

## ESTIMATING GENETIC DISTANCE AMONG MAIZE INBREDS FOR PREDICTING HYBRID MEAN PERFORMANCE AND SPECIFIC COMBINING ABILITY

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**ABSTRACT:** Estimating genetic distance (GD) among lines of maize and the relationship between GD estimates and hybrid performance might be utilized to categorize inbred lines, create heterotic groups, and predict future hybrid performance. A lab experiment used ten inter-simple sequence repeats (ISSR) primers to identify polymorphism in ten inbred lines. In a one-year field trial with a randomized complete blocks design with triplicates, the F<sub>1</sub> diallel crosses were assessed under well-watered and severe stress conditions. Across the ten maize-inbreds, these ten ISSR primers generated 132 amplified fragments, 67 (52.4%) of which, were polymorphic, with an average of 6.7 polymorphic fragments per primer. The range of amplified fragments was eight (ISSR-14) to 19 (ISSR-11). Based on ISSR markers, the genetic similarity coefficients varied from 0.72 (between P<sub>5</sub> and P<sub>6</sub>) to 0.88 (between P<sub>7</sub> and P<sub>10</sub>), with an average of 0.78, among the ten inbreds of maize. Specific bands related to inbred lines of corn were discovered. The findings demonstrated a non-significant and negative correlation between the genetic distance among inbred lines based on ISSR markers and any of the mean performance or specific combining ability of grain yield/fad under severely stressed or well-watered conditions. The findings might assist breeders of maize in a more skillful choose of parental inbred lines to produce hybrids with high mean grain yields.

**Keywords:** *Zea mays*, ISSR, well-watered, and severely stressed.

### INTRODUCTION

Maize (*Zea mays*, L.) is the most widely grown cereal in the world, and it has become known as the "Queen of Cereals" due to its high yield potential. In Egypt, the maize area during the 2023 season was 3.20 million feddans with an overall grain production of 7.6 million tons of an average of 2.375 tons/fad (Egypt State Information Service, 2023). In maize breeding programs, identifying parental inbred lines that create superior hybrids is the most expensive and time-consuming step, so comprehensive yield trials are necessary to assess hybrid performance. The performance of the inbred lines alone does not predict the grain yield performance of maize hybrids (Sadek and Ibrahim, 2018).

A fundamental understanding of the genetic distance among maize germplasm is necessary for a successful breeding program (Patel *et al.*, 2024).

This information makes it possible to monitor the degree of polymorphism and heterozygosity as well as the inheritance pattern. Utilizing marker-assisted methods such as morphological, biochemical, phenological, and molecular (DNA-based) markers, maize genetic distance and population structure among germplasm are investigated. Even so, there were some drawbacks to using phenotypic analysis to measure genetic distance, including low polymorphism as well as the environmental influence on morphological expression. Phenotypic information is important for a primary estimation of maize genetic distance since it provides practical and useful information to evaluate germplasm that is currently accessible (Al-Naggar *et al.*, 2022). To circumvent these restrictions, DNA-based markers were used to identify varieties and expedite breeding programs by early selection of maize lines or segregants

with desired traits (Peric *et al.*, 2021). Various molecular markers were used to assess maize genetic diversity, including simple sequence repeats (SSR), amplified fragment length polymorphism (AFLP), inter-simple sequence repeats (ISSR), and random amplified polymorphic DNA (RAPD) (Sadek and Ibrahim, 2018 and Tanvir *et al.*, 2018).

ISSR markers were used in the study of genetic coding phylogeny, genome mapping, genetic diversity, and evolutionary biology due to their high polymorphism and simplicity. The genomic regions separating intimately spaced, reversely oriented microsatellite sequences were used to create these markers. This method might be utilized for the identification of any individual harboring SSR motifs without any knowledge of

the sequencing data (El-Hosary and El-Akkad, 2015 and Tanvir *et al.*, 2018).

This study's objectives were to: (I) use the ISSR markers to estimate the genetic distance between ten inbred lines of maize, and (II) validate the relationship between genetic distance and both of hybrid performance and specific combining ability.

## MATERIALS AND METHODS

### Plant materials

A half diallel study was conducted using ten yellow maize (*Zea mays*, L.) inbred lines in the 7<sup>th</sup> selfed generation (S<sub>7</sub>), which were established by the Maize Research Program, Field Crops Research Institute (FCRI), Agricultural Research Center (ARC), Egypt. Designation of parental source and origin were listed in Table 1.

**Table 1. Designation parental source and origin of ten inbred lines used in study.**

Inbred line code	Parental source	Country of origin	Inbred line code	Parental source	Country of origin
P <sub>1</sub>	V.N.Jing K868	China	P <sub>6</sub>	Comp#45	ARC-Egypt
P <sub>2</sub>	V.N.K869	China	P <sub>7</sub>	SK-21	ARC-Egypt
P <sub>3</sub>	Pop-32	CIMMYT	P <sub>8</sub>	G.M.3.Y.Pop	ARC-Egypt
P <sub>4</sub>	Gm.Y.Pop	ARC-Egypt	P <sub>9</sub>	Pop-38	CIMMYT
P <sub>5</sub>	P-3444	DuPont Pioneer	P <sub>10</sub>	TWC-360	ARC-Egypt

### Field experiment

A field experiment was conducted at the Experimental Farm, Faculty of Agriculture, Menoufia University, Shebin El-Kom, Egypt (30°31'42"N latitude and 31°04'08"E longitude), during the 2021 and 2022 seasons. Forty-five crosses were evaluated under two irrigation treatments: every 10 days (well-watered) and every 20 days (severe stress). The experimental design was a randomized complete block design (RCBD) with three replications. Each genotype (45 F<sub>1</sub> crosses) was allotted to three ridges of 3 m long and 0.7 m wide, *i.e.*, the experimental plot area was 6.3 m<sup>2</sup>. Kernels were sown in hills 20 cm apart. The recommendations of ARC, Egypt for growing maize were followed. Grain yield was estimated as 15.5% moisture content and expressed as tons/fad. The value of specific

combining abilities (SCA) was computed based on grain yield. The analysis of specific combining abilities was estimated using Model I, Method IV (Griffing, 1956).

$$s_{ij} = y_{ij} - \frac{1}{P-2}(y_{i.} - y_{.j}) + \frac{2}{(P-1)(P-2)}y_{..}$$

### Biometrical analysis

F<sub>1</sub> crosses were subjected to RCBD analysis of variance. The CoStat package application, version 6.311 (Cohort Software, USA), was used to perform the statistical analysis.

### Laboratory experiment

The ISSR technique was performed in the Molecular Markers Laboratory of the Agricultural Genetic Engineering Research Institute, ARC,

Giza, Egypt. Fresh leaves of the ten inbred lines of maize were collected at 10-day-old seedlings and maintained at -80°C for DNA extraction.

### DNA isolation

The DNeasy Mini Kit (Qiagen Santa Clarita, CA) was used to extract and purify genomic DNA according to standard protocol. DNA was observed through 1% agarose gel with ethidium bromide and quantity determined using NANODROP 2000 (Thermo Scientific, USA).

### ISSR amplification

The polymorphism was detected using ten ISSR primers as illustrated in Table (2), according to (Ibrahim *et al.*, 2019). 20 µl of PCR reaction volume containing, 10 µl Master Mix (Sigma), 2.5 µl primer (10 pmol), 2.5 µl template DNA (10 ng), and 5 µl dH<sub>2</sub>O was used in the amplification procedure. A Perkin-Elmer/GeneAmp® PCR System 9700 (PE Applied Biosystems) was used to do the PCR amplification. It was set up to run 40 cycles following a 5-min denaturation cycle at 94°C. A denaturation stage at 94°C for one minute, an annealing phase at 45°C for one minute, and an elongation step at 72°C for 1.5 minutes made up each cycle. In the last cycle, the primer extension phase was extended to 7 min at 72°C. Electrophoresis was used to resolve the amplification products on a 1.5% agarose gel with 0.5 µg/ml of ethidium bromide in 1X TBE buffer at 95 volts. PCR results were exposed to UV light for visualisation, and a Gel Documentation System (BIO-RAD 2000) was used for taking pictures.

### ISSR data analysis

In the ISSR analysis, only distinct and easily identifiable bands were visually graded as present (1) or absent (0) for all samples, and both polymorphic and monomorphic bands were present in the final data sets. Then, a binary statistic matrix was constructed. After that, a binary statistic matrix was built. Next, using the unweighted pair group technique with arithmetic averages (UPGMA), Dice's similarity matrix coefficients among genotypes were determined. Using this matrix, a phylogenetic tree

(dendrogram) was created. Using the PAST software Version 1.91, it was carried out by Dice's similarity index (Hammer *et al.*, 2001). To measure the informativeness of the ISSR marker, the polymorphic information content (PIC) values were determined using the online program for calculating polymorphic information content and resolving power (<https://irscope.shinyapps.io/iMEC/>). Based on Spearman's rank correlation coefficient, the genetic distance and hybrid performance, as well as the genetic distance and specific combining ability for grain yield, were correlated.

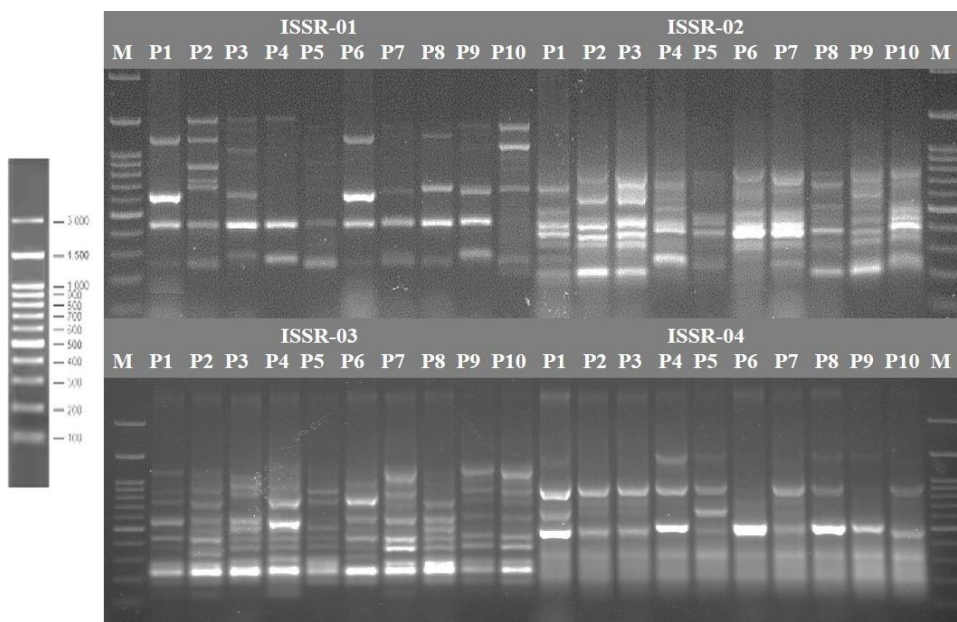
## RESULTS AND DISCUSSION

### Polymorphism detection by ISSR markers

Ten ISSR primers with observable amplification profiles were used to investigate genetic variability among the ten maize inbred lines (Table 2, Fig 1). The ISSR amplification using ten primers resulted in 132 bands of DNA with 13.2 bands/ primer. Among 132 amplified fragments, 67 fragments were detected as polymorphic, with polymorphism average percentage of 52.4%. The bands number per primer varied from eight (ISSR-14) to nineteen (ISSR-11) over the various inbred lines. Nevertheless, the polymorphic bands number ranged from four (ISSR-04) to nine (ISSR-10 and ISSR-11), with a polymorphic bands average number about 6.7 fragments/primer. Among the ten primers, only one displayed 63% high polymorphism (ISSR-14), while the primer ISSR-04 exhibited low polymorphism (40%). The polymorphism information content (PIC) varied from 0.30 (ISSR-04) to 0.37 (ISSR-11 and ISSR-19), with an average PIC value for the amplification products was 0.35. The bands number and the polymorphism percentages obtained in this work were adequate to the estimate of genetic distance as compared to other ISSR markers research. (Lenka *et al.*, 2015; Soliman *et al.*, 2021 and Al-Naggar *et al.*, 2022). SCoT are polymorphic markers that are important for the differentiation of intimately associated maize genotypes (Sadek and Ibrahim, 2018).

**Table 2: The list of primers, sequence of primers, total number of bands (TB), monomorphic bands (MB), polymorphic bands (PB), percentage of polymorphism (%P), frequency (F) and polymorphism information content (PIC) as revealed by ISSR analysis for ten genotyping maize.**

Primer	Sequence	TB	MB	PB	% P	F	PIC
ISSR-01	5'-AGAGAGAGAGAGAGAGTC-3'	11	5	6	55	0.47	0.36
ISSR-02	5'-AGAGAGAGAGAGAGAGTG-3'	10	4	6	60	0.65	0.35
ISSR-03	5'-ACACACACACACACTT-3'	15	7	8	53	0.71	0.33
ISSR-04	5'-ACACACACACACACTG-3'	10	6	4	40	0.72	0.30
ISSR-05	5'-GTGTGTGTGTGTGTGTTG-3'	14	7	7	50	0.72	0.32
ISSR-10	5'-GACAGACAGACAGACAAT-3'	16	7	9	56	0.44	0.35
ISSR-11	5'-ACACACACACACACTA-3'	19	10	9	47	0.44	0.37
ISSR-14	5'-CTCCTCCTCCTCCTCTT-3'	8	3	5	63	0.50	0.36
ISSR-18	5'-ACACACACACACACACAT-3'	11	6	5	45	0.72	0.32
ISSR-19	5'-ACATCCTCCTCCTCCTCC-3'	18	10	8	44	0.58	0.37
<b>Total</b>		132	65	67	-	-	-
<b>Average</b>		13.2	2.9		52.4	0.59	0.35



**Fig. 1: Banding patterns of ten maize inbred lines amplified with the ISSR primers (ISSR-01, ISSR-02, ISSR-03 and ISSR-04) M: 100bp DNA ladder, Lanes “P<sub>1</sub>, P<sub>2</sub>, P<sub>3</sub>, P<sub>4</sub>, P<sub>5</sub>, P<sub>6</sub>, P<sub>7</sub>, P<sub>8</sub>, P<sub>9</sub> and P<sub>10</sub>.”**

**Maize inbred line identification by unique ISSR markers**

As shown in Table 3, the ISSR assay identified nine of ten maize inbred lines using unique positive and/or negative markers. The findings exhibited twenty unique ISSR markers; among them fifteen were positive and the other five markers were negative. The parental inbred line P<sub>1</sub> was characterized through four unique positive markers that amplified using the primers ISSR-01-190bp, ISSR-10-1350bp, ISSR-11-910bp, and ISSR-14-230bp, while one unique negative marker amplified using the primer ISSR-18-510bp. The parental line P<sub>2</sub> was characterized via 2 unique positive markers that amplified using the primers ISSR-01-820bp and ISSR-01-730bp. While two unique negative markers amplified using the primers ISSR-03-710bp and ISSR-19-400bp were used to characterize the parental line P<sub>3</sub>. The parental line P<sub>4</sub> was characterized via two unique positive markers amplified using the primers ISSR-10-210bp and ISSR-19-240bp. The parental line P<sub>5</sub> was characterized using two unique positive markers amplified with the primers ISSR-05-890bp and ISSR-14-500bp, as

well as one unique negative marker ISSR-03-550bp. The parental line P<sub>6</sub> was characterized using two distinct positive markers amplified with the primers ISSR-11-450bp and ISSR-19-280bp. The parental line P<sub>7</sub> was characterized by a single unique negative marker that was amplified with the ISSR-11-380bp primer. The parental line P<sub>9</sub> was characterized via two unique positive markers amplified by the primers ISSR-10-670bp and ISSR-10-270bp. Finally, the parental line P<sub>10</sub> was characterized by only one unique positive marker that was amplified using the primer ISSR-19-1350bp. Positive unique markers were bands that were detected in one genotype but not in the others; negative unique markers, on the other hand, were absent in a certain genotype. These bands might be utilized to determine a person's genotype (Al-Naggar *et al.*, 2022). We discovered 20 unique bands connected to nine maize inbred lines using ISSR analysis. The current findings were consistent with the hypothesis that ISSR analysis can quickly identify ISSR markers associated with genotypes in maize. These markers would be beneficial for maize breeding programs.

**Table 3: Unique positive and negative inter-simple sequence repeat markers generated for ten maize genotypes, along with marker size (bp) and the total number of markers identifying each genotype.**

Maize inbred	Positive unique markers		Negative unique markers		Total
	Primer	Total	Primer	Total	
P <sub>1</sub>	ISSR-01-190bp ISSR-10-1350bp ISSR-11-910bp ISSR-14-230bp	4	ISSR-18-510bp	1	5
P <sub>2</sub>	ISSR-01-820bp ISSR-01-730bp	2			2
P <sub>3</sub>			ISSR-03-710bp ISSR-19-400bp	2	2
P <sub>4</sub>	ISSR-10-210bp ISSR-19-240bp	2			2
P <sub>5</sub>	ISSR-05-890bp ISSR-14-500bp	2	ISSR-03-550bp	1	3
P <sub>6</sub>	ISSR-11-450bp ISSR-19-280bp	2			2
P <sub>7</sub>			ISSR-11-380bp	1	1
P <sub>9</sub>	ISSR-10-670bp ISSR-10-270bp	2			2
P <sub>10</sub>	ISSR-19-1350bp	1			1
<b>Total</b>		<b>15</b>		<b>5</b>	<b>20</b>

### Genetic relationships among maize inbred lines

The obtained results of ISSR analysis were used to calculate the similarity matrices. As represented in Table 4, the genetic similarity varied from 0.72 (among P<sub>5</sub> and P<sub>6</sub>) to 0.88 (among P<sub>7</sub> and P<sub>10</sub>) with genetic similarity average about 0.78. These findings showed differences

among the ten parental inbred lines at the DNA level. In this context, according to ISSR markers El-Hosary and El-Akkad, 2015; Santos *et al.* (2017) and Al-Naggar *et al.* (2022), found that maize genotypes differed greatly hybridization genetically. Corn breeders could use genetic dissimilarity in hybridization procedures to take an advantage of heterosis phenomenon.

**Table 4: Genetic similarity coefficients among ten maize inbred lines, as determined by ISSR analysis.**

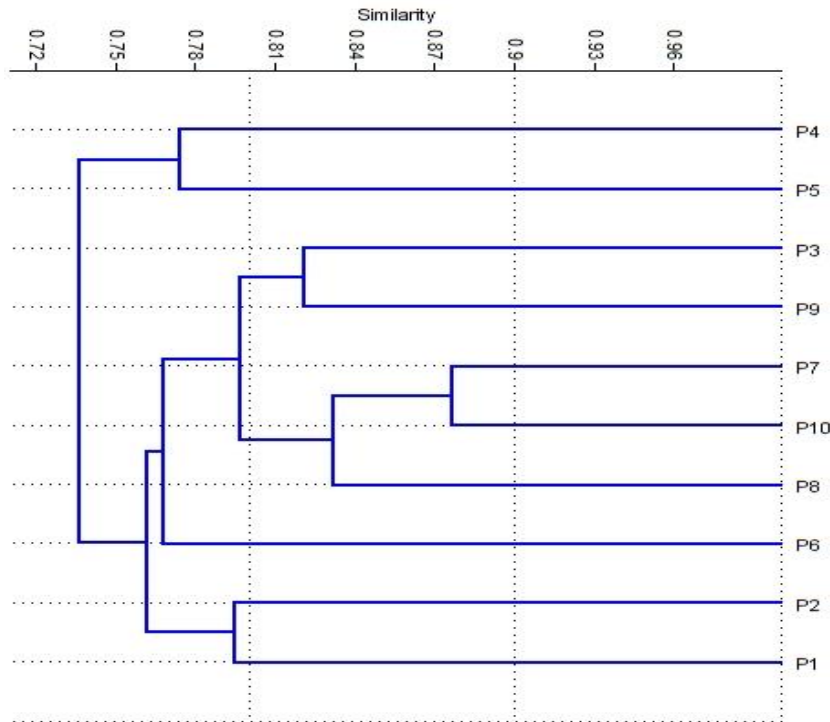
Inbred	P <sub>1</sub>	P <sub>2</sub>	P <sub>3</sub>	P <sub>4</sub>	P <sub>5</sub>	P <sub>6</sub>	P <sub>7</sub>	P <sub>8</sub>	P <sub>9</sub>	P <sub>10</sub>
P <sub>1</sub>	<b>1.00</b>									
P <sub>2</sub>	0.82	<b>1.00</b>								
P <sub>3</sub>	0.78	0.84	<b>1.00</b>							
P <sub>4</sub>	0.79	0.75	0.76	<b>1.00</b>						
P <sub>5</sub>	0.79	0.73	0.75	0.81	<b>1.00</b>					
P <sub>6</sub>	0.77	0.76	0.77	0.80	0.72	<b>1.00</b>				
P <sub>7</sub>	0.78	0.77	0.77	0.75	0.74	0.74	<b>1.00</b>			
P <sub>8</sub>	0.78	0.78	0.78	0.79	0.76	0.79	0.81	<b>1.00</b>		
P <sub>9</sub>	0.82	0.80	0.82	0.75	0.72	0.77	0.80	0.80	<b>1.00</b>	
P <sub>10</sub>	0.81	0.81	0.81	0.77	0.77	0.77	0.88	0.86	0.82	<b>1.00</b>

### Cluster analysis as revealed by ISSR

Figure 2 depicts a dendrogram of ten maize inbred lines based on SCoT markers generated with UPGMA and a similarity matrix derived from the Dice coefficient.

The dendrogram comprised of two main clusters; the first cluster grouped two inbred lines; P<sub>4</sub> and P<sub>5</sub> that were drought tolerant. The second cluster was divided into two sub-cluster; a sub-cluster contained two inbred lines; P<sub>1</sub> and P<sub>2</sub> that were drought tolerant. The other sub-cluster grouped six inbred lines in two groups as follows; the first group included inbred line P<sub>6</sub> in a single group, and the other five inbred lines in another sub-cluster and distributed to two sub-groups;

inbred lines P<sub>3</sub> and P<sub>9</sub> in a single sub-group, and the other sub-group contained three inbred lines (P<sub>7</sub>, P<sub>10</sub>, and P<sub>8</sub>). Based on the overall results, it appeared that ISSR analyses might be used to identify species-specific markers for the ten inbred lines of maize that might be used for genotype discrimination and to identify genetic relationships among genotypes that might be utilized in breeding programs. The molecular genetic results of these ten maize inbred lines are effective tools for the characterization of these genotypes. Similar results have been reported in other studies of genetic distance in maize using ISSR markers El-Hosary and El-Akkad, (2015); Santos *et al.* (2017); Tanvir *et al.* (2018); Soliman *et al.* (2021) and Al-Naggar *et al.* (2022).



**Fig. 2: Dendrogram of ten maize inbred lines based on ISSR markers and the average clustering method.**

**Mean performance and specific combining ability of F<sub>1</sub> crosses under well-watered and severe stress conditions**

The grain yield of crosses varied from 1.62 ton for P<sub>7</sub> × P<sub>9</sub> to 5.22 ton for P<sub>3</sub> × P<sub>5</sub> under well-watered and 1.15 ton for P<sub>7</sub> × P<sub>9</sub> to 3.36 ton for P<sub>3</sub> × P<sub>5</sub> under severe stress conditions, while the total average values were 4.25 and 2.78 t/fed under well-watered and severe stress conditions, respectively. The mean grain yield under severe stress represented 65% of the average yield in the same environments under well-watered conditions. On average, induced moisture stress reduced grain yield by 35%. The severe grain yield reduction of 35% observed under severe water stress in the present study falls within the range reported by earlier workers (AL-Deeb *et al.*, 2023 and Emam *et al.*, 2023). The values of specific combining abilities (SCA) varied from -2.093 (P<sub>7</sub> × P<sub>9</sub>) to 0.931 (P<sub>3</sub> × P<sub>5</sub>) under well-watered and -1.469 (P<sub>7</sub> × P<sub>9</sub>) to 0.585 (P<sub>9</sub> × P<sub>10</sub>) under severe stress conditions (Table 5).

**Correlation between genetic distance (GD) and hybrid mean performance and specific combining ability (SCA) under well-watered and severe stress conditions.**

Genetically different parental pairings are thought to produce hybrids with significant heterotic responses, although selecting parents for a hybridization program for any crop may involve considerations other than genetic divergence. Furthermore, some combinations perform better or worse than expected based on the average performance of the genotypes involved, while a few parents throughout cross combinations may produce stronger F<sub>1</sub>'s. The hybrid mean performance and specific combining ability for grain yield/fad under well-watered and severe stress conditions were negatively correlated with non-significant values of the Spearman's rank correlation coefficient between the genetic dissimilarity among inbred lines based on the ISSR markers (Table 6). Our findings referred to the highest cross for grain yield under well-watered and severe stress conditions as P<sub>3</sub> × P<sub>5</sub> with a genetic similarity of 0.75.

**Table 5: Mean performance and values of specific combining abilities for grain yield (t/fad) of F<sub>1</sub> crosses under well-watered (WW) and severe stress (SS) conditions.**

Crosses	Mean performance		Specific combining ability		Crosses	Mean performance		Specific combining ability	
	WW	SS	WW	SS		WW	SS	WW	SS
P <sub>1</sub> × P <sub>2</sub>	3.01	2.52	-1.645	-0.188	P <sub>3</sub> × P <sub>10</sub>	3.07	2.25	-1.030	-0.364
× P <sub>3</sub>	4.49	3.07	0.169	0.376	P <sub>4</sub> × P <sub>5</sub>	4.11	3.07	-0.609	-0.114
× P <sub>4</sub>	5.02	2.98	0.270	0.165	× P <sub>6</sub>	3.55	2.69	-0.743	-0.127
× P <sub>5</sub>	4.91	3.14	0.084	0.094	× P <sub>7</sub>	4.19	3.02	0.082	0.267
× P <sub>6</sub>	4.38	2.29	-0.018	-0.401	× P <sub>8</sub>	4.73	3.08	0.328	0.153
× P <sub>7</sub>	5.01	3.00	0.801	0.372	× P <sub>9</sub>	4.15	2.94	-0.103	0.129
× P <sub>8</sub>	4.85	3.05	0.343	0.257	× P <sub>10</sub>	5.10	2.86	0.566	0.135
× P <sub>9</sub>	5.09	2.41	0.735	-0.263	P <sub>5</sub> × P <sub>6</sub>	4.24	3.07	-0.135	0.014
× P <sub>10</sub>	3.90	2.18	-0.738	-0.412	× P <sub>7</sub>	4.62	3.09	0.439	0.090
P <sub>2</sub> × P <sub>3</sub>	4.14	2.98	0.015	0.255	× P <sub>8</sub>	3.50	2.92	-0.977	-0.250
× P <sub>4</sub>	4.49	3.05	-0.061	0.213	× P <sub>9</sub>	4.22	3.09	-0.107	0.042
× P <sub>5</sub>	5.03	3.05	0.401	-0.028	× P <sub>10</sub>	4.59	2.83	-0.026	-0.138
× P <sub>6</sub>	4.40	2.98	0.192	0.261	P <sub>6</sub> × P <sub>7</sub>	3.58	2.66	-0.184	0.024
× P <sub>7</sub>	4.48	3.08	0.460	0.427	× P <sub>8</sub>	4.36	2.80	0.302	-0.006
× P <sub>8</sub>	3.69	2.23	-0.621	-0.591	× P <sub>9</sub>	4.49	3.12	0.578	0.440
× P <sub>9</sub>	4.77	2.77	0.611	0.064	× P <sub>10</sub>	4.25	2.60	0.064	-0.004
× P <sub>10</sub>	5.09	2.21	0.649	-0.413	P <sub>7</sub> × P <sub>8</sub>	4.36	2.61	0.496	-0.127
P <sub>3</sub> × P <sub>4</sub>	4.48	2.00	0.270	-0.822	× P <sub>9</sub>	1.62	1.15	-2.093	-1.469
× P <sub>5</sub>	5.22	3.36	0.931	0.290	× P <sub>10</sub>	4.34	2.95	0.340	0.410
× P <sub>6</sub>	3.81	2.50	-0.056	-0.201	P <sub>8</sub> × P <sub>9</sub>	4.15	2.98	0.146	0.189
× P <sub>7</sub>	3.34	2.65	-0.340	0.007	× P <sub>10</sub>	3.90	2.91	-0.390	0.200
× P <sub>8</sub>	4.34	2.98	0.373	0.175	P <sub>9</sub> × P <sub>10</sub>	4.71	3.18	0.566	0.585
× P <sub>9</sub>	3.49	2.97	-0.331	0.283	L.S.D .05	0.215	0.273	0.135	0.173

**Table 6: Pearson correlation coefficients between molecular genetic dissimilarity and each hybrid mean performance and specific combining ability for grain yield/fed under well-watered and severe stress conditions.**

Parameter	Mean performance	Specific combining ability
GD (mol)	Well-watered	
	-0.172	-0.153
	Severe stress	
	-0.194	-0.002

GD: Genetic dissimilarity.



Genetic distance (GD) was not a reliable indicator of hybrid performance or specific combining ability (SCA) in maize under well-watered and severe stress conditions. These findings contradict the belief of some researchers that the genetic distance is positively and statistically significantly correlated with grain yield and specific combining abilities (Gichuru *et al.*, 2017 and Peric *et al.*, 2021). Other investigators (Dhliwayo *et al.*, 2009; Oyekunle *et al.*, 2015; Bhusal and Lal, 2017 and Krishna *et al.*, 2021), reported non-significant or no association with hybrid mean performance and specific combining ability. The lack of association between the microsatellite-based GD estimates of the parental inbreds and the mean grain yield of their F<sub>1</sub> crosses in contrasting environments implied that the microsatellite-based GD between pairs of inbreds could not be used to predict the performance of crosses under severe stress and well-watered conditions. It could be attributed to the absence of linkage between genes controlling the trait and markers used to estimate GD, inadequate genome coverage, different levels of dominance among crosses, and epistasis (Oyekunle *et al.*, 2015). Krishna *et al.* (2021) reported that parents with moderate genetic diversity but high per se performance may be more valuable than parents with high parental diversity alone. To accurately understand the genetic distance of the maize crop, it is necessary to conduct extensive research on a wide variety of inbred lines from different populations and to employ a substantial number of primers.

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## تقدير المسافة الوراثية بين سلالات الذرة الشامية للتنبؤ بمتوسط أداء الهجين والقدرة الخاصة على التآلف

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### الملخص العربي

تقدير التباعد الوراثي بين سلالات الذرة الشامية والارتباط بين التباعد الوراثي ومتوسط أداء الهجين من شأنه أن يحدد استراتيجيات التربية، ويصنف السلالات النقية، ويحدد المجموعات الهجينة ويتنبأ بأداء الهجين المستقبلي. كانت أهداف هذه الدراسة هي تقدير التباعد الوراثي بين عشرة سلالات نقية صفراء الحبوب من الذرة الشامية باستخدام المعلمات الجزيئية (ISSR) وتقدير الارتباط بين التباعد الوراثي ومتوسط أداء الهجين والقدرة الخاصة على التآلف. تم استخدام عشرة معلمات جزيئية ISSR للكشف عن تعدد الأشكال للسلالات العشرة في تجربة معملية. تم تقييم هجن الجيل الأول (F<sub>1</sub>) في تجربة حقلية لمدة عام واحد في تصميم القطاعات الكاملة العشوائية في ثلاث مكررات تحت ظروف الري الطبيعي (الري كل ١٠ أيام) والاجهاد الشديد (الري كل ٢٠ يوم). انتجت معلمات ISSR العشرة إجمالي ١٣٢ قطعة مكبرة منها ٦٧ (٥٢,٤%) كانت متعددة الأشكال بمعدل ٦,٧ قطعة/معلم ISSR وتراوح عدد القطع المكبرة من ٨ (ISSR-14) إلى ١٩ (ISSR-11). بناءً على المعلمات الجزيئية ISSR تراوحت معاملات التماثل الوراثي بين سلالات الذرة الشامية العشرة من ٠,٧٢ (بين P<sub>5</sub> و P<sub>6</sub>) إلى ٠,٨٨ (بين P<sub>7</sub> و P<sub>10</sub>) بمتوسط قدره ٠,٧٨. تم تحديد البانادات الغزيرة المصاحبة لسلالات الذرة الشامية. أظهرت النتائج أن التباعد الوراثي بين السلالات بناءً على معلمات ISSR العشرة كان مرتبطاً ارتباطاً سلبياً وغير معنوياً مع متوسط الأداء والقدرة الخاصة على التآلف لمحصول الحبوب/القدان تحت ظروف كل من الري الطبيعي والاجهاد الشديد. ستساعد النتائج مربي الذرة الشامية في اختيار السلالات النقية بشكل أكثر مهارة للحصول على هجن ذات محصول حبوب عال من القدان