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Utilization of different Graphical and Simplified Statistical Model to Analyse The Stability of Various Summer Forage Genotypes

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ABSTRACT

Plant breeders are very concerned about the presence of genotype environment (G E) interaction since it can significantly lower selection gains and make it more difficult to identify superior genotypes. As an attempt to solve the problem of summer fodder in Egypt, an evaluation was made. Nine genotypes (six teosinte (T)-maize(M) genotypes (T x M (W)106, T x M 202-A, T x M Hytech 2031, T x M Pioneer 30k8(W), T x M pioneer 3444 (Y),T x M SC Giza 168, Pearl millet, Fodder maize and Sudan grass) were evaluated in three nitrogen level (0, 50 and 100 Kg N Fed^{-1}) through 2021 and 2022 summer seasons. The aim of this work is to assess the forage yield performance, determine the magnitude of (G × E) interaction and investigate the stability derived from regression and variance analyses besides using graphical analysis. The crosses T x M SC pioneer 3444 and M (W) 106 and M (Y) 202-A exhibited a significant increase in the fresh and dry matter yield followed by Sudan grass and Pearl millet. Low S^{2}d and value of b around one with high yield over mean were found by T x M Y202-A, T x M pioneer for fresh yield and Pearl millet for dry matter. Graphical analysis confirmed the aforementioned results in addition it showed that fodder maize had the lowest values for fresh yield; meanwhile the highest values were detected by genotypes T x M W106, and T x M Pioneer 3444 for fresh and dry matter yield.

Keywords: Teosinte-maize cross, Pearl millet, Fodder maize and Sudan grass, stability, GGE biplot

INTRODUCTION

One of Egypt's national programs to increase food and feed potentialities gives a lot of thought to improving agricultural productivity and quality using affordable, sustainable alternatives to traditional agronomic methods. In this regard, there is a serious lack of forage crop production throughout the year, especially during the summer months when there is no supply of protein-rich fodder plants to be cultivated.

In other words, it's essential to choose fodder plants with high absorption rates since they produce more and of higher quality with less farming inputs. Finding native plants that are suited to the current environmental circumstances, where plant energy will be used for growth, production, and quality rather than for survival, is therefore imperative. Also, there aren't many recognized commercial suppliers of fodder seeds, particularly in the summer.

The closest relative of maize is teosinte, which is easily hybrid seed with maize and produces a fertile offspring seeds. Nonetheless, the matter has proven contentious for other crops, especially maize where it coexists with a number of species known as "teosintes," which are its wild cousins (Serratos *et al.* 1997).

According to research by Ellstrand *et al.* (2007), Mexicana teosinte and maize can spontaneously hybridize with the wild, although only at very low rates (less than 1% each generation). Although reciprocal introgression has occurred infrequently, in some conditions favor gene flow from teosinte to maize rather than from maize to teosinte (Baltazar *et al.* 2005). In some populations of *Z. mays teosintes*, there is evidence of a restriction to cross ability

when teosinte is the female parent and maize is the male parent. This has been linked to a teosinte gene or gene cluster known as teosinte crossing barrier1 (Tcb1) (Evans and Kermicle, 2001). When teosinte is the pollen parent, there is less incompatibility than when maize is the pollen parent (Baltazar *et al.* 2005). Maize Teosinte hybrids have drawn a lot of interest from both teosinte and maize. The ssp. *mays* x ssp. *mexicana* hybrids do not show statistically significant heterosis when compared to the wild teosinte, but they do when compared to the cultivated parent (Guadagnuolo *et al.* 2006). The genetic distance (GD) between the germplasm lines has been calculated using morphological, biochemical, molecular, and heterosis research (Menkir *et al.* 2004 and Laborda *et al.* 2005).

The two sub species share a tight genetic link, which has sparked interest in adding valuable maize genes to the gene pool. Similarly, attention has been drawn to maize-teosinte or teosinte-maize hybrids for their potential to increase the fodder output of teosinte by utilizing the hybrid vigor displayed by the hybrids. Open cross-breeding reduces expenses by producing hybrids, but plant breeders are primarily concerned with finding the best hybrid seeds. Additionally, the conditions in which the breeding populations will be studied will have a significant impact on the genotypes that are modified by environmental flexions for various characteristics. When this information is available, the breeder can choose from a number of breeding methods that have the highest likelihood of being successful. Many statistical methods may be used to assess stability by modelling the (GxE) interaction. Yet, methods based on variance measures and regression models are those that are most often used. Regression statistics were initially proposed

as a stability parameter by Yates and Cochran (1938); this notion was subsequently rediscovered by Finlay and Wilkinson (1963) and was then improved by Eberhart and Russell (1966). Moreover, Tai offered two stability factors that were on par with those of Eberhart and Russell (1966). The three metrics employed by the regression approach to characterize stability are mean performance, slope of the regression line, and deviation from regression.

Due to the overlap in how their statistics were calculated, they discovered that different stability models likely assess the same stability feature. No references have been discovered on the aforementioned claim regarding fodder crops in Egypt. Consequently, the goals of this study were to evaluate the specific properties of growth behavior, forage yield and quality of some summer forage and some new hybrids between maize and teosinte and to assess the stability of all studied genotypes and to use Spearman rank correlation coefficient to look at the relationships between various stability data.

MATERIALS AND METHODS

Throughout the three seasons 2020, 2021 and 2022, this experiment was conducted at the Experiment, Research Station of Moshtohor Faculty of Agriculture, Benha University, Qalyubia Governorate, Egypt.

Plant Materials

For the study, A local ecotype of teosinte (*Zea mays* spp. mexicana) and six different maize genotypes (*Zea mays* L.) including two inbred lines (M White (W)106 & M yellow (Y) 202-A), four single crosses *i.e.,* Hytech 2031 (W), Pioneer 30k8(W), Pioneer 3444 (Y) and SC Giza 168 (Y) were used in this investigation as well as three summer forage crops i.e. Pearl millet, Fodder maize and Sudan grass.

Maize-Teosinte Hybrids formation

In 2020 growing season, at 10th, 17th and 21th July in isolated area grains from each of teosinte (male) and the six aforementioned maize genotypes (Females) are planted in sequential ridges (4 m) patterns, each planting date including four times as many female plants as male ones. Before pollen is discharged, the male flower (tassel) of the female plant is cut off (detasseled), leaving the tassels on the male plants as the only source of pollen for the female flower (the cob or ear) on the female plants. To stop any female pollen from fertilizing the female silks, the female must be detasseled. During this season, all possible top crosses were made giving a total of six crosses i.e. teosinte 1(teosinte x M 106), teosinte 2(teosinte x M 202-A), teosinte 3(teosinte x Hytech 2031), teosinte 4(teosinte x Pioneer 30k8), teosinte 5(teosinte x pioneer 3444) and teosinte 6(teosinte x SC Giza 168).

Experimental practices and design:

In evaluation successive seasons of 2021 and 2022, the six teosinte-maize hybrids beside Pearl millet, Fodder maize and Sudan grass were sown. The planting dates were on two sowing dates i.e. 17th May 2021 and 16th May 2022. In each season treatments were arranged in a split-plot design in three replicates, three nitrogen levels (0, 50 and 100 Kg N/ fed.) assigned in main plots and forage crops genotypes arranged in split–plots. The area of each plot was 10.5 m² (5 ridges of 3.5 m length and 60 cm width), the other suggested agronomic techniques for cultivating fodder in the summer and winter were commonly used in the area. Pearl millet and Sudan grass were cut twice at cutting intervals after 50, and

90 days from sowing date. However, teosinte-maize hybrids and Fodder maize were cut after 90 days from sowing date.

Soil Analysis and Meteorological DataParticle size distribution (%) analysis of the experimental soil across evaluation seasons according to Jackson (1973) and Black *et al*. (1982), indicated that the soil is clay (2.07%, 24.3%, 21.7% and 52.44% for coarse sand, fine sand, silt, and clay, respectively), the pH (1: 2.5 w/v paste extract) is 7.61, the EC is 0.97 dS m^{-1}, calcium carbonate is 1.07%, the available nutrients in mg kg-1were Nitrogen, Phosphorous, and Potassium were 0.89, 0.34 and 0.74 mg kg^{-1} respectively.

Meteorological variables in the 2020 and 2021 growing season were obtained from Agrometeorological Mostohor Station. For May, June and July in 2020 mean temperature was 25.43, 27.54, and 29.11°C maximum temperature was 34.41, 34.97, and 35.12 °C and relative humidity was 45.0, 50.0 and 64.13, respectively. Meanwhile, in 2021 mean temperature were 27.98, 29.71 and 29.55°C maximum temperature was 35.58, 35.01, and 36.01 °C and relative humidity was 50.0, 54.2 and 68.02, respectively.

The studied parameters: Fresh forage yield (ton/ fed) and dry matter (ton/ fed) as follows: All studied forage genotypes had their fresh forage production calculated for the first and subsequent cuts in each experimental unit, and the results were converted to tons fed^{-1} as total production. Following the selection of 200 g fresh forage samples at random from each experimental unit and accurate weighting with an electric balance with 0.01 g sensitivity were chosen to determine the dry matter content, the obtained fresh samples were dried in an air forced drying oven at 70° C for 3 days until constant weight. Finally, the dry yield of studied forage genotypes was estimated.

Statistical analysis

1- Analysis of variance

According to the proposed design, a statistical analysis of each of the two previously stated seasons was done separately. According to the method outlined by Snedecor and Corchran (1982), the analysis of variance was conducted, and the differences between means of genotypes and nitrogen level in each season as well as interactions were carried out according to Duncan's method at the 5% level (Duncan 1955).

Combined analysis across all studied environments

Prior to doing the combined analysis, the Bartelett test (1937) was run to determine whether the variances were homogeneous based on the homogeneity of the individual error factors. Accordingly, the combined analysis of variance across six environments *i.e.,* 3 nitrogen levels x 2 years was worked out. In the present investigation, environments (combinations of years x nitrogen levels) were viewed as random effects, whereas genotypes were assumed to be fixed effects overall.

Significant genotype x environment interactions was detected and consequently, stability of yield performance was investigated for all studied genotypes. Also, the two-way data were subjected to the Zobel *et al*. (1988) who suggested Tukey test (1949), which divided one degree of freedom for the non-additive component to test for the presence of multiplicative (G x E) interaction.

2- Stability analyses

To find stable genotypes to include in the breeding programs of fodder crops, four commonly used stability approaches were utilized. Regression model and variance

measurements were the two primary classes into which the employed stability approaches were divided. The genotype is regarded as stable under the regression technique if its reaction to the environmental indicator is parallel to the mean response of all genotypes and its departure from the regression model is as little as feasible. This group comprised two stability methods were described by Eberhart & Russell (1966) and Tai (1971). Two stability models of Wricke (1962) and Shukla (1972) were included in the category of stability parameters based on variance measurements. A genotype was deemed stable if it had a low variance measure across several contexts. A brief summary of each method is shown in Table 1.

The high yielding capacity of a genotype is a prerequisite for the stability concept over the two sets of stability factors. In several earlier works, the calculations of the present stability algorithms were described in detail. The following is a quick summary of each.

The regression model proposed by Eberhart and Russell (1966) uses the linear regression coefficient (b), which indicates the genotype response to the environmental indicator, and the deviation from regression mean square (S^2d).

The genotype is said to be adapted in all contexts if the regression coefficient (b value) does not deviate noticeably from unity. Any genotype with b less than 1.0 is adaptable to low yielding conditions, whereas genotypes with b > 1.0 are more sensitive to high yielding situations.

Regarding Tai (1971), The phrases "genetic stability parameters" refer to two components, namely " α and λ ". The first statistic, " α ", measures the linear response of environmental factors, and " λ " illustrates the departure from linear response in terms of magnitude of error variance. In actuality, b and S^2d may be thought of as modified forms of the parameters of α and λ, respectively. A genotype that is entirely stable would not function differently in different environments. This is the same as saying that = -1 and = 1. Since ideal stable genotypes are uncommon, plant breeders must settle for levels of stability that are statistically acceptable.

Average stability will be defined as the values ($\alpha = 0$ & $\lambda = 1$), while below average stability will be defined as the values ($\alpha > 0$ & $\lambda = 1$), and above average stability will be defined as the values ($\alpha < 0$ & $\lambda = 1$).

In the current investigation, the eco-valence stability indicator, W2, or the genotype's contribution to the G x E interaction sum of squares as described by Wricke (1962) were used. There is no way to assess the relevance of W2 for each genotype since the value of W2 is given as a sum of squares. Thus, the genotype was deemed stable if it had a minimal W2 value.

Shukla (1972) created a neutral stability variance estimate known as σ^2. To get around the linear impact from the G x E interaction, the Shukla technique can be expanded to include a covariate. Each genotype can get the remaining G x E interaction variance as the second stability parameter S^2. The two stability variance parameters (S^2 and σ^2) versus the error variance are given for the test of significance.

Table 1. The principles of stability decision-making based on two sets of stability models' parameters (regression and variance).

Stability models				
I. Models based on regression approach				
	1- Eberhart & Russell (1966)		2- Tai (1971)	
Parameters	1- b	2 - S^2d	3 – α	4 – λ
The ideas behind stable decision-making	no significant differ from 1	no significant differ from 0 (low value)	no significant differ from 0	no significant differ from 1
	II. Models based on variance approach			
	3- Wricke (1962)		4- Shukla (1972)	
Parameters	5 - W^2		6 – σ^2	7 – S^2
The ideas behind stable decision-making	Choose the minimum values		No significant	No significant

The two aforementioned qualities were subjected to the combined ANOVA analysis. With the use of an ANOVA, the variations from the grand mean caused by the genotype, environment, and GE were separated. The multi-environment yield trails (MEYTs) data were graphically analyzed using the GGE—biplot approach, which combines two ideas (Gabriel, 1971) and the GGE concept (Yan *et al* 2000). To display the variables (genotype and genotype by environment interaction), which are also the sources of variation, the approach employs a biplot. In this work, visualizing for genotypic comparison and visualizing for environmental comparison both employed genotype-focused scaling. Also, the which—won—where pattern of the MEYTs yield data was best shown using symmetric scaling (Yan and Rajcan, 2002).

RESULTS AND DISCUSSION

Evaluation of the potential for fodder crops
Response to N-fertilization levels addition:-

Add N-fertilization increased fresh forage yield (ton/ fed) and dry matter (ton/ fed). The increase in fresh forage yield magnitude occurred due to increasing N levels with averaged of 12.2%, and 29.27% in the first season (2020) and 11.89% and 26.45% in the second season (2021) due to N_{50} and N_{100}, respectively, compared with control treatment (N0). Also, Add N increased dry matter weight. The increase averaged of 18.82%, and 44.01% in the first season (2020) and 20.51% and 45.51% in the second season (2021) due to N_{50} and N_{100}, respectively, compared with control treatment (N_0), as shown in Table 2.

Effect of genotypes:

The results in Table 2 showed that, the cross between teosinte and each of SC pioneer 3444 and M (W)106 and M (Y) 202-A gave a significant increase in the fresh weight reached 24.44, 24.27 and 24.04 tons fed[-1] in the first season and 23.32, 23.14 and 22.92 tons fed[-1] in the second season, respectively. Regarding dry matter, the cross teosinte x M (W) 106 was given the highest and significant value reached 5.96 and 5.17 tons fed[-1] dry matter , followed by Sudan grass and T x M Pioneer 3444 in the first season and Pearl millet, Sudan grass and M Pioneer 3444 in the second season.

Interaction between Nitrogen levels and genotypes

The interaction between studied genotypes and nitrogen levels showed that increasing nitrogen rate was associated with a progressive significant increase in forage yield and dry matter yield in each genotype. However the highest values for both studied traits were detected by T x M W106 with 100kg N addition in both seasons followed by T x M Pioneer 3444 with 100 kg N. Meanwhile fodder maize showed the low values without and add of nitrogen fertilizer in both season for mention traits.

Table 2. Fresh forage and dry matter yield mean values throughout the six environments, as well as genotype mean values across environments.

Genotypes	Season 2020				Season 2021			
	N0	N50	N100	Mean	N0	N50	N100	Mean
Forage yield (tons/ fed^{-1})								
Pearl millet	17.40kl	20.30hi	22.13eg	19.94C	16.34jl	17.50ij	21.87de	18.57C
Fodder maize	12.93n	13.87mn	14.67m	13.82E	12.03n	12.95mn	13.73m	12.91D
Sudan grass	16.53l	18.93ij	22.67ef	19.38CD	15.56l	17.92hi	21.57ef	18.35C
TxM W106	22.40eg	23.33de	27.07a	24.27A	21.31ef	22.23ed	25.89a	23.14A
TxM Y202-A	21.73fg	24.27cd	26.13ab	24.04A	20.66ef	23.14cd	24.97ab	22.92A
TxM hytech 2031	17.07kl	19.20ij	20.13hi	18.80D	16.08jl	18.18hi	19.09gh	17.78C
TxM pioneer 30K8	16.67l	18.13jk	22.00eg	18.93D	15.69kl	17.13ik	20.92ef	17.92C
TxM Pioneer 3444	21.20gh	24.93bc	27.20a	24.44A	20.14fg	23.79bc	26.02a	23.32A
TxM Giza 168	20.13hi	23.33de	25.47bc	22.98B	19.09gh	22.23de	24.32bc	21.88B
Mean	18.45C	20.70B	23.05A	-	17.43C	19.45B	22.04A	-
Dry matter (tons/ fed^{-1})								
Pearl millet	3.63kl	4.39gi	6.78a	4.93D	3.35hi	4.37de	6.01a	4.58B
Fodder maize	3.46l	3.95il	4.45gi	3.96F	2.96i	3.40h	3.85fg	3.40E
Sudan grass	4.15gk	5.16cf	6.43a	5.25BC	3.92fg	4.88bc	6.12a	4.97AB
TxM W106	5.41bd	5.66bd	6.81a	5.96A	4.68bd	4.90bc	5.95a	5.17A
TxM Y202-A	4.21gj	4.73eg	5.26ce	4.73DE	3.58gh	4.02eg	4.50cd	4.03D
TxM hytech 2031	3.82jl	4.69fg	5.10df	4.54E	3.25hi	4.04ef	4.41de	3.90D
TxM pioneer 30K8	3.97hl	4.53gh	5.72bc	4.74DE	3.40h	3.90fg	4.97b	4.09CD
TxM Pioneer 3444	4.26gj	5.39bd	6.63a	5.43B	3.63fh	4.64bd	5.77a	4.68B
TxM Giza 168	3.90il	5.19cf	5.87b	4.99CD	3.30hi	4.48cd	5.08b	4.28C
Mean	4.09C	4.86B	5.89A	-	3.56C	4.29B	5.18A	-

Notes, the letters denote a sizable difference in means (Dancan test, LSR value: P>0.05). The mean value from high to low is what the alphabets descending from A to Z allude to.

Stability analysis

The 9 forage genotypes (G) across the 6 environments (E), as well as their interaction (G x E), were subjected to the standard combined analysis of variance for forage fresh weight and dry matter yield. The outcomes showed distinct genotypic behavior in addition to a broad range of variability between genotypes and environments (years and nitrogen levels). The extremely significant (G x E) interaction effect demonstrated that the studied genotypes did not respond to environments in a same manner. Thus, stability analysis was performed on the data on the average mention traits in the investigated settings.

In Table 3, the pooled analysis of variance is displayed. The findings demonstrated that for mention characteristics under study, mean squares resulting from environments, genotypes, and genotype-environment interaction (linear) were extremely significant. These findings showed that different genotypes' reactions to various environmental factors are linear. On the other hand, the level of stability of each genotype under examination is determined by the extremely significant pooled departure from linear regression.

The results of stability statistics based on regression and variance models for nine forage genotypes in addition to their fresh and dry yield/ fed are shown in Table 4. Significant differences among genotypes in terms of mention studies were determined. The highest out-yield forage fresh yield from over all mean were obtained by genotypes TxM W106,

TxM Y202-A, TxM Pioneer 3444 and TxM Giza 168 recording 23.70, 23.48, 23.88 and 22.43 ton/ fed, respectively. Meanwhile, the genotypes, Pearl millet, Sudan grass, TxM W106 and TxM Pioneer 3444 exhibited the highest values for dray matter yield and surpassed the overall mean recording 4.75, 5.11, 5.57, and 5.06 ton fed^{-1}, respectively.

Table 3. Mean squares of stability analysis of forage fresh yield and dry matter yield for 9 genotypes across 6 environments.

Source of variation	df	Forage yield (tons/ fed^{-1})	Dry matter (tons/ fed^{-1})
Genotype	8	73.33**	1.86**
Environment+ G*E	45	5.15**	0.81**
Environment	5	41.47**	6.29**
Genotype x Env.	40	0.61**	0.12**
a) Env . (linear)	1	207.33**	31.46**
b) V x Env. (linear)	8	1.93**	0.34**
c) pooled deviations	36	0.25**	0.06**
Genotypes			
Pearl millet	4	0.38**	0.21**
Fodder maize	4	0.10**	0.02**
Sudan grass	4	0.13**	0.08**
TxM W106	4	0.50**	0.07**
TxM Y202-A	4	0.09**	0.04**
TxM hytech 2031	4	0.20**	0.05**
TxM pioneer 30K8	4	0.36**	0.01**
TxM Pioneer 3444	4	0.33**	0.00**
TxM Giza 168	4	0.19**	0.06**
poled error	96	0.001	0.0124

Table 4. Based on regression and variance component models, the average forage and dry matter yield (tons fed⁻¹) and stability data were calculated for nine soybean genotypes cultivated in six different environment.

Genotypes	Mean	Stability parameters (regression models)				Stability parameters (variance components models)		
		Eberhart & Russell (1966)		Tai (1971)		Wricke (1962)	Shukla (1972)	
		b	S^2d	α	λ	W^2	σ^2	S^2
Forage yield (tons/ fed⁻¹)								
Pearl millet	19.26	1.14	0.376	0.14	1.41	1.94	0.41**	6.24**
Fodder maize	13.36	0.41	0.094	-0.60	0.25	8.48	2.09**	0.84
Sudan grass	18.86	1.29*	0.131	0.30	0.47	2.51	0.56**	7.81**
TxM W106	23.70#	1.02	0.496**	0.02	1.87	2.00	0.43**	5.16**
TxM Y202-A	23.48#	0.95	0.085	-0.05	0.33	0.41	0.02	4.20
TxM hytech 2031	18.29	0.67	0.197	-0.33	0.72	3.26	0.75**	2.25
TxM pioneer 30K8	18.42	1.14	0.355 **	0.14	1.34	1.87	0.39**	6.26**
TxM Pioneer 3444	23.88#	1.26*	0.327 **	0.26	1.22	2.88	0.65**	7.58**
TxM Giza 168	22.43#	1.13	0.185	0.13	0.70	1.13	0.20**	6.01**
Mean	20.19	1.00		0.00			0.61	
Dry matter (tons/ fed)								
Pearl millet	4.75#	1.54**	0.205*	0.55	8.82	1.86	0.46**	1.83**
Fodder maize	3.68	0.61	0.017	-0.40	0.68	0.61	0.14**	0.27
Sudan grass	5.11#	1.17	0.083	0.18	3.59	0.44	0.09**	1.03**
TxM W106	5.57#	0.88	0.070	-0.13	3.04	0.33	0.07**	0.59
TxM Y202-A	4.38	0.66	0.040	-0.34	1.68	0.56	0.13**	0.34
TxM hytech 2031	4.22	0.75	0.045	-0.25	1.96	0.40	0.09**	0.43
TxM pioneer 30K8	4.41	0.99	0.014	-0.01	0.60	0.06	0.00	0.70
TxM Pioneer 3444	5.06#	1.30*	0.004	0.31	0.12	0.34	0.07*	1.19**
TxM Giza 168	4.63	1.09	0.060	0.09	2.61	0.27	0.05*	0.88*
Mean	4.65	1.00		0.00			0.12	

Regression coefficients for fresh and dry matter yields, ranged from 0.41 to 1.29 and 0.61 to 1.54, respectively. The Eberhart and Russell model shows that genotypes already behaved differentially to environmental changes. With the exception of Sudan grass and TxM Pioneer 3444 for fresh yield and Pearl millet and TxM Pioneer 3444 for dry matter, the values of regression coefficient (b) did not substantially deviate from one for any of the genotypes that were evaluated. For all genotypes with the exception of three genotypes (TxM W106, TxM Pioneer 30K8, and TxM Pioneer 3444) for fresh yield and Pearl millet for dry matter, the values of deviation from regression (S^2d) were substantially different from zero. It is evident that both genotypes TxM Y202-A, TxM for fresh and dry matter yield, respectively, pioneer 30K8 exhibited values of b and S^2d that did not substantially deviate from unity and zero. Also, their average performance was higher than the average of all genotypes. In light of this, the genotypes mentioned were regarded as phenotypically stable under the Eberhart & Russell (1966) model. On the other hand, as the genotype TxM Giza 168 had b values that were much higher than unity and their yields were higher than the average forage fresh yield, they would be well-suited for high yielding settings. The estimations genotypic stability as defined by Tai (1971) are shown in Table 4 and visually shown in Figs 1 and 2. The findings showed that whereas genotypes TxM hytech 2031 for fresh yield and TxM Y202-A and TxM hytech 2031 for dry matter yield exhibited degrees of above average stability, genotypes TxM W106 for fresh yield and TxM pioneer 30K8 for dry matter yield were found in the average stability range. Fortunately, the fresh and dry matter of TxM Y202-A exceeded the mean of all genotypes. Thus, the area where it hit the upper confidence limit of was extremely near to becoming steady. For the other genotypes, when their values were considerably more than unity, as shown in Figs 1 and 2, the unexpected component of the GxE interaction was more significant than the predictable component. Due to the novelty of the topic, there are no references for comparisons of the stability of different summer forage crops.
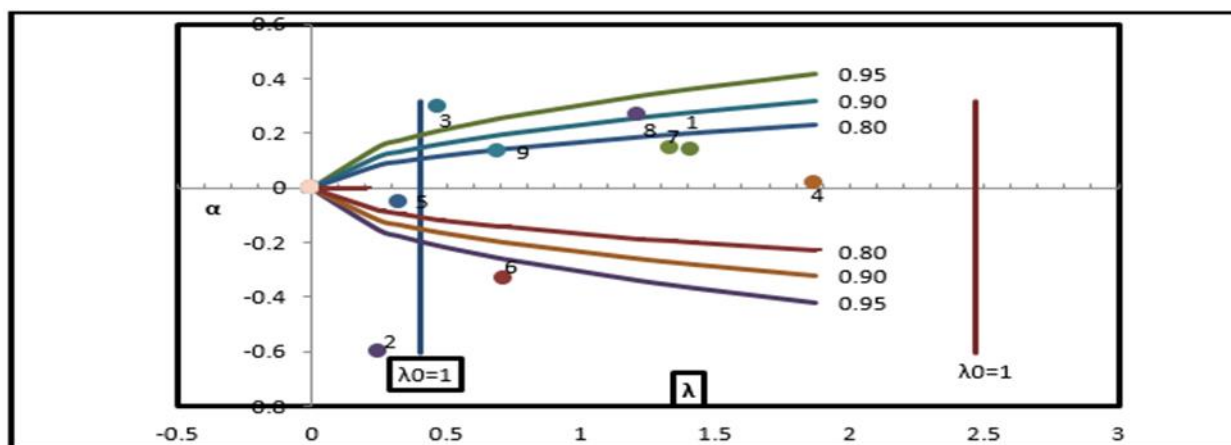
Fig .1. Distribution of genotypic stability statistics for forage fresh yield (ton fed⁻¹).
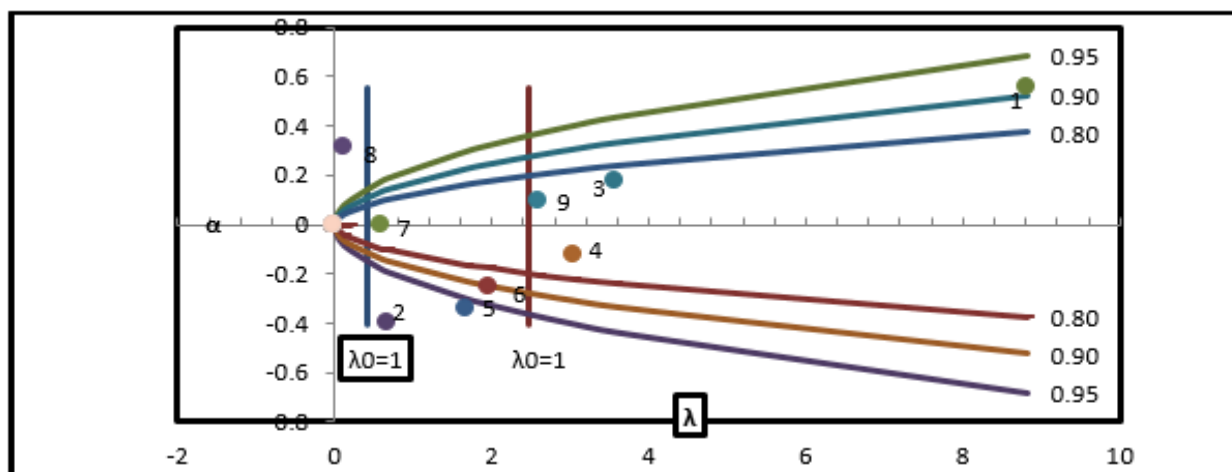
Fig .2. Distribution of genotypic stability statistics for dry matter (ton fed^{-1}).

Using the stability models developed by Wricke (1962) and Shukla, similar stability case findings were observed (1972). The findings showed that only the TxM Y202-A genotype for fresh yield and the TxM pioneer 30K8 for dry matter were determined to be the most stable, with the genotype having the lowest eco-valence statistic W2 and the least significant values of 2 and S^2. Due to their high W2 values and highly significant values of 2, the remaining genotypes were unstable. The analyzed S^2 values demonstrated that the aforementioned genotypes continued to be unstable even when the linear component of the environmental influence (as a covariate) was eliminated.

The results of combined analysis for days to fresh forage yield and dry matter yield was significantly affected by environment changes, genotype and genotype x environment interaction which accounted for 22.04%, 11.07% and 32.58% for forage fresh yield of the total (G + E + G x E interaction) variation, meanwhile, the proportion of mean squares reached 50.82%, 31.54% and 6.89% for dry matter yield, in the order already aforementioned (Table 5) and showed the effect of changes in environments on fresh and dry matter performance of the evaluated genotypes. Other invesigators reported GxE interactions for different summer crops like, Kanfany, *et al.* (2021) reported that rice grain yield was significantly affected by environment, genotype × environment (G × E) interaction and genotype and there explained 67.9%, 23.6% and 8.5% of the total variability, respectively. Bose *et al.* (2017) tested 17 rice genotypes over four environments. AMMI analysis of variance revealed that 74.67% of the total variation was attributable to the genotypes (G), 13.60% to the environments (E) and approximately 11.73% to GE interaction effects. According to Bose *et al.* (2014), the GGE biplot method demonstrated that the first two principal components regression model account for 96.15% of the variance (76.04% for PCA 1 and 20.11% for PCA2), and its graph was plotted to show which genotypes performed better and to determine how environments interact.

A huge amount of environmental squares revealed that the variations in forage fresh and dry matter yield were responsible for the diverse environments' significant differences in environmental means. There was a significant variation in genotypic response between environments, as evidenced by the quantum of the G x E interaction sum of squares being 1.47 times bigger than for genotypes approved for forage fresh yield. According to Mostafavi *et al.* (2014),

the G x E interaction was highly significant. Sabaghnia *et al.* (2008) illustrated the significance of application-direct GEl analysis as it relates to genotype performance and testing environment categorization.

Table 5. Combined analysis of variation for fresh and dry yield fed^{-1} **of nine genotypes across the studied six environments according to GGE biplot method.**

SOV	DF	Forage yield (tons/ fed^{-1})			Dry matter (tons/ fed)		
		SS	Ms	SS%	SS	MS	SS%
E	5	558.89	111.78	11.07	103.02	20.60	31.54
G	8	1112.50	139.06	22.04	166.03	20.75	50.82
GXE	40	1644.62	41.12	32.58	22.49	0.56	6.89
PCI	12	1019.09	84.92	20.19	19.76	1.65	6.05
PC2	10	594.72	59.47	11.78	2.00	0.20	0.61
PC3	8	25.30	3.16	0.50	0.72	0.09	0.22
PC4	6	5.52	0.92	0.11	0.01	0.00	0.00
PC5	4	0.00	0.00	0.00	0.00	0.00	0.00
PC6	2	0.00	0.00	0.00	0.00	0.00	0.00
Residuals	108	87.09	0.81	1.73	12.64	0.12	3.87

**= Significant at the 0.01 level.

The GGE biplot model accounts for 85.34% of the overall variation in the standardized data, with 62.65% and 22.69% of the variance for forage fresh yield being accounted for by the first and second principal components, respectively. For the dry matter yield, PC1 and PC2 are responsible for 95.86% and 2.92%, respectively, of the total variances of the standardized data. The variation for overall variability is substantially proportionate (36.22% for fresh yield and 3.05% for dry matter yield), reflecting the intricacy of the interaction between genotypes and environment.

GGE biplot analyses represent high and low and staple genotypes for fresh yield

Regarding, fresh yield, the mean values of the 9 forage genotypes ranged from 12.93 ton for fodder maize in E0 (0N in the first season) to 27.20 day for the genotype T x M pioneer 3444 in E3 (100N in the first season) (Table 3).

Moreover, the significance and high genotypes were detected by T x M Pioneer 3444and T x M W106 in E1; T x M Pioneer 3444 in E2; T x M W106, T x M Y202-A and T x M Pioneer 3444 in E3; T x M W106, T x M Y202-A, T x M Pioneer 3444 in E4; T x M Y202-A , T x M W106, T x M Pioneer 3444, and T x M Giza 168 in E5; T x M Pioneer 3444, T x M W106 and T x M Y202-A in E6

However, the low yield genotypes were exhibited by genotype fodder maize in all studied environments. GGE biplot analysis Figures 3 and 4 shows the ranking of 9 genotypes base on their mean values and stability.

In this fig. 3, the top two PCs (PC1=62.65%, PC2=22.69%) explained 85.43% of the total GGE variance in the data. It was noted that PC2 must approximate the GE effects connected to each genotype, which is a measure of instability, if PC1 of a GGE bi-plot approximately approximates the genotype main effects (mean performance) (Yan *et al*., 2000; Yan 2007). The average environment coordinate (AEC) axis, which is determined by the average PC1 and PC2 scores across all environments, is the line that connects the bi-plot origin with the average environment denoted by the circle. Hence, projection of genotype markers onto this axis should roughly represent the genotypes' mean yield. Thus, the G2 (fodder maize) have the lowest values for fresh yield, Meanwhile the highest values were detected by genotypes G4 and G8. The process of genotype stability (fig 4) is depicted by the line with two arrows that runs through the origin and perpendicular to the AEC. On this axis, movement in either direction away from the bi-plot origin denotes more G–E interaction and decreased stability (Yan, 2007). As a result, G5, and G2, which are located close to the top of the bi-plot, are less stable and changeable than other genotypes (Fig. 4). Genotypes 1 and 4, which were towards the bottom and close to the AEC abscissa, had higher fresh yield and were more stable than the other genotypes. Because they had the best fresh mean performance and were completely stable, the two genotypes (1 and 4) constituted an optimum genotype for fresh production. All results obtained from the GGE biplot analysis are largely identical to what was mentioned in the results of the mean performance.

GGE biplot analyses represent high and low and staple genotypes for dry matter

Regarding, dry matter, the mean values of the 9 forage genotypes ranged from 2.96 ton for fodder maize in E4 (0N in the second season) to 5.95 day for the genotype T x M w106 in E6 (100N in the second season) (Table 3). Moreover, the significance and high genotypes were detected by T x M

W106 in E1; T x M W106 and T x M Pioneer 3444 in E2; Pearl millet, Sudan grass, T x M W106, and T x M Pioneer 3444 in E3 ;, T x M W106 in E4 ; Sudan grass, T x M W106 and T x M Pioneer 3444 in E5; Pearl millet, Sudan grass, T x M W106 and T x M Pioneer 3444 in E6.

However, the low dry matter yield genotypes were exhibited by genotype fodder maize in all studied environments. GGE biplot analysis Figures 5 and 6 shows the ranking of 9 genotypes base on their mean values and stability.

In this fig. 5, the top two PCs (PC1=95.86%, PC2=2.92%) explained 98.35% of the total GGE variance in the data. It was noted that PC2 must approximate the GE effects connected to each genotype, which is a measure of instability, if PC1 of a GGE bi-plot approximately approximates the genotype main effects (mean performance) (Yan *et al*., 2000; Yan 2007). The average environment coordinate (AEC) axis, which is determined by the average PC1 and PC2 scores across all environments, is the line that connects the bi-plot origin with the average environment denoted by the circle. Hence, projection of genotype markers onto this axis should roughly represent the genotypes' mean yield. Thus, the G2 (fodder maize) followed by G6, G7 and G9 have the lowest values for dry matter yield; Meanwhile the highest values were detected by genotypes G4 and G1 (fig. 5).The line which passes through the origin and is perpendicular to the AEC with double arrows represents the process of stability genotypes. Either direction away from the bi-plot origin, on this axis, indicates greater G×E interaction and reduced stability (Yan, 2007). Therefore, G2 and G9 near the top of the bi-plot are more variable and less stable than others genotypes (fig. 6). Genotypes 4 near the bottom and placed close to the AEC abscissa, were more stable than others and higher fresh yield. Therefore, the genotypes 4 represented an ideal genotype in dry matter yield because it have the highest fresh mean performance and be absolutely stable. All results obtained from the GGE biplot analysis are largely identical to what was mentioned in the results of the mean performance.
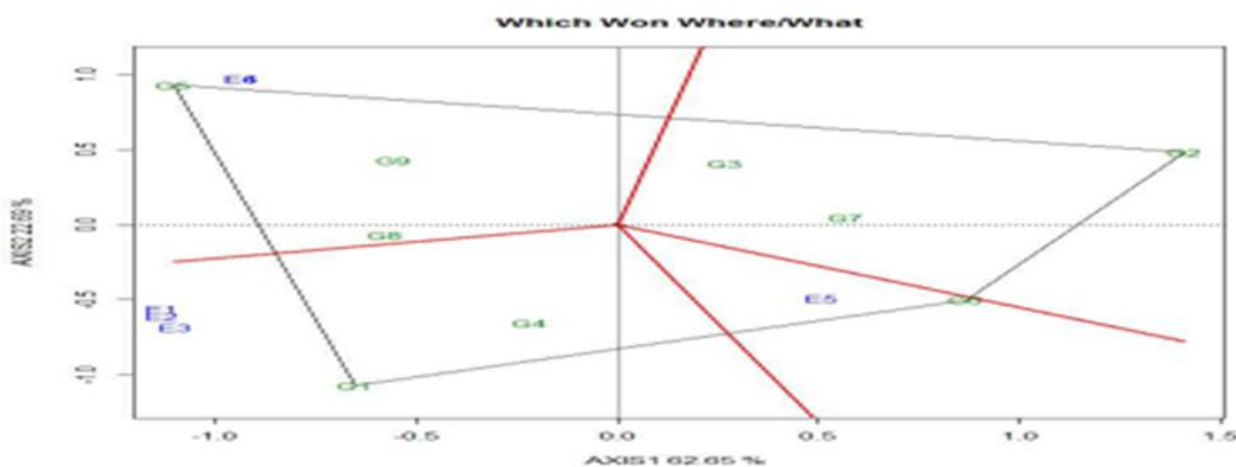
Fig. 3. Polygon view of the GGE bi-plot show the "which-won-where pattern" The GGE bi-plot based on the 9 foder genotypes forage fresh yield performance experiment for 6 environments. The 6 environments in E letter and number (E1 –E6). The genotypes G1= Pearl millet, G2= Fodder maize, G3= Sudan grass, G4= TxM W106, G5 =TxM Y202-A G6= TxM hytech 2031, , G7=TxM pioneer 30K8, G8= TxM Pioneer 3444and G9= TxM Giza 168.
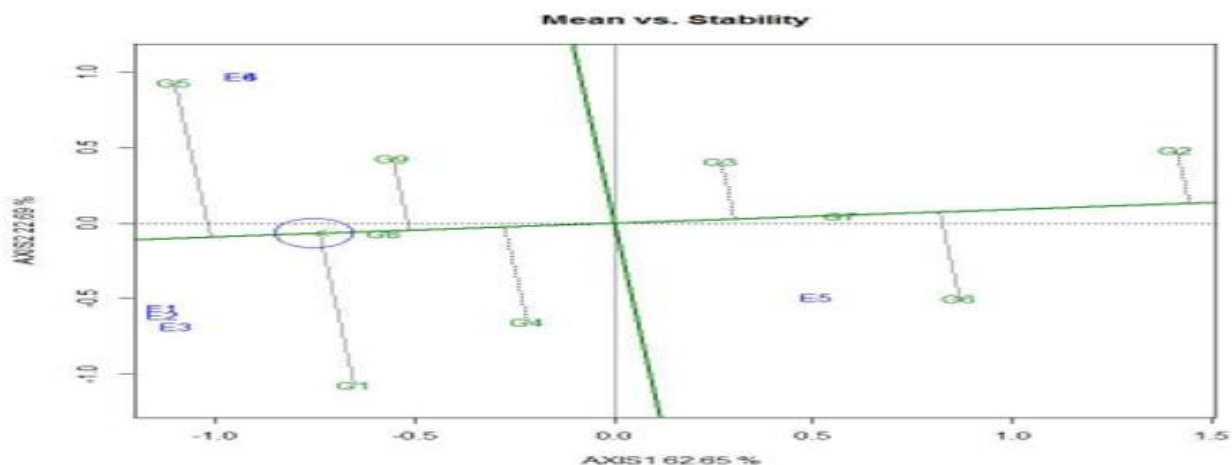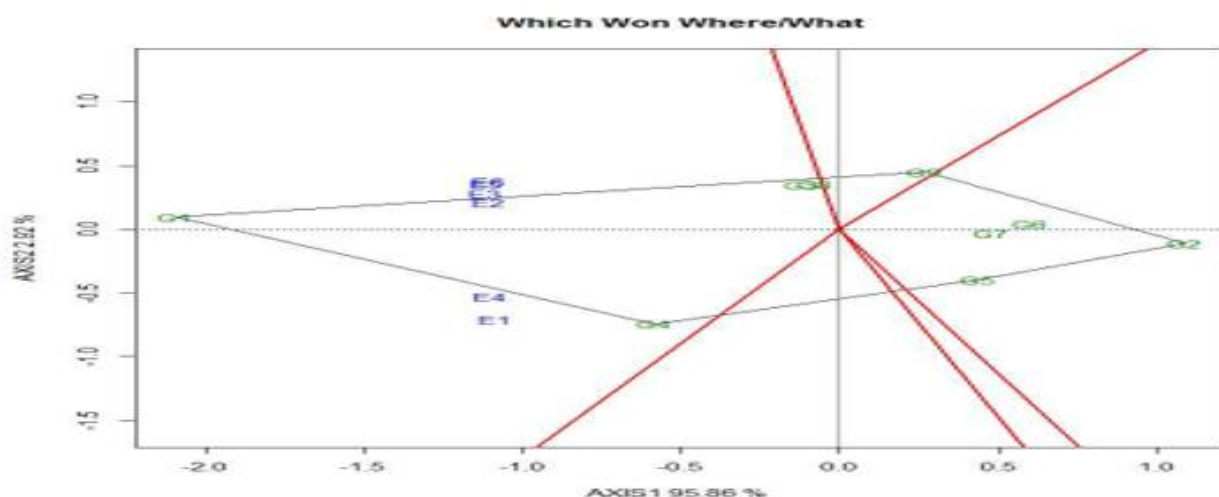
Fig. 4. Average-environment coordinate (AEC) view of the GGE bi-plot for Ranking of 9 genotypes based on mean and stability. The 6 environments in E letter and number (E1 –E6). The genotypes G1= Pearl millet, G2= Fodder maize, G3= Sudan grass, G4= TxM W106, G5 =TxM Y202-A G6= TxM hytech 2031, , G7=TxM pioneer 30K8, G8= TxM Pioneer 3444and G9= TxM Giza 168.

Fig. 5. Polygon view of the GGE bi-plot show the "which-won-where pattern" The GGE bi-plot based on the 9 fodder genotypes forage yield performance experiment for 6 environments. The 6 environments in E letter and number (E1 –E6). The genotypes G1= Pearl millet, G2= Fodder maize, G3= Sudan grass, G4= TxM W106, G5 =TxM Y202-A G6= TxM hytech 2031, , G7=TxM pioneer 30K8, G8= TxM Pioneer 3444and G9= TxM Giza 168.
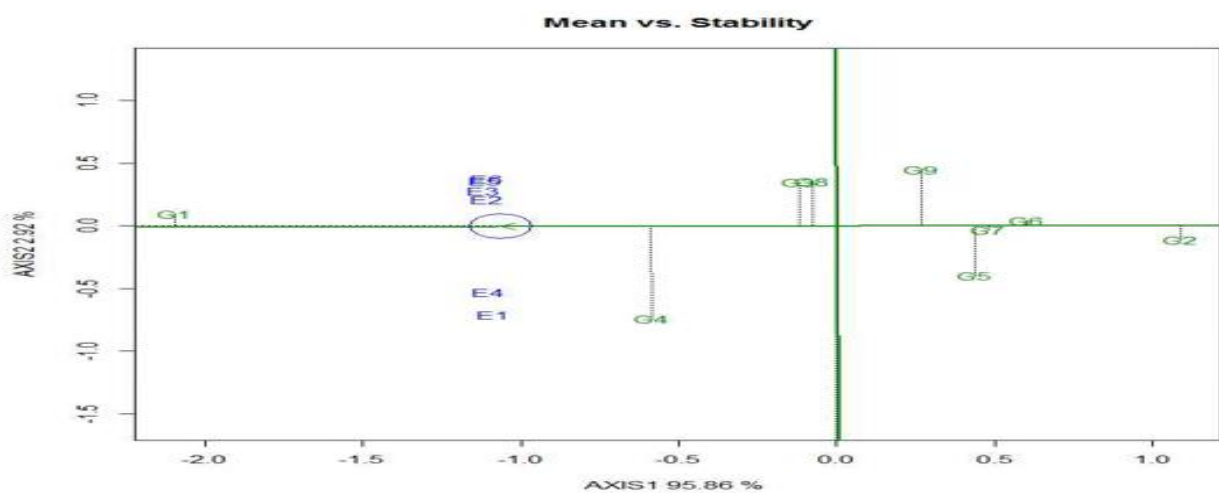

Fig. 6. Average-environment coordinate (AEC) view of the GGE bi-plot for Ranking of 9 genotypes based on mean and stability, The 6 environments in E letter and number (E1 –E6). The genotypes G1= Pearl millet, G2= Fodder maize, G3= Sudan grass, G4= TxM W106, G5 =TxM Y202-A G6= TxM hytech 2031, , G7=TxM pioneer 30K8, G8= TxM Pioneer 3444and G9= TxM Giza 168.

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استخدام نماذج إحصائية و رسومية مختلفة لتحليل ثبات أنواع مختلفة من الأعلاف الصيفية

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قسم المحاصيل بكلية الزراعة جامعة بنها

الملخص

يهتم مربى النبات بتقدير تفاعل البيئة مع الوراثة لأن التفاعل يمكن أن يقلل بشكل كبير من مكاسب الانتخاب ويجعل من الصعب تحديد التراكيب الوراثية المتفوقة في البيئات المختلفة. وكمحاولة لحل مشكلة قلة الاعلاف الصيفية في مصر، تم تقييم تسعة تراكيب وراثية (ستة تراكيب وراثية ناتجة من تهجين الذرة الشامية بالريانة و هي maize (M)- (T) 106 (W) (TxM) ، TxM 202-A، TxM Hytech 2031، TxM Pioneer 30k8 (W) ، TxM Pioneer 3444 (Y)، TxM SC Giza 168 و تم تقييم الدخن والدراوة و حشيشة السودان) تحت ثلاثة مستويات من النيتروجين (0، 50، 100 كجم نيتروجين / فدان) خلال الموسمين الصيفيين 2021 و 2022. لتقييم أداء محصول العلف، وتحديد حجم التفاعل (G × E) وتحديد الثبات المستمد من تحليلات الانحدار والتباين بالإضافة إلى استخدام التحليل البياني، أظهرت الهجن الريانة x بيونير 3444 و الريانة x السلالة 106 و الريانة x السلالة 202 زيادة معنوية في إنتاجية المادة الطازجة والجافة تليها حشيشة السودان ثم الدخن. تم العثور على قيم منخفضة لـ S²d وقيمة b حول الواحد مع محصول عالي على المتوسط بواسطة الريانة x السلالة 202 ، الريانة x بيونير 3444 للمحصول الطازج والدخن للمادة الجافة. أكد التحليل البياني للنتائج المذكورة أعلاه أن الدراوه لديها أقل القيم للمحصول الطازج ، بينما أعلى القيم سجلت بواسطة التركيب الوراثي الريانة x السلالة 106 و الريانة x بيونير 3444 لإنتاج الأعلاف الطازجة والجافة.