Chen, Y., Feng, H., Yu, L., Li, W. & Zhou, L. (2022). Frequency and spectrum of mutations induced by gamma rays revealed by phenotype screening and whole-genome re-sequencing in *Arabidopsis thaliana*. *International Journal of Molecular Sciences*, **23**(2): 654.

Hameed, A., Shah, T. M., Atta, B. M., Haq, M. A. & Sayed, H. I. N. A. (2008). Gamma irradiation effects on seed germination and growth, protein content, peroxidase and protease activity, lipid peroxidation in *desi* and kabuli *Kabuli* chickpea. *Pakistan Journal of Botany*, **40**(3): 1033–1041.

Holme, I. B., Gregersen, P. L. & Brinch-Pedersen, H. (2019). Induced genetic variation in crop plants by random or targeted mutagenesis: convergence and differences. *Frontiers in Plant Science*, **10**: 1468.

Layek, S., Pramanik, S., Das, A., Gupta, A. K., Bhunia, A. & Pandit, M. K. (2021). Effect of gamma radiation on seed germination and seedling growth of snake gourd (*Trichosanthes anguina* L.). *South African Journal of Botany*, **145**: 320–322.

Ling, A. P. K., Chia, J. Y., Hussein, S. & Harun, A. R. (2008). Physiological responses of *Citrus sinensis* to gamma irradiation. *World Applied Sciences Journal*, **5**(1): 12-–19.

Ma, L., Kong, F., Sun, K., Wang, T. & Guo, T. (2021). From classical radiation to modern radiation: past, present, and future of radiation in mutation breeding. *Frontiers in Public Health*, 9.

Mashev, N., Vassilev, G. & Ivanov, K. (1995). A study of N-allyl N-2 pyridyl thiourea and gamma radiation treatment on growth and quality of peas and wheat. *Bulgarian Journal of Plant Physiology*, **21**(4): 56–63.

Mba, C., Afza, R., Bado, S. & Jain, S. M. (2010). Induced mutagenesis in plants using physical and chemical agents. In: Plant cell culture: essential methods, pp. 111–130.

Mukri, G., Prabha, C., Mondal, S., Bhat, J.S., Raju, D., Gadag, R.N., Shilpa, K., Singh, C. & Sharma, J. (2021). Electron beam effects and determination of GR50 dose in tropical field corn, *Maize Journal*, **10**(1): 24–29.

Qun, S., Wang, J. H. & Sun, B. Q. (2007). Advances on seed vigor physiological and genetic mechanisms. *Agricultural Sciences in China*, **6**(9): 1060–1066.

Shrivastava, R., Mondal, S., Patel, N. B., Purkayastha, S. & Devi, Y. L. (2021). Standardization of GR50 dose of gamma rays for mutation breeding experiments in safflower (*Carthamus tinctorious* L.). *Indian Journal of Genetics and Plant Breeding*, **81**(3): 474–477.

Sidhya, P. & Pandit, M. K. (2015). Mutagenic effectiveness and efficiency of gamma rays in snake gourd (*Trichosanthes anguina* L.). *Journal of Applied and Natural Sciences*, **7**(2): 649–651.

Sünnetcioglu, M. M., Dadayli, D., Celik, S. & Köksel, H. (1998). Application of the electron paramagnetic resonance spin probe technique for detection of irradiated wheat. *Cereal Chemistry*, **75**(6): 875–878.

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RESEARCH PAPER

Genotype × environment interaction and stability studies in sweet corn hybrids using Eberhart and Russell model

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Abstract: The present study was carried out to estimate genotype × environment interaction and stability for qualitative and quantitative traits in sweet corn hybrids (*Zea mays* L. var *saccharata*). Forty-five hybrids using line × tester mating design were developed, which along with their eighteen parents and three checks (Priya, Madhuri and Sugar-75) were evaluated at three different locations during *Kharif* 2019 (E1 and E2) and *Rabi* 2019-20 (E3), in randomized block design with three replications. Stability analysis was done using Eberhart and Russell (1966) model on a pooled basis for twenty different characters. The results of the analysis of variance over the three environments for phenotypic stability revealed that variance due to genotypes and environment (linear) were significant for all the studied characters. Further, stability analysis revealed that all the genotypes possessed non-significant deviations from regression (S^2d_i) reflecting their predictable behaviour for the trait green cob yield. Only the hybrid $L_{12} \times T_1$ showed stable performance for protein content over the three environments. A study of data for green cob weight/plant revealed that two sweet corn hybrids $L_7 \times T_2$ and $L_7 \times T_3$ possessed non-significant deviations from regression (S^2d_i) along with a regression coefficient value nearly equivalent to unity (b_i=1) and a mean greater than the population mean. The performances of these two hybrids thus could be predictable as well as stable for cultivation in various environments. Analysis for quality characters showed that for TSS content of the green grain, sweet corn hybrids $L_1 \times T_1$ and $L_{11} \times T_1$ showed non-significant deviations from regression (S^2d_i) and regression coefficient equivalent to unity (b_i=1) with greater mean than the population mean, thus signifying their predictable performances and stability for different environments for sweetness.

Keywords: Green cob yield · Regression · Stability · Sweet corn · TSS

Introduction

Sweet corn (*Zea mays* L. var *saccharata*) is field corn in an arrested state of development (Erwin, 1951). With high nutritional values, delicate texture and sweet taste within pericarp and endosperm, it is treated as a vegetable (Kwiatkowski and Clemente, 2007). The most useful mutations resulting in its sweetness are due to genes *sh2*, *bt1*, *su1* and *se*, which function either by accumulating sugar at the expense of starch or by changing the types and proportions of different polysaccharides stored in the endosperm (Boyer and Shannon, 1984). Due to the sweetness and tenderness of its kernels and its appetizing taste, which has in turn resulted in its increased cultivation in the country and ensuring a good return to the farmers, the popularity of sweet corn is increasing in the national and international market. Further, the leftover plant after the harvest of cobs can be used as fresh or dry fodder for the animals. Recombining the same inbreds repeatedly without the infusion of new heterotic combinations may lead to the depletion of heterosis (Revilla *et al.*, 2000). The evaluation of genotype environmental interactions gives an idea about the stable performance of the genotype under

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varying environmental conditions, which in turn helps in assessing the genetic potential of the genotype and its nature. A lower magnitude of genotype environmental interactions indicates the consistent performance of a genotype over a wide range of environments. A study of the magnitudes of genotype × environmental interactions for yield and yield-related characters and quality parameters is a must for any breeding programme aiming to develop stable hybrids.

Material and methods

Eighteen diverse sweet corn inbred lines, collected from different parts of the country were used as parents (fifteen females and three testers) (Table 1). The crosses were made in line × tester matting design at Instructional Farm, RCA, Udaipur during *Kharif* 2018. Total 66 genotypes comprising 45 sweet corn hybrids, 18 parental lines and 3 standard checks (Priya, Madhuri and Sugar-75) were evaluated in three different environments (E_1 at Instructional Farm, RCA, Udaipur during *Kharif* 2019, E_2 at ARS, Banswara during *Kharif* 2019 and E_3 at Instructional Farm, RCA, Udaipur during *Rabi* 2019-20) in randomized block design with three replications.

Table 1. List of genotypes used

S.No.	Symbol	Pedigree
1.	L_1	SC-7-2-1-2-6-1
2.	L_2	SC-18728
3.	L_3	BAJ-SC-17-6
4.	L_4	BAJ-SC-17-10
5.	L_5	BAJ-SC-17-12
6.	L_6	BAJ-SC-17-9
7.	L_7	BAJ-SC-17-11
8.	L_8	BAJ-SC-17-8
9.	L_9	BAJ-SC-17-4
10.	L_{10}	BAJ-SC-17-2
11.	L_{11}	BAJ-SC-17-1
12.	L_{12}	DMSC-28
13.	L_{13}	Mas Madu (sh2 sh2)
14.	L_{14}	MRCSC-12
15.	L_{15}	SC-33
16.	T_1	SC-35
17.	T_2	SC-32
18.	T_3	DMRSC-1

Recommended agronomic practices were used to raise a healthy crop. Observations were recorded for 20 yields attributing quantitative and qualitative characteristics like days to 50% tasseling, days to 50% silking, plant height, ear height, number of leaves/plant, length of leaf, breadth of leaf, days to green cob harvest, number of ears/ plant, ear length, ear girth, number of grain rows/ear, number of grains/row, 100 fresh seed weight, green cob weight/plant, moisture per cent of green grain, green cob yield, green fodder yield, TSS content of green grain and protein content. Ten plants were taken from each row for recording observations from each replication. TSS content was recorded using a hand refractometer.

Estimation was done over the three environments on a pooled basis. The procedure proposed by Eberhart and Russell (1966) was used to estimate the stability and study different characteristics of genotypes.

Result and discussion

In the present study, genotype × environment interaction was shared by both predictable (linear) and unpredictable (deviation) components for different traits. Eberhart and Russell model (1966) considered both linear (b_i) and non-linear (S^2d_i) components of genotypes × environment interaction for predicting the performance of a genotype. According to this model, any genotype possessing a unit regression coefficient (b_i=1) and non-significantly deviation from regression (S^2d_i=0) along with higher mean performance than the population mean is regarded as a stable or ideal genotype. Further, non-significant deviation from regression (S^2d_i) indicates the predictable and stable performance of any genotype in a given set of environments.

The variance due to genotypes and environment (linear) was found significant for all the characters included in the study. The variance due to E + (G × E) interactions were found significant for most of the characters, except for the number of leaves/plant, breadth of leaf, ear length, ear girth and TSS content of green grain. The mean sum of squares due to G × E (linear) interactions were reported significant for all the characters, except for the number of leaves/plant, breadth of leaf, ear length, ear girth, 100 fresh seed weight and TSS content of green grain. Further, the analysis revealed that the characters days to 50% silking, number of leaves/ plant, length of leaf, breadth of leaf, ear length, ear girth, number of grains/row, 100 fresh seed weight, green fodder yield and TSS content of green grain had significant mean sums of squares due to pooled deviations, suggesting that prediction for these characters would be difficult as the genotypes differed considerably with respect to their stability.

Analysis for yield characters revealed that for green cob weight/plant two sweet corn hybrids $L_7 \times T_2$ and $L_7 \times T_3$ possessed non-significant deviations from regression (S^2d_i) along with regression coefficient value nearly equivalent to unity (b_i=1) and mean greater than the population mean (Table 2). The performances of these two hybrids thus could be predictable as well as stable for cultivation in various environments. A study for stability parameters for green cob yield revealed that all the genotypes possessed non-significant deviations from regression (S^2d_i) reflecting their predictable behaviour (Table 3). Only one sweet corn hybrid $L_6 \times T_1$ possessed non-significant deviation from regression (S^2d_i) along with a regression coefficient nearly equivalent to unity (b_i=1) and mean higher than the population mean, thus making it stable performer and suitable for all the environments for the number of grains/row. One sweet corn hybrid $L_{13} \times T_1$ exhibited non-significant deviation from regression (S^2d_i) along with a regression coefficient value nearly equivalent to unity (b_i=1) and mean more than the population mean indicating its predictable nature and stable performance in various environments for 100 fresh seed weight. None of the sweet corn hybrids possessed a regression coefficient nearly equal to unity (b_i=1) for the number of ears/plant, ear girth, number of grain rows/ear and green fodder yield.

Analysis for quality characters (Table 4) showed that for TSS content of the green grain, sweet corn hybrids $L_1 \times T_1$ and $L_{11} \times T_1$ showed non-significant deviations from regression (S^2d_i) and regression coefficient equivalent to unity (b_i=1) with greater mean than the population mean, thus signifying their predictable performances and stability for different environments for sweetness. While for protein content, the sweet corn hybrids $L_2 \times T_1$, $L_6 \times T_1$, $L_8 \times T_1$, $L_{10} \times T_1$, $L_{12} \times T_1$, $L_2 \times T_2$, $L_4 \times T_2$, $L_5 \times T_2$, $L_8 \times T_2$, $L_9 \times T_2$, $L_{10} \times T_2$, $L_{11} \times T_2$, $L_{14} \times T_2$, $L_{15} \times T_2$, $L_1 \times T_3$, $L_2 \times T_{3,}$ $L_4 \times T_3$, $L_5 \times T_3$ and $L_{10} \times T_3$ showed non-significant deviations from regression (S^2d_i) and regression coefficient equivalent to unity (b_i=1) with mean at par from the population mean, thus signifying their predictable performances and stability in various environments. Only the hybrid $L_{12} \times T_1$ showed stable performance for protein content over the three environments.

Similar results for the identification of stable genotypes under different environments were reported by Sowmya *et al*. (2018); Kumar *et al.* (2019); Machado *et al.* (2019);

Table 2. Best sweet corn hybrids for green cob weight/plant on the basis of stability parameters with the corresponding value of economic heterosis and combining ability effects

S.No.	Hybrids	Mean	Suitability forenvironment	Economic heterosis (%)	SCA effects
1	$L_7 \times T_2$	0.26	All environments (b_i=1)	36.8**	-0.02**
2	$L_7 \times T_3$	0.26	All environments (b_i=1)	36.8**	-0.01*
3	$L_7 \times T_1$	0.33	Unfavourable environments (bi<1)	73.7**	0.03**
4	$L_3 \times T_1$	0.27	Unfavourable environments (bi<1)	42.1**	0.01**
5	$L_{12} \times T_1$	0.26	Favourable environments (bi>1)	36.8**	0.01**
6	$L_{10} \times T_1$	0.25	Favourable environments (bi>1)	31.6**	0.06**

**Significant at 1% level of significance

Table 3. Five best sweet corn hybrids for green cob yield on the basis of stability parameters with the corresponding value of economic heterosis and combining ability effects

S.No.	Hybrids	Mean	Suitability forenvironment	Economic heterosis (%)	SCA effects
1	$L_{12} \times T_1$	15061.1	All environments (b_i=1)	33.7**	832.6**
2	$L_7 \times T_1$	19305.6	Unfavourable environments (bi<1)	71.4**	1550.7**
3	$L_9 \times T_3$	15646.7	Unfavourable environments (bi<1)	38.9**	1999.6**
4	$L_7 \times T_3$	15314.4	Favourable environments (bi>1)	36.0**	-281.5
5	$L_{10} \times T_1$	14695.6	Favourable environments (bi>1)	30.5**	3551.1**

**Significant at 1% level of significance

Table 4. Best sweet corn hybrids for TSS content of green grain on the basis of stability parameters with the corresponding value of economic heterosis and combining ability effects

S.No.	Hybrids	Mean	Suitability forenvironment	Economic heterosis (%)	SCA effects
1	$L_1 \times T_1$	15.9	All environments (b_i=1)	10.5*	-0.07
2	$L_{11} \times T_1$	17.0	All environments (b_i=1)	17.9**	0.33
3	$L_2 \times T_3$	16.0	Favourable environments (bi>1)	11.2**	1.34**
4	$L_5 \times T_2$	15.9	Favourable environments (bi>1)	9.9**	0.92**
5	$L_{10} \times T_3$	16.4	Unfavourable environments (bi<1)	13.7**	-0.23
6	$L_1 \times T_3$	16.3	Unfavourable environments (bi<1)	13.3**	1.22**

**Significant at 1% level of significance

Pinto *et al.* (2019); Raj *et al.* (2019) and Boreddy *et al.* (2020).

Conclusion

Among all the sweet corn hybrids, $L_{12} \times T_1$ was identified as a stable performer in various environments (b_i=1) with a higher mean than the population mean for green cob yield. For unfavourable environments (b_i<1), the sweet corn hybrids $L_7 \times T_1$ and $L_9 \times T_1$ revealed stable performance with a high mean value for green cob yield. Within favourable environments (b_i>1), hybrids $L_7 \times T_3$ and $L_{10} \times T_1$ showed stable performances along with a higher mean for green cob yield. All these sweet corn hybrids also exhibited positively significant standard heterosis over the best check Sugar-75 on a pooled basis. These parents and sweet corn hybrids can be used in future breeding programmes and further multi-location testing programmes, respectively.

The quality parameters are relatively more important, especially because of the direct consumption of sweet corn as a vegetable and the preference of the consumers. The overall results indicated that emphasis on green cob yield, green fodder yield and kernel sweetness may be considered in the objective of sweet corn hybrid development.

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Declaration

The authors do not have any conflict of interest.

References

Boreddy, S. R., Ganesan, K. N., Ravikesavan, R., Senthil, N. & Babu, R. (2020). Genotype-by-environment interaction and yield stability of maize (*Zea mays* L.) single cross hybrids. *Electronic Journal of Plant Breeding*, **11**(1): 184–191.

Boyer C. D. & Shannon J. C. (1984). The use of endosperm genes for sweet corn improvement. *Plant Breeding Reviews*, **1**: 193–161.

Eberhart, S. A. & Russell, W. A. (1966). Stability parameters for comparing varieties. *Crop Science*, **6**: 36–40.

Erwin, A. T. (1951). Sweet corn- Mutant or historic species? *Economic Botany*, **5**(3): 302–306.

Kumar, S., Chandel, U., Guleria, S. K. & Devlash, R. (2019). Combining ability and heterosis for yield contributing and quality traits in medium maturing inbred lines of maize (*Zea mays* L.) using line × tester. *International Journal of Chemical Studies*, **7**(1): 2027–2034.

Kwiatkowski, A. & Clemente, E. (2007). Características do milho doce (*Zea mays* L.) para industrialização. *Revista Brasileira de Tecnologia Agroindustrial*, **1**: 93–103.

Machado, N. G., Neto, N. L. & Hongyu, K. (2019). Statistical analysis for genotype stability and adaptability in maize yield based on environment and genotype interaction models. *Ciencia Natura*, **41**(25): 1–9.

Pinto, J. F. N., Candido, W. S., Pinto, J. F. N. & Reis, E. F. (2019). Adaptability and stability in maize populations. *Journal of Agricultural Science*, **11**(14): 23–31.

Raj, R. N., Devi, C. P. R. & Gokulakrishnan, J. (2019). G × E interaction and stability analysis of maize hybrids using Eberhart and Russell Model. *International Journal of Agriculture, Environment and Biotechnology*, **12**(1): 1–6.

Revilla, P., Velasco, P., Vales, M. I., Malvar, R. A. & Ordas, A. (2000). Cultivar heterosis between sweet and Spanish field corn. *Journal of American Society of Horticulture Science,* **125**: 684–688.

Sowmya, H. H., Kamatar, M. Y., Shanthakumar, G., Brunda, S. M., Shadakshari, T. V., Babu, B. M. S. & Rajput, S. S. (2018). Stability analysis of maize hybrids using Eberhart and Russel Model. *International Journal of Current Microbiology and Applied Sciences*, **7**(2): 3336–3343.

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