

GENE ACTION OF MAIZE TRAITS AND RESISTANT SOURCE DETECTION AGAINST STALK ROT USING DEEP LEARNING TECHNIQUE

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Abstract. The early selection of pure lines against stalk rot and inheritance pattern of physiological and nutritional traits under disease stress is the main problem faced by the breeders in developing countries. One hundred maize lines were assessed for stalk rot using both artificial and natural inoculation. Six generations (P₁, P₂, F₁, F₂, BC₁, and BC₂) produced from the pure lines showing consistent resistance (Y11, EL7) and susceptible (DR59, DR69) responses during two growing seasons. Genetic images of these lines were obtained using DNA-based makers (SSRs) by performing polymerase chain reaction in the department of Medicinal Chemistry, University of Minnesota, USA. Studied traits showed the dominating impact of additive gene action in both seasons. Nutritional traits (protein, oil and starch contents) mostly exhibited negative correlation with lesion length while other showed non-significant correlation during spring and autumn. A deep learning model (Inception-V3) was trained with genetic images to distinguish between resistant and susceptible lines. The model showed 95% accuracy in resistant line detections. Considering the impact of the illness on physiological and nutritional traits, the current study favored phenotypic based selection in physiological traits. The study also showed the adverse impact of disease on nutritional traits. The current research not only aids in the management of the disease in high-yielding varieties, but also aids in identifying the resistant lines earlier against stalk rot using image processing model.

Keywords: *additive, genetic images, deep learning, physiological, nutritional*

Introduction

Maize quantity and quality can be improved by exploring its genetic potential (Shahini et al., 2023). Underdeveloped nations frequently, experience malnutrition (Rahut et al., 2024). The world population that rely on maize for their livelihoods have

achieved significant progress in the field of maize genomics research (Chakraborty et al., 2023). About 70% increase in staple foods would be required by 2050 to keep up with the population's increasing demand (Soma et al., 2023; Li et al., 2024). Corn grains will supply more than half of the demands (Yan et al., 2011). Since corn's oil is used as fuel in industry, the increase in oil prices after 1970 has given it more significance (Singh et al., 2001).

Early maturing cultivars of maize differ in their physiological traits (Akamatsu et al., 2024). The improvement in these traits might leave the field in time. Moreover, corn is an excellent source of proteins, vitamins, fats and minerals. The difference in biochemical composition of maize hybrids are observed significantly even cultivated on the same site (Shahini et al., 2023). This might be caused by the samples' genetic makeup, management techniques and environmental factors (Harrelson et al., 2019; Idikut et al., 2009).

Some breeders emphasized the role of additive gene effects for physiological traits while others focused on non-additive gene actions (Mir et al., 2015; Rastgari et al., 2014). Genetic interactions with the environment influence the amount of carbohydrates in maize kernels (Mattoo et al., 2023). Grain sugar concentration is regulated by both additive and non-additive genetic activity (Adu et al., 2023). The conversion of proteins to starch is also influenced by high moisture concentrations (Benton et al., 2005). Some found the environment role on protein content, while others explained the significance of the action of additive and non-additive genes (García Bravo et al., 2023). Numerous researchers have reported positive association between oil and protein contents (Dubey et al., 2009; Kashyap et al., 2023; Li et al., 2024).

Numerous biotic and abiotic factors influence plants (Liu et al., 2024). One of the main biotic constraints that has resulted in losses globally is stalk rot (*Fusarium species*) (Neish et al., 1983). The genes that are most desired and have the highest genetic variability determine the outcome of breeding programs. Programs including hybridization can obtain desired genes from these differences. Locus (qRfg1) was identified for stalk rot resistance in maize (Yang et al., 2010). Multidisciplinary cooperation among plant breeding, plant pathology, agronomy, environmental science, soil science, social sciences and economics is required to address the sustainable plant disease management. Plant diseases involve the complex interactions between biotic and abiotic factors comprising hosts, environments and pathogens. These interactions are favored by human interaction by using same cropping system, improper handlings of plant wastes and extensive use of pesticides. To increase the protein, oil, and starch content of maize, researchers have used several breeding techniques (Li et al., 2023; Murphy, 2023; Liang et al., 2023).

The determination of resistant lines earlier using the power of image processing models can minimize the time of resistant lines detection. It is undeniable that genome-based technologies, including as sequencing and genotyping, play a significant role in contemporary plant breeding. Resistance breeding programs have been improved because of advances in molecular approaches. Global research on the genetic makeup of maize lines is underway (Garg et al., 2023; Liu et al., 2023) which serves to mitigate the need for conventional inbreeding selection techniques. Additionally, it is thought that genotypes have an impact on the variance in maize strains' resistance to diseases.

The genetic makeup of various plant populations is ascertained by the application of SNP (single nucleotide polymorphism) molecular markers in unsupervised artificial neural network methods (Yoosefzadeh Najafabadi et al., 2023; Wang et al., 2025).

Accurately assessing *Oleaeuropaea*'s genetic diversity also heavily depends on computer tools (Slobodova et al., 2023). In addition to helping with the correct application of pesticides in the field, deep learning image processing approaches may detect weeds in vegetable fields with accuracy (Jin et al., 2021; Ma et al., 2024). Image-based disease classification has been made possible by deep learning algorithms, particularly CNN (Attallah, 2023).

In identification and classification tasks, a CNN with the fewest layers produces accurate results (Alhazmi, 2023; Ghosh et al., 2023). In order to apply pesticides correctly and accurately, a deep learning technique (a drone equipped with a Yolo-V3 neural network model) is utilized to take images of the pest's position (Al Hiary et al., 2011). ConvNet has demonstrated outstanding performance in image classification, localization, and identification tasks that have been investigated (Simonyan et al., 2015).

The only way to increase the crop yield is to respond appropriately against the diseases considering the physiological and nutritional traits. Disease resistant strains are the major component of breeding programs used to enhance high-yielding cultivars. Knowledge about the mode of gene action in the improvement of physiological and nutritional traits and the use of machine learning algorithms in early detection of plant diseases would not only assist in developing disease-resistant breeding programs but also give farmers a practical remedy at their doorstep.

In maize cultivation, stalk rot is a drastic and pervasive disease (Duan et al., 2022). It poses a serious danger to maize production due to recent changes in climate and agricultural practices (Duan et al., 2019). *Fusarium* and *Pythium* species are the primary motives behind maize stalk rot (Song et al., 2015). Multiple genes are thought to provide stalk rot resistance in maize, which has been classified as a quantitative trait (Ye et al., 2019). Selecting appropriate lines for hybridization programs under stressful conditions requires a thorough understanding of the additive or non-additive genetic impact (Mukaro et al., 2023). Implementing a breeding strategy to create extremely prolific hybrids in an unfavorable environment is more challenging than in a favorable one (Al-Falahy, 2015). Some researchers have highlighted the significance of non-additive gene action (Kamal et al., 2023) while others have concentrated on the relevance of dominant gene action (Mukaro et al., 2023). Next-generation sequencing (NGS) technologies have completely changed crop improvement strategies (Jamil et al., 2019; Ma et al., 2025). Numerous significant genes have been made easier to map and clone because to these methods (Lü et al., 2018). The convolutional neural network (image processing technique) has simplified the process of comparing and identifying disease-resistant cultivars. (Bao et al., 2021) investigated head blight disease with the spatial attention module. By minimizing the background influence, this strategy enabled them to extract the necessary characteristics. They were able to get 94.1% accuracy with the suggested classifier. Disease detection can benefit from knowledge of the lesion area's color, texture, and structure. (Jin et al., 2021) identified weeds in the field by utilizing genetic algorithms. (Zou et al., 2021; Han et al., 2024) detected a number of disorders using the DesnseNet model. They said that the accuracy of their suggested model was 95%. Using CNN, (Hidayat et al., 2022) were able to assess the quality of rice seeds with 93% accuracy compared to other suggested model. In the light of these facts, the objective of the research is to (1) determine the genetic inheritance of disease resistance in addition to the physiological and nutritional traits of maize. (2) Correlate

lesion length (stalk rot) with other traits 3) determine the role of deep learning model in earlier identification of resistant lines against stalk rot.

Materials and methods

Both field and laboratory studies were involved in the current research. Field trial was performed for physiological traits while laboratory studies were carried out for nutritional traits at Maize and Millet Research Institute (MMRI), Yousafwala, Pakistan. Later on, genetic image-based resistance source identification was carried out using UV tray images at University of Minnesota, USA. Six generations (P_1 , P_2 , F_1 , F_2 , BC_1 , BC_2) of two crosses were grown in Randomized Complete Block Design with three repeats. Two seeds were planted by hand in each hill and pruned to one plant at seedling stage. In each experimental plot, the spacing between plants and rows was kept at 20 and 75 cm respectively. To produce F_1 generations, Y11 and EL7 (a female parent) crossed with DR59 and DR69 (male parent) respectively. To create the BC_1 and BC_2 generations, the F_1 of both hybrids backcrossed to their respective parent (P_1 , P_2) in the spring season. F_2 generations produced by selfing a specific percentage of F_1 seeds. Two distinct studies carried out in the autumn and spring to investigate the inheritance of attributes of six generations. One row for the parental and F_1 generations, ten rows for the hybrid generations and fifteen rows for the F_2 generations were maintained.

Thirty (30) plants from parents and F_1 generation, 150 plants from backcross generations and 300 plants from F_2 generations were selected to record different physiological and nutritional traits. The different maize traits like days to 50% emergence, days to 50% tasseling, days to 50% silking, lesion length, protein, oil, starch and moisture content were studied. For model training, genetic images were cropped and processed before training and testing of the proposed model. TensorFlow, Google Colaboratory hardware and Python were utilized to detect genetic image based resistant sources using the Inception-V3 model. The stages involved in resistant source detection are described in *Figure 1*. The significance of differences between generational means was studied using the analysis of variance technique (Steel et al., 1996). The model was checked by accuracy percentage.

Results

Days to 50% emergence

The combined analysis of variance showed highly significant results ($P < 0.01$) for the mean square values of days to 50% emergence (*Table 1*). Both hybrids showed non-significant results in autumn while results were significant ($P < 0.01$, $P < 0.05$) in spring (*Tables 2 and 3*). The Scaling test (*Table 4*) for both hybrids showed no value on any measure providing a simple dominance model for the trait. The genetic effect was governed by two variables m, [d] in spring (*Tables 5 and 6*). The generation variance analysis showed the effect of the additional gene (D) having a more pronounced effect than the effect of the dominant gene (H) in cross-1 (*Table 7*). Days to 50% emergence showed a greater value of H over D in cross-2. The degree of dominance was recorded ((H/D) $1/2$) -1.41 and 3.64 in cross-1 and cross-2, respectively.

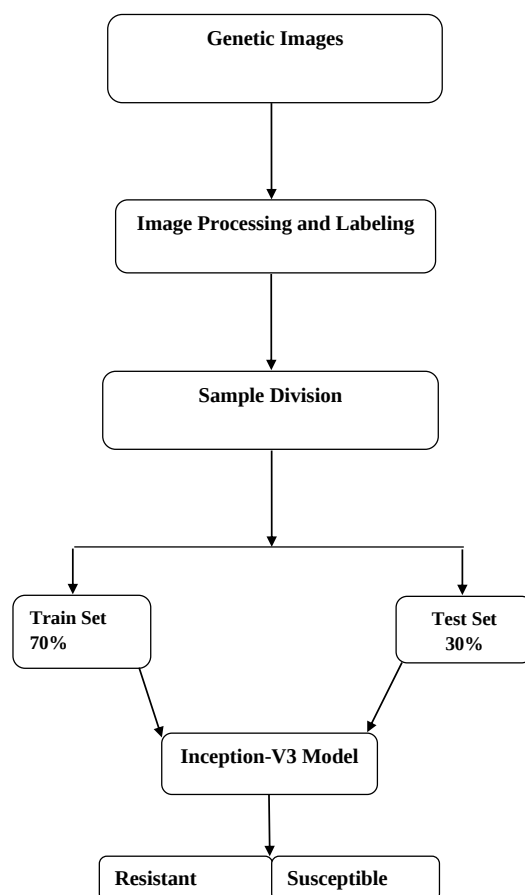


Figure 1. Stages of image processing model

Table 1. Combined analysis of variance for different traits in two crosses

Crosses	S.O.V	D.F	1	2	3	4	5	6	7	8
Y11 × DR59	T	5	1.17**	5.09**	3.64**	6.97**	1.54**	36.29**	1.54**	188.91**
	T × S	5	1.00**	25.23**	20.44**	1.44**	0.10 ^{NS}	4.04**	0.26 ^{NS}	0.49 ^{NS}
	Error	20	0.23	0.57	0.72	0.35	0.04	0.77	0.33	0.29
EL7 × DR69	T	5	0.71*	32.27**	40.73**	6.09**	2.18**	24.62**	3.65**	186.33**
	T × S	5	1.38*	5.47**	5.80**	0.49 ^{NS}	0.11 ^{NS}	3.84**	3.92**	0.06 ^{NS}
	Error	20	0.26	0.49	0.48	0.72	0.15	0.91	0.89	0.38

S.O.V = source of variation, D.F = degree of freedom, 1 = days to 50% emergence, 2 = days to 50% silking, 3 = days to 50% tasseling, 4 = protein contents, 5 = oil contents, 6 = starch contents, 7 = moisture contents, 8 = lesion length, T = treatments, T X S = treatment-season interaction, ** = highly significant at 1% level of significance, * = significant at 5% level of significance, NS = non-significant

Table 2. Analysis of variance for different traits in autumn season for both crosses

Crosses	S.O.V	D.F	1	2	3	4	5	6	7	8
Y11 × DR59	Generations	5	0.32 ^{NS}	6.45**	8.72**	5.30**	0.43**	11.13**	0.84**	101.34**
	Error	10	0.18	0.38	0.28	0.44	0.02	0.60	0.12	0.23
EL7 × DR69	Generations	5	4.0 ^{NS}	6.85**	9.65 **	3.72**	1.00**	15.51**	4.78**	92.24 **
	Error	10	3.0	0.85	0.78	0.41	0.09	0.61	0.83	0.32

S.O.V = source of variation, D.F = degree of freedom, 1 = days to 50% emergence, 2 = days to 50% silking, 3 = days to 50% tasseling, 4 = protein contents, 5 = oil contents, 6 = starch contents, 7 = moisture contents, 8 = lesion length, ** = highly significant at 1% level of significance, * = significant at 5% level of significance, NS = non-significant

Table 3. Analysis of variance for different traits in spring season for both crosses

Crosses	S.O.V	D.F	1	2	3	4	5	6	7	8
Y11 × DR59	Generations	5	1.02*	23.86**	18.08**	3.11**	1.21**	29.21**	0.95 ^{NS}	88.05**
	Error	10	0.25	0.83	1.18	0.28	0.06	0.94	0.58	0.41
EL7 × DR69	Generations	5	1.70**	30.76**	34.08**	2.85*	1.30*	12.95**	2.80 ^{NS}	94.15**
	Error	10	0.16	0.26	0.55	1.17	0.24	1.34	0.86	0.52

S.O.V = source of variation, D.F = degree of freedom, 1 = days to 50% emergence, 2 = days to 50% silking, 3 = days to 50% tasseling, 4 = protein contents, 5 = oil contents, 6 = starch contents, 7 = moisture contents, 8 = lesion length, ** = highly significant at 1% level of significance, * = significant at 5% level of significance, NS = non-significant

Table 4. Scaling test for important maize plant traits in two seasons for two crosses

Traits	Season	Cross 1			Cross 2		
		A	B	C	A	B	C
1	SP						
2	AU	-2.00 ± 0.94	-4.66 ± 1.45	-4.00 ± 1.91			
	SP			6.66 ± 2.78		-2.00 ± 0.74	
3	AU		2.33 ± 0.55	8.33 ± 1.52	2.33 ± 1.00		8.00 ± 2.90
	SP		-5.33 ± 1.94			-7.00 ± 1.37	
4	AU						
	SP						
5	AU						
	SP					-1.80 ± 0.58	
6	AU				-8.66 ± 1.63	-7.66 ± 0.78	-7.00 ± 2.08
	SP				-5.00 ± 1.22		
7	AU		-1.00 ± 0.47		-1.33 ± 0.66	1.00 ± 0.47	
8	AU	1.04 ± 0.35		8.37 ± 1.34			4.32 ± 0.81
	SP		-2.48 ± 0.96	5.41 ± 1.10			2.91 ± 1.11

1 = days to 50% emergence, 2 = days to 50% silking, 3 = days to 50% tasseling, 4 = protein contents, 5 = oil contents, 6 = starch contents, 7 = moisture contents, 8 = lesion length, AU = Autumn, SP = Spring, Scales having the values are significant at 5% significant level

Table 5. Estimates of genetic effects for generation means for important maize plant traits for Cross-1 (Y₁₁ * DR₅₉)

Traits	Season	M	[d]	[h]	[i]	[j]	[l]
1	SP	13.00 ± 1.50	0.66 ± 2.35				
2	AU	62.33 ± 1.90	2.00 ± 0.23	-12.00 ± 5.00	-6.00 ± 1.88		
	SP	89.33 ± 1.92	-4.00 ± 0.37	-12.66 ± 4.96			9.33 ± 3.28
3	AU	56.33 ± 0.33	-1.00 ± 0.47	-7.83 ± 1.67	-6.00 ± 1.63	-1.16 ± 0.50	
	SP	87.83 ± 2.34	-3.5 ± 0.40	-14.16 ± 6.39			10.33 ± 4.24
4	AU	9.00 ± 3.33	1.16 ± 0.23				
	SP	9.83 ± 3.89	0.50 ± 0.28				
5	AU	3.50 ± 0.28	-0.40 ± 0.03				
	SP	3.85 ± 0.42	0.31 ± 0.10				
6	AU	41.08 ± 3.94	1.48 ± 0.17				
	SP	40.16 ± 0.44	2.66 ± 0.48				
7	AU	15.00 ± 0.28	1.26 ± 0.22				
8	AU	8.50 ± 0.29	-6.46 ± 0.13	-15.60 ± 1.24	-7.8 ± 1.19	0.76 ± 0.33	7.23 ± 1.85
	SP	7.06 ± 0.18	-5.33 ± 0.13	-14.46 ± 1.26	-7.30 ± -1.05		9.18 ± 1.44

1 = days to 50% emergence, 2 = days to 50% silking, 3 = days to 50% tasseling, 4 = protein contents, 5 = oil contents, 6 = starch contents, 7 = moisture contents, 8 = lesion length, AU = Autumn, SP = Spring

Table 6. Estimates of genetic effects for generation means for important maize plant traits for Cross-2 (EL₇ * DR₆₉)

Traits	Season	M	[d]	[h]	[i]	[j]	[l]
1	SP	13.50 ± 1.63	1.00 ± 0.47				
2	AU	59.50 ± 2.53	-1.83 ± 0.47				
	SP	85.66 ± 0.33	-3.00 ± 0.47			1.50 ± 0.47	6.33 ± 2.40
3	AU	57.00 ± 2.86	-2.33 ± 0.22		-4.00 ± 2.82		
	SP	84.33 ± 0.33	-1.33 ± 0.66		-4.00 ± 1.88	3.33 ± 0.70	11.33 ± 3.29
4	AU	9.00 ± 0.50	1.05 ± 0.26				
	SP	7.16 ± 3.12	1.23 ± 0.56				
5	AU	3.12 ± 0.19	-0.39 ± 0.03				
	SP	3.23 ± 0.14	-0.48 ± 0.14			1.05 ± 0.50	
6	AU	37.16 ± 0.44		-5.83 ± 2.42	-9.33 ± 2.35		25.66 ± 3.75
	SP	39.50 ± 0.86	2.66 ± 0.51			0.86 ± 0.80	
7	AU	14.66 ± 0.33	1.56 ± 0.31				
8	AU	7.67 ± 0.12	-6.73 ± 0.59	-11.60 ± 1.32	-4.41 ± 1.28		
	SP	6.86 ± 0.19	-6.99 ± 0.70	-10.87 ± 1.65	-3.39 ± 1.61		

1 = days to 50% emergence, 2 = days to 50% silking, 3 = days to 50% tasseling, 4 = protein contents, 5 = oil contents, 6 = starch contents, 7 = moisture contents, 8 = lesion length, AU = Autumn, SP = Spring

Table 7. Estimates of genetic effects for generation variance for important maize plant traits

Traits	Season	Cross 1				Cross 2			
		D	E	H	(H/D) ^{1/2}	D	E	H	(H/D) ^{1/2}
1	SP	0.66	0.33	-1.33	-1.41	0.10	0.00	1.33	3.64
2	AU	-1.33	1.66	-2.66	1.41	2.66	1.00	-5.33	-1.41
	SP	-1.33	0.88	0.44	-0.57	0.53	0.11	0.88	1.28
3	AU	8.66	0.22	-8.88	-1.02	4.00	1.00	-6.66	-1.29
	SP	-4.00	1.00	5.33	-1.15	-1.33	0.66	1.33	-1.00
4	AU	4.33	0.13	-2.22	-0.71	-0.33	0.25	2.66	-2.82
	SP	-1.66	0.41	8.66	-2.28	-7.50	0.47	15.44	-1.43
5	AU	-0.006	0.11	0.53	-8.98	-0.29	0.01	0.96	-1.81
	SP	0.02	0.15	-0.56	-4.61	-1.17	0.16	1.92	-1.28
6	AU	6.89	0.15	-4.30	-0.79	-1.33	0.63	2.44	-1.35
	SP	-1839.14	1.63	3674.07	-1.41	6.66	1.25	-9.33	-1.18
7	AU	0.66	0.11	-0.44	-0.81	0.33	0.13	-0.22	-0.81
8	AU	0.92	0.39	-2.41	-1.61	-1.92	0.35	2.63	-1.16
	SP	-0.41	0.62	-1.25	1.73	-0.70	0.11	1.03	-1.21

1 = days to 50% emergence, 2 = days to 50% silking, 3 = days to 50% tasseling, 4 = protein contents, 5 = oil contents, 6 = starch contents, 7 = moisture contents, 8 = lesion length, AU = Autumn, SP = Spring

Days to 50% silking

The treatment as well as treatment × season were significant ($P < 0.01$) for days to 50% silk in both hybrids in Table 1. Significant results for the trait in each season were also studied in both hybrids (Tables 2 and 3). During the autumn, cross-1 (Y11 x DR59) showed four model parameters m, [d], [h] and [i] while in the spring, m, [d], [h] and [l] provided a good fit for days to 50% silk (Table 5). The trait in cross-2 (El7 x DR69) showed a slight additive dominance pattern during the autumn. However, additive genetic action with greater contribution from the inferior parent was noted. Four parameter model m, [d], [j] and [l] elaborated the gene effect for the trait during spring

(Table 6). Cross-1 and cross-2 showed greater value of D over H in autumn while D is less than H in spring season as mentioned in Table 7. The correlation between lesion length and days to 50% silk was non-significant (Table 8).

Table 8. Correlation between lesion length and investigated traits for both crosses under two seasons

Trait	Lesion length			
	Cross-1		Cross-2	
	Autumn	Spring	Autumn	Spring
1	-	-0.42 ^{NS}	-	-0.12 ^{NS}
2	-0.25 ^{NS}	0.27 ^{NS}	0.23 ^{NS}	0.21 ^{NS}
3	-0.46 ^{NS}	0.22 ^{NS}	0.18 ^{NS}	0.15 ^{NS}
4	-0.64**	-0.44 ^{NS}	-0.61*	-0.27 ^{NS}
5	-0.83**	-0.74**	0.01 ^{NS}	-0.13 ^{NS}
6	-0.81**	-0.87**	-0.43 ^{NS}	-0.76**
7	-0.43 ^{NS}	-	0.23 ^{NS}	-

1 = days to 50% emergence, 2 = days to 50% silking, 3 = days to 50% tasseling, 4 = protein contents, 5 = oil contents, 6 = starch contents, 7 = moisture contents. ** = highly significant at 1% level of significance. * = significant at 5% level of significance. NS = Non-significant

Days to 50% tasseling

Days to 50% tassels in Table 1 provided significant results ($P < 0.01$) for treatment as well as treatment $\times$ season. The results were also significant for the trait in both hybrids when analyzed separately in autumn and spring (Tables 2 and 3). The trait in cross-1 showed a five-parameter model m , $[d]$, $[h]$, $[i]$, and $[j]$ and four-parameter model m , $[d]$, $[h]$, $[l]$ in autumn and spring respectively (Table 5). Cross-2 exhibited genetic influence of m , $[d]$, $[i]$, and m , $[d]$, $[i]$, $[j]$ and $[l]$ in autumn and spring respectively (Table 6). Both crosses showed greater value of D over H in autumn while H was greater than D in spring season (Table 7). The degree of dominance was less than unity in both crosses. A non-significant relationship was observed between lesion length and days to 50% tassel (Table 8).

Protein contents

In the case of protein contents, the treatment and treatment $\times$ season analysis were significant in cross-1. Cross-2 revealed significant results for treatment only (Table 1). Seasonal analysis during the autumn and spring seasons showed significant results for the treatment in cross-1 and cross-2 (Tables 2 and 3). The protein contents in both hybrids showed an additive gene action without dominance (Tables 5 and 6). H was greater than D in both hybrids except cross-1 during autumn (Table 7). Correlation study between lesion length and protein contents exhibited negative relation ($r = -0.64$, $r = -0.61$) in both crosses during autumn (Table 8).

Oil contents

In the case of oil contents, significant mean square values were observed for treatment only in both crosses (Table 1). Significant variation studied in each season for both hybrids (Tables 2 and 3). Oil contents are controlled by m and $[d]$ in both hybrids except cross-2 where $[j]$ is also involved in the spring (Tables 5 and 6). The value of H was greater than D in autumn and less in spring in cross-1. Cross-2 showed greater

value of H compared to D during autumn and spring seasons. The degree of dominance was less than unity in both hybrids (*Table 7*). Correlation study between lesion length and oil contents exhibited negative value of -0.83 and -0.74 in cross-1 during autumn and spring respectively (*Table 8*).

Starch contents

Starch contents showed variation due to treatment as well as environment (*Table 1*). Both hybrids showed significant differences for treatment in each season (*Tables 2 and 3*). The trait in cross-1 is governed by m and [d] in autumn and spring (*Table 5*). Cross-2 exhibited m, [h], [i] and [l] genetic influence in the autumn. In spring, the three-parameter model m, [d], and [j] explained the effect of the gene better (*Table 6*). The degree of dominance was less than unity in both hybrids (*Table 7*). Correlation study between lesion length and starch contents exhibited negative value of -0.81 and -0.87 in cross-1 during autumn and spring respectively. Likewise, the value of -0.76 was noted in cross-2 (*Table 8*).

Moisture contents

In the case of moisture contents, treatment mean square was significant in both crosses. Only for cross-2, the treatment and environment interaction was significant (*Table 1*). In autumn, both crosses demonstrated notable intergenerational differences (*Table 2*). Genetic effects m and [d] regulate the moisture contents of both crosses (*Tables 5 and 6*). In both crosses, the degree of dominance is below unity (*Table 7*).

Lesion length

In the case of lesion length, *Table 1* showed significant differences for treatment only. In a similar vein, *Tables 2 and 3* demonstrated notable generational variations in both crosses. The six-parameter model m, [d], [h], [i], [j], and [l] was seen during the autumn for lesion length in cross-1, whereas the five-parameter model Parameters was observed during the spring. A good fit to the observed values was given by the model parameters m, [d], [h], [i], and [l] (*Table 5*). In both autumn and spring, the trait in cross-2 displayed the four-parameter pattern m, [d], [h], and [i] (*Table 6*). In cross-1, H has a lower value than D, while in cross-2, it has a larger value (*Table 7*).

Model predictions

The majority of farmers visually monitor the crop to recognize pathogen infection status. The use of pre-trained model was explored to distinguish between susceptible and resistant lines based on genetic images. Preprocessed images after proper cropping were fed to the model to minimize the computational time. The model results elaborated in *Figure 2* show the training and validation accuracy of the model. The training accuracy was up to the mark while validation accuracy showed 95%. The model predictions on unseen images are shown in *Figure 3*.

Discussion

Breeding programs are advantageous for researchers only, if there exist genetic differences among the planting materials (Reddy et al., 2018). The differences are an

essential source for introducing desired changes in plants (Abdul Aziz et al., 2024). Generation mean analysis was carried out to obtain information about the genetic composition of the trait. The days to 50% emergence in the spring, days to 50% silk in the autumn, protein content in both seasons, oil content in both seasons while autumn in cross-2, and starch contents for cross-1 in both seasons exhibited non-significant scaling tests, indicating the dominant additive model satisfies these features. All other traits had significant values in at least one of the scaling tests and showed a cognitive interaction elaborating the presence of epistasis (Table 4). The results of the analysis of the mean generation of days to 50% emergence in the spring showed the importance of the additive dominance model. Generation variance analysis demonstrated both additive type and over dominance of genetic action for the trait in cross-1 and cross-2 respectively. Similar kind of findings are observed by Amegbor et al. (2023). Cross-1 showed a non-allelic interaction with a greater contribution of the additive gene effect in the autumn for 50% day to silking. A negative value of [h] showed a lesser contribution by the dominant parent. Dominance reduces silk days. The sign of [h] and [l] are opposite in Table 5 demonstrated the manifestation of epistasis which might show a disadvantage in early selection. In cross-2, additive and non-additive genetic action played a role in inheriting the trait during the autumn and spring seasons, respectively. The results of generation variance analysis exhibited the contribution of both additive and over dominance gene action. The results of the study are supported by Onejeme et al. (2020) and Lal et al. (2023). Non-additive gene action in both seasons for 50% days to tasseling was observed in cross-1. A negative value of [h] showed a lesser contribution by the dominant parent. Therefore, selection must be made carefully in future generations. In spring, the sign of [h] and [l] are opposite and elaborate duplicate epistasis, which might cause problems in early selection. Additive gene action during autumn was involved in cross-2. The negative value of [d] and [i] in cross-2 during spring demonstrated the presence of alleles with a decreasing effect indicating careful selection in advanced generations. Analysis of generation variance favored the contribution of genetic action as well as the influence of dominant genes in both crosses. Similar kind of results were also achieved by Yadav et al. (2023). The importance of the Season $\times$ Treatment analysis in cross-1 demonstrated the involvement of the environment in controlling protein contents. The trait in both hybrids exhibited the additive gene action with no dominance. Therefore, simple selection followed by relative breeding is appropriate to improve the trait. The negative association of the trait with lesion length justifies the negative effect of the disease on the trait. Similar kind of results has been elaborated by Lobulu et al. (2023). The study indicated the non-involvement of environment in controlling the oil contents. With the exception of cross-2, which also exhibited epistasis relations during the spring, the oil contents in both hybrids demonstrated an additive dominance model with a distinct influence of additive genetic role in both seasons. A negative [d] value indicated that the inferior parent contributed more. In order to improve the characteristic, careful selection followed by pedigree breeding is appropriate. The characteristic's negative connection with the lesion length indicated that the disease had a negative impact on the trait. The current findings are in accordance with the findings of Luo et al. (2023). Starch content further demonstrated how the environment affected the characteristic. A simple additive model was seen in the characteristic in cross-1, with the additive impact contributing in both growth seasons. Autumn starch content revealed a complicated non-additive gene action in cross-2. Duplicate epistasis was present due to opposite sign of [h] and [l], suggesting

that selection need to be postponed until later generations. Additive gene action was observed during spring. The disease's detrimental impact on the characteristic was explained by the trait's negative connection with lesion length. The study endorsed the findings of Wu et al. (2023). A straightforward additive dominance model was shown by the mean generation analysis for both hybrids in the autumn for moisture contents. Partial dominance gene action was observed due to lesser value of degree of dominance from unity. Ohunakin et al. (2023) reported similar results.

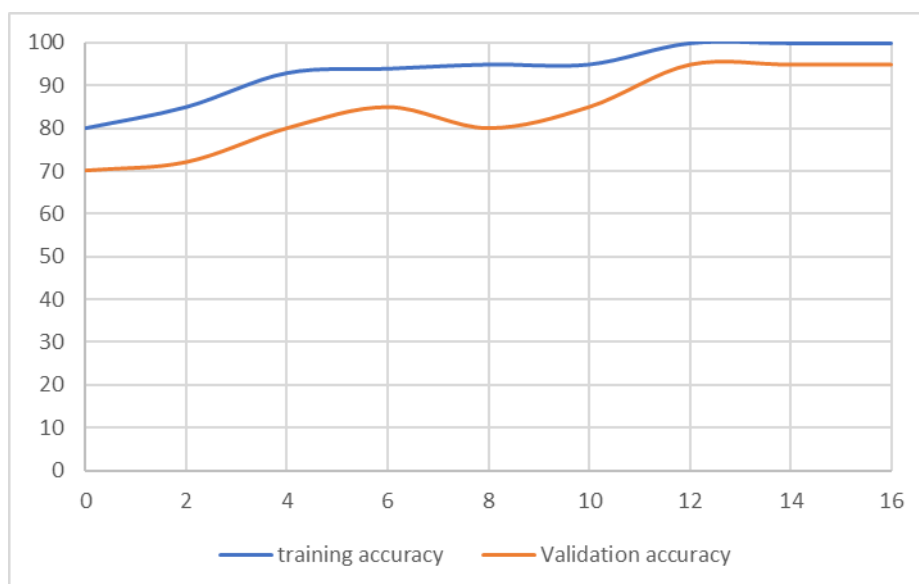


Figure 2. Model training and validation accuracy

Over the course of two seasons, crosses between lines with consistently resistant and susceptible responses were developed. The non-significant treatment x season means square results were due to this activity. The lesion length is the result of a complicated non-additive gene action throughout the autumn in cross-1. The negative values of [h] and [I] represented the more contribution of lower parent. As a result, careful selection is required in succeeding generations. Duplicate epistasis was present which was indicated by opposite signs of [h] and [I]. It will be problematic for early selection. A non-additive genet action in lesion length exhibited in the spring. Duplicate epistasis observed indicating that selection ought to be postponed until later generations. In both seasons, Cross-2 shown non-allelic interaction with more additive genetic impact, the negative values of [h] and [i] showed lesser contribution from the greater parent. As a result, careful selection is required in succeeding generations. The same significant findings were observed by Hou et al. (2023) and Ali Khan et al. (2023). The current study was also able to reach up to 95% accuracy using image-processing model (Guerrero-Ibañez et al., 2023; Zhou et al., 2024) applied a CNN model for the diagnosis and categorization of tomato diseases. They got 99% classification accuracy. Our results endorsed the findings of Mohanty et al. (2016), who detected 26 distinct plant diseases with 99.35% accuracy. The requirement for cameras has been replaced by the emergence of android phones. To detect infections early, farmers can snap images of the affected region and upload them to the main server (Ranjith et al., 2017).

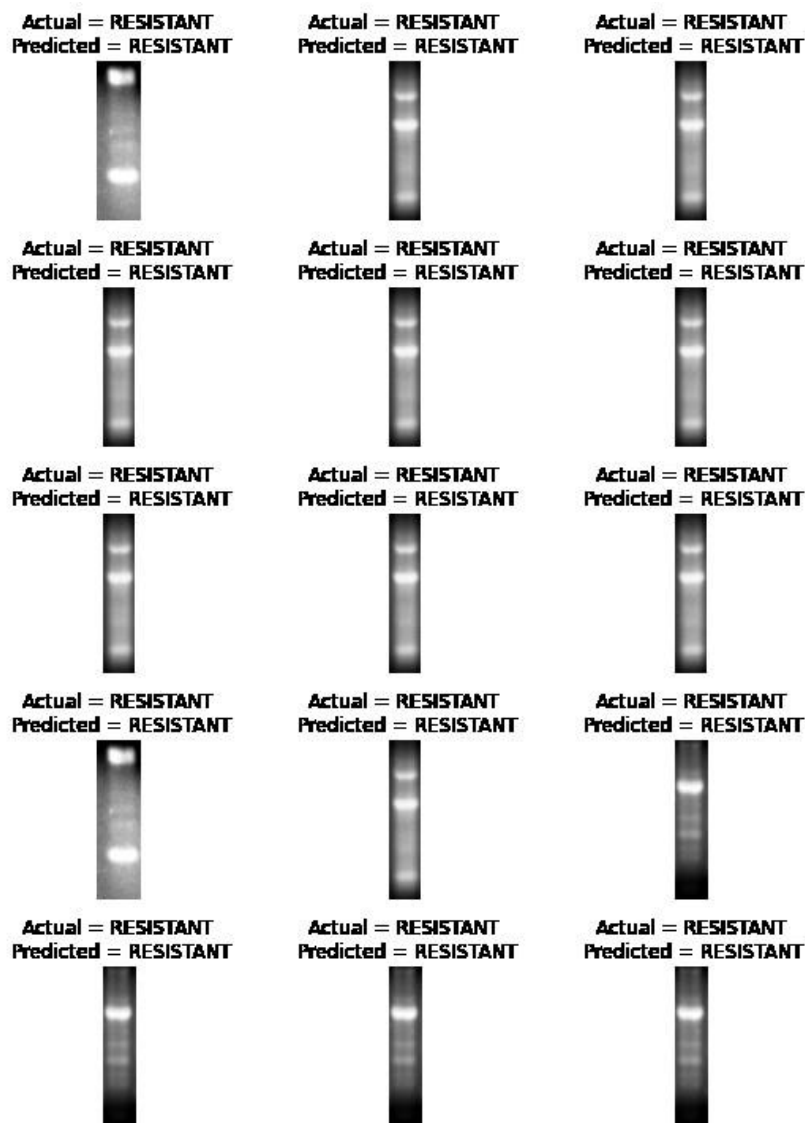


Figure 3. Model predictions on unseen images

Research limitations

The limitations of the research are as under:

1. The disease (stalk rot) requires favorable environment to show its pandemic impact. We were unable to maintain it in natural environment.
2. The research focused on grayscale images, which may limit the model performance on RGB images.
3. The more training can enhance model performance. However, it requires more image data, high power GPU machine and additional memory.

Conclusions

Some differences in gene action in the results of generation mean and variance analysis elaborated in this research might be due to difference in the statistical methods used. The current study helps in identifying disease resistant lines using the power of

artificial intelligence. Inheritance pattern also helps in the improvement of physiological and nutritional traits. By examining disease resistance alone, it became clear that lesion length was not significantly correlated with physiological and nutritional traits. These resistant lines may provide a gene or genes for high-yielding cultivars. Using the suggested model on a smartphone can assist pathologists and breeders in creating high-yielding varieties in addition to helping farming communities in solving their problems at their doorstep.

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REFERENCES

- [1] Abdul Aziz, M., Masmoudi, K. (2024): Molecular breakthroughs in modern plant breeding techniques. – Horticultural Plant Journal. DOI: 10.1016/j.hpj.2024.01.004.
- [2] Adu, J., Nyadanu, D., Nyarko, A., Quaye, M. O., Kuor, F., Menka, C. A. (2023): Identification of high-yielding landraces and hybrids of maize (*Zea mays* L.) and the heritability of yield-related traits in Ghana. – Asian Journal of Advances in Agricultural Research 22(4). DOI: 10.9734/ajaar/2023/v22i4447.
- [3] Akamatsu, Y., Morita, S., Sunaga, Y., Kanno, T. (2024): Variations in the yield and moisture content of ears of forage corn varieties with different relative maturity. – Grassland Science 70(1). DOI: 10.1111/grs.12414.
- [4] Al Hiary, H., Bani Ahmad, S., Reyalat, M., Braik, M., ALRahamneh, Z. (2011): Fast and accurate detection and classification of plant diseases. – International Journal of Computer Applications 17(1). DOI: 10.5120/2183-2754.
- [5] Al-Falahy, M. A. H. (2015): Estimation combining ability, heterosis and some genetic parameters across four environments using full diallel cross method. – International Journal of Pure and Applied Sciences and Technology 26(1).
- [6] Alhazmi, S. (2023): Different stages of watermelon diseases detection using optimized CNN. – Lecture Notes in Networks and Systems 627 LNNS. DOI: 10.1007/978-981-19-9858-4_11.
- [7] Ali Khan, H., Siddiqui, D. A. (2023): The effect of corporate diversification, investment, capital structure and dividend policies on firms' financial performance: a global sectorial analysis. – SSRN Electronic Journal. DOI: 10.2139/ssrn.4432371.
- [8] Amegbor, I. K., van Biljon, A., Shargie, N. G., Tarekegne, A., Labuschagne, M. T. (2023): Combining ability estimates for quality and non-quality protein maize inbred lines for grain yield, agronomic, and quality traits. – Frontiers in Sustainable Food Systems 7. DOI: 10.3389/fsufs.2023.1123224.
- [9] Attallah, O. (2023): Tomato leaf disease classification via compact convolutional neural networks with transfer learning and feature selection. – Horticulturae 9(2). DOI: 10.3390/horticulturae9020149.
- [10] Bao, W., Yang, X., Liang, D., Hu, G., Yang, X. (2021): Lightweight convolutional neural network model for field wheat ear disease identification. – Computers and Electronics in Agriculture 189. DOI: 10.1016/j.compag.2021.106367.

- [11] Benton, J. R., Klopfenstein, T. J., Erickson, G. E. (2005): Effects of corn moisture and length of ensiling on dry matter digestibility and rumen degradable protein. – Nebraska Beef Cattle Reports, January.
- [12] Chakraborty, M., Munshi, S. K., Haque, A., Azad, M. A. K., Islam, T., Alam, M., Shiddiky, M. J. A. (2023): Current Biotechnological Approaches in Maize Improvement. – In: Wani, S. H. et al. (eds.) Maize Improvement: Current Advances in Yield, Quality, and Stress Tolerance under Changing Climatic Scenarios. Springer, Cham. DOI: 10.1007/978-3-031-21640-4_8.
- [13] Duan, C., Song, F., Sun, S., Guo, C., Zhu, Z., Wang, X. (2019): Characterization and molecular mapping of two novel genes resistant to *Pythium* stalk rot in maize. – *Phytopathology* 109(5). DOI: 10.1094/PHYTO-09-18-0329-R.
- [14] Duan, C., Cao, Y., Dong, H., Xia, Y., Li, H., Hu, Q., Yang, Z., Wang, X. (2022): Precise characterization of maize germplasm for resistance to *Pythium* stalk rot and *Gibberella* stalk rot. – *Scientia Agricultura Sinica* 55(2). DOI: 10.3864/j.issn.0578-1752.2022.02.003.
- [15] Dubey, R. B., Joshi, V. N., Verma, M. (2009): Heterosis for nutritional quality and yield in conventional and nonconventional hybrids of maize (*Zea mays* L.). – *Indian Journal of Genetics and Plant Breeding* 69(2).
- [16] García Bravo, L. A., Vega-Murillo, V. E., Villagómez- Cortes, J. A., Zárate-Martínez, J. P., Leyva-Ovalle, O. R., Calderón Robles, R. C., Ríos-Utrera, Á., Bermúdez, M. M., Martínez-Velázquez, G. (2023): Additive and non-additive genetic effects for reproductive traits in a Holstein-Brown Swiss diallel in humid subtropical climate. – *Revista Mexicana De Ciencias Pecuarias* 14(3). DOI: 10.22319/rmcp.v14i3.6247.
- [17] Garg, R., Subudhi, P. K., Varshney, R. K., Jain, M. (2023): Editorial: abiotic stress: molecular genetics and genomics. Vol. II. – *Frontiers in Plant Science* 13. DOI: 10.3389/fpls.2022.1101139.
- [18] Ghosh, S., Singh, A., Kumar, S. (2023): PB3C-CNN: an integrated parallel big bang-big crunch and CNN based approach for plant leaf classification. – *Inteligencia Artificial* 26(72). DOI: 10.4114/intartif.vol26iss72pp15-29.
- [19] Guerrero-Ibañez, A., Reyes-Muñoz, A. (2023): Monitoring tomato leaf disease through convolutional neural networks. – *Electronics (Switzerland)* 12(1). DOI: 10.3390/electronics12010229.
- [20] Han, H., Sha, R., Dai, J., Wang, Z., Mao, J., Cai, M. (2024): Garlic origin traceability and identification based on fusion of multi-source heterogeneous spectral information. – *Foods* 13(7): 1016. DOI: <https://doi.org/10.3390/foods13071016>.
- [21] Harrelson, F. W., Erickson, G. E., Klopfenstein, T. J., Jackson, D. S., Clark, P. M., Fithian, W. A. (2019): Influence of corn hybrid, kernel traits, location, and dry rolling or steam flaking on ruminal digestibility in beef cattle. – *Applied Animal Science* 35(1). DOI: 10.15232/aas.2018-01778.
- [22] He, Q., Zhan, J., Liu, X., Dong, C., Tian, D., Fu, Q. (2025): Multispectral polarimetric bidirectional reflectance research of plant canopy. – *Optics and Lasers in Engineering* 184: 108688. DOI: <https://doi.org/10.1016/j.optlaseng.2024.108688>.
- [23] Hidayat, I., Dewi, F. O. S. (2022): Effect of liquidity, leverage, and working capital turn on profitability. – *APTISI Transactions on Management (ATM)* 7(1). DOI: 10.33050/atm.v7i1.1832.
- [24] Hou, M., Cao, Y., Zhang, X., Zhang, S., Jia, T., Yang, J., Han, S., Wang, L., Li, J., Wang, H., Zhang, L., Wu, X., Duan, C., Li, H. (2023): Genome-wide association study of maize resistance to *Pythium aristosporum* stalk rot. – *Frontiers in Plant Science* 14. DOI: 10.3389/fpls.2023.1239635.
- [25] Idikut, L., Atalay, A. I., Kara, S. N., Kamalak, A. (2009): Effect of hybrid on starch, protein and yields of maize grain. – *Journal of Animal and Veterinary Advances* 8(10).
- [26] Jamil, M., Ali, A., Gul, A., Ghafoor, A., Napar, A. A., Ibrahim, A. M. H., Naveed, N. H., Yasin, N. A., Mujeeb-Kazi, A. (2019): Genome-wide association studies of seven

- agronomic traits under two sowing conditions in bread wheat. – *BMC Plant Biology* 19(1). DOI: 10.1186/s12870-019-1754-6.
- [27] Jin, X., Che, J., Chen, Y. (2021): Weed identification using deep learning and image processing in vegetable plantation. – *IEEE Access* 9. DOI: 10.1109/ACCESS.2021.3050296.
- [28] Kamal, N., Khanum, S., Siddique, M., Saeed, M., Ahmed, M. F., Kalyar, M. T. A., Rehman, S. U., Mahmood, B. (2023): Heterosis and combining ability studies in a 5x5 diallel crosses of maize inbred lines. – *Journal of Applied Research in Plant Sciences* 4(01). DOI: 10.38211/joarps.2022.3.1.50.
- [29] Kashyap, S., Kumar, R., Ram, H., Kumar, A., Basak, N., Sheoran, P., Bhattacharjee, S., Biswal, B., Ali, G., Kumar, B., Bhakuni, K., Hindoriya, P. S., Birbal, P. S., Min, D. (2023): Quantitative and qualitative response of fodder maize to use of bulk and nano-fertilizers in north western plains of India. – *Agronomy* 13(7). DOI: 10.3390/agronomy13071889.
- [30] Lal, K., Kumar, S., Shrivastav, S. P., Singh, L., Singh, V. (2023): Combining ability effects and heterosis estimates in maize (*Zea mays* L.). – *Electronic Journal of Plant Breeding* 14(1). DOI: 10.37992/2023.1401.001.
- [31] Li, H., Fernie, A. R., Yang, X. (2023): Using systems metabolic engineering strategies for high-oil maize breeding. – *Current Opinion in Biotechnology* 79. DOI: 10.1016/j.copbio.2022.102847.
- [32] Li, Z., Xiang, F., Huang, X., Liang, M., Ma, S., Gafurov, K., Gu, F., Guo, Q., Wang, Q. (2024): Properties and characterization of sunflower seeds from different varieties of edible and oil sunflower seeds. – *Foods* 13(8): 1188. DOI: <https://doi.org/10.3390/foods13081188>.
- [33] Liang, M., Li, T., Qu, Y., Qin, J., Li, Z., Huang, X., Zhang, Q., Zhang, Y., Guo, Q., Wang, Q. (2023): Mitigation mechanism of resveratrol on thermally induced trans- α -linolenic acid of trilinolenin. – *LWT* 189: 115508. DOI: <https://doi.org/10.1016/j.lwt.2023.115508>.
- [34] Liu, S., Bai, H., Li, F., Wang, D., Zheng, Y., Jiang, Q., Sun, F. (2023): An apple leaf disease identification model for safeguarding apple food safety. – *Food Science and Technology (Brazil)* 43. DOI: 10.1590/fst.104322.
- [35] Liu, Y., Shi, A., Chen, Y., Xu, Z., Liu, Y., Yao, Y., Wang, Y., Jia, B. (2024): Beneficial microorganisms: regulating growth and defense for plant welfare. – *Plant Biotechnology Journal*. DOI: <https://doi.org/10.1111/pbi.14554>.
- [36] Lobulu, J., Shimelis, H., Laing, M. D., Mushongi, A. A., Shayanowako, A. I. T. (2023): Progeny testing of maize (*Zea mays*) genotypes for grain yield and yield components, Striga resistance and Fusarium oxysporum f. sp. strigae compatibility. – *Plant Breeding* 142(3). DOI: 10.1111/pbr.13087.
- [37] Lü, H., Yang, Y., Li, H., Liu, Q., Zhang, J., Yin, J., Chu, S., Zhang, X., Yu, K., Lv, L., Chen, X., Zhang, D. (2018): Genome-wide association studies of photosynthetic traits related to phosphorus efficiency in soybean. – *Frontiers in Plant Science* 9. DOI: 10.3389/fpls.2018.01226.
- [38] Luo, M., Lu, B., Shi, Y., Zhao, Y., Liu, J., Zhang, C., Wang, Y., Liu, H., Shi, Y., Fan, Y., Xu, L., Wang, R., Zhao, J. (2023): Genetic basis of the oil biosynthesis in ultra-high-oil maize grains with an oil content exceeding 20%. – *Frontiers in Plant Science* 14. DOI: 10.3389/fpls.2023.1168216.
- [39] Ma, S., Guo, Y., Zhang, T., Liu, D., Wang, L., Hu, R., Zhou, D., Zhou, Y., Chen, Q., Yu, L. (2024): Comprehensive Identification and expression analysis of the multidrug and toxic compound extrusion (MATE) gene family in *Brachypodium distachyon*. – *Plants* 13(18): 2586. DOI: <https://doi.org/10.3390/plants13182586>.
- [40] Mattoo, A. K., Cavigelli, M. A., Mišić, D. M., Gašić, U., Maksimović, V. M., Kramer, M., Kaur, B., Matekalo, D., Nestorović Živković, J., Roberts, D. P. (2023): Maize

- metabolomics in relation to cropping system and growing year. – *Frontiers in Sustainable Food Systems* 7. DOI: 10.3389/fsufs.2023.1130089.
- [41] Mir, S. D., Ahmad, M., Parray, G. A., Zaffar, G., Dar, S. H. (2015): Heterosis studies in single crosses of inbred lines in maize (*Zea mays* L.). – *Electronic Journal of Plant Breeding* 6(4).
- [42] Mohanty, S. P., Hughes, D. P., Salathé, M. (2016): Using deep learning for image-based plant disease detection. – *Frontiers in Plant Science* 7(September). DOI: 10.3389/fpls.2016.01419.
- [43] Mukaro, R., Kamutando, C. N., Magorokosho, C., Mutari, B., Zaidi, P. H., Kutwayo, D., Sibiya, J. (2023): Genetic potential of tropically adapted exotic maize (*Zea mays* L.) heat-tolerant donor lines in sub-tropical breeding programs. – *Agronomy* 13(8). DOI: 10.3390/agronomy13082050.
- [44] Murphy, D. J. (2023): Impact of Genomics on Improving the Quality of Agricultural Products. – In: Copping, L. G. et al. (eds.) *Genomics: Commercial Opportunities from a Scientific Revolution*. Garland Science, London. DOI: 10.1201/9781003423782-23.
- [45] Neish, G. A., Farnworth, E. R., Greenhalgh, R., Young, J. C. (1983): Observations on the occurrence of fusarium species and their toxins in corn in eastern Ontario. – *Canadian Journal of Plant Pathology* 5(1). DOI: 10.1080/0706068309501647.
- [46] Ohunakin, A. O., Odiyi, A. C., Fayeun, L. S. (2023): Genetic analysis of resistance to northern leaf blight of tropical maize inbred lines. – *Journal of Crop Science and Biotechnology*. DOI: 10.1007/s12892-023-00202-7.
- [47] Onejeme, F. C., Okporie, E. O., Eze, C. E. (2020): Combining ability and heterosis in diallel analysis of maize (*Zea mays* L.) lines. – *International Annals of Science* 9(1). DOI: 10.21467/ias.9.1.188-200.
- [48] Rahut, D. B., Mishra, R., Bera, S. (2024): Geospatial and environmental determinants of stunting, wasting, and underweight: empirical evidence from rural South and Southeast Asia. – *Nutrition* 120. DOI: 10.1016/j.nut.2023.112346.
- [49] Ranjith, Anas, S., Badhusha, I., Ot, Z., Faseela, K., Shelly, M. (2017): Cloud based automated irrigation and plant leaf disease detection system using an android application. – *Proceedings of the International Conference on Electronics, Communication and Aerospace Technology, ICECA 2017, January*. DOI: 10.1109/ICECA.2017.8212798.
- [50] Rastgari, M., Ahmadi, H., Zebarjadi, A. R. (2014): Combining ability analysis and gene effects in maize (*Zea mays* L.) using line $\times$ tester crosses. – *Research on Crops* 15(3). DOI: 10.5958/2348-7542.2014.01386.2.
- [51] Reddy, B. J., Mandal, R., Chakroborty, M., Hijam, L., Dutta, P. (2018): A review on potato (*Solanum tuberosum* L.) and its genetic diversity. – *International Journal of Genetics* 10(2). DOI: 10.9735/0975-2862.10.2.360-364.
- [52] Shahini, E., Shehu, D., Kovalenko, O., Nikonchuk, N. (2023): Comparative analysis of the main economic and biological parameters of maize hybrids that determine their productivity. – *Scientific Horizons* 26(4). DOI: 10.48077/scihor4.2023.86.
- [53] Simonyan, K., Zisserman, A. (2015): Very deep convolutional networks for large-scale image recognition. – *3rd International Conference on Learning Representations, ICLR 2015, Conference Track Proceedings*.
- [54] Singh, V., Moreau, R. A., Hicks, K. B., Eckhoff, S. R. (2001): Effect of alternative milling techniques on the yield and composition of corn germ oil and corn fiber oil. – *Cereal Chemistry* 78(1). DOI: 10.1094/CCHEM.2001.78.1.46.
- [55] Slobodova, N., Sharko, F., Gladysheva-Azgari, M., Petrova, K., Tsiupka, S., Tsiupka, V., Boulygina, E., Rastorguev, S., Tsygankova, S. (2023): Genetic diversity of common olive (*Olea europaea* L.) cultivars from Nikita Botanical Gardens collection revealed using RAD-seq method. – *Genes* 14(7). DOI: 10.3390/genes14071323.
- [56] Soma, K., Hennen, W., van Berkum, S. (2023): Can domestic food production provide future urban populations with food and nutrition security?—Insights from Bangladesh, Kenya and Uganda. – *Sustainability (Switzerland)* 15(11). DOI: 10.3390/su15119005.

- [57] Song, F. J., Xiao, M. G., Duan, C. X., Li, H. J., Zhu, Z. D., Liu, B. T., Sun, S. L., Wu, X. F., Wang, X. M. (2015): Two genes conferring resistance to *Pythium* stalk rot in maize inbred line Qi319. – *Molecular Genetics and Genomics* 290(4). DOI: 10.1007/s00438-015-1019-5.
- [58] Steel, R. G. D., Torrie, J. H. (1996): *Principles and Procedures of Statistics. A Biometrical Approach*. 3rd Ed. – McGraw Hill Book Company Inc., New York.
- [59] Wang, M., Lin, H., Lin, H., Du, P., Zhang, S. (2025): From species to varieties: how modern sequencing technologies are shaping medicinal plant identification. – *Genes* 16(1): 16. DOI: <https://doi.org/10.3390/genes16010016>.
- [60] Wu, W., Zhong, Y., Liu, Y., Xu, R., Zhang, X., Liu, N., Guo, D. (2023): A new insight into the biosynthesis, structure, and functionality of waxy maize starch under drought stress. – *Journal of the Science of Food and Agriculture* 103(11). DOI: 10.1002/jsfa.12599.
- [61] Yadav, P. K., Tripathi, M. K., Tiwari, S., Chauhan, S., Tripathi, N., Sikarwar, R. S., Solanki, R. S., Yadav, S., Singh, A. K. (2023): Genetic components and variability assessment for grain yield and its accrediting traits in maize (*Zea mays* L.). – *International Journal of Environment and Climate Change* 13(9). DOI: 10.9734/ijecc/2023/v13i92298.
- [62] Yan, J., Warburton, M., Crouch, J. (2011): Association mapping for enhancing maize (*Zea mays* L.) genetic improvement. – *Crop Science* 51(2). DOI: 10.2135/cropsci2010.04.0233.
- [63] Yang, Q., Yin, G., Guo, Y., Zhang, D., Chen, S., Xu, M. (2010): A major QTL for resistance to *Gibberella* stalk rot in maize. – *Theoretical and Applied Genetics* 121(4). DOI: 10.1007/s00122-010-1339-0.
- [64] Ye, J., Zhong, T., Zhang, D., Ma, C., Wang, L., Yao, L., Zhang, Q., Zhu, M., Xu, M. (2019): The auxin-regulated protein ZmAuxRP1 coordinates the balance between root growth and stalk rot disease resistance in maize. – *Molecular Plant* 12(3). DOI: 10.1016/j.molp.2018.10.005.
- [65] Yoosefzadeh Najafabadi, M., Hesami, M., Eskandari, M. (2023): Machine learning-assisted approaches in modernized plant breeding programs. – *Genes* 14(4). DOI: 10.3390/genes14040777.
- [66] Zhou, Y., Zhou, H., Chen, Y. (2024): An automated phenotyping method for Chinese *Cymbidium* seedlings based on 3D point cloud. – *Plant Methods* 20(1): 151. DOI: 10.1186/s13007-024-01277-1.
- [67] Zou, K., Chen, X., Zhang, F., Zhou, H., Zhang, C. (2021): A field weed density evaluation method based on UAV imaging and modified u-net. – *Remote Sensing* 13(2). DOI: 10.3390/rs13020310.