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Stability Analysis in Hedge Lucerne (*Desmanthus virgatus* (L.) Willd) for Yield and Quality

Arun Chacko[1*], Mareen Abraham[2] and Shahiba A.M.[1]

[1]M.Sc. Plant Breeding and Genetics, Department of Plant Breeding and Genetics, College of Agriculture,
Vellayani, Thiruvananthapuram, Kerala- 695522, India,

[2]Professor and Officer i/c, AICRP on Forage Crops and Utilization, College of Agriculture, Vellayani,
Thiruvananthapuram, Kerala- 695522, India

*Corresponding Author E-mail: arun7joseph@gmail.com

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ABSTRACT

Eight hedge lucerne genotypes were evaluated over four locations for analyzing stability for yield and quality. As the G x E interactions were significant for all the characters, further analysis was done for estimating the stability parameters according to Eberhart and Russell model (1966). 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. T_1 (IC 345276), T_4 (IC 261839), T_6 (IC 421199) and T_7 (TNDV 1) were stable over the four different locations. 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.

Key words: *G x E interaction, Stability analysis, Hedge lucerne*

INTRODUCTION

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. Hedge lucerne is a forage legume which is preferred by cattle for its palatable green fodder and adequate amount of crude protein[2]. Comparative evaluation of chemical composition (dry matter percentage, crude protein, calcium and phosphorous) of hedge lucerne with other tropical and sub-tropical forage legumes reveal it to be a nutritious feed[4]. The pithy stem of the fodder makes it easier to harvest and frequent cuts can be taken. Hedge lucerne is observed as potential fodder legume that can substitute leucaena for ruminant feed due to its versatile nature.

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Many fodder crops are under-utilized and their cultivation is reduced due to the fluctuant performance of diverse varieties. Being a promising fodder legume with ample advantages, hedge lucerne demands genetic improvement in terms of productivity. Information on adaptability and stability with regard to performance of genotypes can be drawn from the analysis of interaction of genotypes with locations and other agro-ecological conditions. In this perspective, the present investigation was conducted across four locations in Kerala to study the genotype x environment interaction in hedge lucerne for yield and quality.

MATERIAL AND METHODS

Eight hedge lucerne genotypes were evaluated at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani. Randomized block design with eight treatments and four replication was followed across the four locations in Kerala *viz.*, College of Agriculture, Vellayani, Krishi Vigyan Kendra, Kollam, College of Horticulture, Thrissur and Regional Agricultural Research Station, Ambalavayal . The eight treatments were the accessions namely, T_1 (IC 345276), T_2 (IC 343710), T_3 (IC 89910), T_4 (IC 261839), T_5 (IC 90934), T_6 (IC 421199), T_7 (TNDV 1) and T_8 (Thumburmuzhi local). Seeds were sown in continuous line and row spacing of 50 cm. Yield and quality attributes *viz.*, green fodder yield, dry matter production, crude protein and crude fibre were observed for the four harvests. The Eberhart and Russell model was used to analyze the data.

RESULTS AND DISCUSSION

The analysis of variance showed significant differences among the eight hedge lucerne genotypes for yield and quality characters studied across four environments (Table 1). The pooled analysis of variance revealed that for the genotypes, G x E interactions was significant for all the characters studied. As the G x E interactions were significant for all the characters, further analysis was done for estimating the stability parameters (Table 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 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 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[7] in rice, Bikash *et al.*[1] in pearl millet, Preeti *et al.*[10] in wheat, Mehraj *et al.*[5], in oats and Patil *et al.*[8], 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 4).

Eberhart and Russell model, 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 poor environments.

Mean performance and stability parameters for yield and quality traits in hedge lucerne over four locations (Table 5) :

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_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[6]. in forage maize and Mehraj *et al.*[5] in oats.

Dry matter production

The dry matter production ranged from 40.62g (T_6) to 28.89g (T_3). The genotype T_1 (μ=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 (μ=40.62, b_i=1.34, S^2_{di} = 0.47) and T_8 (μ=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 was observed by Preeti *et al.*[10] 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 (μ=13.12, b_i=0.97, S^2_{di} = 0.01) and T_8 (μ=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 (μ=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.*[11] in sorghum, Peterson *et al*[9]. in wheat, Shi *et al.*[12] in rice, Gurmu *et al*.[3] 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 (μ=23.35, b_i=0.97, S^2_{di} = 0.098), T_5 (μ=28.21, b_i=0.96, S^2_{di} = 0.054) and T_7 (μ=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 were identified as stable across environment. The genotype T_2 (μ=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.

Table 1. Analysis of variance (mean square) for individual locations

Table 1.1. Location-I (COA, Vellayani)

Source of variation	df	Green fodder yield	Dry fodder yield	Crude protein	Crude fibre
Replication	3	37.45	1.51	3.07	2.36
Genotypes	7	340.78^{**}	48.42^{**}	84.53^{**}	28.79^{**}
Error	21	8.66	0.33	0.26	1.01

Table 1.2. Location-II (KVK, Kottarakkara)

Source of variation	df	Green fodder yield	Dry matter production	Crude protein	Crude fibre
Replication	3	21.81	0.03	0.34	2.99
Genotypes	7	259.97^{**}	120.02^{**}	76.98^{**}	34.25^{**}
Error	21	19.17	0.15	0.26	0.57

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

Table 1.3. Location-III (COH, Thrissur)

Source of variation	df	Green fodder yield	Dry matter production	Crude protein	Crude fibre
Replication	3	8.52	0.27	0.24	0.16
Genotypes	7	398.24^{**}	93.07^{**}	81.96^{**}	26.65^{**}
Error	21	9.27	0.15	0.13	0.11

Table 1.4. Location-IV (RARS, Ambalavayal)

Source of variation	df	Green fodder yield	Dry matter production	Crude protein	Crude fibre
Replication	3	2.41	1.68	0.47	0.15
Genotypes	7	308.83^{**}	84.41^{**}	90.13^{**}	27.71^{**}
Error	21	8.72	0.45	0.35	0.33

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

Table 2. Pooled Analysis of Variance (mean square) for different quantitative traits of hedge lucerne over four locations

Source of variation	df	Green fodder yield	Dry matter production	Crude protein	Crude fibre
Genotypes	7	1145.58^{**}	357.00^{**}	331.14^{**}	114.93^{**}
Environment	3	249.09^{**}	152.39^{**}	56.74^{**}	51.39^{**}
G x E interaction	21	54.08^{**}	6.43^{**}	0.82^{**}	0.82^{**}
Error	96	12.21	0.25	0.35	0.62

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

Table 3. Analysis of Variance (mean square) for mean data of different quantitative traits of hedge lucerne over four locations

Source of variations	df	Green fodder yield	Dry matter production	Crude protein	Crude fibre
Genotypes	7	286.39^{**}	89.25^{**}	82.78^{**}	28.73^{**}
E+ (G x E)	24	19.61^{*}	6.17^{**}	1.95^{**}	1.79^{**}
Environments	3	62.27^{**}	38.09^{**}	14.18^{**}	12.84^{**}
Environments (Lin)	1	186.82^{**}	114.29^{**}	42.55^{**}	38.54^{**}
G x E(Lin)	7	32.80^{**}	2.15	0.27	0.38
Pooled deviation	16	3.39	1.17^{**}	0.15	0.10
Pooled error	96	3.05	0.25	0.35	0.62
Total	31	79.86	24.93	20.21	7.87

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

Table 4. Estimates of environmental indices (I_j) for each character of hedge lucerne under different locations

Sl. No.	Character	Vellayani	Kottarakkara	Thrissur	Ambalavayal
1.	Green fodder yield	2.36	-0.66	-3.68	1.95
2.	Dry matter production	2.22	-0.21	-2.91	0.91
3.	Crude protein	1.34	-0.03	-1.81	0.49
4.	Crude fibre	1.26	-0.10	-1.70	0.58

Table 5. Mean performance and stability parameters for yield and quality traits in hedge lucerne over four locations

Genotype	Green fodder yield			Dry matter production			Crude protein			Crude fibre		
	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	112.35	1.12	-0.62	39.93	0.97	0.09	21.38	1.42	0.02	23.35	0.97	0.098
T_2	101.28	1.34	-0.30	32.62	0.99	0.98*	15.51	0.92	0.29	22.71	1.26	0.004
T_3	90.45	2.38	-2.55	28.89	1.50	1.13*	14.59	1.21	-0.08	26.83	1.41	-0.139
T_4	100.67	1.74	0.001	37.59	0.94	1.04*	13.12	0.97	0.01	23.59	0.45	-0.143
T_5	98.75	-1.45	9.20	31.37	0.70	0.71*	13.91	0.69	0.02	28.21	0.96	0.054
T_6	110.48	1.26	-2.54	40.62	1.34	0.47	20.26	0.89	-0.01	24.06	0.95	-0.116
T_7	109.02	0.07	1.15	40.32	0.27	3.95**	23.48	0.95	0.32	27.44	1.09	-0.027
T_8	115.42	1.52	-1.61	40.04	1.25	0.49	24.39	0.91	-0.06	29.95	0.89	-0.145
Grand mean	104.93			36.42			18.34			25.77		

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

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.

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