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MAPPING OF ASSOCIATIONS AND GENETIC STABILITY IN MAIZE

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Abstract

The analysis of variance showed that there were substantial differences between all of the maize and sweet corn genotypes for all of the characteristics across all three settings. All maize characters showed a small difference between phenotypic and genotypic variance, with the exception of grain yield per plant and ear girth in E1, and the number of kernel rows per ear and test weight in E2, E3, where environmental variations had less of an impact. High genotypic and phenotypic variation for ears per plant was found in sweet corn, suggesting a moderate environmental effect on expression of this characteristic in generations E1, E2, and E3. Except for ear girth, number of kernel rows per ear, and grain yield per plant in E1, maize phenotypes were highly heritable and advanced genetically by a large percentage in all three environments.

Keywords: *Mapping, Associations, Genetic, Stability, Maize*

1. Introduction

Maize, a staple food crop, has a 2.36 Gb genome and a chromosomal number of 2n=20, placing it in the grass family Poaceae. Native to Mexico and Central America are the annual and perennial grasses of the genus Zea. Both wild species known together as Teosintes and domesticated maize belong to the genus Zea. The Teosintes people of Mexico are credited for domesticating maize 6,300 years ago. Although some sources claim that maize was first domesticated in the Americas about 9000 b.c.[1-2]

The high yield potential of this crop earned it the moniker "Queen of Cereals." Since maize is the only cereal crop that can be grown in such a wide range of temperatures and habitats, there are many different landraces of maize. Maize also offers a wide range of variants with specific agricultural benefits, such as the more common yellow/white grain, sweet corn, baby corn, popcorn, waxy corn, high amylase corn, high oil corn, quality protein maize, and a few more. Because of its potential for value addition in the bioethanol sector, maize is an important industrial raw material. [3]

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The maize plant is monoecious, meaning that it produces both male and female flowers, but they do so on different inflorescences. The tassel, also called the male inflorescence, is found at the very tip and consists of a "central spike and 10-50 lateral branches". There are two florets and three anthers on each tassel spikelet. Due to their diminutive size and light weight, the pollen grains produced by anthers are readily carried by the wind to new sites. The female inflorescence, also known as the silk, cob, or ear, is located about halfway up the main stem. Two florets emerge from the axillary bud during the time of ear development, however only the top floret is used. Each ear's functioning floret gives rise to an ovary with a hairy (trichome-covered), elongated style called silk. In most cases, the male spikelets develop before the female ones.[4-5]

Pollens from anemophiles and protandrous flowers help increase cross-pollination, whereas reports of self-pollination average about 5%. Grains are produced in ears or cobs, typically one per stalk, and account for around 42% of a plant's dry weight.[6]

Maize's superior physiological efficiency stems from the fact that it's a C4 plant. Its morphological and phenotypic variety is unparalleled among cereals. New, improved maize varieties and reliable access to irrigation have made rabi a viable time for its production in many parts of India, despite the fact that maize has traditionally been grown during the kharif season. Higher maize yields in the Rabi season may be attributed to more effective water and fertiliser use.[7]

2. Literature review

Dubois, M. & Smith, F. (2019) The F2 and F3 generations of four different crosses of quality protein maize (QP) were evaluated for their variability in terms of "days to 50% silking, plant height, number of leaves, cob length, cob girth, number of grain rows per cob, number of grains per row, hundred grain weight, grains per cob, grain protein, grain tryptophan, and grain yield". The PCV and GCV estimates for each feature were deemed moderate. The predicted GCV was less than the PCV for most quantitative traits, indicating that environmental variables are important in the expression of these traits. Overall, heritability was found to be low, moderate, or high..[8]

Cole, C. T. (2018) Among 20 genotypes and 3 controls, we determined heritabilities, coefficients of variation, and rates of genetic progress for a total of 14 characteristics. The time between "anthesis and silking, grain yield per plant, ear height, harvest index, number of

grain rows per cob, number of grains per row, and 100 seed weight were all predicted to have high to moderate GCV and PCV. Plant height, ear height, and ear girth" were all shown to have high heritabilities. Estimates of genetic progress in terms of biological output, grain production per plant, plant height, and ear height were all modest, indicating that they would be amenable to improvement by selection.[9]

Bernardo, R. (2017)evaluated heritability and genetic advancement in a set of 65 newly developed maize strains, among other metrics of genetic variety. The average sum of squares for all eleven characteristics was found to differ significantly as a function of genotype, as determined by analysis of variance. The GCV and PCV estimations were moderate to high for "grain production, number of kernels per row, 100-kernel weight, ear length, and plant height", all of which indicate "considerable variability and prospects for genetic improvement" via selection. [10]

De Oliveira & Pinheiro, J. B. (2016) The estimated genetic diversity, broad sense heritability, and genetic advancement of 86 maize genotypes developed during rabi, 2012-2013 were studied. An analysis of variance showed that there were substantial differences between genotypes for each of the 12 variables considered. "Plant yield, ear height, number of kernels per row, and 100-kernel weight" are all examples of high heritability characteristics that might be improved by early generation selection. These traits have a high to moderate coefficient of variation and a moderate rate of genetic advancement. [11]

Ebdon, J. S., &GauchJr (2015)60 inbred maize lines were evaluated for 12 quantitative traits, and genetic diversity, heritability, and genetic advancement were computed. data on "plant height, ear size, number of kernel rows per ear", weight of 100 seeds, yield per plant, and percentage of grain that is shelled; and data on when the plant will reach 50% tasseling, 50% silking, and maturity. Statistical study revealed an increase in genetic heterogeneity. "Genotypic coefficients of variation (GCV) were lower than phenotypic coefficients of variation (PCV)" across the board, indicating that environmental factors had a role in shaping the traits in question. [12]

3. Methodology

The goal of this research, titled "Genetic Variability, Stability, and Association Mapping in Maize (Zea mays L.)," was to collect information on quantitative and qualitative traits in maize, as well as their heritability, genetic progress, correlation, stability analysis across

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different locations, and SSR marker-based diversity. The research was conducted in three different regions of Gujarat during rabi 2019-20 under the supervision of Anand Agricultural University (AAU).

3.2 Experimental materials

Both the Main Maize Research Station at Agra University (AAU) in Godhra and the ICARIndian Institute of Maize Research (IIMR) in Ludhiana provided the maize (Zea mays L.) and sweet maize (Zea mays L. saccharata) genotypes utilised in this research..

3.3 Experimental details

The crop was cultivated by randomly scattering maize seeds. The experiment was protected against harm and the edge effect by a row of guards. The crop was successfully grown by using the advised agronomic and plant protection techniques.

3.4 Statistical procedure

The statistical and genetic analysis of the various traits relied on the mean values across replicates for each genotype and environment. The computer facilities were made available by the Department of Agricultural Statistics at the University of Agriculture and Veterinary Science in Anand. An summary of the study's numerous statistical methodologies is provided below.

- Analysis of Variance
- Critical difference of the estimates
- Coefficient of variation
- Estimation of Variance Components

4. Results

Studying "Genetic Variability, Stability, and Association Mapping in Maize (Zea mays L.)" was the purpose of this investigation. The tests used 51 varieties of maize and 45 varieties of sweet corn. Both maize and sweet corn underwent their own sets of statistical analysis for variability, correlation, and stability, while phenotypic data for similar traits was pooled for molecular marker research into genetic diversity, population structure, and GWAS.

4.1 Analysis of variance (anova)

In rabi 2019-20, scientists from Anand Agricultural University collected data on a wide variety of characters at their three different research stations (E1: Experimental Farm, Department of Genetics and Plant Breeding, B. A. College of Agriculture, AAU, Anand; E2: Main Maize Research Station, AAU, Godhra; E3: Agricultural Research Station, AAU, Sansoli). Tables 4.1 and 4.2 provide the mean squares for all variables in sweet corn that may be ascribed to different causes of variance.

Table 4.1: ANOVA mean squares for maize features in three habitats

Sources	**d.f.**	**Days to 50% tasseling**			**Days to 50% silking**			**Plant height (cm)**		
		E_1	**E_2**	**E_3**	**E_1**	**E_2**	**E_3**	**E_1**	**E_2**	**E_3**
Replications	1	106.03**	5.64	8.24	148.32**	7.68	27.53*	2033.23**	46.03	1289.36**
Genotypes	50	58.65**	51.38**	57.34**	54.29**	50.68**	59.55**	969.83**	3064.50**	1076.68**
Error	50	5.21	4.28	4.92	6.00	3.52	5.23	79.86	172.36	113.83
Sources	**d.f.**		**Earheight(cm)**			**Earsper plant**			**Earlength(cm)**	
			E_2	**E_3**	**E_1**	**E_2**	**E_3**	**E_1**	**E_2**	**E_3**
Replications	1	429.07**	27.11	352.58**	0.21	0.12	0.17**	3.22	5.66**	16.27**
Genotypes	50	281.00**	1131.31**	406.92**	0.20**	0.32**	0.13**	9.87**	16.05**	11.10**
Error	50	18.83	78.99	30.38	0.08	0.07	0.01	1.34	0.54	1.12
Sources	**d.f**	**E1**	**Ear girth E2**	**E3**	**E1**	**Ear weight (g) E2**	**E3**	**E1**	**Number of kernel rows per ear E2**	**E3**
Replications	1	0.02	5.68**	1.24	39.84	971.07*	235.87	0.65	8.04**	1.78
Genotypes	50	5.42**	6.60**	2.67**	1477.28**	2481.09**	1616.34**	4.56**	9.97**	10.73**
Error	50	1.71	0.63	0.66	107.49	156.80	91.83	2.24	0.86	0.90

Table 4.2: Mean squares from an ANOVA on 51 maize genotypes in three settings

Sources	**d.f.**	Number of kernels per row			Number of kernels per ear			Shelling (%) **(cm)**		
		E_1	**E_2**	**E_3**	**E_1**	**E_2**	**E_3**	**E_1**	**E_2**	**E_3**

Replications	1	36.79*	16.19**	87.01**	5153.00	16377.5**	6254.00	1.42	2.38	2.90
Genotypes	50	56.95**	73.59**	72.14**	14203.50**	23771.9**	18776.3**	95.48**	91.81**	93.06**
Error	50	5.63	1.85	5.21	2270.80	1355.2	1647.70	1.19	0.97	0.84
Sources	**d.f.**		Test weight (g) **E_2**	**E_3**	**E_1**	Grain yield per plant (g) **E_2**	**E_3**	**E_1**	Protein content (% **E_2**	**E_3**
Replications	1	190.29**	189.91**	190.13**	3372.8**	1329.2*	530.51	3.97**	0.60	0.001
Genotypes	50	42.20**	42.99**	42.56**	801.7**	3733.2**	2860.81**	8.32**	9.52**	8.19**
Error	50	12.09	12.06	12.05	223.2	197.8	131.69	0.31	0.67	0.34

Sources	**d.f.**	**Total soluble sugars (%)**			**Lysine content (µg/ml)**			**Tryptophan content (µg/ml)**			**β-Carotene (ppm)**		
		E1	**E2**	**E3**	**E1**	**E2**	**E3**	**E1**	**E2**	**E3**	**E1**	**E2**	**E3**
Replications	1	0.00011	0.047**	0.022**	0.011	0.008	0.04**	0.00076**	0.01**	0.001**	1.68	8.91**	0.18
Genotypes	50	0.04271**	0.043**	0.040**	0.402**	0.417**	0.37**	0.0485**	*0.04**	0.46**	38.71**	26.15**	29.44**
Error	50	0.00025	0.0004	0.0002	0.003	0.013	0.005	0.00008	0.0002	0.00008	0.50	0.47	0.43

4.2Correlation coefficients

It is important to gather data on the correlations between yield and contributing factors prior to initiating a breeding effort in order to expedite the assessment of high-yielding genotypes in selection programmes.

In order to forecast grain production and its contributing components, this study analysed the correlation coefficients (Tables 4.3) between 19 phenotypic and genotypic parameters of 51 maize genotypes.

Table 4.3:Correlation correlations between genotype and phenotype for a number of maize traits (E1: Anand).

		TA	**SI**	**PH**	**EH**	**EPP**	**EL**	**KPR**	**EG**	**KRP**	**NKE**	**EW**	**SH**	**TW**	**Pro**	**TSS**	**LYS**	**TRP**	**Car**	**GY**
TA	r	1.0	0.98*	-	0.05	0.28	-0.05	0.00	0.48*	0.51*	0.16	-0.12	-	-	-	-	-	-	0.24	-0.24

	g	0	*	0.09		*			*	*			0.33**	0.53**	0.49**	0.11	0.35**	0.39**		
	rp	1.00	0.97**	-0.08	0.04	0.18	-0.07	0.00	0.27**	0.24*	0.11	-0.09	-0.28**	-0.28**	-0.44**	-0.11	-0.32**	-0.35**	0.22*	-0.18
SI	rg		1.00	-0.10	0.05	0.32*	-0.07	-0.02	0.51**	0.55**	0.16	-0.11	-0.33*	-0.51**	-0.52**	-0.11	-0.38**	-0.40**	0.28*	-0.21
	rp		1.00	-0.09	0.04	0.21*	-0.08	-0.01	0.28**	0.26**	0.11	-0.08	-0.28**	-0.27**	-0.46**	-0.11	-0.33**	-0.36**	0.26**	-0.15
PH	rg			1.00	0.82**	0.14	0.47**	0.55**	0.12	0.15	0.50**	0.60**	0.08	0.40**	0.15	-0.02	0.37**	0.31*	-0.22	0.50**
	rp			1.00	0.82**	0.08	0.37**	0.43**	0.09	0.09	0.38**	0.51**	0.06	0.25**	0.15	-0.02	0.33**	0.29**	-0.20*	0.34**
EH	rg				1.00	0.06	0.41**	0.44**	0.19	0.07	0.40**	0.40**	0.01	0.31*	0.27*	-0.11	0.29*	0.28*	-0.25	0.36**
	rp				1.00	0.01	0.34**	0.38**	0.15	0.07	0.33**	0.36**	0.01	0.22*	0.23*	-0.10	0.27**	0.27**	-0.23*	0.27**
EPP	rg					1.00	-0.02	0.04	0.28*	0.11	0.03	0.24	0.14	0.01	-0.07	0.27*	-0.20	-0.13	0.48**	0.00
	rp					1.00	0.04	0.08	0.03	-0.09	0.03	0.09	0.10	-0.04	-0.04	0.19	-0.15	-0.09	0.31**	0.02
EL	rg						1.00	0.64**	0.10	-0.07	0.54**	0.61**	0.00	0.05	0.18	-0.08	0.30*	0.22	-0.24	0.59**
	rp						1.00	0.63**	0.06	0.05	0.55**	0.52**	-0.01	0.04	0.12	-0.06	0.25**	0.19	-0.20*	0.51**
KPR	rg							1.00	0.13	0.25	0.94**	0.56**	0.03	0.14	0.22	-0.07	0.26	0.21	0.03	0.89**
	rp							1.00	0.00	0.12	0.87**	0.49**	0.02	0.10	0.16	-0.04	0.23*	0.19	0.04	0.70**
EG	rg								1.00	0.67**	0.33*	-0.07	-0.23	-0.41**	-0.32*	-0.14	-0.23	-0.30*	-0.07	0.03
	rp								1.00	0.75**	0.36**	0.10	-0.17	-0.20*	-0.20*	-0.11	-0.16	-0.21*	-0.07	0.19*
KRP	rg									1.00	0.53**	-0.20	-0.17	-0.32*	-0.53**	-0.26	-0.30*	-0.39**	0.24	0.25

	rp									1.00	0.567**	0.09	-0.11	-0.08	-0.26**	-0.17	-0.16	-0.22*	0.12	0.38**
NKE	rg										1.00	0.42**	-0.01	0.01	-0.01	-0.13	0.11	0.04	0.10	0.86**
	rp										1.00	0.44**	-0.02	0.05	-0.01	-0.10	0.10	0.03	0.09	0.76**
EW	rg											1.00	-0.08	0.25	0.02	0.00	0.21	0.11	-0.10	0.39**
	rp											1.00	-0.07	0.24*	0.02	0.00	0.19*	0.10	-0.09	0.40**
SH	rg												1.00	0.45**	0.12	-0.07	-0.02	0.06	0.13	0.29*
	rp												1.00	0.34**	0.10	-0.07	-0.02	0.06	0.13	0.22*
TW	rg													1.00	0.07	0.13	0.24	0.24	-0.12	0.37**
	rp													1.00	0.02	0.07	0.18	0.17	-0.09	0.30**
Pro	rg														1.00	0.05	0.26	0.47**	-0.17	0.19
	rp														1.00	0.05	0.24*	0.45**	-0.16	0.12
TSS	rg															1.00	0.16	0.21	0.04	-0.08
	rp															1.00	0.16	0.20*	0.04	-0.05
LYS	rg																1.00	0.86**	-0.30*	0.26
	rp																1.00	0.86**	-0.30**	0.18
TRP	rg																	1.00	-0.32*	0.33*
	rp																	1.00	-0.32**	0.24*
Car	rg																		1.00	-0.08

	rp																		1.00	-0.05
GY	rg																			1.00
	rp																			1.00

4.3 Genetic diversity using ssr markers

In this study, SSR molecular markers were employed to analyse the genetic diversity present in 96 maize genotypes. The results obtained by using this marker system are discussed below.

Total genomic DNA was recovered using the CTAB method described by Doyle and Doyle (1990), and its purity and integrity were verified by visual inspection of the DNA on an agarose gel (0.8%) with DNA standard uncut lambda DNA. DNA from each genotype was separated into a single band on Plate 4.6. Spectrophotometric analysis of DNA quality revealed a 260/280 ratio ranging from 1.63 (1820194/T1) to 2.13 (I-07-62-22-5).

DNA extracted from maize leaves had an average concentration of 2704.12 ng/l, as measured by the Nano Quant spectrophotometer (NanoDropTM 1000). The GWQPM-22-5 genotype had a DNA concentration of 836.20 ng/l, whereas the IL-17-28 genotype had a DNA concentration of 4852.10 ng/l.

Table 4.6:Genomic DNA is analysed qualitatively and quantitatively

Sr. No	**Genotypes**	**Concentration of stocksolution(ng/µl)**	**$\lambda_{260/280}$ Ratio**	**Preparation of workingsolution(50ng/µl,150µl)**	
				Stocksolutiontaken(µl)	**Water(nucleasefree)added(µl)**
1	I-07-14-1-2	3057.10	1.88	2.45	147.55
2	I-07-28-3-2	3072.50	2.01	2.44	147.56
3	I-07-29-1-3	2592.80	2.10	2.89	147.11
4	I-07-66-1-2	2774.50	1.78	2.70	147.30

5	I-07-66-2-3	4738.70	1.70	1.58	148.42
6	I-07-66-3-2	3836.20	1.79	1.96	148.04
7	I-07-66-4-1	2276.20	2.06	3.29	146.71
8	I-07-56-4-3	2157.30	1.91	3.48	146.52
9	I-077-59-5	2568.30	1.97	2.92	147.08
10	I-07-60-4-3	1995.40	2.11	3.76	146.24
11	I-07-65-44-4	3668.40	1.98	2.04	147.96
12	I-07-6-4-4	2092.90	2.02	3.58	146.42
13	I-07-6-4-5	2664.50	2.00	2.81	147.19
14	I-07-9-5	2806.00	2.00	2.67	147.33
15	I-07-13-1-3	2117.90	2.01	3.54	146.46
16	IL-14-28	1942.10	2.10	3.86	146.14
17	IL-14-48	4194.20	2.02	1.79	148.21
18	IL-14-60	3412.40	2.00	2.20	147.80
19	LM-5	2765.00	1.90	2.71	147.29
20	H07R-1-3	2156.10	1.88	3.48	146.52
21	GWQPM-	1796.20	2.	4.18	145.82

	5-3		0 1		
22	GWQPM-11	1440.30	2. 0 0	5.21	144.79
23	GWQPM-17-2	1690.90	1. 9 5	4.44	145.56
24	GWQPM-22-5	836.20	1. 9 5	8.97	141.03

Systems theory and population density are important in determining structure and variability. The use of molecular markers is a major step forward in plant breeding. In order to improve agricultural output and ensure the efficient management, use, and conservation of germplasm resources, an accurate assessment of genetic diversity is required. Investigations of genetic diversity benefit from PCR-dependent co-dominant marker based fingerprinting techniques due to their higher polymorphic loci and easier processing. Data given by molecular markers may help avoid the G E interaction seen with morphological/biochemical markers.

Differences in the number of repetitions across alleles were mirrored by a wide range in the molecular weight of the amplified PCR products, which ranged from 100 bp (umc2129) to 930 bp (umc1480). From a total of 96 maize genotypes, 118 distinct alleles were isolated. From 2 (umc1262) to 3 (umc1552), Table 4.7 reveals that the average number of alleles present at each location was 2.14. One possible explanation is that different sets of SSR markers were used to evaluate individuals with potentially vastly different genotypes.

Table 4.7:The SSR Marker Analysis Outcomes

Sr.No.	Locusname	Chr	Ampliconsize(bp)	Alleles	MAF	H_e	H_I	PIC	IC
1	umc1756	2	164-170	3	0.78	0.35	0.02	0.29	0.94
2	umc1552	2	130-170	3	0.54	0.60	0.04	0.54	0.93
3	umc1262	2	157-170	2	0.65	0.46	0.00	0.35	1.00
4	umc2252	2	112-145	3	0.41	0.65	0.82	0.58	-0.25
5	umc1535	2	155-170	2	0.53	0.50	0.00	0.37	1.00
6	umc1831	7	184-206	2	0.60	0.48	0.00	0.37	1.00
7	umc2380	2	121-132	3	0.63	0.53	0.02	0.48	0.96
8	umc2129	2	100-166	3	0.53	0.53	0.08	0.43	0.84
9	umc1256	2	173-200	2	0.51	0.50	0.00	0.37	1.00
10	umc1746	3	105-112	2	0.73	0.40	0.07	0.32	0.81
11	umc1641	3	111-134	2	0.63	0.47	0.09	0.36	0.80
12	umc1010	3	116-130	2	0.68	0.44	0.04	0.34	0.90
13	umc1813	3	123-134	2	0.69	0.43	0.01	0.34	0.98
14	umc1136	3	145-168	2	0.60	0.48	0.04	0.36	0.91
15	umc1489	3	128-146	2	0.54	0.50	0.07	0.37	0.85

16	umc1690	3	110-116	2	0.52	0.50	0.13	0.37	0.74
17	umc2258	3	151-160	2	0.65	0.46	0.01	0.35	0.98
18	umc2101	3	157-180	2	0.64	0.46	0.10	0.36	0.78
19	umc2103	3	156-175	2	0.59	0.48	0.02	0.37	0.96
20	umc1757	4	147-165	2	0.70	0.42	0.04	0.33	0.90
21	umc1294	4	150-175	2	0.77	0.35	0.01	0.29	0.97
22	umc2282	4	335-420	2	0.83	0.29	0.07	0.25	0.75
23	umc2038	4	150-160	2	0.51	0.50	0.06	0.37	0.89
24	dupssr34	4	177-233	2	0.70	0.42	0.16	0.33	0.63
25	umc2384	4	100-117	3	0.56	0.54	0.05	0.45	0.90
26	umc2388	5	257-400	2	0.78	0.35	0.14	0.29	0.60
27	umc2296	5	133-155	2	0.67	0.44	0.13	0.34	0.71
28	umc1060	5	167-246	3	0.45	0.60	0.00	0.51	1.00
29	umc2201	5	190-210	2	0.74	0.39	0.01	0.31	0.97
30	umc1941	5	106-131	3	0.56	0.55	0.00	0.46	1.00
31	phi087	5	116-129	2	0.76	0.37	0.02	0.30	0.94
32	umc2136	5	149-181	2	0.66	0.45	0.04	0.35	0.91
33	umc2223	1	166-180	2	0.64	0.46	0.00	0.35	1.00
34	umc1122	1	150-170	2	0.79	0.33	0.00	0.28	1.00
35	umc2151	1	125-140	2	0.55	0.49	0.00	0.37	1.00
36	umc2083	1	122-143	2	0.55	0.49	0.13	0.37	0.74
37	umc1446	1	156-168	2	0.64	0.46	0.00	0.36	1.00
38	umc1558	1	123-151	2	0.70	0.42	0.02	0.33	0.94
39	umc1353	1	232-260	2	0.60	0.48	0.00	0.37	1.00
40	umc2204	1	149-160	2	0.64	0.46	0.00	0.35	1.00
41	umc2226	1	100-115	2	0.51	0.50	0.07	0.37	0.87
42	umc1480	7	100-930	3	0.66	0.49	0.02	0.43	0.96
43	umc2392	7	250-270	2	0.57	0.49	0.00	0.37	1.00
44	umc2220	2	114-127	2	0.67	0.44	0.00	0.35	1.00
45	umc1578	3	168-185	2	0.83	0.28	0.00	0.24	1.00
46	umc2050	3	131-140	2	0.70	0.42	0.06	0.33	0.85
47	umc1228	4	141-156	2	0.60	0.48	0.00	0.36	1.00
48	umc2295	5	129-136	2	0.56	0.49	0.00	0.37	1.00
49	umc2298	5	100-110	2	0.80	0.32	0.06	0.27	0.80
50	umc1429	5	235-260	2	0.60	0.48	0.00	0.36	1.00
51	umc1153	5	117-128	2	0.63	0.46	0.01	0.36	0.98
52	umc2189	1	163-175	2	0.58	0.49	0.00	0.37	1.00
53	umc1452	1	118-124	2	0.64	0.46	0.00	0.36	1.00
54	umc1796	6	127-141	2	0.64	0.46	0.00	0.35	1.00
55	umc2104	3	126-130	2	0.68	0.43	0.00	0.34	1.00
56	phi193225	3	145-153	2	0.59	0.48	0.02	0.37	0.96
57	umc2137	4	138-156	2	0.58	0.49	0.00	0.37	1.00
58	umc1629	5	120-125	2	0.70	0.42	0.00	0.33	1.00
59	umc2143	5	156-166	2	0.52	0.50	0.00	0.37	1.00
60	umc2240	1	160-165	2	0.53	0.50	0.00	0.37	1.00
61	umc1303	4	113-120	2	0.65	0.46	0.00	0.35	1.00
Min.				2	0.41	0.28	0.00	0.24	-0.25
Max.				3	0.83	0.65	0.82	0.58	1.00
Average				2.14	0.63	0.46	0.04	0.36	0.90

averaged 0.60 with a range of 0.019 to 0.91%; Sa et al. (2018) reported a PIC average of 0.67%, which is higher than the result of the current study's investigation. When calculating association using the same genotypic data, this research included fewer alleles within genotypes, which may be the cause of the lower PIC value that was found..

ISSN 2515-8260 Volume 07, Issue 03, 2020

5. Conclusion

It was discovered that the sweet corn genotypes 1820228/T2, 1820231/T1, and I-07-37-6-1 had a good potential for green cob yield. On the other hand, it was discovered that the sweet corn genotypes GWQPM22-5, GWQPM-11, GWQPM-26-1, GWQPM-17-2, and I-07-9-5 had a promising potential for grain output per plant. It was shown that the ear height, the number of kernels per row, the number of kernels per ear, the proportion of shelled kernels, and the test weight all showed a positive link with the amount of grain produced by each maize plant. All contexts and degrees of analysis showed this link..

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