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Eberhart and Russell Approach of Genotype Environment Interaction for Yield and Quality Traits in Forage Legume - Hedge Lucerne (*Desmanthus virgatus* (L.) Willd.)

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Abstract

The present work 'Eberhart and Russell approach of Genotype - Environment interaction for yield and quality traits in forage legume-Hedge Lucerne (*Desmanthus virgatus* (L.) Willd.)' was carried out across four locations in Kerala viz., College of Agriculture, Vellayani, College of Horticulture, Thrissur, Krishi Vigyan Kendra, Kottarakkara and Regional Agricultural Research Station, Ambalavayal, Wayanad during 2017-2018 with an objective to identify stable genotypes of *Desmanthus virgatus* in varied environments with respect to yield and quality. Eberhart and Russell model (1966) was used to analyze the stability and adaptability of yield and yield related characters of these genotypes. Based on the environmental indices, COA, Vellayani and RARS, Ambalavayal was found most favourable for all of the characters. Stability analysis revealed that the genotypes T₁ (IC 345276), T₄ (IC 261839), T₆ (IC 421199) and T₇ (TNDV 1) were stable over the four different locations.

Key words: Stability analysis, Gx E interaction, Environmental indices, Hedge lucerne

Introduction

The phenotypic expression of a character is influenced by the genotype and environmental factors. The correlation between genotype and phenotype get reduced in the presence of G x E interaction which makes it difficult to assess the genetic potential of a particular genotype whose relative ranking will be altered in different environments. This forges need to determine G x E magnitude in varying environments to identify the stable genotypes. Several methods were proposed to analyze Gx E interaction and to determine the stability in performance of genotypes (Becker and Leon, 1988).

The linear regression model proposed by Eberhart and Russell (1966) is the most commonly used method for analysis of genotype x environment interaction.

Development of improved varieties showing stable performance across wide environmental conditions is a necessity to increase the productivity. *Desmanthus virgatus* commonly known as hedge lucerne is a perennial shrub legume belonging to the family *Fabaceae* and subfamily *Mimosoideae*. It is a native of tropics and subtropics of new world. The fodder can be safely fed to ruminants and non ruminants as it is palatable, aggressive, persistent and tolerant to grazing. It contains high condensed tannins and is devoid of toxicants like mimosine.

Currently, there is a need to develop and identify hedge lucerne genotypes with higher yield potential.

Objective

The present investigation was conducted across four locations in Kerala to study the genotype x environment interaction in hedge lucerne for yield, quality and identifying the stable genotypes.

Materials and methods

The field experiment was conducted at four locations of Kerala to determine the stability of eight genotypes of *Desmanthus virgatus* for yield and its component traits. The eight genotypes of hedge lucerne viz., T₁ (IC 345276), T₂ (IC 343710), T₃ (IC 89910), T₄ (IC 261839), T₅ (IC 90934), T₆ (IC 421199), T₇ (TNDV 1) and T₈ (Thumburmuzhi local) were evaluated in a Randomized Block Design (RBD) with four replications over four locations during 2017-2018. The spacing of 50 cm between the rows and continuous line sowing with a plot size of 3 m x 1 m was followed in the field experiment. The observations were recorded on the characters such as plant height, number of branches, length of branches, number of leaves per plant, leaf to stem ratio, number of pods per plant, green fodder yield, dry matter production, crude protein and crude fibre content during the 90 (first cut), 140 (second cut), 190 (third cut) and 240 (fourth cut) DAS (Days After Sowing).

SPAR 2.0 software was used to analyze the stability using Eberhart and Russell model.

Results and Discussion

The analysis of variance showed significant differences among the eight hedge Lucerne genotypes for yield and its component characters studied across four environments (Table 5.1). The pooled analysis of variance revealed that the genotypes, G x E interactions was significant for all the characters studied. As the G x E interactions was significant for all the characters, further analysis was done for estimating the stability parameters (Table 5.2). The total sum of squares is partitioned into genotypes, Environments + (Genotype x Environment) and pooled error in the ANOVA. The mean squares due to E+(G x E) were significant for the characters green fodder yield, dry matter production, crude protein and crude fibre content prioritizing the presence of G x E interaction for these traits. The mean sum of squares due to genotype was significant for the characters under study (Table 5.3). The sum of squares due to E+ (G x E) was further partitioned into that of Environment (Linear), Genotype x Environment linear and pooled deviation (Table 5.3).

The linear component of Environment was significant for the characters like green fodder yield, dry matter production, crude protein and crude fibre content. The variation due to G x E (linear) were significant for the characters green fodder yield and dry fodder yield. The non linear component and pooled deviation were significant for the character dry matter production indicating the importance of both linear and non linear components. Similar findings were also reported by Palathingal (2003) in rice, Bikash *et al.* (2013) in pearl millet, Preeti *et al.* (2016) in wheat, Mehraj *et al.* (2017) in oats and Patil *et al.* (2017) in okra. It was found that Vellayani was favourable for all of the characters whereas Thrissur was unfavourable for all the characters based on the environmental indices calculated (Table 5.4).

Eberhart and Russell model (1966) considered three stability parameters like (i) mean performance (μ), (ii) regression coefficient (b_i) and (iii) deviation from regression (S^2_{di}). Linear component of G x E interaction is measured by using b_i value and also gives an idea about response of genotype. G x E interaction of unpredictable type (*i.e.*, predictable or unpredictable type) is measured from S^2_{di} value.

The result interpretation of present study was done by using the parameters like regression coefficient, mean value and deviation from regression for stability. Once the genotypes were found to be stable based on non-significant deviation from regression ($S^2_{di}=0$), then the type of stability was based on regression coefficient and mean value. If b_i is equal to unity, a genotype is considered as stable or has the same performance in all the environment, if b_i is more than unity, it is considered to have less than average stability or good performance in favourable environments and if b_i is less than unity, it is suggested to have above average stability or good performance under unfavourable environments.

Mean performance and stability parameters for yield and its component traits in hedge lucerne over four locations (Table 5.5):

Plant height

The maximum plant height was observed for the genotype T₈ (116.75 cm) followed by T₁ (112.87 cm) and the lowest was observed for the genotype T₃ (71.03 cm).

Among the genotypes, T₁ genotype ($\mu=112.87$, $b_i=1.07$, $S^2_{di}=0.30$) and the genotype T₆ ($\mu=110.31$, $b_i=0.89$, $S^2_{di}=-0.32$) were identified as stable ones with regression coefficient near unity and non-significant deviation from regression. The genotypes T₂, T₃ and T₄ recorded b_i value more than one (1.41, 1.46, 1.75 respectively) with non-significant minimum deviation from the regression (0.56, 3.11, 2.11 respectively). The genotypes T₅ and T₈ recorded b_i value of 0.75 and 0.58 with non-significant deviation from regression -0.21 and 1.44 respectively. Similar results were observed by Saranya (2016) in neelamari, Preeti *et al.* (2016) in wheat, Patil *et al.* (2017) in oats.

Table 5.1: Analysis of variance (mean square) for individual locations

Table 5.1.1: Location-I (COA, Vellayani)

Source of variation	df	Plant height (cm)	Number of branches plant ⁻¹	Length of branches plant ⁻¹ (cm)	Number of leaves plant ⁻¹	Leaf to stem ratio	Number of pods cluster ⁻¹	Green fodder yield (g)	Dry matter production (g)	Crude protein (%)	Crude fibre (%)
Replication	3	3.48	0.21	2.73	3.16	0.0035	0.0067	37.45	0.26	3.07	2.36
Genotypes	7	973.25**	26.21**	1226.21**	1138.22**	0.032**	3.68**	340.78**	78.79**	84.53**	28.79**
Error	21	1.81	0.59	0.18	6.29	0.0028	0.84	8.66	0.07	0.26	1.01

Table 5.1.2: Location-II (KVK, Kottarakkara)

Source of variation	df	Plant height (cm)	Number of branches plant ⁻¹	Length of branches plant ⁻¹ (cm)	Number of leaves plant ⁻¹	Leaf to stem ratio	Number of pods cluster ⁻¹	Green fodder yield (g)	Dry matter production (g)	Crude protein (%)	Crude fibre (%)
Replication	3	1.16	1.48	2.55	14.80	0.0094	0.0056	21.81	0.03	0.34	2.99
Genotypes	7	1075.01**	29.20**	1184.41**	1274.32**	0.034**	3.07**	259.97**	120.02**	76.98**	34.25**
Error	21	1.11	0.45	0.17	19.99	0.0011	0.0071	19.17	0.15	0.26	0.57

** Significant at 1%, * Significant at 5%

Table 5.1.3: Location-III (COH, Thrissur)

Source of variation	df	Plant height (cm)	Number of branches plant ⁻¹	Length of branches plant ⁻¹ (cm)	Number of leaves plant ⁻¹	Leaf to stem ratio	Number of pods cluster ⁻¹	Green fodder yield (g)	Dry matter production (g)	Crude protein (%)	Crude fibre (%)
Replication	3	0.87	0.95	0.28	7.27	0.0027	0.035	8.52	0.27	0.24	0.16
Genotypes	7	1054.30**	31.30**	1155.50**	1502.46**	0.044**	3.04**	398.24**	93.07**	81.96**	26.65**
Error	21	1.03	0.21	0.20	12.39	0.0016	0.046	9.27	0.15	0.13	0.11

Table 5.1.4: Location-IV (RARS, Ambalavayal)

Source of variation	df	Plant height (cm)	Number of branches plant ⁻¹	Length of branches plant ⁻¹ (cm)	Number of leaves of plant ⁻¹	Leaf to stem ratio	Number of pods cluster ⁻¹	Green fodder yield (g)	Dry matter production (g)	Crude protein (%)	Crude fibre (%)
Replication	3	1.22	0.43	0.30	3.74	0.0016	0.02	2.41	1.68	0.47	0.15
Genotypes	7	893.12**	22.08**	1242.09**	1026.62**	0.031**	2.89**	308.83**	84.41**	90.13**	27.71**
Error	21	1.08	0.38	0.43	16.56	0.0016	0.01	8.72	0.45	0.35	0.33

** Significant at 1%, * Significant at 5%

Source of variation	df	Plant height (cm)	Number of branches plant ⁻¹	Length of branches plant ⁻¹ (cm)	Number of leaves of plant ⁻¹	Leaf to stem ratio	Number of pods cluster ⁻¹	Green fodder yield (g)	Dry matter production (g)	Crude protein (%)	Crude fibre (%)
Genotypes	7	3946.99**	105.44**	4781.32**	4494.68**	0.13**	12.38**	1145.58**	357.00**	331.14**	114.93**
Environment	3	285.86**	20.33**	14.26**	468.87**	0.03**	0.50**	249.09**	152.39**	56.74**	51.39**
G x E interaction	21	16.23**	1.12**	8.96**	148.98**	0.004**	0.09**	54.08**	6.43**	0.82**	0.82**
Error	96	1.31	0.46	0.40	12.99	0.0021	0.02	12.21	0.25	0.35	0.62

** Significant at 1%, * Significant at 5%

Table 5.2: Pooled Analysis of Variance (mean square) for yield and its component traits of hedge lucerne over four locations

Table 5.3: Analysis of Variance (mean square) for mean data of yield and its component traits of hedge lucerne over four locations

Source of variations	df	Plant height (cm)	Number of branches plant ⁻¹	Length of branches plant ⁻¹ (cm)	Number of leaves plant ⁻¹	Leaf to stem ratio	Number of pods cluster ⁻¹	Green fodder yield (g)	Dry matter production (g)	Crude protein (%)	Crude fibre (%)
Genotypes	7	986.74**	26.36**	1195.33**	1123.67**	0.0321**	3.09**	286.39**	89.25**	82.78**	28.73**
E+ (G x E)	24	12.48**	0.88**	2.41	47.24*	0.0012	0.04	19.61*	6.17**	1.95**	1.79**
Environments	3	71.46**	5.08**	3.56	117.22**	0.0017	0.13**	62.27**	38.09**	14.18**	12.84**
Environments (Lin)	1	214.39**	15.25**	10.70*	351.65**	0.0185**	0.37**	186.82**	114.29**	42.55**	38.54**
G x E(Lin)	7	7.88**	0.56**	2.78	63.53*	0.0015**	0.03	32.80**	2.15	0.27	0.38
Pooled deviation	16	1.87	0.12	1.72**	21.08**	0.0007	0.02	3.39	1.17**	0.15	0.10
Pooled error	96	1.31	0.11	0.40	3.25	0.0005	0.02	3.05	0.25	0.35	0.62
Total	31	232.48	6.63	271.78	290.31	0.0085	0.73	79.86	24.93	20.21	7.87

** Significant at 1%, * Significant at 5%

Table 5.4: Estimates of environmental indices (I_j) for each character of hedge lucerne under different locations

Sl. No.	Characters	Vellayani	Kottarakkara	Thrissur	Ambalavayal
1.	Plant height (cm)	2.28	-0.52	-4.03	2.26
2.	Number of branches	0.56	-0.20	-1.04	0.68
3.	Length of branches (cm)	0.47	0.08	-0.96	0.44
4.	Number of leaves	0.40	4.62	-4.73	0.27
5.	Leaf to stem ratio	0.85	-0.01	-0.03	0.03

6.	Number of pods	0.15	0.63	-0.12	0.04
7.	Green fodder yield (g)	2.36	-0.66	-3.68	1.95
8.	Dry matter production (g)	2.22	-0.21	-2.91	0.91
9.	Crude protein (%)	1.34	-0.03	-1.81	0.49
10.	Crude fibre (%)	1.26	-0.10	-1.70	0.58

Table 5.5: Mean performance and stability parameters for yield and its component traits in hedge lucerne over four locations

Genotype	Plant height (cm)			Number of branches			Length of branches (cm)			Number of leaves		
	Mean	b _i	S ² _{di}	Mean	b _i	S ² _{di}	Mean	b _i	S ² _{di}	Mean	b _i	S ² _{di}
T ₁	112.87	1.07	0.30	5.10	1.10	-0.09	22.96	0.62	0.05	145.03	0.58	-2.56
T ₂	86.81	1.41	0.56	6.40	1.58	0.11	34.78	3.31	4.60**	119.66	3.91	70.07**
T ₃	71.03	1.46	3.11	10.31	1.30	-0.04	35.53	-1.7	5.77**	99.69	0.86	31.00
T ₄	94.53	1.75	2.11	4.29	1.05	-0.03	54.49	1.12	0.92	124.86	0.66	16.47
T ₅	101.10	0.75	-0.21	6.29	0.92	-0.10	62.49	2.09	1.48*	139.84	0.06	26.98
T ₆	110.31	0.89	-0.32	4.56	1.42	-0.02	47.66	1.05	-0.02	141.04	0.82	1.41
T ₇	86.56	0.10	5.37	3.98	0.78	0.08	33.41	0.29	0.26	112.17	0.46	-2.03
T ₈	116.75	0.56	1.44	10.34	-0.17	0.14	74.65	1.21	-0.09	143.33	0.66	1.39
Grand mean	97.49			6.41			45.75			128.20		

** Significant at 1%, * Significant at 5%

Table 5.5: continued

Genotype	Leaf to stem ratio				Number of pods				Green fodder yield (g)				Dry matter production (g)			
	Mean	b _i	S ² _{di}	Mean	b _i	S ² _{di}	Mean	b _i	Mean	b _i	S ² _{di}	Mean	b _i	Mean	b _i	S ² _{di}
T ₁	0.89	0.75	0.0005	1.51	2.12	0.011	112.35	1.12	39.93	0.97	-0.62	0.09	0.97	0.09		
T ₂	0.71	2.52	-0.0004	1.58	0.24	0.001	101.28	1.34	32.62	0.99	-0.30	0.98*	0.99	0.98*		
T ₃	0.92	-0.17	-0.0002	1.43	1.30	0.019	90.45	2.38	28.89	1.50	-2.55	1.13*	1.50	1.13*		
T ₄	0.76	1.09	0.0004	2.77	1.79	0.056*	100.67	1.74	37.59	0.94	0.001	1.04*	0.94	1.04*		
T ₅	0.67	0.37	-0.0004	2.14	1.23	-0.003	98.75	-1.45	31.37	0.70	9.20	0.71*	0.70	0.71*		
T ₆	0.88	1.56	0.000	0.00	0.00	-0.005	110.48	1.26	40.62	1.34	-2.54	0.47	1.34	0.47		
T ₇	0.84	1.18	0.0007	2.52	0.89	0.015	109.02	0.07	40.32	0.27	1.15	3.95**	0.27	3.95**		
T ₈	0.83	0.68	0.0008	2.38	0.42	0.031	115.42	1.52	40.04	1.25	-1.61	0.49	1.25	0.49		
Grand mean	0.81			1.79			104.93		36.42							

** Significant at 1%, * Significant at 5%

Table 5.5: continued

Genotype	Crude protein (%)			Crude fibre (%)		
	Mean	b_i	S^2_{di}	Mean	b_i	S^2_{di}
T ₁	21.38	1.42	0.02	23.35	0.97	0.098
T ₂	15.51	0.92	0.29	22.71	1.26	0.004
T ₃	14.59	1.21	-0.08	26.83	1.41	-0.139
T ₄	13.12	0.97	0.01	23.59	0.45	-0.143
T ₅	13.91	0.69	0.02	28.21	0.96	0.054
T ₆	20.26	0.89	-0.01	24.06	0.95	-0.116
T ₇	23.48	0.95	0.32	27.44	1.09	-0.027
T ₈	24.39	0.91	-0.06	29.95	0.89	-0.145
Grand mean	18.34			25.77		

** Significant at 1%, * Significant at 5%

Number of branches per plant

The number of branches ranged from 4.29 (T₄) to 10.34 (T₈). The genotype T₁ ($\mu = 5.10$, $b_i = 1.10$, $S^2_{di} = -0.09$), T₄ ($\mu = 4.29$, $b_i = 1.05$, $S^2_{di} = -0.03$) and genotype T₅ ($\mu = 6.29$, $b_i = 0.92$, $S^2_{di} = -0.10$) recorded near unit regression with minimum non-significant deviation from regression. These genotypes were stable for different environments. The genotypes T₂, T₃ and T₆ showed b_i value more than one (1.58, 1.30 and 1.42 respectively) and minimum deviation from regression (0.11, -0.04 and -0.02 respectively) hence are stable and adaptable for rich environment. Regression coefficient less than one with minimum deviation from linearity was observed for the genotype T₇ ($\mu = 3.98$, $b_i = 0.78$, $S^2_{di} = 0.08$). Similar findings were recorded by Abou *et al.* (2006) in white mustard and Patil *et al.* (2017) in okra.

Length of branches

Length of the branches ranged from 74.65 cm (T₈) to 22.96 cm (T₁). T₃ ($b_i = 1.05$) was the genotype with near unit regression and non-significant deviation from regression, so T₃ was the stable genotype. T₈ was the genotype with more than unit regression and non-significant deviation from regression indicating high responsiveness towards the rich environment. The genotypes T₁ ($b_i = 0.62$) and T₇ ($b_i = 0.29$) showed less than unit regression with minimum non-significant deviation from regression. They were highly responsive in unfavourable environment. Similar results for variation in stability parameters for the character length of branches plant⁻¹ were observed by Singh and Arya (2014) in *Vigna radiata* and Ramesh *et al.* (2017) in pigeon pea.

Number of leaves per plant

The number of leaves varied from 145.03 (T₁) to T₃ (99.69). The genotype T₆ was identified as stable genotype with near unit regression ($b_i = 0.82$) and non-significant deviation from regression. The genotype T₁ ($b_i = 0.58$, $S^2_{di} = -2.56$) and T₇ ($b_i = 0.46$, $S^2_{di} = -2.03$) were suitable for poor environment. They were performs under unfavourable environment. Similar results for variability in stability parameters for the trait number of leaves plant⁻¹ was reported by Saranya (2016) in neelamari, Nanavati (2016) in maize.

Leaf to stem ratio

The leaf to stem ratio was highest for the genotype T_3 (0.92) and the lowest for T_5 (0.67). The genotype T_4 ($b_i=1.09$, $S^2_{di} = 0.0004$) and T_7 ($b_i=1.18$, $S^2_{di} = 0.0007$) showed near unit regression with non-significant deviation from regression, which were considered as stable genotypes across the environment. The genotype T_6 was identified as the genotype favourable for rich environment, with regression of more than one and non-significant deviation from regression. The genotype T_1 was identified as stable genotype under unfavourable environment. These results were in accordance with the results of Nanavati (2016) in maize, and Mehraj *et al.* (2017) in oats.

Number of pods

The number of pods ranged from 0.00 (T_6) to 2.77 (T_4). The genotypes T_5 ($b_i=1.23$, $S^2_{di} = -0.003$) and T_7 ($b_i=0.89$, $S^2_{di} = 0.015$) identified as stable genotypes with near unit regression and minimum non-significant deviation from regression. The genotypes T_1 and T_3 were showed high mean, more than one regression coefficient and minimum non-significant deviation indicates high responsiveness towards environmental factors and performs well under rich environments. The genotype T_8 was stable for unfavourable environment with $b_i=0.42$ and $S^2_{di}=0.031$. These findings are in agreement with Ramesh *et al.* (2017) in pigeon pea.

Green fodder yield

The green fodder yield varied from 90.45g (T_3) to 115.42g (T_8). The genotype T_1 had regression coefficient near unity with minimum non-significant deviation from regression, which specifies that the genotype was stable across the environment. The genotypes T_2 , T_4 and T_8 showed more than one regression coefficient with non-significant deviation from regression, which indicates the high responsiveness of these genotypes for rich environment. The variable stability parameters were reported in green fodder yield by Nanavati (2016) in forage maize and Mehraj *et al.* (2017) in oats.

Dry matter production

The dry matter production ranged from 40.62g (T_6) to 28.89g (T_3). The genotype T_1 ($\mu=39.93$, $b_i=0.97$, $S^2_{di} = 0.09$) was identified as stable genotype with unit regression coefficient and minimum non-significant regression from deviation. The genotype T_6 ($\mu=40.62$, $b_i=1.34$, $S^2_{di} = 0.47$) and T_8 ($\mu=40.04$, $b_i=1.25$, $S^2_{di} = 0.49$) were stable for rich environment. They had more than one regression coefficient and non-significant deviation from regression. The same findings for variation in stability parameters were observed by Preeti *et al.* (2016) in wheat.

Crude protein content

The crude protein content varied from 24.39% (T_8) to 13.12% (T_4) in the present study. The genotypes T_4 ($\mu = 13.12$, $b_i = 0.97$, $S^2_{di} = 0.01$) and T_8 ($\mu = 24.39$, $b_i = 0.91$, $S^2_{di} = -0.06$) recoded high mean, near unit regression coefficient and non-significant deviation from regression for this trait. The genotype T_1 showed more than one regression coefficient and non-significant deviation from regression and was identified for rich environment. The genotype T_5 ($\mu = 13.91$, $b_i = 0.69$, $S^2_{di} = 0.02$) exhibited

less than unit value of regression and non-significant deviation from regression and hence the genotype was suitable for poor environment. Comparable findings for the variable stability parameters for protein content was reported by Saeed *et al.* (1985) in sorghum, Peterson *et al.* (1992) in wheat, Shi *et al.* (1999) in rice, Gurmu *et al.* (2009) in soybean.

Crude fibre content

The highest crude fibre content was recorded for the genotype T_8 (29.95%) and the lowest for the genotype T_2 (22.71%). The genotypes T_1 ($\mu = 23.35$, $b_i = 0.97$, $S^2_{di} = 0.098$), T_5 ($\mu = 28.21$, $b_i = 0.96$, $S^2_{di} = 0.054$) and T_7 ($\mu = 27.44$, $b_i = 1.09$, $S^2_{di} = -0.027$) showed high mean, near unit regression and minimum non-significant deviation from regression. These genotypes hence identified as stable across environment. The genotype T_2 ($\mu = 22.71$, $b_i = 1.26$, $S^2_{di} = 0.004$) was identified for rich environment based on stability parameters. The genotype T_4 showed regression coefficient less than one with non-significant deviation from regression, which was stable for unfavourable environments.

Identification of character imparting stability

Based on the regression coefficient, deviation from regression and environmental indices, the characters plant height, green fodder yield, dry fodder yield, dry matter production and crude protein content can be accounted as the stability imparting characters.

Conclusion

The genotype T_1 (IC 345276) was stable over all locations for the characters green fodder yield, dry matter production and crude fibre. The genotype T_4 (IC 261839) and genotype T_7 (TNDV 1) was stable for the character crude protein across the locations.

The genotypes T_2 (IC 343710) and T_8 (Thumburmuzhi local) were stable genotypes for favourable environment. The genotype T_2 (IC 343710) showed stable performance for the characters green fodder yield and crude fibre. The genotype T_8 (Thumburmuzhi local) was stable in favourable environment for green fodder yield and dry matter production. The genotype T_5 (IC 90934) was found to be stable for the character crude fibre in unfavourable environments.

The present study revealed that the genotypes T_1 (IC 345276), T_4 (IC 261839), T_6 (IC 421199) and T_7 (TNDV 1) were stable over the four different locations *viz.*, College of Agriculture, Vellayani, College of Horticulture, Thrissur, Krishi Vigyan Kendra, Kottarakkara and Regional Agricultural Research Station, Ambalavayal, Wayanad. The genotypes T_2 (IC 343710) and T_8 (Thumburmuzhi local) showed stable performance under favourable environments *viz.*, College of Agriculture, Vellayani and Regional Agricultural Research Station, Ambalavayal, Wayanad, while the genotype T_5 (IC 90934) was suitable for unfavourable environment. The superior genotypes identified in the present study can be used for further breeding programme.

Among the several methods were proposed to analyze G×E interaction and to determine the stability in performance of genotypes, the model proposed by Eberhart

and Russell (1966) is the most commonly used method for analysis of genotype x environment interaction in which environmental index was formulated instead of environmental mean and a new parameter in the form of non-linear response was also used that partitioned variance due to environment and g x e interaction into linear and deviation from linear components. Thus Eberhart and Russell (1966) model can be considered better than the other methods but it uses environmental index as an independent variable and regression of genotype mean on environmental index could not define the entire variation due to g x e interaction.

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