GENOTYPE×ENVIRONMENT INTERACTION IN HEDGE LUCERNE (*Desmanthus virgatus* (L.) Willd.) FOR YIELD AND QUALITY

by

ARUN CHACKO
(2016-11-034)

THESIS

Submitted in partial fulfilment of the

requirements for the degree of

MASTER OF SCIENCE IN AGRICULTURE

Faculty of Agriculture

Kerala Agricultural University

DEPARTMENT OF PLANT BREEDING AND GENETICS

COLLEGE OF AGRICULTURE

VELLAYANI, THIRUVANANTHAPURAM -695522

KERALA, INDIA

2018

DECLARATION

I, hereby declare that this thesis entitled **"GENOTYPE×ENVIRONMENT INTERACTION IN HEDGE LUCERNE (*Desmanthus virgatus* (L.) Willd.) FOR YIELD AND QUALITY"** is a bonafide record of research work done by me during the course of research and the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title, of any other University or Society.

Arun Chacko

Vellayani,
Date: 06/08/2018

Arun Chacko
(2016 - 11-034)

CERTIFICATE

Certified that this thesis entitled **"GENOTYPE×ENVIRONMENT INTERACTION IN HEDGE LUCERNE (*Desmanthus virgatus* (L.) Willd.) FOR YIELD AND QUALITY"** is a record of research work done independently by **Mr. Arun Chacko (2016-11-034)** under my guidance and supervision and that it has not previously formed the basis for the award of any degree, diploma, fellowship or associateship to him.

Vellayani,
Date: 6/8/2018

Dr. Mareen Abraham
(Major Advisor, Advisory Committee)
Professor and Officer (i/c)
AICRP on Forage Crops and Utilization
College of Agriculture, Vellayani

CERTIFICATE

We, the undersigned members of the advisory committee of Mr. Arun Chacko a candidate for the degree of **Master of Science in Agriculture** with major in Plant Breeding and Genetics, agree that the thesis **"GENOTYPE×ENVIRONMENT INTERACTION IN HEDGE LUCERNE (*Desmanthus virgatus* (L.) Willd.) FOR YIELD AND QUALITY"** may be submitted by Mr. Arun Chacko, in partial fulfilment of the requirement for the degree.

6/8/2018

Dr. Mareen Abraham
Professor & Officer (i/c)
AICRP on Forage crops and Utilization
College of Agriculture,
Vellayani
Thiruvananthapuram – 695522

06/8/18

Dr. Vijayaraghava Kumar
Professor (RC) and Head
Department of Agricultural Statistics
College of Agriculture,
Vellayani
Thiruvananthapuram – 695522

6/8/18

Dr. Arya K.
Professor and Head
Department of Plant Breeding and Genetics
College of Agriculture,
Vellayani
Thiruvananthapuram – 695522

Dr. Bindhu J.S.,
Assistant Professor (Agronomy)
AICRP on IFS
On Farm Research Centre
College of Agriculture,
Vellayani
Thiruvananthapuram - 695522

External Examiner

Professor & Head
Biotechnology & Crop Improvement
College of Horticulture, Bagalkot

Acknowledgement

*First and foremost, praises and thanks to the **Almighty**, for everything that happens to me...*

*With great respect and devotion, I would like to record my deep sense of gratitude and indebtedness to my major advisor **Dr. Mareen Abraham**, Professor and Officer i/c, Forage crops and utilization for her valuable guidance, constant inspiration, abundant encouragement, critical scrutiny of the manuscript and valuable suggestions which render me to accomplish the research work successfully. I extend my sincere gratitude for the care and affection bestowed on me throughout the study period.*

*It gives me immense pleasure to express my deep sense of gratitude to **Dr. Arya K**, Professor and Head, Department of Plant Breeding and Genetics, for her motherly approach, valuable advices and whole hearted approach right from the beginning, which helped me in the successful completion of the thesis.*

*I consider it as my privilege to express my deep felt gratitude to **Dr. Vijayaraghavakumar**, Professor (RC) and Head, Department of Agricultural Statistics, for his valuable suggestions, technical advices, statistical interpretation of the experiment data and incessant motivation throughout the research work.*

I convey my heartfelt gratitude to Dr. Bhindhu J. S, Assistant professor (Agronomy), AICRP on IFS, OFRC for her generous timely help, unstinting support, suggestions and passionate approach rendered during the period of research work.

*I am deeply grateful to my beloved teachers of Plant Breeding and Genetics, **Dr. C. Lekha Rani, Dr.Jayalekshmi V. G.** and **Dr.Beena Thomas** for generous support, continues and timely advice, constructive criticisms and constant encouragement rendered to me during the course of my study and research work.*

*I take this opportunity to sincerely acknowledge **Dr. Rajendran P.**, Associate Director, RARS, Ambalavayal, **Dr. George Thomas**, Associate Dean, COH, Vellanikkara, **Dr. Poornima**, KVK Kollam and **Mr. Liffey**, Farm Manager, RARS, Ambalavayal for the valuable suggestions, cooperation and providing me with facilities for completion of the research programme.*

*I would like express my sincere gratitude to Dr. **Usha Thomas, Anitha mam** and **Babitha mam** for the valuable suggestions and whole hearted cooperation and support rendered throughout the research programme.*

*My heartfelt thanks to **Dr.Babu**, Professor and Head, Department of Forage Crops, TNAU, Coimbatore, **Dr. Juliet Hepziba** and **Dr. Jeyakumar**, for their valuable suggestions, timely help and affection during the course of study and the research programme.*

No choice of words will suffice to express thanks to my ever loving friend **Shahi** *for being with me from the beginning of course study till now and played a big part in completion of the research programme. Without her persistent help and care, this would not have been possible.*

A very special thanks to **Nayana Jyothibas** *and* **Ivy Mary Rajan** *for being the best batchmates, whose cooperation, love, support and affection helped me through many hardships.*

Words are inadequate to express my thanks to **Rahul Guptha, Divya Hari, Arjun T.P, Akhil Ajith, Agnes Jose, Prabhu M, Gokul Raj, Manju chechi** *and* **Arya chechi** *for their unbound love and big hearted support.*

I wish to express my heartful thanks to my seniors **Saranya chechi, Sreenivas chettan, Hari chettan, Athulettan, Sudhrik bayya, Vinay bayya, Siddesh bayya, Brunda chechi, Praveena chechi, Rahana chechi, Thejasree chechi, Asoontha chechi, Namitha chechi, Thouseem chechi, Manu chettan** *and* **Prathibha chechi,** *and vibrant juniors* **Anand, Govind, Vinod, Christy, Ankitha** *and* **Swathy** *for their help and support throughout the study period. It is my pleasure to express my special thanks to* **Sini chechi, Santhosh chettan** *and* **Suja chechi** *for their sincere cooperation and kindly approach offered during the study period.*

My loving gratitude to my dear friends **Ajil, Gokul, Fallu, Naveen, Abhinav, Ajmal, Fazee, Suru, Vishnu, Avinash, Ravi, Suman, Reddy, Hampi, Mathew, Madhu, Nivya, Geethu Jacob** *for their love, care and support. I express my special thanks to* **Nishanth bro, Dhaneshettan, Nibin bro, Jaslam ikka, Rejinettan, Nikhi bro, Vishnu chettan, Arjunettan, Amjath, Aabith ikka, Adarsh, Amal, Sijith,** *for their timely help, valuable suggestions and support during period of work. I cherish with appreciation the joyful company of my friends* **Anitta Jose, Jisna** *and* **Amaljith** *throughout my career for their unbound love and wholehearted support.*

I am thankful to **Kerala Agricultural University** *for the technical and financial assistance for carrying out my study and research work. I would like to express my thanks to* **Librarian** *and* **library staffs** *of COA, Vellayani for their support and assistance during the study period.*

It would be impossible to list out all those who have helped me in one way or another in successful completion of this work. I once again express my heartful thanks to all those who helped me in completing this venture in time.

Words are not enough to express my whole-hearted and affectionate gratitude to my **Pappa** *and* **Mummy** *for their unconditional love, sacrifices and support bestowed on me throughout my career. I am affectionately dedicating this thesis to my dear sister* **Pinky** *and* **Grandmother** *for their selfless sacrifice, moral support, constant prayers and inspiring encouragement in all my endeavours.*

Arun Chacko.

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LIST OF ABBREVIATIONS AND SYMBOLS USED

%	Per cent
G x E	Genotype x Environment
CD	Critical Difference
C.V	Coefficient of variation
cm	Centimetre
mg	Milligram
RBD	Randomised Block Design
Cluster^{-1}	Per cluster
DAS	Days After Sowing
^{0}C	Degree Celsius
g m^{-2} day^{-1}	gram per meter square per day
g dm^{-2} day^{-1}	gram per decimetre square per day
et al.	And others
Fig.	Figure
g	Gram
g^{-1}	Per gram
Kg	Kilo gram
ha^{-1}	Per hectare
KAU	Kerala Agricultural University
t ha^{-1}	Tonne per hectare
kg ha^{-1}	Kilogram per hectare

kg $plot^{-1}$	Kilogram per plot
$Plant^{-1}$	Per plant
$Plot^{-1}$	Per plot
Day^{-1}	Per day
Via	Through
Mm	Millimetre
No.	Number
CGR	Crop Growth Rate
cv	Cultivar
NAR	Net Assimilation Rate
Sl.	Serial
sp. or spp.	Species (Singular and Plural)
LAI	Leaf Area Index
viz.	Namely
i.e	that is
d.f	Degrees of freedom
S. E	Standard Error
mg g^{-1}	Milligram per gram

INTRODUCTION

1. 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 (Deepthi *et al.*, 2013). 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 (Johri *et al.*, 1987). 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.

In Kerala, only 40 per cent of green and dry fodder requirement is roughly met from the available feed resources (NDDB, 2016). To narrow the demand supply gap in feed and fodder, genetic improvement of fodder crops with regard to high yield and quality is essential. 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.

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 the need to determine G x E magnitude in

varying environments to identify the stable genotypes. Several methods were proposed to analyze G×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. Currently, there is a need to develop and identify hedge lucerne genotypes with higher yield potential.

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.

The main objective of this study was

- To identify stable genotypes of *Desmanthus virgatus* in varied environments with respect to yield and quality.

REVIEW OF LITERATURE

2. REVIEW OF LITERATURE

Hedge lucerne (*Desmanthus virgatus* (L.) Willd) is a tropical forage legume native of tropics and sub tropics of new world. The word 'Desmanthus' originates from the Greek terms '*desme*' meaning bundle and '*anthos*' meaning flower.

Hedge lucerne belongs to the family Fabaceae, subfamily Mimosoideae. It's a small shrub, 2-3 m tall and roughly resembles Leucaena. No poisonous principle is observed in the foliage (KAU, 2016).

Being a palatable, aggressive, persistent, grazing tolerant perennial browse shrub free from anti-nutritional factors and from which frequent cuts can be taken, it's a potential forage legume. However the genetic improvement achieved in terms of its productivity is very low. Hence this investigation aims at the study of genotype-environment interaction in hedge lucerne genotypes under varied climatic conditions to identify stable genotypes with respect to yield and quality.

The plant is a herbaceous perennial, branched and suffruticose at the base with a height upto 0.5 to 2.5 m. It posses deep woody tap root. The stems are slender, pithy in center, angular, green turning brown. The leaves are 2-8 cm long, compound, bipinnate, bearing 10-25 pairs of linear-oblong leaflets. The leaves posses nyctinastic leaf movements. The inflorescence bears 9-11 whitish mimosoid flowers. The fruits are linear, dehiscent, 5.5-8.5 cm long pods which contain 11-26 reddish brown or golden brown U-shaped seeds (Gutteridge and Shelton, 1994).

2.1. GROWTH, YIELD AND QUALITY ATTRIBUTES OF HEDGE LUCERNE

The comparison between the lucerne and hedge lucerne revealed that optimum biomass, dry matter and crude protein were obtained at 45 days cutting interval for hedge lucerne. Thus hedge lucerne can be considered as a better substitute for lucerne due to its versatile nature (Khan and Bose, 1994).

Shanthi (1995) studied the genetic variability in forty types of hedge lucerne (*Desmanthus virgatus* (L.) Willd) and observed the maximum plant height of genotypes in first cutting followed by a reduction in the second cutting. A linear increase in number of branches, leaf to stem ratio, crude protein and crude fibre was observed from first cutting to second cutting. A general reduction in green fodder yield from first cutting to the second cutting was also observed.

The effect of height and frequency of cutting on yield, quality and persistence of hedge lucerne (*Desmanthus virgatus* (L.) Willd) accession IRFL 1857 over two years. Plants harvested every two weeks at a stubble height of 100 cm gave the highest leaf yield and total dry matter (Trujillo *et al.,* 1996)

Suksombat and Buakeeree (2006) conducted an experiment to determine the effects of cutting interval and cutting height on the yield and nutrient composition of hedge lucerne (*Desmanthus virgatus* (L.) Willd). They found that significant increase in dry matter and nutrient yield were observed with increased cutting of hedge lucerne stand every 40 to 50 days. The cutting height during harvest had no effect on dry matter or nutrient content.

The biomass yield, palatability, chemical composition and nutritive value of hedge lucerne (*Desmanthus virgatus* (L.) Willd) in sheep was studied and obtained a biomass yield of 39.81 t ha^{-1}. The mean crude fibre and crude protein content were 19.77% and 15.20% respectively. The experiment revealed that hedge lucerne can be used as a potential leguminous fodder for small ruminants (Radhakrishnan *et al.*, 2007)

The plant height of hybrid napier exhibited significant differences between the varieties. Growth was slow during the initial stages as evidenced by low plant height. The maximum plant height was observed during the fourth harvest and a gradual decrease in further harvests. Crude fibre content did not show any significant differences among different cultivars. With respect to leaf area index, green fodder yield, dry matter yield, crude protein content, relative growth rate

and net assimilation rate significant differences were observed between the cultivars. Green fodder yield was comparatively less during the initial harvests and highest yield was observed during the third harvest (Soumya, 2011).

Deepthi *et al.* (2013) conducted a study on genetic divergence and association analysis in hedge lucerne (*Desmanthus virgatus* (L.) Willd) in which twenty mutants along with control of variety TNDV-1 were evaluated for twelve traits. The simple correlation estimates revealed that green fodder yield plant^{-1} was significant and positively correlated with number of branches plant^{-1}, leaf to stem ratio and dry matter yield plant^{-1}. The path analysis results showed the high positive direct effect of dry matter yield on green fodder yield plant^{-1} followed by number of branches plant^{-1}, plant height, leaf to stem ratio and pods cluster^{-1}.

An effect of date of sowing and cutting intervals on growth attributes and yield in lucerne (*Medicago sativa* L.) was evaluated under North Gujarat agro-climatic conditions. Significantly higher plant height, mean number of leaves plant^{-1}, mean leaf area plant^{-1} and higher dry forage yield was observed by 30 days cutting interval after common cut (Kumar and Patel, 2013).

Shashikanth *et al.* (2013) evaluated the performance of eight guinea grass varieties in Southern dry zone of Karnataka during *kharif* season over three years. From the pooled data, significantly higher green fodder yield (1007.04 q ha^{-1}year^{-1}), dry matter yield (147.72 q ha^{-1}year^{-1}), crude protein yield (12.99 q ha^{-1}year^{-1}) along with growth parameters like plant height (78.47 cm) and leaf to stem ratio (0.71) were recorded in the variety JHGG-08-1.

Jindal *et al.* (2015) conducted a varietal evaluation trial on three entries of lucerne (*Medicago sativa*) namely, BAIF Lucerne, Anand-21 and Anand 22 along with two national checks viz., RL-88 and Anand-2 under three different agro-ecological zones for assessing quality parameters and forage yield potential. The green fodder yield, dry fodder yield and crude protein content pooled over three years recorded highest at Coimbatore in South zone.

Ishrath (2016) conducted a study on cutting intervals and additives for quality silage production using hybrid Bajra Napier variety Suguna. The cutting interval 75 days recorded highest green fodder yield. The highest crude protein (10.56%) and the lowest crude fibre content (26.81%) were observed from 45 days cutting interval.

Green fodder yield, chemical and nutrient composition and nutrient uptake potential of fifteen sorghum varieties belonging to sweet sorghum, dual purpose and forage types under double cut system with 75 days interval were studied. Green fodder yield showed significant difference among the sorghum varieties. The highest green fodder yield (71.28 t ha^{-1}) was obtained from sweet sorghum variety CSH 22 SS which was on par with forage varieties HC 308 and CSV 21F. Forage variety HJ 513 was observed with high green fodder yield (69.48 t ha^{-1}). For dry matter yield and crude protein content, non-significant differences were observed among the sorghum varieties. For crude protein, significant differences were obtained among the varieties. SPV 462 recorded the highest crude protein percentage (7.08 %) which was on par with varieties Phule Revati, CSV 19 SS, Pant Chari 5 and CSV 15. Crude fibre percentage recorded the highest in HJ 513 (33.11%) and the lowest in CSV 27 (22.71%). Forage varieties showed significantly higher values in dry matter percentage. Dry matter percentage was observed higher in SSG 898 (33.11 %) and the lowest in CSH 22 SS (25.91 %) (Singh and Chauhan, 2017).

Forage nutritional quality of ten Bajra x Napier hybrids (B x N hybrids) along with their eleven parents and four checks were assessed. Hybrids GB x FD-444 and GB x FD-436 recorded the highest dry matter per cent. Highest crude protein per cent (9.63 %) was recorded from male parent TNCN-011 and check CO -3 (Gate *et al.,* 2018).

2.2. GENOTYPE X ENVIRONMENT INTERACTION AND STABILITY ANALYSIS

Plant breeders aim at developing new varieties with high yield stability over wide range of environments. Genotype-environment interaction is one of the basic reasons for the difference in high performance in genotype for the yield and other essential agronomic traits.

Genotype of an individual is its genetic constitution while phenotype is the observable characteristics and phenotypic value is the observed value of a particular characteristic. Phenotypic value of an individual is affected partly by the genotype and partly by the environment which it grows.

An environment is referred as all the external agencies which determine the performance at the phenotypic level. According to Comstock and Moll (1963), the environment can be micro and macro. A potential environment which changes over locations or time is referred as a macro-environment while micro-environment is the special environment circumstances confined to an individual which have very small contribution to the genotypic expression. Environmental variation can be divided as predictable and unpredictable (Allard and Bradshaw, 1964). All the permanent characters of an environment such as climate, soil type along with characters which show fluctuation in a systematic manner can be referred as predicable environment. Unpredictable environment includes changes that are uncontrollable such as the amount and distribution of rainfall in a given area, temperature and atmosphere. Only the macro-environment and its interaction with genotype can be studied since it has major contribution to the final expression of a genotype.

The performance of a genotype with respect to changing environmental factors over time within a given location is referred to as stability of a genotype whereas adaptability refers to the stability in performance of genotypes with respect to changes across locations. Thus a stable variety is less sensitive to the environmental changes taking place.

Genotype-environment interaction is the interplay of genetic and non-genetic effects causing differential relative genotypic responses in different environments. The presence of genotype-environment interaction can be confirmed from the analysis of variance developed by Sprague and Federer (1951). Other approach makes use of regression technique in which G x E interaction is partitioned into linear and non-linear components. Ecovalence measure is the contribution of a genotype to the interaction sum of squares (Wricke, 1962). The genotype with least ecovalence is considered most stable.

Differential responses of improved genotypes to change in environments were initially interpreted by Finlay and Wilkinson (1963). In this approach the components of a genotype and environment interaction were linearly related to environmental effects when measured on small scale as the genotypic effects. An improvement in Finlay and Wilkinson model was done by Eberhart and Russell (1966) by adding a stability parameter, which shows the deviation from regression. According to Eberhart and Russell (1966), a stable genotype exhibits high mean yield, regression coefficient around unity and deviation from regression near zero. Shukla (1972) used the term 'stability variance' an estimate of variance in terms of the residuals in a two-way classification for indentifying the stability of a particular genotype.

Mini (1989) conducted a comparative study of genotype environment interaction in sesame grown over three different locations. Stability analysis methods of Eberhart and Russell (1966), Perkins and Jinks (1968), Freeman and Perkins (1971), Wricke (1962) and Shukla (1972) were used. By examining the stability parameters, variety IS 284 was found to be more stable for most of the characters.

Moneim *et al.* (1990) evaluated twenty-five types of forage peas (*Pisum sativum* L.) across four locations for two years to study the genotype-environment interaction for herbage and seed yield under rainfed conditions. The

accession 88/335 was identified for wide adaptation and stability for high herbage yield and seed yield.

Jyothi (2002) evaluated eight Kunjukunju rice cultures across three locations of Palghat for identifying the stable culture. For many of the yield and yield related traits, Kunjukunju rice culture K-6 was identified as stable in different environments. For many yield traits, variety Kanchana was found specifically adapted only to favourable environments. Nine rice cultures from F_6 generation of wide crosses were evaluated across three locations to study the stability for characters. For most of the yield contributing traits, Culture C 26T (b) was stable over three locations (Palathingal, 2003).

Fourteen mutants of coleus were evaluated across four locations of Kerala for analysing the stability. Significant differences in most of the economic traits were observed among the selected mutants. Mutants '641' and '352' were identified as high yielding and well adapted over locations for many of the economic traits (Shinoj, 2003).

Seven commercial rice hybrids and two check varieties were used for genotype x environment interaction study across three farming situations of Kerala during *kharif* season. Based on the stability analysis, the hybrid KRH-2 was well suited under poor management conditions as it recorded highest mean value and regression coefficient less than unity. Hybrid NSD-2 was identified well suited for better management conditions (Chandrashekhar, 2004).

Sastry (2005) studied sixteen isabgol genotypes across three environments for analysing the stability using Eberhart and Russell (1966) method. Significance for linear component of G x E interaction was observed in number of effective spikes, seed yield and disease index. For the non-linear components, days to 50 per cent flowering and husk content was found to be significant. Genotypes RI-9809, EC-124345 and DM-4 were identified stable for all environments. Genotypes DM-2 and Niharika were stable for seed yield.

Genotype GI-2 was found to be unstable but having more husk than other genotypes.

To determine genotype-environment interaction and stability, fourteen cotton genotypes were evaluated across four locations. Significant differences in mean yield over the environments were observed. Significance in deviation from regression was found only for four genotypes and regression coefficients ranged between 0.23 to 1.46. Genotypes SG-1001, SG-125 and DLP-5409 which are high yielding were identified as stable genotypes (Killi and Harem, 2006).

Ten varieties of cowpea were raised in four environments to assess the selection techniques in genotype-environment interaction. Based on the environment index best and poorest environment was selected. Significant difference in effects of genotype and environment were obtained. Presence of genotype-environment interaction was confirmed from the joint regression analysis. Regression coefficient, non-parametric statistic, superiority measure can be used together to select genotypes based on yield and environmental response (Aremu *et al.*, 2007).

Marimuthu (2007) studied the genotype x environment interaction in eight selected New Plant Type (NPT) lines of rice along with Jyothi as check variety across three low land rice ecosystems. NPT-7 been had identified with better performance based on performance for yield, agronomic characters, grain characteristics and stability.

For analysing the stability in Black gram, twenty genotypes were evaluated over three environments. Eberhart and Russell (1966) method and genotype grouping technique by Francis and Kannenberg model (1978) were used to analyse the data. Higher mean seed yield, average responsiveness to season and stability was recorded in the genotypes VBG 89, VBG (Bg) 4 and VBG 62 (Shanthi *et al.*, 2007).

Seventeen genotypes of brinjal were evaluated over four environments for stability analysis. Mean squares due to genotypes and environments were significant for all the characters studied. Non-significance in genotype x environment (linear) mean sum of squares for most of the characters showed that variation in performance of genotypes is entirely unpredictable. The genotypes PB-66, PbS, PB-67, PB-60 and PB-4 were found to be stable for number of fruits per plant and yield per hectare (Bora, 2010).

Jagjivan (2010) compared different methods for stability analysis in rice (*Oryza sativa* L.) and observed that Eberhart and Russell model (1966) was on par with latest AMMI model. For predicting the stability in performance of a genotype, Eberhart and Russell model (1966) was found preferable than other methods.

Haridas (2011) evaluated stability of fifty ground nut genotypes having bunch type growth habit over three environments for pod yield per plant and its related characters. Pooled analysis showed significance in mean square values due to genotypes. Mean squares due to G x E interaction were significant for all the characters except oil content. Mean squares due to environments were significant for all the characters in the pooled analysis over environments. Environment E3 was observed with high performance for most of the characters.

Singh (2011) evaluated thirty chilli genotypes along with three checks across three different environmental conditions to study the genotype x environment interaction. Around seventeen genotypes were found stable for yield. Genotype PC-2507 showed the highest yield and identified as the most stable genotype. Indo sem, PC-10 and AC-150 were the genotypes found to be specifically adapted to favourable environment.

The Genotype x Environment study in aromatic rice to analyse the stability over three environments depicted that genotype GT 6 had more adaptable characters over the three environments. More stable grain characters were observed in genotype GT 1 over the two locations (Ram, 2012).

Bikash *et al.* (2013) evaluated 30 hybrids of pearl millet during *kharif* season across four locations for dry fodder yield stability. High significance in mean squares due to genotypes and environments together with G x E interaction from the analysis of variance for stability indicated significant differences among genotypes. The mean squares due to G x E interaction was partitioned into linear and non-linear components and G x E (linear) was predominant for characters like days to 50 percent flowering, plant height and dry fodder yield and the performance of which could be predicted across the environments. The estimation of environmental index helped in selection of the most favourable environment for all the characters as E_1 (irrigated condition). The hybrids found to be stable over the environments are 94111A x 1250 and 96111A x (G73-107 x bsectap 1). For the poor environment, hybrid ICMA97444 x ICMR0/035 was the best suited. The hybrids studied did not exhibit uniform pattern of environment response (linear). For identifying stable hybrid by selection, genotypes with average response for different characters and phenotypic stability of characters should be given importance.

Singh and Arya (2014) evaluated thirty-six genotypes of *Vigna radiata* (L.) to analyse the stability under three environments using methodology of Eberhart and Russell model (1966). The genotype-environment interaction effect was analysed using the additive mean effect and multiplicative interaction effects (AMMI) model. Two genotypes G2 and G36 with high mean seed yield showed non-significant deviation from regression. The genotype G33 with average mean seed yield showed non-significant deviation from regression. Environment A (early sown) and B (timely sown) were favourable for most of the yield component traits, environment C (late sown) was unfavourable for almost all the yield and yield related traits. For seed yield, genotypes G1, G2, G3, G4, G18, G22, G24 and G25 were found to be stable based on AMMI 1. Based on AMMI 2, genotypes G14, G22 and G25 were found to be stable for seed yield. Based on analysis, genotypes and environments were grouped into nine sectors.

Anarase *et al.* (2015) conducted an experiment with five male sterile lines, fourteen testers, resultant seventy hybrids and two checks of rabi sorghum across three different locations for examining the genotype-environment interaction for yield and yield related traits. The study on stability parameters depicted that eight parents were found to be average stable for grain yield.

Ten black gram cultures along with four check varieties were raised during kharif, rabi and summer seasons under open and shaded conditions for analyzing the stability by using Eberhart and Rusell's model. The data analysed as pooled over open condition as well as shaded condition did not show any variation between genotypes under three seasons for number of seeds pod^{-1} and none of the genotypes showed stability in protein content. The data pooled over six environments depicted that all the traits showed variation between genotypes under the environments studied. Ranking of genotypes were done based on stability, yield and yield contributing characters and the least ranked genotypes T_6, T_5 and T_3 were recommended for cultivation under open and shaded conditions (Bhagwat, 2015).

Stability analysis study in ten F_1 hybrids and two check varieties of okra over four locations obtained significant differences among genotypes and environments for all the characters in the pooled analysis of variance for evaluation of F_1 hybrids over locations and seasons. The hybrids Thirumala local x Mallapalli local, Thirumala local x Kattakada and Thirumala local x Punjab Phalgani local were stable over different locations and seasons (Gogineni, 2015).

To identify stability for green fodder yield in forage maize (*Zea mays* L.) forty five hybrids and fourteen parents were evaluated during kharif (E_1), rabi (E_2) and summer (E_3). For fresh green stem weight $plant^{-1}$ and green forage yield $plant^{-1}$ significance was observed in G x E (linear) and G x E (non-linear). The hybrids with average stability such as IC-170121 x GWC-0511 and African Tall x GWC-0401 would be well adapted over a range of environments. Hybrids such

as IC-130726 x GWC-0512, GM-6 x IC-130693 with below average stability were specifically adapted to favourable environment. The hybrid IC-130726 x GWC-9603 with above average stability was specifically adapted to poor environment (Nanavati, 2016).

Preeti *et al.* (2016) conducted a study on effects of changing environments on wheat dry matter yield. Forty-two genotypes were grown across four different locations during rabi season to identify the stable genotypes. Non-linear component accounted a major portion of G x E for dry fodder yield plant^{-1}. Environment E_1 was identified as the most favourable environment for all characters from the estimates of environment additive effects. The genotypes WH 1098, WH1126, PBW 343, WH 1081, WH 542 and HD 2851 were identified as stable for dry matter yield in all environments and were more adaptive.

Pangti (2016) examined the stability parameters in thirty bread wheat (*Triticum aestivum* L. em Thell) genotypes to for yield and quality attributes in two environments. More than eleven genotypes were found to be stable for grain yield. For both the environments *viz.*, E1 (timely sown) and E2 (late sown), all the characters exhibited significant differences.

Saranya (2016) studied stability analysis in nine neelamari mutants over four locations for yield and indigotin content. In the pooled analysis of variance, significant differences for all the characters were observed among the genotypes studied. This indicated that the genotypes interacted significantly with environments. Mutants It-1, It-2 and It-8 were identified as stable mutants for favourable environments. The stable mutants identified over different locations during the summer season are It-3, It-6 and It-9. Mutant It-10 was the mutant suitable for unfavourable environment.

Baranda (2017) evaluated thirty genotypes of cowpea (*Vigna unguiculata* (L.) Walp) under three environments for analyzing stability using Eberhart and Russell model (1966). Environment-2 was found to be the most suitable for many of the characters based on the mean performance. High consistent

expression for yield character in all environments was observed in genotype CPD-197. Poor yielding genotypes were CPD-115 (Environment E_1, E_2 and on pooled basis) and CPD-127 (Environement-E_3). Wide adaptability under desired environments was shown by the genotype CPD-201. Genotypes CPD-17, CPD-196, CPD-78 and CPD-200 were observed with desired response moisture stress condition.

The existence of genotype x environment interactions and stability were assessed for yield and quality in four Pineapple varieties over seven locations. From the pooled analysis of variance all the characters showed significant difference in genotypic variances over the seven locations. Varieties Amritha and Mauritius were stable for all quantitative and qualitative traits. The stability type was determined based on regression coefficient and mean values (Manivannan *et al.*, 2017).

Mehraj *et al.* (2017) studied genotype-environment interaction in twelve different genotypes of oats (*Avena sativa* L.) for forage yield and its related traits. The genotypes SKO-90, SKO-96 and Sabzaar were identified as stable across the environments. For favourable environments, genotypes SKO-148, SKO-160, SKO-166 and SKO-167 were the most suited while genotype SKO-20 was found to be suited for poor environments for forage yield.

Patil *et al.* (2017) evaluated thirty-seven entries of okra *viz.*, eight parents, twenty eight F_1's and one standard check over four season for developing stable hybrids for fruit yield plant^{-1} and its related traits. From the pooled analysis of variance, high significance for the mean squares for genotypes was obtained which indicated the variability for all the characters among the genotypes. Highly significant differences obtained for environments and genotype x environment except for ascorbic acid indicated the divergence among growing environments and differential response of genotypes to various environments. Environment E2 was found to be most favourable whereas E3 most unfavourable. Eight hybrids were identified as stable for fruit yield plant^{-1} and its components.

AMMI analysis was used to study the stability of twenty genotypes of bio-fortified red kernel rice (*Oryza sativa* L.) across three environments and three locations. First interaction principle axis was favourable for all characters whereas second interaction principle axis are favourable for characters such as spikelet fertility, grain yield plot^{-1}(kg), iron content (ppm), protein and amylose content (%) and grain yield plant^{-1}. For grain yield plot^{-1}, grain yield plant^{-1} and protein content, the genotype RTN-1211-4-2-1-1 was found to be stable. For all the characters across three environments, the genotype RTN-1201-13-2-2-1-32 was found to be most favourable (Rajaram, 2017).

Assessment of stability for forage yield in ten genotypes of *Cenchrus ciliaris* was carried under rainfed conditions for four years. Except green fodder yield at first cut, all other characters were significant for gxe interaction which depicted the differential behaviour of genotype over the time. For green fodder production, genotypes CAZRI 231 and CAZRI 2177 were found to be stable, whereas for higher dry matter production over wide environmental conditions genotypes CAZRI 231 and CAZRI 2177 were found stable (Rajora *et al.*, 2017).

Ramesh *et al.* (2017) investigated twenty genotypes of Pigeon pea (*Cajanus cajan* (L.) Mill sp.) for analysing stability for yield and its components during kharif season over three years. Among the varieties high significant differences were obtained for all the characters except pod bearing length, number of pods plant^{-1} and seed yield. Except 100 seed weight, all other characters showed significant differences in different environment. For seed yield, the genotypes ICP-9691 and ICP-12654 were on par with check and the genotype ICP-13270 was stable for pod length across the environments.

For analysing the yield and micronutrient stability in Mung bean (*Vigna radiata* L.), thirty genotypes were raised across six artificial environments. Majority of the genotypes exhibited high significant difference in deviation from regression which depicted the suitability of these genotypes for better environment and their unpredictable response. Genotypes ML-1108, SMH-99-2,

MH-124, PDM-9-249 and ML-759 were recommended for better environment with high seed yield and iron content (Singh *et al.*, 2018).

Ten hybrids along with one check variety in Brinjal (*Solanum melongena* L.) was raised across four locations in Kerala for analyzing the stability and adaptability of yield and yield attributing characters using Eberhart and Russell model. Significant differences among genotypes, environments and genotype x environment interaction for all the characters were obtained from the pooled analysis of variance. Stability parameters like overall mean, regression coefficient (b_i) and deviation from regression (S^2_{di}) were used to identify the promising hybrids. The significance in mean squares due to Environments + (Genotype x Environment) revealed the existence of genotype x environment interaction. In *kharif* season, the stable hybrid identified was Wardha local x Palakurthi local (SMV1 x SMV2), widely adapted to all environments for days to first flowering, number of fruits plant^{-1}, fruit weight, fruit length, calyx length, yield plant^{-1}, yield plot^{-1}and plant height. The hybrid with regression coefficient lower than unity and non-significant deviation from regression for days to first flowering, Surya x Vellayani local (SMV3 x SMV6) was found to be suited for poor environments. The hybrid NBR-38 x Vellayani local (SMV4 x SMV6) had high mean values, regression coefficient greater than unity and non-significant deviation from regression for days to first harvest and found stable for favourable environments (Vishwanath, 2018).

MATERIALS AND METHODS

3. MATERIALS AND METHODS

The present investigation on "Genotype×Environment interaction in Hedge lucerne (*Desmanthus virgatus* (L.) Willd.) for yield and quality" was conducted in the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani, Thiruvananthapuram during 2016-2018. The field experiment was conducted at four locations of Kerala to determine the stability of eight genotypes of *Desmanthus virgatus* for yield and quality.

The details of materials used and methodologies adopted in the present study are described below.

3.1. EXPERIMENTAL SITE

The present work was carried out in four locations of Kerala.

Location I: College of Agriculture, Vellayani.

Location II: Krishi Vigyan Kendra, Kottarakkara.

Location III: College of Horticulture, Thrissur.

Location IV: Regional Agricultural Research Station, Ambalavayal.

3.2. EXPERIMENTAL DESIGN

The experiment was laid out in Randomized Block Design (RBD) with eight treatments and four replications. The spacing of 50 cm x continuous line sowing with a plot size of 3 m x 1 m was followed in the field experiment.

3.3. CULTURAL OPERATIONS

The land was prepared thoroughly by digging and leveling. The seeds collected were treated with hot water for 3 minutes followed by water soaking over night, shade dried and sown in the field in continuous line with 50 cm spacing between the lines.

3.4. RECORDING OF OBSERVATIONS

The list of hedge lucerne genotypes used as treatments in the study are described in Table 1. From each replication five competitive plants per treatment were randomly selected and tagged. From these plants observations with respect to different characters were recorded and the mean values of five plants were considered for statistical analysis. Observations were recorded on the following characters during 90 (first cut), 140 (second cut), 190 (third cut) and 240 (fourth cut) DAS (Days After Sowing).

3.4.1. Growth Characters

3.4.1.1. Plant Height (cm)

The height of the plant was measured from the base of the plant to the tip of the tallest branch at the time of each harvest using measuring scale and their mean values was expressed in centimeter.

3.4.1.2. Number of Branches Plant^{-1}

The total number of branches in a plant was counted at each harvest.

3.4.1.3. Length of Branches (cm)

The length of the branches was measured from the main stem to the tip of the branch at the time of each harvest using measuring scale and their mean value was expressed in centimeter.

3.4.1.4. Number of Leaves Plant^{-1}

The total number of leaves produced in a plant was counted at each harvest.

3.4.1.5. Leaf to Stem Ratio

The sample plants were cut at the base. The leaves and the stem were separated and oven dried for 5 days till constant weight was obtained. The dry weight of leaves and stem of individual plants were recorded. The ratio was computed by dividing leaf dry weight by the stem dry weight.

Table 1. List of hedge lucerne (*Desmanthus virgatus* L. (Willd)) genotypes used in the study

Sl. No.	Genotypes	Genotype name	Source
1.	T_1	IC 345276	IGFRI, Jhansi
2.	T_2	IC 343710	IGFRI, Jhansi
3.	T_3	IC 89910	IGFRI, Jhansi
4.	T_4	IC 261839	IGFRI, Jhansi
5.	T_5	IC 90934	IGFRI, Jhansi
6.	T_6	IC 421199	IGFRI, Jhansi
7.	T_7	TNDV 1	Tamil Nadu Agricultural University
8.	T_8	Thumburmuzhi local	Cattle Breeding Farm, Thumburmuzhi

Plate 1. General field view

a) **COA, Vellayani**

b) **KVK, Kottarakkara**

Plate 2. General field view

c) COH, Thrissur

d) RARS, Ambalavayal

3.4.1.6. Number of Pods Cluster^{-1}

The number of pods in each cluster was counted in a plant at harvest and mean values were measured.

3.4.2. Yield Attributes

3.4.2.1. Green Fodder Yield (g plant^{-1})

At regular cutting intervals the crop was harvested and fresh weight of the plants in the net plot was recorded and expressed in g plant^{-1}.

3.4.2.2. Dry Fodder Yield (g plant^{-1})

From each harvest crop samples were collected and dried in a hot air oven at 70^{0}C to a constant weight and expressed in g plant^{-1}.

3.4.3. Quality Aspects

3.4.3.1. Crude Protein Content (%)

The crude protein content was calculated by multiplying the nitrogen content of the plant by the factor 6.25 (Simpson *et al.*, 1965) and expressed in percentage (%).

3.4.3.2. Crude Fibre Content (%)

The crude fibre content was determined by AOAC method (AOAC, 1975) and expressed in percentage (%).

3.4.4. Physiological Characters

3.4.4.1. Dry Matter Production (g plant^{-1})

During the seed maturation stage five observational plants from each replication were uprooted. Shoot, leaves and roots were separated and dried to a constant weight at 70^{0}C in a hot air oven. The sum of these individual components gave total dry matter production.

3.4.4.2. Leaf Area Index

Leaf area of observational plants was measured using Leaf area meter LI-COR 3100 available at Department of Crop Physiology, Tamil Nadu Agricultural University, Coimbatore. The leaf area index was obtained from the formula according to Watson (1952).

$$LAI = \frac{\text{Leaf area of the plant } (cm^2)}{\text{Ground area occupied } (cm^2)}$$

3.4.4.3. Crop Growth Rate (g m^{-2} day^{-1})

CGR was computed using the formula of Watson (1958) and expressed as g m^{-2} day^{-1}.

$$CGR = \frac{W_2 - W_1}{P(t_2 - t_1)}$$

Where,

W_1 and W_2 = Plant dry weights at times t_1 and t_2

t_1 and t_2 = time interval in days

P = ground area on which W_1 and W_2 have been estimated.

3.4.4.4. Net Assimilation Rate (g dm^{-2} day^{-1})

Net Assimilation Rate (NAR) refers to the change in dry weight of the plant per unit leaf area per unit time. The procedure given by Gregory (1917) and modified by Williams (1946) was followed for calculating NAR.

$$NAR = \frac{w_2 - w_1}{t_2 - t_1} \text{ — } \frac{\log_e L_2 - \log_e L_1}{L_2 - L_1}$$

Where, W_1- dry weight of plant (g) at time t_1, L_1- leaf area (dm^2) at t_1

W_2- dry weight of plant (g) at time t_2, L_2- leaf area (dm^2) at t_2

t_2- t_1 :- time interval in days

3.5 STATISTICAL ANALYSIS

The data recorded on different traits were subjected to the following statistical analysis.

1. Analysis of Variance
2. Stability Analysis

3.5.1 Analysis of Variance

3.5.1.1 *Analysis in Randomized Block Design (RBD)*

The Randomized Block Design (RBD) was adopted with four replications. As per the method outlined by Panse and Sukhatme (1985) the analysis of variance was carried out.

$$Y_{ij} = m + g_i + r_j + e_{ij}$$

Where, Y_{ij} = Phenotypic observation of i^{th} genotype in j^{th} replication

M = General mean

g_i = True effect of i^{th} genotype

r_j = True effect of j^{th} replication

e_{ij} = Random error associated with i^{th} genotype and j^{th} replication

For each character Analysis of Variance (ANOVA) was carried out as indicated below:

Source of variation	d.f.	SS	MSS	F-ratio
Replications	r-1	RSS	M_r	M_r/M_e
Genotypes	g-1	TSS	M_g	M_g/M_e
Error	(r-1) (g-1)	ESS	M_e	
Total	rg-1			

Where,

r = Number of replications

t = Number of treatments (genotypes)

M_r = Mean sum of squares of replications

M_g = Mean sum of squares of treatments

M_e = Mean sum of squares of error

d.f = Degrees of freedom

The significance of mean sum of squares for each character was tested against the corresponding error degrees of freedom using 'F' test (Fisher and Yates, 1967).

$$\text{Standard Error Mean (SE(m))} = (M_e/r)^{1/2}$$

Where,

M_e = Error mean of squares

r = Number of replications

C.D = S.E (d) x t

Where,

$S.E\ (d) = (2\ M_e/r)^{1/2}$

't' = t Table value at error degrees of freedom

$C.V = (S.D/\overline{X}) \times 100$

Where, S.D = Standard deviation of the population

$\overline{X}$ = Population mean

3.5.2 Stability Analysis

3.5.2.1 Methods to Measure Stable Performance of Genotypes

Analysis of variance of genotypic mean was computed for each agronomic variable in each environment. The data were pooled over environments as the coefficient of variation values in each environment was generally low.

3.5.2.2 Eberhart and Russell's model (1966)

To study the stability of genotypes under different environments the methodology of Eberhart and Rusell's model is used. The parameters estimated are the following (i) overall mean genotype over a range of environments, (ii) the regression of each genotype on the environmental index and (iii) a function of squared deviation from the regression.

$$Y_{ij} = m + B_i I_j + \delta_{ij} \qquad (i = 1,2,\ldots, g \text{ and } j = 1,2,\ldots, e)$$

Where, Y_{ij} = mean of i^{th} genotype in j^{th} environment

m = mean of all genotypes over all the environments

B_i = regression coefficient of the i^{th} genotype on the environmental index which measures the response of this genotype to varying environments

I_j = environmental index which is defined as the deviation of the mean of all the genotypes at a given location from overall mean

$$I_j = \frac{\sum_i Y_{ij}}{t} - \frac{\sum_i \sum_j Y_{ij}}{ge}$$

With $\sum_j I_j = 0$

δ_{ij} = The deviation from regression of the i^{th} genotype at j^{th} environment

3.5.2.3 Analysis of Variance for Stability

The analysis of variance proposed by Eberhart and Russell (1966) is given below.

ANOVA to estimate stability parameters (Eberhart and Russell, 1966)

Source	d.f	Sum of squares	Mean sum of squares
Total	(ge-1)	$\sum\sum Y_{ij}^2$ - CF	
Genotype	(g-1)	$\frac{\sum Y_i^2}{e}$ – CF	MS_1
Environment + (Genotype x Environment)	g(e-1)	$\sum\sum Y_{ij}^2 - \frac{\sum Y_i^2}{e}$	
Environment Linear	1	$\frac{\sum(Y_{ij}I_j)^2}{g(\sum I_j^2)}$	
Genotype + Environment (Linear)	(g-1)	$\sum\left[\frac{(\sum_j Y_{ij}I_j)^2}{\sum_j I_j^2}\right] - \frac{(\sum_j Y_j I_j)^2}{g\sum_j I_j^2}$	MS_2
Pooled deviation	g(e-2)	$\sum\sum \delta_{ij}^2$	MS_3
Deviation due to Genotype 1 Genotype 2 : Genotype g	(e-2)	$\left[\sum Y_{ij}^2 - \frac{Y_i^2}{e}\right] - \left[\frac{(\sum Y_i I_j)^2}{\sum I_j^2}\right]$	
Pooled error	ge(r-1)		S_e^2

g = No. of genotypes = 8, r = No. of replications = 4

e = No. of environments = 4

3.5.2.4 Estimation of stability parameters

The two stability parameters, regression coefficient (b_i) and deviation from regression (S_{di}^2) were estimated as follows :

3.5.2.5 Computation of regression coefficient (b_i) for each genotype

$$b_i = \frac{\sum_j Y_{ij} I_j}{\sum_j I_j^2}$$

Where,

b_i = regression coefficient of i^{th} genotype

$\sum I_j^2$ = The sum of squares of environmental indices (I_j) which are common to each value of b_i

$\sum_j Y_{ij} I_j$ = (for each genotype) = The sum of products of environmental index (I_j) and the corresponding means of that genotypes t for each environment (Y_{ij}).

3.5.2.6 Computation of Mean Square Deviation S^2_{di} from Linear Regression

In regression analysis, the variance of dependent variable (Y) is partitioned into two parts, the one which explains the linearity between dependent and independent variables (variance due to regression) and the other which explains the variance due to deviations from linearity symbolically.

$\sigma^2 Y = \sigma^2$(regression) + σ^2 (deviation from regression)

For estimating S^2_{di} values, the variance due to deviation from regression can be obtained by subtracting the variance due to regression from $\sigma^2 Y$. The variance of means of individual genotypes over different locations can be obtained by,

$$\sigma_i^2 = \sum_j Y_{ij}^2 - \left(\frac{Y_i^2}{g}\right)$$

Where, Y_{ij} and Y_i are the mean values of genotypes in each location and total value of a variety in all the locations respectively.

The variance due to deviations from regression $\left(\sum_j \delta_{ij}^2\right)$ for a genotype being:

$$\sum_j \delta_{ij}^2 = \left[\sum_j Y_{ij}^2 - \frac{Y_i^2}{g}\right] - \frac{\left(\sum_j Y_{ij} I_j\right)^2}{\sum_j I_j^2}$$

Where,

$\left[\sum_j Y_{ij}^2 - \frac{Y_i^2}{g}\right]$ = The variance due to dependent variable

$\frac{\left(\sum_j Y_{ij} I_j\right)^2}{\sum_j I_j^2}$ = The variance due to regression

From which it can be obtained as

$$S^2 d_i = \left[\frac{\sum_j \delta_{ij}^2}{e-2}\right] - \left(\frac{S_e^2}{r}\right)$$

3.5.2.7 Test of Significance

The mean sum of squares due to genotypes and environments were tested against pooled deviation. Whereas, mean sum of squares due to G x E interaction was tested against pooled error. Environment (linear) and G x E (linear) were tested against pooled deviation. If pooled deviation is non-significant both these linear components were tested against pooled error. Mean sum of squares due to pooled deviations were tested against pooled error.

The following tests of significance were carried out:

1. To test the significance of difference among genotypes means i.e.,

   $H_o = \mu_1 = \mu_2 = \mu_3 \ldots = \mu_g$

$$F = \frac{MS_1}{MS_3}$$

2. To test that the genotypes did not differ for their regression on environmental index, i.e., $H_o = b_1 = b_2 = b_3 \ldots = B_e$

$$F = \frac{MS_2}{MS_3}$$

3. Individual deviation from linear regression was tested as follows:

$$F = \left[\left(\sum_j \delta_{ij}^2\right)/(e-2)\right]/pooled\ error$$

Against F table value at (e-2), ge (r-1), at 5% or 1% probability level.

3.5.2.8 Stable Genotype

A stable genotype with unit response was the genotype with unit regression coefficient ($b_i = 1$) and deviation not significantly different from zero ($S_{di}^2 = 0$).

Mean and standard error of 'b'

$$\text{Mean of b} = \bar{b} = \sum_i \frac{b_i}{v}$$

$$\text{S.E. (b)} = \sqrt{\frac{\text{Mean Sum of square due to pooled deviation}}{\sum_j I_j^2}}$$

$$\text{S.E. } b_i = \sqrt{\sum_j \delta_{ij}^2/(e-2)/\sum_j I_j^2}$$

3.5.2.9 Population mean

Population mean (μ) and standard error was calculated as

Population mean (μ) = Grand total/Number of observation s

$$\text{S.E. (mean)} = \sqrt{\frac{\text{Mean sum of square due to pooled deviation}}{\text{Number of environments} - 1}}$$

RESULTS

4. RESULTS

The present study was conducted to evaluate the performance of eight hedge lucerne genotypes (*Desmanthus virgatus* (L.) Willd.) over four locations *viz.*, College of Agriculture, Vellayani, College of Horticulture, Thrissur, Krishi Vigyan Kendra, Kottarakkara and Regional Agricultural Research Station, Ambalavayal, Wayanad in Kerala with an objective to identify stable genotypes of *Desmanthus virgatus* in varied environments with respect to yield and quality. The results obtained from the study are presented below under the following titles.

1. Analysis of variance
2. Mean performance
3. Stability parameters (Eberhart and Russell, 1966)

4.1 ANALYSIS OF VARIANCE

The analysis of variance showed significant differences among the eight hedge lucerne genotypes for all the characters studied across four environments (Table 2.1 – 2.4).

4.2 MEAN PERFORMANCE

4.2.1 Mean performance of hedge lucerne at College of Agriculture (COA), Vellayani

The mean performances of eight hedge lucerne genotypes for different parameters of growth, yield, quality and physiological characters at COA, Vellayani were recorded and presented below.

4.2.1.1. Growth characters

The mean performance of growth characters of hedge lucerne for different cuttings at COA, Vellayani are given in the Table 3.

Table 2. Analysis of variance (mean square) for individual locations

Table 2.1. Location-I (COA, Vellayani)

Source of variation	df	Plant height	Number of branches plant^{-1}	Length of branches plant^{-1}	Number of leaves plant^{-1}	Leaf to stem ratio	Number of pods cluster^{-1}	Green fodder yield	Dry fodder yield	Dry matter production	Crude protein	Crude fibre
Replication	3	3.48	0.21	2.73	3.16	0.0035	0.0067	37.45	1.51	0.26	3.07	2.36
Genotypes	7	973.25**	26.21**	1226.21**	1138.22**	0.032**	3.68**	340.78**	48.42**	78.79**	84.53**	28.79**
Error	21	1.81	0.59	0.18	6.29	0.0028	0.84	8.66	0.33	0.07	0.26	1.01

Table 2.2. Location-II (KVK, Kottarakkara)

Source of variation	df	Plant height	Number of branches plant^{-1}	Length of branches plant^{-1}	Number of leaves plant^{-1}	Leaf to stem ratio	Number of pods cluster^{-1}	Green fodder yield	Dry fodder yield	Dry matter production	Crude protein	Crude fibre
Replication	3	1.16	1.48	2.55	14.80	0.0094	0.0056	21.81	0.07	0.03	0.34	2.99
Genotypes	7	1075.01**	29.20**	1184.41**	1274.32**	0.034**	3.07**	259.97**	46.32**	120.02**	76.98**	34.25**
Error	21	1.11	0.45	0.17	19.99	0.0011	0.0071	19.17	0.09	0.15	0.26	0.57

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

Table 2.3. Location-III (COH, Thrissur)

Source of variation	df	Plant height	Number of branches plant^{-1}	Length of branches plant^{-1}	Number of leaves plant^{-1}	Leaf to stem ratio	Number of pods cluster^{-1}	Green fodder yield	Dry fodder yield	Dry matter production	Crude protein	Crude fibre
Replication	3	0.87	0.95	0.28	7.27	0.0027	0.035	8.52	0.13	0.27	0.24	0.16
Genotypes	7	1054.30**	31.30**	1155.50**	1502.46**	0.044**	3.04**	398.24**	54.11**	93.07**	81.96**	26.65**
Error	21	1.03	0.21	0.20	12.39	0.0016	0.046	9.27	0.12	0.15	0.13	0.11

Table 2.4. Location-IV (RARS, Ambalavayal)

Source of variation	df	Plant height	Number of branches plant^{-1}	Length of branches plant^{-1}	Number of leaves plant^{-1}	Leaf to stem ratio	Number of pods cluster^{-1}	Green fodder yield	Dry fodder yield	Dry matter production	Crude protein	Crude fibre
Replication	3	1.22	0.43	0.30	3.74	0.0016	0.02	2.41	0.09	1.68	0.47	0.15
Genotypes	7	893.12**	22.08**	1242.09**	1026.62**	0.031**	2.89**	308.83**	60.83**	84.41**	90.13**	27.71**
Error	21	1.08	0.38	0.43	16.56	0.0016	0.01	8.72	0.14	0.45	0.35	0.33

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

Table. 3 Mean performance of biometric characters of different cuttings of hedge lucerne at COA, Vellayani

Genotypes	Plant Height (cm)				Number of Branches Plant^{-1}				Length of Branches (cm)			
	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut
T_1	104.3	110.9	113.7	115.9	3.758	4.158	4.955	5.705	15.38	19.64	20.39	23.66
T_2	75.42	79.46	82.69	89.12	5.190	5.710	6.230	7.258	26.66	30.94	35.97	38.07
T_3	60.35	66.34	70.95	75.31	8.640	9.232	10.94	12.26	22.94	25.91	28.64	32.80
T_4	89.29	90.84	95.39	98.16	3.680	4.120	4.900	5.503	44.21	46.52	50.29	54.26
T_5	91.23	96.00	100.9	102.8	5.490	6.039	6.940	7.273	53.33	56.62	60.75	63.82
T_6	101.9	105.9	110.9	112.2	4.120	4.743	4.950	5.395	36.28	40.92	42.87	48.34
T_7	77.59	80.79	83.75	85.71	3.990	4.150	4.830	5.465	24.91	27.34	30.85	33.38
T_8	102.9	111.1	114.3	118.7	9.100	9.610	10.94	11.63	64.55	67.62	70.94	75.32
S.E (m)	**1.038**	**0.725**	**0.937**	**0.671**	**0.043**	**0.070**	**0.070**	**0.134**	**0.304**	**0.381**	**0.479**	**0.217**
C.D (0.05)	**3.072**	**2.146**	**2.775**	**1.988**	**0.127**	**0.206**	**0.206**	**0.280**	**0.900**	**1.128**	**1.419**	**0.642**

Genotypes	Number of Leaves Plant^{-1}				Leaf to Stem Ratio				Number of Pods Cluster^{-1}			
	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut
T_1	112.3	124.6	139.5	146.2	0.910	0.914	0.921	0.948	0.000	1.208	1.230	1.758
T_2	86.31	95.64	100.9	113.1	0.650	0.690	0.719	0.765	1.250	1.354	1.550	1.640
T_3	75.61	89.61	98.62	107.9	0.810	0.820	0.880	0.898	1.053	1.183	1.430	1.538
T_4	72.51	85.62	106.3	128.2	0.670	0.700	0.730	0.748	1.853	2.190	2.640	3.083
T_5	88.59	102.9	132.9	136.5	0.630	0.650	0.690	0.685	1.560	1.970	2.148	2.335
T_6	106.3	125.9	139.6	142.7	0.850	0.880	0.900	0.890	0.000	0.000	0.000	0.000
T_7	84.21	91.08	101.6	111.0	0.740	0.790	0.800	0.885	2.150	2.338	2.590	2.718
T_8	99.99	114.9	134.6	146.1	0.780	0.830	0.850	0.823	1.540	1.678	1.958	2.515
S.E (m)	**1.062**	**1.107**	**1.085**	**2.031**	**0.007**	**0.007**	**0.009**	**0.038**	**0.012**	**0.017**	**0.017**	**0.058**
C.D (0.05)	**3.144**	**3.277**	**3.213**	**4.225**	**0.021**	**0.020**	**0.028**	**0.078**	**0.036**	**0.050**	**0.050**	**0.172**

4.2.1.1.1. Plant height (cm)

The plant height showed significant difference in all the genotypes. The genotype T_1 recorded the maximum (104.3cm) plant height, which was on par with T_8 (102.9 cm) and T_6 (101.9 cm) during first cut of hedge lucerne. The plant height of genotypes increased in successive cuttings with the highest plant height recorded for the genotype T_8 during second, third and fourth cuttings (111.1 cm, 114.3 cm and 118.3 cm). The genotype T_8 was on par with the genotype T_1 for plant height at second (110.9 cm) and third (113.7 cm) cuttings of hedge lucerne. The genotype T_3 showed the minimum plant height at four successive cuttings (60.35 cm, 66.34 cm, 70.95 cm and 75.31 cm).

4.2.1.1.2 Number of branches plant^{-1}

The highest number of branches plant^{-1} was observed in genotype T_8 for the successive three cuttings (9.100, 9.610 and 10.94) and the genotype T_3 showed maximum number of branches plant^{-1} during third (10.94) and fourth (12.26) cut of hedge lucerne. The genotype T_4 recorded the minimum number of branches plant^{-1} during first (3.684) and second cut (4.120) of hedge lucerne. The genotype T_7 showed the lowest number of branches plant^{-1} during third cut and the genotype T_6 during fourth cut (5.395).

4.2.1.1.3 Length of branches (cm)

The highest length of branches was observed for the genotype T_8 during first (64.55 cm), second (67.62 cm), third (70.92 cm) and fourth (75.32 cm) cuttings. The genotype T_3 showed the minimum length of branches during all the four cuttings (15.38 cm, 19.64 cm, 20.39 cm and 23.66 cm) of hedge lucerne.

4.2.1.1.4 Number of leaves plant^{-1}

The highest number of leaves plant^{-1} was observed for the genotype T_1 during first (112.3) and fourth (146.2) cut of hedge lucerne. During second (125.9) and third (139.6) cutting, the genotype T_6 showed the maximum number of leaves plant^{-1}. The genotype T_1 was on par with T_6 during second (124.6) and

third (139.5) cut and T_8 (146.1) and T_6 (142.7) were on par with the genotype T_1 during fourth cut of hedge lucerne in number of leaves plant ^{1}. The lowest number of leaves plant^{-1} was observed for the genotype T_4 during first (72.51) and second (85.62) cut and the genotype T_3 (75.61) was on par with T_4 during first cut. The minimum number of leaves plant^{-1} was observed for the genotype T_3 during third (98.62) and fourth (107.9) cut and this was on par with T_7 (101.6) and T_2 (100.9) during third cut and with T_7 (111.0) during fourth cut of hedge lucerne.

4.2.1.1.5 Leaf to stem ratio

The genotype T_1 recorded highest leaf to stem ratio (0.910, 0.914, 0.924 and 0.948) for all the cuttings. The genotype T_6 (0.900) was on par with the genotype T_1 during third cut and T_3 (0.898), T_6 (0.890) and T_7 (0.885) were on par with T_1 during fourth cut. The minimum leaf to stem ratio was observed for the genotype T_5 (0.630, 0.650, 0.690 and 0.685) during all the four cuttings. The genotype T_2 (0.650) was on par with the genotype T_5 during first cut.

4.2.1.1.6 Number of pods cluster^{-1}

The genotype T_7 showed the maximum number of pods cluster^{-1} during first (2.150) and second (2.338) cut whereas, the genotype T_4 recorded the highest number of pods cluster^{-1} during third (2.640) and fourth (3.083) cut. The genotype T_7 (2.590) was on par with T_4 at the third cut for the character number of pods cluster^{-1}.

4.2.1.2 Yield attributes

The mean performances of yield attributes of hedge lucerne for different cuttings at COA, Vellayani are given in the Table 4.

4.2.1.2.1 Green fodder yield (g plant^{-1})

Green fodder yield showed significant variation among the genotypes for different cut in hedge lucerne. Superior yield was reported in the genotype T_6 during first (96.39 g) and second (100.69 g) cut. The genotype T_1 was on par with

Table. 4 Mean performance of yield attributes of different cuttings of hedge lucerne at COA, Vellayani

Genotypes	Green Fodder Yield (g)				Dry Fodder Yield (g)			
	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut
T_1	91.230	98.610	108.94	116.55	25.390	27.638	30.278	34.313
T_2	80.970	84.608	98.640	103.09	18.625	21.368	24.190	28.603
T_3	76.340	81.290	90.283	96.785	18.553	20.818	23.080	26.005
T_4	90.283	95.288	100.94	105.30	23.613	24.320	31.293	32.805
T_5	84.290	90.840	94.860	93.928	21.503	23.220	25.908	27.183
T_6	96.390	100.69	108.89	112.03	24.680	28.880	30.288	31.940
T_7	85.673	91.062	100.79	109.09	26.383	27.340	28.940	30.363
T_8	92.190	97.060	109.75	119.58	27.768	30.820	33.520	35.905
S.E (m)	**0.936**	**0.931**	**0.849**	**1.971**	**0.198**	**0.299**	**0.307**	**0.285**
C.D (0.05)	**2.773**	**2.757**	**2.513**	**4.100**	**0.587**	**0.885**	**0.908**	**0.844**

T_6 (98.61 g) for green fodder yield at the second cut. During the third cut, the genotype T_8 recorded the maximum (109.75 g) yield which was on par with T_6 (108.89 g) and T_1 (108.94 g). The highest green fodder yield was recorded for the genotype T_8 during fourth cut which was on par with T_1 (116.55 g). The lowest yield was recorded for the genotype T_3 during first (76.34 g), second (81.29 g) and third (90.283 g) cut whereas, the minimum yield during fourth cut was observed for the genotype T_5 (93.928 g) which was on par with T_3 (96.785 g).

4.2.1.2.2 Dry fodder yield (g plant^{-1})

The highest dry fodder yield was observed for the genotype T_8 at all the four cuttings (27.768 g, 30.820 g, 33.520 g and 35.905 g). The lowest dry fodder yield was observed for the genotype T_2 (18.625 g) during first cut which was on par with T_3 (18.553 g). The genotype T_3 showed the minimum dry fodder yield during second (20.818 g), third (23.080 g) and fourth (26.005 g) cut. The genotype T_2 was on par with the genotype T_3 (21.368 g) during the second cut of harvest.

4.2.1.3 Quality aspects

The mean performances of quality aspects of hedge lucerne for different cuttings at COA, Vellayani are given in Table 5.

4.2.1.3.1 Crude protein content (%)

Crude protein content was the highest for the genotype T_8 for all the four cuttings i.e., 25.00%, 25.02%, 25.29% and 25.46%. The genotype T_7 was on par with the genotype T_8 (24.58%) during first cut. The lowest crude protein content was observed for the genotype T_4 during first, second, third and fourth cut with 13.95%, 14.00%, 14.02% and 14.16% respectively.

4.2.1.3.2 Crude fibre content (%)

The crude fibre content was the highest for the genotype T_8 for all the four cuttings in hedge lucerne (30.24%, 30.25%, 30.75% and 30.99%) while the

Table. 5 Mean performance of quality aspects of different cuttings of hedge lucerne at COA,Vellayani

Genotypes	Crude Protein Content (%)				Crude Fibre Content (%)			
	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut
T_1	22.44	22.48	22.85	23.61	23.12	24.13	24.50	24.52
T_2	16.01	16.03	16.31	16.93	24.15	24.25	24.59	24.64
T_3	16.02	16.08	16.14	16.16	28.09	28.30	28.31	28.49
T_4	13.95	14.00	14.02	14.16	24.03	24.11	24.19	24.25
T_5	20.43	20.48	14.56	14.99	29.00	29.10	29.22	29.55
T_6	23.49	23.81	21.59	21.66	23.19	24.99	25.03	25.06
T_7	24.58	24.98	24.11	24.44	28.12	28.23	28.59	28.64
T_8	25.00	25.02	25.29	25.46	30.24	30.25	30.75	30.99
S.E (m)	**0.202**	**0.205**	**0.178**	**0.258**	**0.232**	**0.278**	**0.293**	**0.504**
C.D (0.05)	**0.598**	**0.607**	**0.526**	**0.765**	**0.687**	**0.824**	**0.868**	**1.492**

Fig.1 Mean performance of yield attributes of hedge lucerne at COA, Vellayani

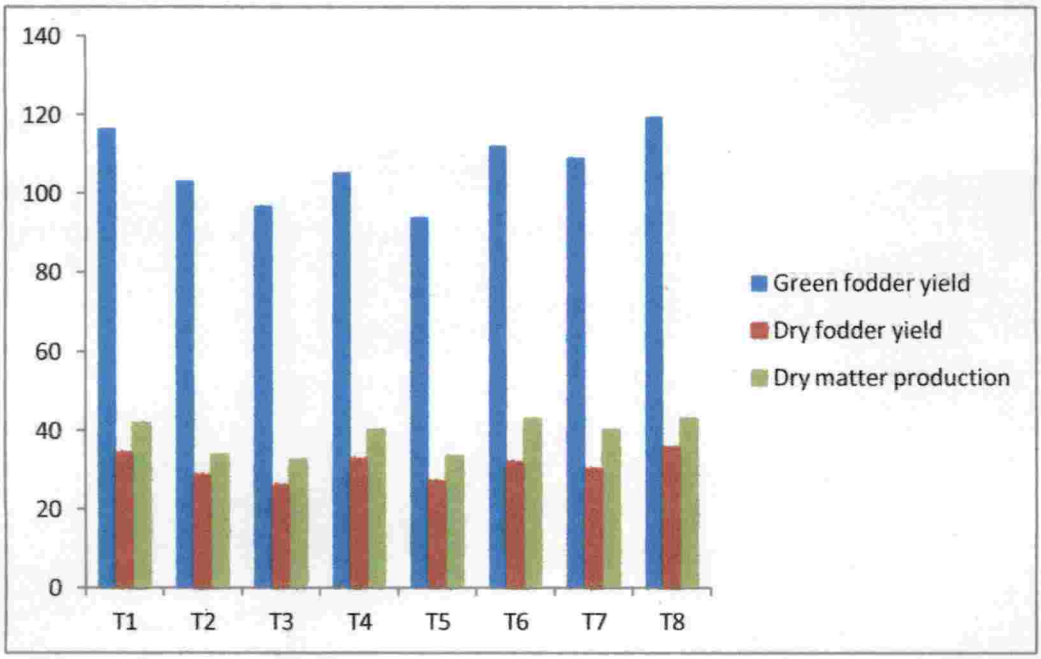
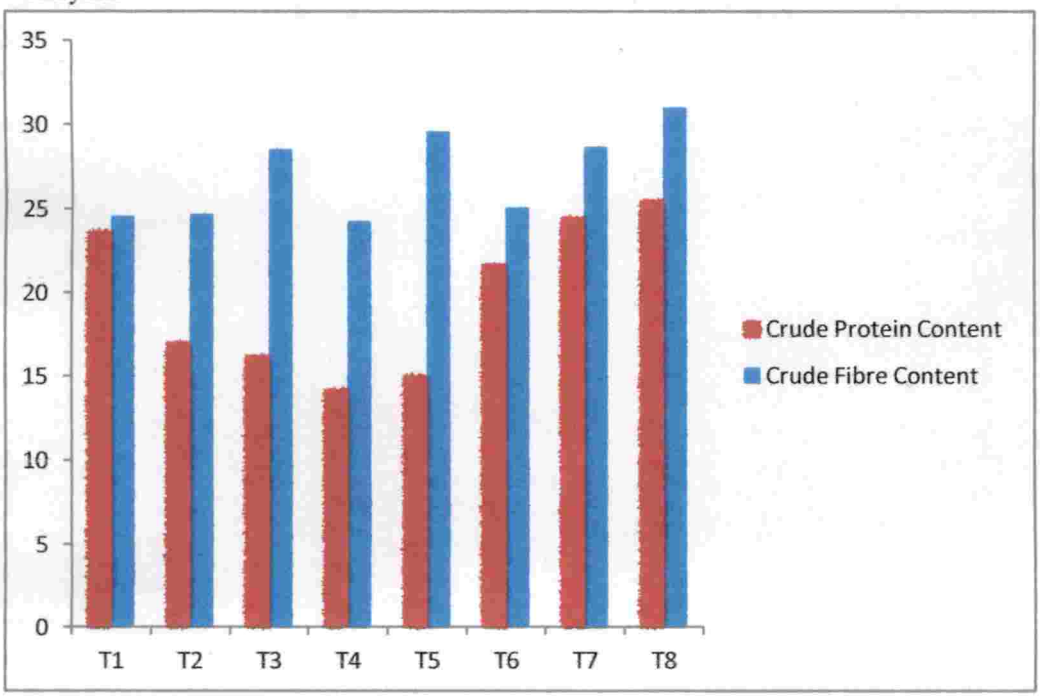


Fig 2. Mean performance of quality characters of hedge lucerne at COA, Vellayani



genotype T_5 (29.55%) was on par with the genotype T_8 for the crude fibre content during fourth of cut. During the first cut, the lowest crude protein content was observed for the genotype T_1 (23.12%) which was on par with the genotype T_6 (23.19%). The lowest crude protein content was observed for the genotype T_4 during second (24.11%), third (24.19%) and fourth (24.25%) stage of cuttings which was on par with T_5 (24.99%, 25.03% and 25.06%), T_1 (24.13%, 24.50% and 24.52%) and T_2 (24.25%, 24.59% and 24.64%) during second, third and fourth cuttings.

4.2.1.4 Physiological characters

The mean performances of physiological characters of hedge lucerne for different cuttings at COA, Vellayani are given in Table 6.

4.2.1.4.1 Dry matter production (g plant^{-1})

T_8 genotype recorded highest dry matter production (35.64 g, 38.69 g, 41.29 g) during the first, second and third cuttings of hedge lucerne. The genotype T_6 (34.82 g) and T_7 (34.62 g) was on par with the genotype T_8 in the first cutting and the genotype T_6 (37.88 g) was on par with the genotype T_8 in the second cutting. During the third and fourth cutting, the maximum dry matter production (41.29 g and 43.08 g) was recorded from T_6 genotype. The lowest dry matter production was recorded from the genotype T_5 (25.64 g), T_2 (28.55 g), T_2 (30.89 g) and T_3 (32.65 g) during first, second, third and fourth cutting respectively. The genotype T_3 (31.19 g) was on par with the genotype T_2 during the third cutting.

4.2.1.4.2 Leaf Area Index

The leaf area index showed significant variation in each genotype. The highest leaf area index was observed for the genotype T_1 (7.418, 8.028, 8.058 and 8.168) and the lowest for the genotype T_3 (2.740, 3.410, 3.430 and 3.453) in all the four cuts of hedge lucerne.

Table. 6 Mean performances of physiological characters of different cuttings of hedge lucerne at COA, Vellayani

Genotypes	Dry Matter Production(g)				Leaf Area Index				Crop Growth Rate ($g\ m^{-2}\ day^{-1}$)				Net Assimilation Rate ($g\ dm^{-2}\ day^{-1}$)			
	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut
T_1	33.59	34.29	36.29	41.96	7.418	8.028	8.058	8.168	2.97	1.50	1.76	2.69	0.02	-0.32	-0.01	0.01
T_2	26.35	28.55	30.89	34.02	3.308	4.110	4.120	4.440	1.65	1.83	1.88	1.59	0.02	-0.63	0.05	-0.01
T_3	28.45	30.15	31.19	32.65	2.740	3.410	3.430	3.453	0.80	1.51	1.51	1.95	0.01	-0.92	-0.05	0.03
T_4	33.91	35.49	38.56	40.22	5.033	5.960	6.003	6.020	0.58	0.47	1.80	1.01	0.02	0.57	0.04	0.05
T_5	25.64	28.61	32.09	33.67	6.230	5.920	5.950	5.958	1.58	1.15	1.79	0.85	0.02	-0.63	-0.05	0.08
T_6	34.82	37.88	41.29	43.08	6.938	7.050	7.123	7.390	1.44	2.03	0.94	1.10	0.03	-0.54	0.03	0.02
T_7	34.62	35.49	38.69	40.48	4.110	4.328	4.353	4.478	1.54	0.64	1.07	0.95	0.02	-0.80	0.37	0.02
T_8	35.64	38.69	41.29	43.04	5.810	6.113	6.310	6.405	3.67	2.80	4.65	2.94	0.03	0.63	1.21	0.08
S.E (m)	**0.366**	**0.268**	**0.363**	**0.133**	**0.059**	**0.089**	**0.067**	**0.236**	**0.341**	**0.234**	**0.325**	**0.292**	**0.002**	**0.037**	**0.019**	**0.023**
C.D (0.05)	**1.085**	**0.793**	**1.074**	**0.394**	**0.125**	**0.187**	**0.142**	**0.490**	**0.973**	**0.732**	**0.936**	**0.837**	**0.007**	**0.109**	**0.057**	**NS**

4.2.1.4.3 Crop Growth Rate (g cm^{-2} day^{-1})

Crop growth rate was highest in the genotype T_8 (3.67 g m^{-2} day^{-1}) in first, second, third and fourth cutting. The genotype T_1 was on par (2.97 g m^{-2} day^{-1} and 2.69 g m^{-2} day^{-1}) with the genotype T_8 in the first and fourth cutting. The lowest crop growth rate was recorded from the genotype T_4 (0.58 g m^{-2} day^{-1}) in the first and second cutting followed by the genotypes T_6 (0.94 g m^{-2} day^{-1}) and T_5 (0.85 g m^{-2} day^{-1}) in the third and fourth cutting respectively. The genotypes T_3 (0.80 g m^{-2} day^{-1}), T_6 (1.44 g m^{-2} day^{-1}) and T_7 (1.54 g m^{-2} day^{-1}) were on par with the genotype T_4 in the first cutting. During the third cutting the genotypes T_1 (1.76 g m^{-2} day^{-1}), T_3 (1.51 g m^{-2} day^{-1}), T_4 (1.80 g m^{-2} day^{-1}), T_5 (1.79 g m^{-2} day^{-1}) and T_7 (1.07 g m^{-2} day^{-1}) was on par with the genotype T_6. The genotypes T_2 (1.59 g m^{-2} day^{-1}), T_4 (1.01 g m^{-2} day^{-1}), T_6 (1.10 g m^{-2} day^{-1}) and T_7 (0.95 g m^{-2} day^{-1}) were on par with the genotype T_5 during the fourth cutting.

4.2.1.4.4 Net Assimilation Rate (g dm^{-2} day^{-1})

The maximum net assimilation rate was recorded in the genotype T_8 (0.03 g dm^{-2} day^{-1}, 0.63 g dm^{-2} day^{-1} and 1.21 g dm^{-2} day^{-1}) for first, second and third cutting. The genotype T_4 (0.57 g dm^{-2} day^{-1}) was on par with the genotype T_8. The lowest net assimilation rate was recorded in the genotype T_3 (0.01 g dm^{-2} day^{-1}, -0.92 g dm^{-2} day^{-1} and -0.05 g dm^{-2} day^{-1}) during first, second and third cutting.

4.2.2 Mean performance of hedge lucerne at KVK, Kottarakkara

The mean performances of eight hedge lucerne genotypes for different parameters of growth, yield, quality and physiological characters at KVK, Kottarakkara were studied.

4.2.2.1 Growth characters

The mean performances of growth characters of hedge lucerne genotypes for different cuttings at KVK, Kottarakkara are given in Table 7.

Table. 7 Mean performances of biometric characters of different cuttings of hedge lucerne at KVK, Kottarakkara

Genotypes	Plant Height (cm)				Number of Branches Plant^{-1}				Length of Branches (cm)			
	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut
T_1	100.7	108.6	110.4	112.6	4.130	4.950	5.125	5.728	15.30	18.34	20.53	22.73
T_2	74.12	80.94	82.01	86.04	4.868	5.110	5.943	6.203	22.41	25.96	27.64	32.62
T_3	54.55	60.88	65.97	68.05	7.150	8.940	9.763	10.11	24.85	28.64	32.19	38.13
T_4	82.96	86.92	90.38	92.00	2.193	2.840	3.213	3.675	43.67	48.21	50.94	55.75
T_5	89.64	95.01	98.64	100.3	4.668	5.128	5.860	6.428	50.21	54.19	56.34	61.13
T_6	97.45	103.9	107.1	109.9	2.990	3.213	3.870	4.138	34.92	39.61	43.85	47.40
T_7	77.91	82.53	85.91	89.40	2.190	2.940	3.160	3.843	20.91	25.95	29.64	34.15
T_8	104.4	110.8	115.9	117.5	8.610	9.430	10.94	11.26	65.29	68.66	70.28	74.70
S.E (m)	**1.067**	**0.914**	**1.001**	**0.527**	**0.046**	**0.059**	**0.061**	**0.087**	**0.240**	**0.390**	**0.432**	**0.211**
C.D (0.05)	**3.160**	**2.706**	**2.964**	**1.559**	**0.135**	**0.174**	**0.181**	**0.178**	**0.710**	**1.153**	**1.280**	**0.626**

Genotypes	Number of Leaves Plant^{-1}				Leaf to Stem Ratio				Number of Pods Cluster^{-1}			
	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut
T_1	109.6	125.9	140.9	147.5	0.840	0.870	0.900	0.890	0.000	1.123	1.250	1.325
T_2	95.21	112.6	135.2	143.9	0.620	0.630	0.650	0.680	1.200	1.233	1.290	1.485
T_3	71.02	89.64	95.32	99.37	0.880	0.900	0.930	0.910	0.953	0.960	1.100	1.353
T_4	75.61	91.20	100.6	124.7	0.850	0.870	0.710	0.770	1.140	1.230	2.490	2.883
T_5	86.38	102.4	128.9	144.1	0.590	0.610	0.650	0.675	1.420	1.850	1.968	2.080
T_6	95.64	119.6	125.9	143.3	0.820	0.830	0.840	0.843	0.000	0.000	0.000	0.000
T_7	81.84	90.26	96.34	114.8	0.750	0.760	0.770	0.790	1.518	1.960	2.150	2.333
T_8	96.39	105.7	132.1	144.9	0.750	0.790	0.801	0.868	1.250	1.450	1.890	2.183
S.E (m)	**1.090**	**1.044**	**1.186**	**3.162**	**0.007**	**0.006**	**0.009**	**0.005**	**0.010**	**0.013**	**0.017**	**0.042**
C.D (0.05)	**3.226**	**3.092**	**3.512**	**6.577**	**0.022**	**0.018**	**0.019**	**0.022**	**0.031**	**0.039**	**0.052**	**0.125**

4.2.2.1.1 Plant height (cm)

The maximum plant height for hedge lucerne was recorded from genotype T_8 (104.4 cm, 110.8 cm, 115.9 cm and 117.5 cm) and the lowest plant height was recorded from the genotype T_3 during all the four cuttings. The genotype T_1 (108.6 cm) was on par with T_8 during the second cutting.

4.2.2.1.2 Number of branches plant^{-1}

The highest number of branches plant^{-1} was obtained in the genotype T_8 (8.61, 9.43, 10.94 and 11.26) in all the four cuttings. The lowest number of branches was observed in the genotype T_7 (2.19 and 3.16) during first and third cutting. The genotype T_4 (2.19 and 3.12) was on par with T_7 for the first and third cutting. The genotype T_4 showed the lowest number of branches (2.84 and 3.68) during second and fourth cutting. The genotype T_7 was on par with T_4 (2.94 and 3.84) for the second and fourth cutting.

4.2.2.1.3 Length of branches (cm)

For length of branches, the highest and lowest value was observed in the genotype T_8 (65.29 cm, 68.66 cm, 70.28 cm and 74.7 cm) and the genotype T_1 (15.3 cm, 18.34 cm, 20.53 cm and 22.73 cm) respectively for the four cuttings in hedge lucerne.

4.2.2.1.4 Number of leaves plant^{-1}

The number of leaves was highest in the genotype T_1 (109.6, 125.9, 140.9 and 147.5) in four cuttings. During the fourth cutting genotypes T_2, T_5, T_6 and T_8 were on par with T_1. Lowest number of leaves was recorded in the genotype T_3 for the four cuttings which was on par with T_7 (90.26 and 96.34) during second and fourth cutting and also with T_4 during the second cut.

4.2.2.1.5 Leaf to stem ratio

Among the genotypes evaluated, highest (0.88, 0.99, 0.93 and 0.91) and lowest (0.59, 0.61, 0.65 and 0.67) leaf to stem ratio was observed in the genotype

T_3 and T_5 respectively for all cuttings. T_1 and T_6 were on par with T_3 and T_2 was on par with T_5 during the fourth cutting.

4.2.2.1.6 Number of pods cluster^{-1}

The maximum number of pods per cluster was obtained from the genotype T_7 (1.52 and 1.96) for the first and second cutting and the genotype T_4 (2.49 and 2.88) during the third and fourth cutting. The genotype T_6 did not produce any pods at the time of four cuttings.

4.2.2.2 Yield attributes

The mean performance of yield attributes of hedge lucerne genotypes for different cuttings at KVK, Kottarakkara are given in Table 8.

4.2.2.2.1 Green fodder yield (g plant^{-1})

The green fodder yield plant^{-1} varied from 70.58 g to 88.89 g in the genotype T_3. The highest green fodder yield was obtained for the genotype T_8 (112.99 g) during the fourth cutting and 110.89 g, 102.97 g and 98.61 g for the third, second and first cutting respectively.

4.2.2.2.2 Dry fodder yield (g plant^{-1})

For the four cuttings, the highest dry fodder yield was obtained from the genotype T_8 (28.51 g, 30.95 g, 32.09 g and 33.13 g) and lowest from the genotype T_3 (18.62 g, 19.63 g, 20.95 g and 22.85 g).

4.2.2.3 Quality aspects

The mean performances of quality aspects of hedge lucerne genotypes for different cuttings at KVK, Kottarakkara are given in Table 9.

4.2.2.3.1 Crude protein content (%)

Among the genotypes, the highest crude protein content was recorded from the genotype T_8 (24.20 %, 24.21 %, 24.35 % and 24.46 %) and the genotype T_4

Table. 8 Mean performance of yield attributes of different cuttings of hedge lucerne at KVK, Kottarakkara

Genotypes	Green Fodder Yield (g)				Dry Fodder Yield (g)			
	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut
T_1	90.280	93.288	102.94	110.69	26.350	28.560	30.818	31.973
T_2	83.238	85.908	89.640	101.99	21.583	23.153	23.608	27.250
T_3	70.588	74.120	80.290	88.893	18.620	19.630	20.950	22.850
T_4	88.670	90.280	95.670	97.420	25.690	27.123	28.640	31.113
T_5	82.910	87.617	92.310	103.91	20.638	23.283	24.923	28.058
T_6	96.578	99.990	105.82	109.93	26.330	28.508	30.620	32.230
T_7	97.380	100.87	106.38	108.37	23.283	25.153	28.510	30.163
T_8	98.610	102.97	110.89	112.99	28.508	30.950	32.090	33.130
S.E (m)	**0.710**	**0.845**	**0.718**	**3.095**	**0.254**	**0.262**	**0.223**	**0.148**
C.D (0.05)	**2.103**	**2.502**	**2.125**	**6.439**	**0.752**	**0.777**	**0.660**	**0.440**

Table. 9 Mean performance of quality aspects of different cuttings of hedge lucerne at KVK, Kottarakkara

Genotypes	Crude Protein Content (%)				Crude Fibre Content (%)			
	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut
T_1	21.00	21.01	21.05	21.17	22.14	22.54	22.67	22.71
T_2	15.62	15.96	16.03	16.02	22.00	22.09	22.15	22.25
T_3	14.20	14.22	14.28	14.54	26.31	26.45	26.52	26.66
T_4	12.94	13.01	13.06	13.14	23.00	23.12	23.23	23.44
T_5	13.00	14.02	14.09	14.15	28.09	28.35	28.41	28.52
T_6	13.99	19.55	19.62	19.93	23.42	23.51	23.58	24.03
T_7	19.52	22.42	22.95	23.06	27.51	27.52	27.64	27.64
T_8	24.20	24.21	24.35	24.46	29.45	29.46	29.58	29.58
S.E (m)	**0.134**	**0.173**	**0.174**	**0.260**	**0.209**	**0.306**	**0.254**	**0.256**
C.D (0.05)	**0.397**	**0.513**	**0.515**	**0.769**	**0.620**	**0.905**	**0.753**	**0.755**

Fig 3. Mean performance of yield attributes of hedge lucerne at KVK, Kottarakkara

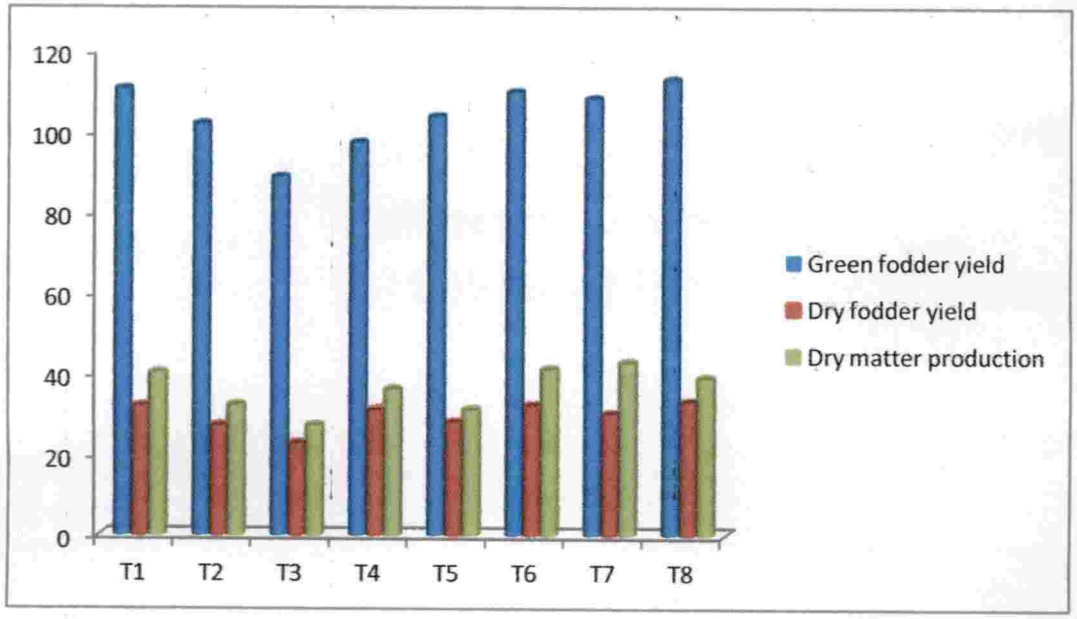
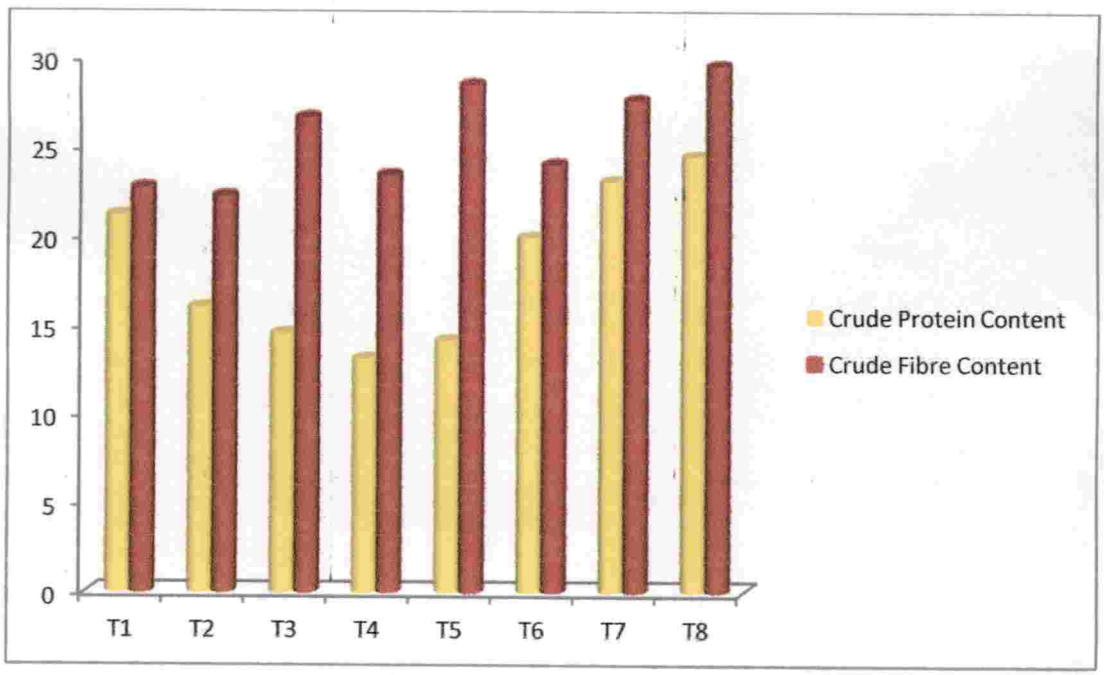


Fig 4. Mean performance of quality characters of hedge lucerne at KVK, Kottarakkara



recorded the lowest crude protein content (12.94 %, 13.01%, 13.06 % and 13.14 %) during the four cuttings. The genotype T_5 was on par with T_4 during the first cutting (13 %).

4.2.2.3.2 Crude fibre content (%)

The highest crude fibre content was obtained from the genotype T_8 (29.45 %, 29.46 %, 29.58% and 29.58%) and lowest crude fibre content was recorded in the genotype T_2 (22%, 22.09%, 22.15% and 22.25%) which was on par with the genotype T_1 (22.14%, 22.54%, 22.67% and 22.71%) during all the four cuttings.

4.2.2.4 Physiological characters

The mean performances of physiological characters of hedge lucerne genotypes for different cuttings at KVK, Kottarakkara are given in Table 10

4.2.2.4.1 Dry matter production (g plant^{-1})

The genotype T_7 recorded the highest dry matter production plant^{-1} in four cuttings (34.29 g, 37.24 g, 40.27 g and 42.69 g). The lowest dry matter production was obtained from the genotype T_3 (21.02 g, 23.95 g, 25.94 g and 27.25 g) in all the four cuttings of hedge lucerne.

4.2.2.4.2 Leaf Area Index

Leaf area index measured the highest values (7.42, 7.54, 7.61 and 7.71) in the genotype T_1 and the lowest values (2.74, 2.75, 2.81 and 2.89) in the genotype T_3 for all four harvest.

4.2.2.4.3 Crop Growth Rate (g m^{-2} day^{-1})

Crop growth rate in the genotype T_8(6.07 g m^{-2} day^{-1}), T_5 (1.76 g m^{-2} day^{-1}), T_8 (2.24 g m^{-2} day^{-1} and 2.43 g m^{-2} day^{-1}) recorded the highest among the genotypes first, second, third and fourth cut respectively. The genotypes T_1 (1.47 g m^{-2} day^{-1}, T_6 (1.45 g m^{-2} day^{-1}), T_7 (1.25 g m^{-2} day^{-1}) and T_8 (1.63 g m^{-2} day^{-1})

Table.10. Mean performances of physiological characters of different cuttings of hedge lucerne at KVK, Kottarakkara

Genotypes	Dry Matter Production (g)				Leaf Area Index				Crop Growth Rate ($g\ m^{-2}\ day^{-1}$)				Net Assimilation Rate ($g\ dm^{-2}\ day^{-1}$)			
	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut
T_1	34.26	36.28	39.21	40.19	7.418	7.540	7.618	7.715	2.90	1.47	1.51	0.77	0.22	0.024	0.011	0.407
T_2	24.52	26.34	30.64	32.29	3.308	3.440	3.540	3.995	3.44	1.05	0.88	1.27	0.21	0.031	0.012	-0.172
T_3	21.02	23.95	25.94	27.25	2.740	2.753	2.813	2.895	2.71	0.67	0.31	0.69	0.26	0.017	0.010	-0.743
T_4	24.39	28.63	30.65	36.12	5.033	5.120	5.240	5.470	3.77	0.95	1.01	1.65	0.22	0.017	0.015	-5.651
T_5	23.95	27.91	29.34	31.17	6.230	6.418	6.510	6.650	1.90	1.76	1.09	2.09	0.17	0.018	0.011	-1.918
T_6	33.92	35.65	38.66	41.12	6.938	7.013	7.090	7.098	4.15	1.45	1.41	1.07	0.18	0.035	0.018	0.313
T_7	34.29	37.24	40.27	42.69	4.110	4.120	4.220	4.230	3.12	1.25	0.76	1.10	0.24	0.027	0.016	-1.044
T_8	28.64	31.92	34.59	38.87	5.810	5.940	6.000	6.020	6.07	1.63	2.24	2.43	0.31	0.039	0.019	1.512
S.E (m)	**0.247**	**0.382**	**0.300**	**0.191**	**0.059**	**0.077**	**0.092**	**0.195**	**0.614**	**0.225**	**0.182**	**0.214**	**0.029**	**0.002**	**0.001**	**0.246**
C.D (0.05)	**0.731**	**1.131**	**0.889**	**0.566**	**0.125**	**0.159**	**0.191**	**0.404**	**1.762**	**0.643**	**0.524**	**0.582**	**NS**	**0.005**	**0.002**	**0.728**

was on par with the genotype T_5 during second cut. The genotype T_5 (2.09 g m^{-2} day^{-1}) was on par with the genotype T_8 during the fourth cutting. The lowest crop growth rate was observed in the genotype T_5 (1.9 g m^{-2} day^{-1}) in the first cutting which was on par with the genotypes T_1 (2.9 g m^{-2} day^{-1}) , T_3 (2.71 g m^{-2} day^{-1}) and T_7 (3.12 g m^{-2} day^{-1}). During the second cutting, the genotype T_3 (0.67 g m^{-2} day^{-1}) recorded the lowest crop growth rate and was on par with the genotypes T_2 (1.05 g m^{-2} day^{-1}) and T_4 (0.95 g m^{-2} day^{-1}). In the third cutting, the genotype T_3 (0.31 g m^{-2} day^{-1}) was recorded lowest CGR and was on par with the genotype T_7 (0.76 g m^{-2} day^{-1}). The genotype T_3 (0.69 g m^{-2} day^{-1}) recorded the lowest crop growth rate which was on par with the genotypes T_1(0.77 g m^{-2} day^{-1}), T_6 (1.07 g m^{-2} day^{-1}) and T_7 (1.1 g m^{-2} day^{-1}).

4.2.2.4.4 Net Assimilation Rate (g dm^{-2} day^{-1})

The highest net assimilation rate was observed in the genotype T_8 (0.039 g dm^{-2} day^{-1}, 0.019 g dm^{-2} day^{-1} and 1.512 g dm^{-2} day^{-1}) during the second third and fourth cutting which was on par with the genotypes T_6 (0.035 g dm^{-2} day^{-1} and 2.9 g dm^{-2} day^{-1}) in the second and third cutting. The lowest net assimilation rate was recorded from the genotypes T_3 (0.017 g dm^{-2} day^{-1} and 0.010 g dm^{-2} day^{-1}) and T_4 (-5.651 g m^{-2} day^{-1}) during the second, third and fourth cuttings. The genotypes T_5 (0.018 g dm^{-2} day^{-1} and 0.011 g m^{-2} day^{-1}) and T_1 (0.011 g m^{-2} day^{-1}) was on par with the genotype T_3 in the second and third cutting.

4.2.3 Mean performance of hedge lucerne at College of Horticulture (COH), Thrissur

The mean performances of eight hedge lucerne genotypes for different parameters of growth, yield, quality and physiological characters at COH, Thrissur were studied.

4.2.3.1 Growth characters

The mean performances of growth characters of hedge lucerne genotypes for different cuttings at COH, Thrissur are presented in Table 11.

4.2.3.1.1 Plant height (cm)

The genotype T_8 showed the maximum plant height during all the four cuttings (99.46 cm, 104.8 cm, 110.7 cm and 114.1 cm). The minimum plant height was observed for the genotypes T_3 for the first (55.12 cm), second (59.16 cm), third (63.59 cm) and fourth (66.13 cm) cuttings.

4.2.3.1.2 Number of branches plant^{-1}

The number of branches plant^{-1} showed significant difference in all the eight genotypes of hedge lucerne. The maximum branches were observed for the genotype T_8 at all the four cuttings (7.910, 8.610, 9.468 and 10.38). The lowest branches were obtained for the genotype T_7 during first (1.878), second (2.104), third (2.760) and fourth (3.200) cut and it was on par with T_4 during first (1.943) and second (2.188) cut of hedge lucerne.

4.2.3.1.3 Length of branches (cm)

The length of branches varied significantly in all the genotypes. The longest branch was observed for the genotype T_8 (61.09 cm, 64.86 cm, 69.37 cm and 73.49 cm) while the genotype T_1 showed the shortest branch (14.26 cm, 15.62 cm, 19.64 cm and 22.44 cm) for all the four cuttings.

4.2.3.1.4 Number of leaves plant^{-1}

For the number of leaves plant^{-1}, the genotype T_6 (108.9) showed maximum number of leaves at first cut, T_1 (115.2 and 125.6) showed more number of leaves during second and third cut, while T_5 (143.3) recorded maximum number of leaves during fourth cut of hedge lucerne. The genotype T_6 was on par with T_1 during second (113.2) and third (123.9) cut, while T_8 (124.6) was on par with T_1 during third cut of hedge lucerne. The genotypes T_1 (142.2)

Table. 11 Mean performances of biometric characters of different cuttings of hedge lucerne at COH, Thrissur

Genotypes	Plant Height (cm)				Number of Branches Plant^{-1}				Length of Branches (cm)			
	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut
T_1	93.29	100.8	104.1	108.4	3.090	3.810	4.123	4.620	14.26	15.62	19.64	22.44
T_2	66.26	71.19	78.64	81.12	3.638	4.090	4.895	5.135	21.05	25.34	28.91	32.23
T_3	55.12	59.16	63.59	66.13	7.208	7.943	8.753	9.675	23.22	26.84	31.29	36.46
T_4	74.59	80.64	84.31	88.18	1.943	2.188	2.945	3.375	40.95	45.20	47.61	53.10
T_5	87.22	91.62	95.82	98.24	4.120	4.818	5.178	5.663	46.38	51.61	55.94	60.87
T_6	94.92	99.81	104.2	106.7	2.100	2.940	3.160	3.633	34.12	38.24	42.09	46.74
T_7	70.66	76.23	80.99	84.92	1.878	2.140	2.760	3.200	21.85	25.64	28.68	32.94
T_8	99.64	104.8	110.7	114.1	7.910	8.610	9.468	10.38	61.09	64.86	69.37	73.49
S.E (m)	**0.840**	**0.961**	**0.851**	**0.507**	**0.030**	**0.057**	**0.045**	**0.081**	**0.349**	**0.480**	**0.521**	**0.225**
C.D (0.05)	**2.488**	**2.844**	**2.519**	**1.501**	**0.090**	**0.169**	**0.133**	**0.170**	**1.032**	**1.421**	**1.542**	**0.665**

Genotypes	Number of Leaves Plant^{-1}				Leaf to Stem Ratio				Number of Pods Cluster^{-1}			
	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut
T_1	98.98	115.6	125.6	142.2	0.810	0.850	0.860	0.868	0.000	0.890	1.100	1.200
T_2	76.38	90.65	98.63	106.6	0.620	0.638	0.642	0.630	1.150	1.283	1.490	1.625
T_3	69.56	75.12	82.39	91.70	0.840	0.872	0.915	0.930	0.980	1.010	1.090	1.180
T_4	94.28	100.6	112.7	118.7	0.650	0.670	0.702	0.715	1.250	1.950	2.120	2.370
T_5	84.95	95.64	109.6	143.3	0.570	0.600	0.630	0.653	1.150	1.490	1.670	1.963
T_6	108.9	113.2	123.9	135.7	0.760	0.780	0.810	0.840	0.000	0.000	0.000	0.000
T_7	74.91	86.31	91.19	110.3	0.680	0.710	0.730	0.810	1.890	2.010	2.130	2.553
T_8	98.65	106.3	124.6	139.2	0.730	0.750	0.790	0.793	1.450	1.850	1.950	2.515
S.E (m)	**0.945**	**0.959**	**0.998**	**2.489**	**0.008**	**0.007**	**0.007**	**0.032**	**0.013**	**0.009**	**0.015**	**0.153**
C.D (0.05)	**2.799**	**2.838**	**2.956**	**5.177**	**0.023**	**0.020**	**0.020**	**0.059**	**0.037**	**0.027**	**0.044**	**0.320**

and T_8 (139.2) were on par with the genotype T_5 at fourth cut of hedge lucerne. The genotype T_3 recorded the minimum number of leaves during first (69.56), second (75.12), third (82.39) and fourth (91.70) cuts.

4.2.3.1.5 Leaf to stem ratio

During all the four cuts the genotype T_3 recorded the highest (0.840, 0.872, 0.915 and 0.930) leaf to stem ratio compared to other genotypes. The lowest leaf to stem ratio was observed for the genotype T_5 at first (0.570), second (0.600) and third (0.630) cut, whereas, T_2 showed the lowest (0.630) ratio during fourth cut. The genotype T_5 (0.653) was on par with T_2 during fourth cut.

4.2.3.1.6 Number of pods cluster^{-1}

The highest pods cluster^{-1} was noticed in the genotype T_7 in all the four cuttings (1.890, 2.010, 2.130 and 2.553). The genotype T_4 was on par with T_7 during third (2.102) and fourth cut (2.370) while the genotype T_8 was on par with the genotype T_7 during fourth cut. No pods were noticed in the genotype T_6 during all the different stage of cuttings.

4.2.3.2. Yield attributes

The mean performances of yield attributes of hedge lucerne genotypes for different cuttings at COH, Thrissur are given in Table 12.

4.2.3.2.1 Green fodder yield (g plant^{-1})

The variation in green fodder yield was noticed during each cut in hedge lucerne. During first cut, the highest yield was observed in case of the genotype T_1 (90.480 g) which was on par with the genotype T_8. For the rest three cuttings, the genotype T_8 showed the maximum green fodder yield of 96.367 g, 100.89 g and 110.54 g respectively, which was on par with the genotype T_1 (95.308 g, 100.58 g and 108.58 g). The lowest yield was performed by the genotype T_3 during all the four cuttings.

Table. 12 Mean performance of yield attributes of different cuttings of hedge lucerne at COH, Thrissur

Genotypes	Green Fodder Yield (g)				Dry Fodder Yield (g)			
	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut
T_1	90.840	95.308	100.58	108.76	22.343	24.250	26.323	29.365
T_2	79.610	84.910	90.673	95.505	17.560	19.880	21.053	23.878
T_3	69.398	75.123	79.420	81.748	17.420	19.120	19.338	19.620
T_4	72.100	82.087	88.640	95.263	20.368	23.580	24.960	27.615
T_5	81.690	89.980	94.940	102.04	19.658	22.150	24.393	26.530
T_6	76.310	84.288	93.293	105.76	20.150	24.560	27.640	29.448
T_7	75.280	81.073	88.642	110.43	18.250	20.330	22.940	27.608
T_8	90.373	96.367	100.89	110.54	21.208	25.220	29.548	31.240
S.E (m)	**0.808**	**0.936**	**0.731**	**2.153**	**0.208**	**0.257**	**0.212**	**0.174**
C.D (0.05)	**2.392**	**2.772**	**2.165**	**4.477**	**0.617**	**0.760**	**0.629**	**0.514**

4.2.3.2.2 Dry fodder yield (g plant^{-1})

The highest dry fodder yield was obtained for the genotype T_1 (22.43 g) during first cut of crop while, the genotype T_8 showed the maximum yield during remaining three cuttings. The lowest dry fodder yield was recorded for the genotype T_3 for all the four cuttings.

4.2.3.3 Quality aspects

The mean performances of quality aspects of hedge lucerne genotypes for different cuttings at COH, Thrissur are presented in Table 13.

4.2.3.3.1 Crude protein content (%)

The crude protein content was highest for the genotype T_8 during first (22.41%), second (22.43%), third (22.58%) and fourth (22.67%) cuttings. Whereas the lowest protein content was observed for the genotype T_4 in all the stages of cuttings (11.00%, 11.00%, 11.19% and 11.26%).

4.2.3.3.2 Crude fibre content (%)

During the four cuttings of hedge lucerne, the highest crude fibre content was observed for the genotype T_8 (27.31%, 27.34%, 27.65% and 28.37% respectively). The lowest crude fibre content was recorded for the genotype T_3 for all the four cuttings (20.42%, 20.45%, 20.69% and 20.76% respectively).

4.2.3.4 Physiological characters

The mean performances of physiological characters of hedge lucerne genotypes for different cuttings at COH, Thrissur was listed in Table 14.

4.2.3.4.1 Dry matter production (g plant^{-1})

The genotype T_8 recorded maximum dry matter production (31.25 g, 33.62 g, 36.52 g and 38.65 g) during first, second, third and fourth cuttings. The lowest dry matter production was obtained from the genotype

Table. 13 Mean performances of quality aspects of different cuttings of hedge lucerne at COH, Thrissur

Genotypes	Crude Protein Content (%)				Crude Fibre Content (%)			
	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut
T_1	18.20	18.24	18.59	18.96	21.32	21.32	21.45	21.83
T_2	13.42	13.54	13.68	13.78	20.42	20.45	20.69	20.76
T_3	12.00	12.09	12.12	12.37	24.00	24.01	24.21	24.39
T_4	11.00	11.00	11.19	11.26	22.51	22.63	22.82	22.86
T_5	12.20	12.21	12.39	12.65	26.22	26.23	26.38	26.50
T_6	18.12	18.14	18.65	18.78	22.00	22.09	22.13	22.36
T_7	21.51	21.52	21.64	21.74	23.24	23.28	23.42	25.41
T_8	22.41	22.43	22.58	22.67	27.31	27.34	27.65	28.37
S.E (m)	**0.204**	**0.158**	**0.158**	**0.185**	**0.196**	**0.202**	**0.174**	**0.172**
C.D (0.05)	**0.604**	**0.467**	**0.469**	**0.549**	**0.581**	**0.597**	**0.516**	**0.510**

Fig 5. Mean performance of yield attributes of hedge lucerne at COH, Thrissur

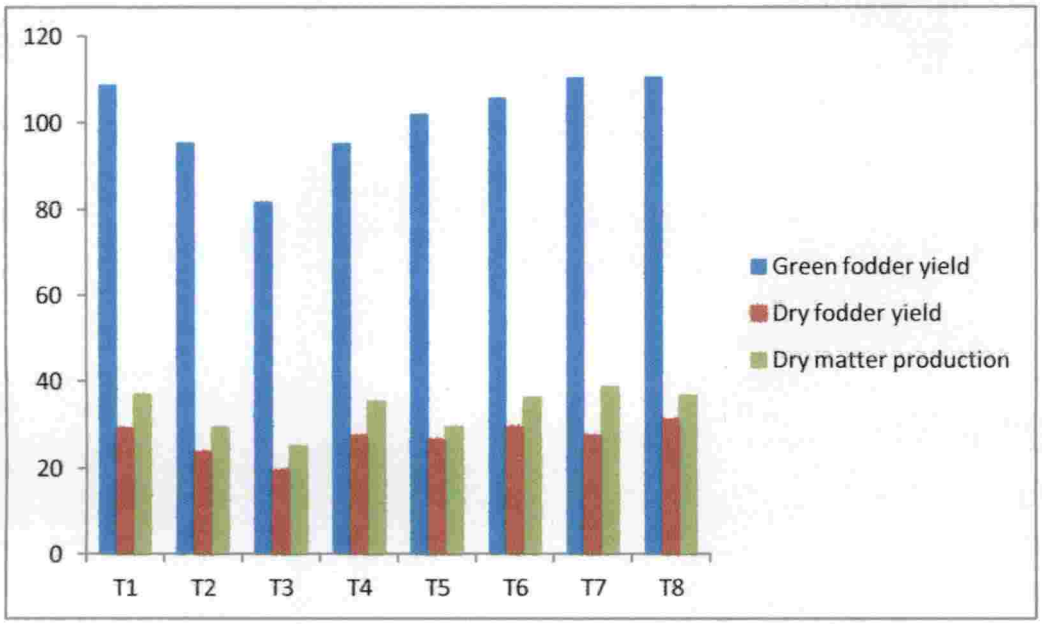


Fig 6. Mean performance of quality attributes of hedge lucerne at COH, Thrissur

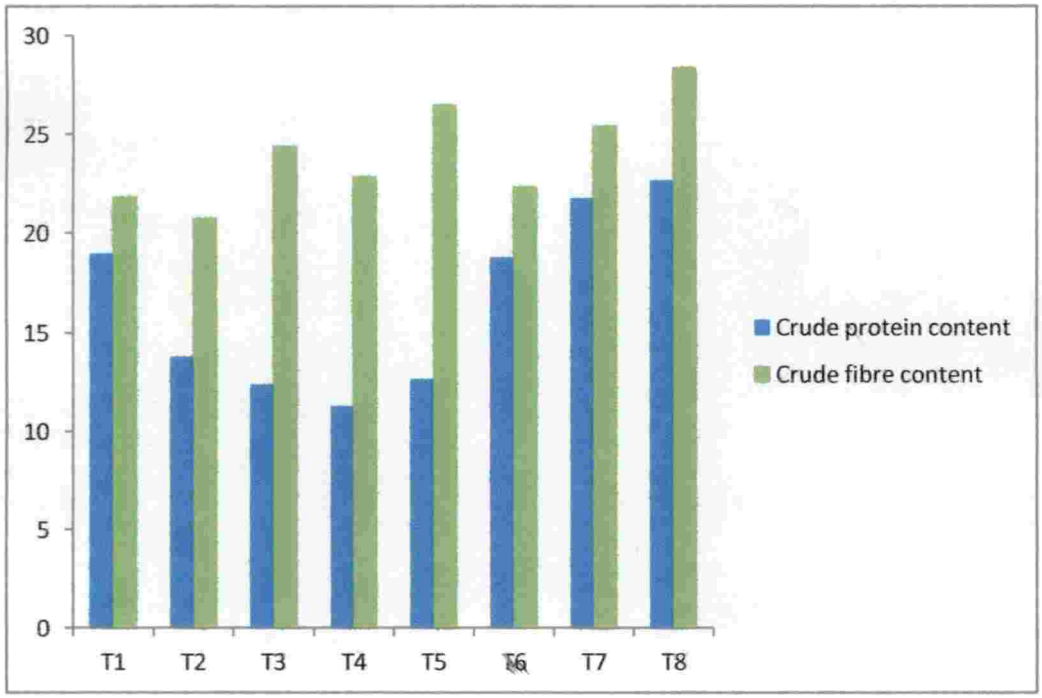


Table. 14 Mean performances of physiological characters of different cuttings of hedge lucerne at COH, Thrissur

Genotypes	Dry Matter Production (g)				Leaf Area Index				Crop Growth Rate ($g\ m^{-2}\ day^{-1}$)				Net Assimilation Rate ($g\ dm^{-2}\ day^{-1}$)			
	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut
T_1	28.62	31.29	34.59	36.91	6.418	6.530	6.620	6.950	3.32	1.27	1.38	2.03	0.056	0.020	0.303	0.088
T_2	20.33	22.45	25.33	29.46	3.228	3.410	3.563	3.813	2.91	1.55	0.78	1.88	0.071	0.018	1.139	0.115
T_3	18.61	20.96	23.01	25.05	2.013	2.123	2.750	2.858	3.60	1.13	0.15	0.19	0.056	0.022	0.061	0.793
T_4	25.96	28.61	23.56	35.37	4.278	4.520	4.650	4.978	3.83	2.14	0.92	1.77	0.076	0.029	0.101	0.499
T_5	20.37	21.09	25.28	29.59	5.010	5.160	5.760	5.835	2.84	1.66	1.41	1.43	0.057	0.060	0.562	0.196
T_6	29.66	31.29	34.52	36.29	6.120	6.240	6.308	6.438	3.01	2.67	1.97	1.20	0.043	0.012	0.408	0.059
T_7	31.25	33.62	36.52	38.65	4.558	4.820	4.860	4.973	3.54	1.39	1.59	1.13	0.039	0.028	0.714	0.819
T_8	28.64	31.24	35.11	36.73	5.120	5.250	5.410	5.535	3.89	2.94	2.89	3.11	0.121	0.064	1.411	0.253
S.E (m)	**0.254**	**0.230**	**0.264**	**0.193**	**0.059**	**0.067**	**0.081**	**0.230**	**0.393**	**0.256**	**0.215**	**0.223**	**0.003**	**0.004**	**0.090**	**0.060**
C.D (0.05)	**0.752**	**0.680**	**0.781**	**0.570**	**0.126**	**0.138**	**0.170**	**0.478**	**0.112**	**0.734**	**0.594**	**0.641**	**0.010**	**0.011**	**0.266**	**0.178**

T_3 (31.25 g, 33.62 g, 36.52 g, 38.65g) during first, second, third and fourth cuttings.

4.2.3.4.2 Leaf Area Index

The genotypes showed significant variation for the character leaf area index. The genotype T_1 showed the maximum leaf area index at all the four cuttings (6.418, 6.530, 6.620 and 6.950 respectively). The genotype T_3 recorded the minimum leaf area index of 2.013, 2.123, 2.750 and 2.858 during first, second, third and fourth cut respectively.

4.2.3.4.3 Crop Growth Rate (g m^{-2} day^{-1})

Among the hedge lucerne genotypes, the maximum crop growth rate was observed in the genotype T_8 (3.89 g m^{-2} day^{-1}, 2.94 g m^{-2} day^{-1}, 2.89 g m^{-2} day^{-1} and 3.11 g m^{-2} day^{-1}) during the first, second, third and fourth cuttings. The genotypes T_4 (3.83 g m^{-2} day^{-1}) and T_6 (2.67 g m^{-2} day^{-1}) were on par with the genotype T_8 during first and second cuttings. The lowest crop growth rate was observed in the genotypes T_5 (2.84 g m^{-2} day^{-1}), T_3 (1.13 g m^{-2} day^{-1}, 0.15 g m^{-2} day^{-1} and 0.19 g m^{-2} day^{-1}) during the first, second, third and fourth cuttings which was on par with T_2 (2.91 g m^{-2} day^{-1}) in the first cutting, T_1 (1.27 g m^{-2} day^{-1}), T_2 (1.55 g m^{-2} day^{-1}), T_5 (1.66 g m^{-2} day^{-1}) and T_7 (1.39 g m^{-2} day^{-1}) during the second cutting.

4.2.3.4.4 Net Assimilation Rate (g dm^{-2} day^{-1})

The maximum net assimilation rate was recorded in the genotype T_8 (0.121 g dm^{-2} day^{-1}, 0.064 g dm^{-2} day^{-1}, 1.411 g dm^{-2} day^{-1}) and T_7 (0.819 g dm^{-2} day^{-1}) during the first, second, third and fourth cuttings. The genotypes T_5 (0.06 g dm^{-2} day^{-1}) and T_3 (0.793 g dm^{-2} day^{-1}) was on par with the genotypes T_8 and T_7 during the second and fourth cuttings respectively. The lowest net assimilation rate was observed in the genotypes T_7 (0.039 g dm^{-2} day^{-1}), T_6 (0.012 g dm^{-2} day^{-1}), T_3 (0.061 g dm^{-2} day^{-1}) and

T_6 (0.059 g dm^{-2} day^{-1}) during the first, second, third and fourth cuttings respectively.

4.2.4 Mean performance of hedge lucerne at RARS, Ambalavayal

The mean performances of eight hedge lucerne genotypes for different parameters of growth, yield, quality and physiological characters at Ambalavayal were studied.

4.2.4.1 Growth characters

The mean performances of growth characters of hedge lucerne genotypes for different cuttings at RARS, Ambalavayal are presented in Table 15.

4.2.4.1.1 Plant height (cm)

The highest plant height was observed for the genotype T_8 during first (100.9 cm) and second (105.3 cm) cut, T_1 during third cut (111.0 cm) and T_8 at fourth cut in hedge lucerne. The genotype T_8 (110.9 cm) was on par with T_1 during third cut, whereas T_3 recorded the lowest plant height during all the cuttings (60.22 cm, 64.12 cm, 70.95 cm and 74.63 cm).

4.2.4.1.2 Number of branches plant^{-1}

During first and second cut, the number of branches was more for the genotype T_8 (8.070 and 8.638), but during third and fourth cut the genotype T_3 (9.845 and 11.35) reported the maximum branches plant^{-1}. The lowest number of branches was recorded for the genotype T_4 at first (2.933) and third (4.573) cut, whereas, during second and fourth cut the minimum branches were reported for the genotype T_7 (3.310 and 5.783).

4.2.4.1.3 Length of branches (cm)

The length of branches showed significant difference among the genotypes. The genotype T_8 reported the maximum length of branches during all the four cut (60.28 cm, 64.25 cm, 70.91 cm and 75.09 cm), while, the genotype T_1 reported

Table. 15 Mean performances of biometric characters of different cuttings of hedge lucerne at RARS, Ambalavayal

Genotypes	Plant Height (cm)				Number of Branches Plant^{-1}				Length of Branches (cm)			
	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut
T_1	90.37	96.52	111.0	114.5	3.750	4.290	5.943	6.325	13.59	16.52	19.34	23.02
T_2	76.33	81.09	85.67	90.96	5.190	5.890	6.315	7.973	24.39	28.68	31.28	36.24
T_3	60.22	64.12	70.95	74.63	7.010	7.690	9.845	11.35	20.94	25.66	30.91	34.76
T_4	87.54	90.85	94.66	99.77	2.933	3.580	4.573	5.855	43.28	46.38	51.82	54.87
T_5	88.64	93.66	97.89	10.29	4.110	5.760	6.818	7.090	50.96	54.44	60.29	64.15
T_6	90.22	94.28	99.09	112.3	3.610	4.670	5.183	5.833	29.64	34.92	41.09	48.19
T_7	74.31	80.94	83.94	86.21	3.090	3.310	4.820	5.783	17.49	21.09	28.55	33.16
T_8	100.9	105.3	110.9	116.7	8.070	8.638	9.410	10.61	60.28	64.25	70.91	75.09
S.E (m)	**0.609**	**0.896**	**0.939**	**0.521**	**0.026**	**0.047**	**0.054**	**0.081**	**0.317**	**0.378**	**0.290**	**0.332**
C.D (0.05)	**1.804**	**2.653**	**2.779**	**1.544**	**0.086**	**0.139**	**0.161**	**0.166**	**0.938**	**1.120**	**0.859**	**0.982**

Genotypes	Number of Leaves Plant^{-1}				Leaf to Stem Ratio				Number of Pods Cluster^{-1}			
	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut
T_1	112.6	124.3	130.2	144.3	0.850	0.900	0.905	0.893	0.000	1.423	1.590	1.754
T_2	72.61	86.34	98.64	115.0	0.690	0.710	0.730	0.780	1.030	1.120	1.218	1.558
T_3	75.94	88.61	94.26	102.8	0.850	0.890	0.910	0.925	1.130	1.380	1.448	1.648
T_4	94.61	104.7	112.9	127.9	0.730	0.750	0.780	0.810	1.850	2.090	2.190	2.733
T_5	88.64	100.3	119.6	135.4	0.600	0.630	0.650	0.675	1.550	1.893	2.103	2.183
T_6	106.5	125.6	139.6	142.5	0.840	0.880	0.900	0.943	0.000	0.000	0.000	0.000
T_7	76.31	86.31	95.62	112.5	0.780	0.810	0.840	0.858	1.413	1.868	2.190	2.483
T_8	101.3	114.6	134.2	143.0	0.750	0.790	0.810	0.858	1.948	2.000	2.010	2.310
S.E (m)	**0.951**	**0.993**	**0.832**	**2.878**	**0.007**	**0.009**	**0.008**	**0.032**	**0.011**	**0.015**	**0.017**	**0.051**
C.D (0.05)	**2.815**	**2.939**	**2.464**	**5.987**	**0.020**	**0.028**	**0.023**	**0.058**	**0.032**	**0.044**	**0.049**	**0.150**

the minimum length of branches at all the four cut (13.59 cm, 16.52 cm, 19.34 cm and 23.02 cm).

4.2.4.1.4 Number of leaves plant^{-1}

The number of leaves was highest for the genotype T_1 at first (112.6), second (124.3) and fourth (144.3) cut and during third cut the genotype T_6 (139.6) recorded the maximum number of leaves. The genotypes T_8 (143.0) and T_6 (142.5) was on par with T_1 during fourth cut of hedge lucerne. The lowest number of leaves was observed in the genotype T_2 (72.61) during first cut, T_7 (86.31) during second cut, and T_3 during third (94.26) and fourth cut (102.8).

4.2.4.1.5 Leaf to stem ratio

The leaf to stem ratio was highest for the genotype T_1 (0.850) and T_3 (0.850) during first cut and T_1 at second (0.900) cut, T_3 at third (0.910) and T_6 at fourth (0.943) cut. The lowest leaf to stem ratio was observed for the genotype T_5 for all the four cuttings in hedge lucerne (0.600, 0.630, 0.650 and 0.675).

4.2.4.1.6 Number of pods cluster^{-1}

The number of pods was highest in the genotype T_8 (1.948) of first cut, in the genotype T_4 (2.090, 2.190 and 2.733) of second, third and fourth cut respectively. No pods were observed in case of the genotype T_6 during all the four cuts and in T_1 during first cut.

4.2.4.2 Yield attributes

The mean performances of yield attributes of hedge lucerne genotypes for different cuttings at RARS, Ambalavayal are given in Table 16.

4.2.4.2.1 Green fodder yield (g plant^{-1})

The green fodder yield was highest for the genotype T_8 at first (95.120 g), second (97.690 g), third (104.81 g) and fourth (118.56 g) cuts, T_1 and T_6 were on par during second (96.340g and 69.373 g) and third (102.85 g and 100.27 g) cut.

Table. 16 Mean performance of yield attributes of different cuttings of hedge lucerne at RARS, Ambalavayal

Genotypes	Green Fodder Yield (g)				Dry Fodder Yield (g)			
	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut
T_1	89.340	96.340	102.85	113.39	28.540	30.290	31.318	34.175
T_2	81.270	90.270	96.380	104.53	21.008	24.810	28.583	30.133
T_3	75.930	80.910	85.910	94.368	18.638	21.580	22.610	25.628
T_4	89.373	95.668	98.620	104.70	24.290	29.993	30.540	33.415
T_5	80.670	84.290	87.460	95.115	21.590	23.558	24.510	26.360
T_6	89.640	96.373	100.27	112.18	24.950	28.540	30.940	33.483
T_7	84.390	94.120	97.613	112.21	24.120	27.693	29.330	32.665
T_8	95.120	97.690	104.81	118.56	30.890	31.850	34.223	36.753
S.E (m)	**0.976**	**1.088**	**1.148**	**2.087**	**0.237**	**0.298**	**0.309**	**0.188**
C.D (0.05)	**2.891**	**3.222**	**3.400**	**4.341**	**0.700**	**0.882**	**0.914**	**0.556**

The lowest green fodder yield was reported for the genotype T_3 at all the four cuttings (75.930 g, 80.910 g, 85.910 g and 94.368 g).

4.2.4.2.1 Dry fodder yield (g plant^{-1})

The highest and lowest dry fodder yield was recorded for the genotype T_8 (30.890 g, 31.850 g, 34.223 g and 36.753 g) and T_3 (18.638 g, 21.580 g, 22.610 g and 25.628 g) during all the cuts in hedge lucerne.

4.2.4.3 Quality aspects

The mean performances of quality aspects of hedge lucerne genotypes for different cuttings at RARS, Ambalavayal are given in Table 17.

4.2.4.3.1 Crude protein content (%)

The highest crude protein content was reported for the genotype T_7 during first three cuttings (24.00%, 24.10% and 24.28% respectively) which was on par with the genotype T_8 (23.94%, 24.00% and 24.16% respectively). During fourth cut the genotypeT_8 showed the maximum crude protein content of 24.98 %. The lowest crude protein content was reported for the genotype T_5 during all the cuts (13.00%, 13.49%, 13.15% and 13.88% accordingly) which was on par with the genotype T_4 (13.40%, 13.49%, 13.58% and 13.95% accordingly) during all the four cuttings in hedge lucerne.

4.2.4.3.2 Crude fibre content (%)

For all the four cuts, the genotype T_8 showed the maximum crude fibre content (30.00%, 30.02%, 30.19% and 31.52% respectively). The lowest crude fibre content was reported by the genotype T_2 for all the four cuts (23.00%, 23.00%, 23.01% and 23.23% respectively), which was on par with the genotype T_4 (23.45%, 23.54%, 23.69% and 23.79% respectively).

Table. 17 Mean performances of quality aspects of different cuttings of hedge lucerne at RARS, Ambalavayal

Genotypes	Crude Protein Content (%)				Crude Fibre Content (%)			
	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut
T_1	21.24	21.26	21.45	21.82	24.11	24.21	24.26	24.35
T_2	15.00	15.00	15.06	15.31	23.00	23.00	23.01	23.23
T_3	15.01	15.03	15.12	15.32	27.13	27.25	27.45	27.78
T_4	13.40	13.49	13.58	13.95	23.45	23.54	23.69	23.79
T_5	13.00	13.11	13.15	13.88	28.00	28.11	28.21	28.28
T_6	20.24	20.41	20.46	20.69	24.11	24.12	24.32	24.79
T_7	24.00	24.10	24.28	24.71	27.12	27.29	27.54	27.97
T_8	23.94	24.00	24.16	24.98	30.00	30.02	30.19	31.52
S.E (m)	**0.228**	**0.169**	**0.165**	**0.299**	**0.195**	**0.256**	**0.267**	**0.288**
C.D (0.05)	**0.674**	**0.501**	**0.489**	**0.885**	**0.577**	**0.758**	**0.791**	**0.854**

Fig 7. Mean performance of yield characters of hedge lucerne at RARS, Ambalavayal

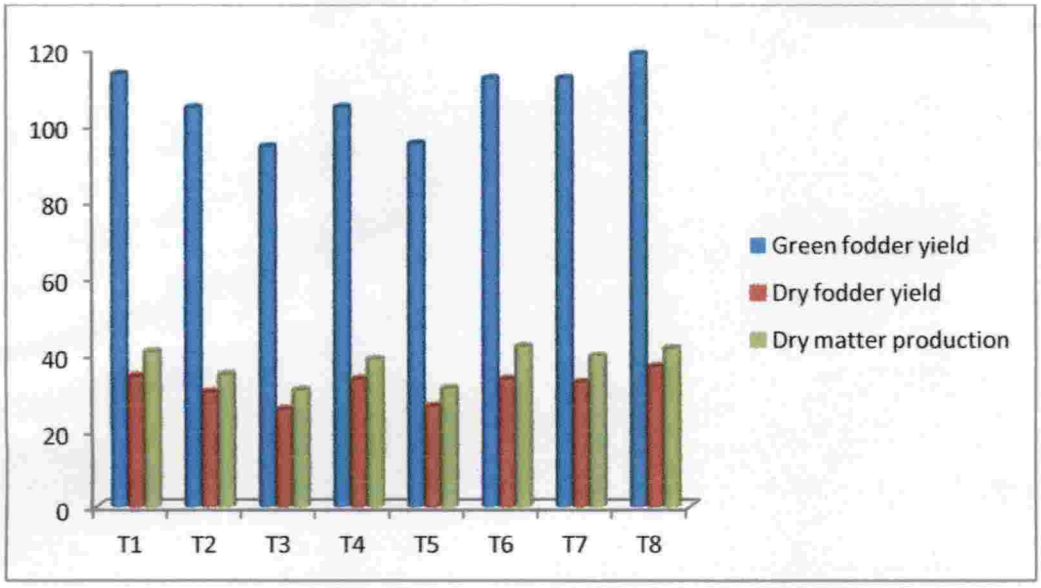
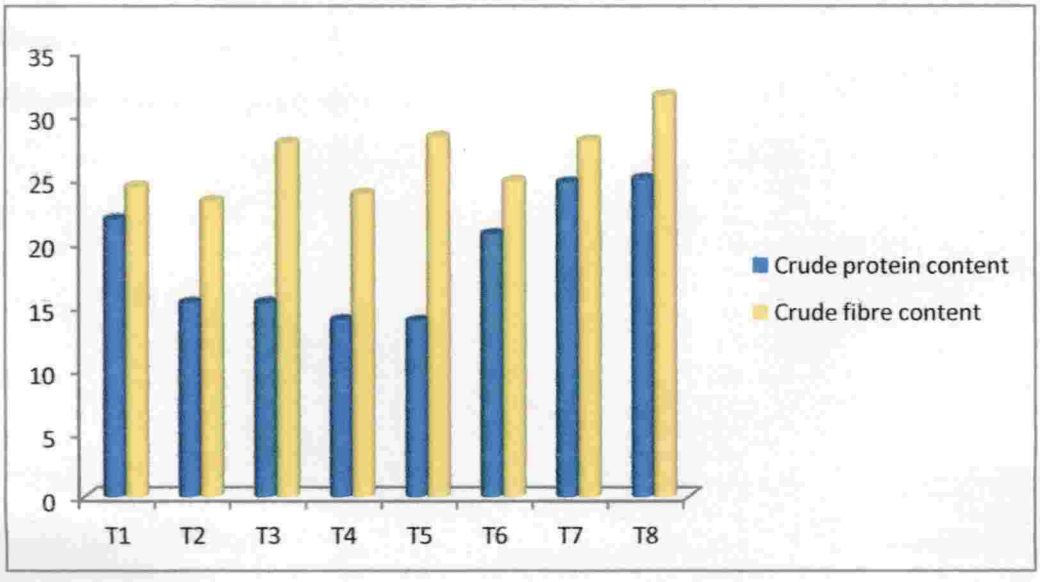


Fig 8. Mean performance of quality characters of hedge lucerne at RARS, Ambalavayal



4.3.4.4 Physiological characters

The mean performances of physiological characters of hedge lucerne genotypes for different cuttings at RARS, Ambalavayal are given in Table 18.

4.2.4.4.1 Dry matter production (g plant^{-1})

Dry matter production recorded maximum in the genotypes T_6 (34.93 g), T_8 (37.26 g and 40.12 g) and T6 (41.99 g). The genotype T_8 (41.53 g) was on par with the genotype T_6 during the fourth cutting. The lowest dry matter production was obtained in the genotypes T_5 (20.67 g), T_3 (24.92 g), T_5 (28.33 g) and T_3 (30.64 g).

4.2.4.4.2 Leaf Area Index

The leaf area index was highest for the genotype T_1 (7.250, 7.440, 7.540 and 7.660) during all the four cuts whereas, the genotype T_3 showed the minimum leaf area index for first (3.240), second (3.358), third (3.490) and fourth (3.585) cuts.

4.2.4.4.3 Crop Growth Rate (g m^{-2} day^{-1})

The highest crop growth rate was obtained from the genotypes T_2 (4.52 g m^{-2} day^{-1}), T_8 (3.80 g m^{-2} day^{-1}, 2.51 g m^{-2} day^{-1} and 2.22 g m^{-2} day^{-1}) during first, second, third and fourth cuttings respectively. The genotypes T_5 (3.54 g m^{-2} day^{-1}), T_6 (3.87 g m^{-2} day^{-1}) and T_8 (3.96 g m^{-2} day^{-1}) were on par with the genotype T_2 during the first cutting. The genotype T_2 (1.58g m^{-2} day^{-1}) and the genotype T_6 (1.6 g m^{-2} day^{-1}) were on par with the genotype T_8. During the fourth cut, the genotypes T_1 (1.9 g m^{-2} day^{-1}), T_2 (2.01 g m^{-2} day^{-1}), T_4 (1.92 g m^{-2} day^{-1}), T_6 (1.7 g m^{-2} day^{-1}) and T_7 (1.69 g m^{-2} day^{-1}) were on par with the genotype T_8.

4.2.4.4.4 Net Assimilation Rate (g dm^{-2} day^{-1})

The highest net assimilation rate was recorded in the genotype T_8 (0.059 g dm^{-2} day^{-1} and 0.021 g dm^{-2} day^{-1}) during first and second cutting

Table. 18 Mean performances of physiological characters of different cuttings of hedge lucerne at RARS Ambalavayal

Genotypes	Dry Matter Production (g)				Leaf Area Index				Crop Growth Rate ($g\ m^{-2}\ day^{-1}$)				Net Assimilation Rate ($g\ dm^{-2}\ day^{-1}$)			
	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut	1st cut	2nd cut	3rd cut	4th cut
T_1	31.64	34.52	38.51	40.64	7.250	7.440	7.540	7.660	4.30	1.17	0.69	1.90	0.028	0.016	0.021	0.012
T_2	28.55	30.56	32.15	34.69	4.163	4.260	4.308	4.468	4.52	2.48	1.58	2.01	0.045	0.014	0.067	0.011
T_3	21.94	24.92	28.62	30.64	3.240	3.358	3.490	3.585	2.47	0.64	0.37	1.03	0.027	0.015	0.013	0.014
T_4	28.54	32.06	34.62	38.64	5.978	6.098	6.130	6.273	3.19	1.96	0.69	1.92	0.026	0.011	0.027	0.011
T_5	20.67	25.95	28.33	31.06	5.840	5.970	6.010	6.240	3.54	1.31	0.63	1.23	0.026	0.015	0.037	0.012
T_6	34.93	36.36	38.64	41.99	7.060	7.120	7.280	7.488	3.87	2.39	1.60	1.70	0.024	0.011	0.034	0.010
T_7	27.59	31.25	35.26	39.48	4.990	5.100	5.118	5.215	2.93	2.38	1.09	1.69	0.058	0.011	0.018	0.012
T_8	34.22	37.26	40.12	41.53	6.480	6.520	6.820	6.908	3.96	3.80	2.51	2.22	0.059	0.021	0.031	0.013
S.E (m)	**0.327**	**0.291**	**0.314**	**0.337**	**0.089**	**0.074**	**0.067**	**0.294**	**0.342**	**0.315**	**0.321**	**0.265**	**0.001**	**0.001**	**0.001**	**0.000**
C.D (0.05)	**0.969**	**0.862**	**0.929**	**0.998**	**0.184**	**0.155**	**0.138**	**0.611**	**0.982**	**0.894**	**0.933**	**0.758**	**0.002**	**0.004**	**0.003**	**0.001**

whereas the genotypes T_2 (0.067 g dm^{-2} day^{-1}) and T_8 (0.013 g dm^{-2} day^{-1}) recorded highest during the third and fourth cutting respectively. The genotypes T_7 (0.059 g dm^{-2} day^{-1}) during the first cutting and T_1 (0.012 g dm^{-2} day^{-1}), T_5 (0.012 g dm^{-2} day^{-1}) and T_7 (0.012 g dm^{-2} day^{-1}) during the fourth cutting was on par with the genotype T_8. The lowest net assimilation rate was recorded in the genotypes T_6 (0.024 g dm^{-2} day^{-1}) in the first cutting, followed by the genotypes T_4 (0.011 g dm^{-2} day^{-1}), T_6 (0.011 g dm^{-2} day^{-1}), T_7 (0.011 g dm^{-2} day^{-1}) in the second cutting. The genotypes T_3 (0.013 g dm^{-2} day^{-1}) and T_6 (0.010 g dm^{-2} day^{-1}) during third and fourth cutting respectively. The genotypes T_4 (0.026 g dm^{-2} day^{-1}) and T_5 (0.026 g dm^{-2} day^{-1}) were on par with the genotype T_6 during the first cutting. The genotypes T_2 (0.014 g dm^{-2} day^{-1}), T_3 (0.015 g dm^{-2} day^{-1}) and T_5 (0.015 g dm^{-2} day^{-1}) were on par with the genotype T_4 in the second cutting. The genotypes T_2 (0.011 g dm^{-2} day^{-1}) and T_4 (0.011 g dm^{-2} day^{-1}) were on par with the genotype T_6 during the fourth cutting.

4.3 STABILITY ANALYSIS

4.3.1 Pooled Analysis of Variance

Eight genotypes of hedge lucerne were subjected to pooled analysis of variance for different characters *viz.*, plant height, number of branches $plant^{-1}$, length of branches $plant^{-1}$, number of leaves $plant^{-1}$, leaf to stem ratio, number of pods $cluster^{-1}$, green fodder yield, dry fodder yield, dry matter production, crude protein and crude fibre content over four locations. The analysis revealed that for the genotypes, G x E interactions were significant for all the characters studied. As the G x E interactions were significant for all the characters, further analysis were done for estimating the stability parameters (Table 19).

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 like plant height, number of branches $plant^{-1}$, number of leaves $plant^{-1}$, green fodder yield, dry fodder yield, dry matter production, crude protein and crude fibre content prioritizing the

Table 19 . Pooled Analysis of Variance (mean square) for different quantitative traits of hedge lucerne over four locations

Source of variation	df	Plant height	Number of branches plant^{-1}	Length of branches plant^{-1}	Number of leaves plant^{-1}	Leaf to stem ratio	Number of pods cluster^{-1}	Green fodder yield	Dry fodder yield	Dry matter production	Crude protein	Crude fibre
Genotypes	7	3946.99**	105.44**	4781.32**	4494.68**	0.13**	12.38**	1145.58**	195.43**	357.00**	331.14**	114.93**
Environment	3	285.86**	20.33**	14.26**	468.87**	0.03**	0.50**	249.09**	135.69**	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**	4.75**	6.43**	0.82**	0.82**
Error	96	1.31	0.46	0.40	12.99	0.0021	0.02	12.21	0.20	0.25	0.35	0.62

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

presence of G x E interaction for these traits. The mean sum of squares due to genotype was significant for the eleven characters under study (Table 20). 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 20). The linear component of Environment were significant for the characters like plant height, number of branches plant^{-1}, length of branches plant^{-1}, number of leaves plant^{-1}, leaf to stem ratio, number of pods cluster^{-1}, green fodder yield, dry fodder yield, dry matter production, crude protein and crude fibre content. The variation due to G x E (linear) were significant for the characters like plant height, number of branches plant^{-1}, number of leaves plant^{-1}, leaf to stem ratio, green fodder yield and dry fodder yield. The non linear component, pooled deviation were significant for the characters like length of branches plant^{-1}, number of leaves plant^{-1}, dry fodder yield and dry matter production indicating the importance of both linear and non linear components.

4.3.2 Environmental indices

The environmental indices of eleven characters is described in the Table 21. It was found that Vellayani was favourable for all of the characters whereas Thrissur was unfavourable for all the characters. Kottarakkara was highly favourable for number of leaves and number of pods while, Ambalavayal was favourable for number of branches and dry fodder yield.

4.3.3 Stability parameters

The estimation of stability parameters i.e., mean(μ), regression coefficient (b_i) and deviation from regression (S^2_{di}) for eleven characters are furnished below (Table 22).

4.3.3.1 Plant height

The maximum plant height was observed for the genotype T_8 (116.75 cm) followed by T_1 (112.87 cm) and the lowest was observed for the genotype T_3 (71.03 cm).

Table 20. Analysis of Variance (mean square) for mean data of different quantitative traits of hedge lucerne over four locations

Source of variations	df	Plant height	Number of branches plant^{-1}	Length of branches plant^{-1}	Number of leaves plant^{-1}	Leaf to stem ratio	Number of pods cluster^{-1}	Green fodder yield	Dry fodder yield	Dry matter production	Crude protein	Crude fibre
Genotypes	7	986.74**	26.36**	1195.33**	1123.67**	0.0321**	3.09**	286.39**	48.86**	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*	5.27**	6.17**	1.95**	1.79**
Environments	3	71.46**	5.08**	3.56	117.22**	0.0017	0.13**	62.27**	33.92**	38.09**	14.18**	12.84**
Environments (Lin)	1	214.39**	15.25**	10.70*	351.65**	0.0185**	0.37**	186.82**	101.77**	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**	2.52**	2.15	0.27	0.38
Pooled deviation	16	1.87	0.12	1.72**	21.08**	0.0007	0.02	3.39	0.46**	1.17**	0.15	0.10
Pooled error	96	1.31	0.11	0.40	3.25	0.0005	0.02	3.05	0.20	0.25	0.35	0.62
Total	31	232.48	6.63	271.78	290.31	0.0085	0.73	79.86	15.12	24.93	20.21	7.87

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

Table 21. Estimates of environmental indices (I_j) for each character of hedge lucerne under different locations

Sl. No.	Character	Vellayani	Kottarakkara	Thrissur	Ambalavayal
1.	Plant height	2.28	-0.52	-4.03	2.26
2.	Number of branches	0.56	-0.20	-1.04	0.68
3.	Length of branches	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	2.36	-0.66	-3.68	1.95
8.	Dry fodder yield	1.15	-0.15	-2.83	1.83
9.	Dry matter production	2.22	-0.21	-2.91	0.91
10.	Crude protein	1.34	-0.03	-1.81	0.49
11.	Crude fibre	1.26	-0.10	-1.70	0.58

Table 22. 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 22. continued

Genotype	Leaf to stem ratio			Number of pods			Green fodder yield			Dry fodder yield			Dry matter production		
	Mean	b_i	S^2_{di}	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	0.89	0.75	0.0005	1.51	2.12	0.011	112.35	1.12	-0.62	32.45	1.11	0.22	39.93	0.97	0.09
T_2	0.71	2.52	-0.0004	1.58	0.24	0.001	101.28	1.34	-0.30	27.46	1.28	0.05	32.62	0.99	0.98*
T_3	0.92	-0.17	-0.0002	1.43	1.30	0.019	90.45	2.38	-2.55	23.52	1.40	0.54	28.89	1.50	1.13*
T_4	0.76	1.09	0.0004	2.77	1.79	0.056*	100.67	1.74	0.001	31.23	1.27	-0.03	37.59	0.94	1.04*
T_5	0.67	0.37	-0.0004	2.14	1.23	-0.003	98.75	-1.45	9.20	27.03	0.02	0.83*	31.37	0.70	0.71*
T_6	0.88	1.56	0.000	0.00	0.00	-0.005	110.48	1.26	-2.54	31.77	0.77	0.42	40.62	1.34	0.47
T_7	0.84	1.18	0.0007	2.52	0.89	0.015	109.02	0.07	1.15	30.12	0.94	0.65*	40.32	0.27	3.95**
T_8	0.83	0.68	0.0008	2.38	0.42	0.031	115.42	1.52	-1.61	34.25	1.93	0.55	40.04	1.25	0.49
Grand mean	0.81			1.79			104.93			29.74			36.42		

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

Table 22. 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%

Among the genotypes, T_1 genotype (μ= 112.87, b_i = 1.07, S^2_{di}= 0.30) and the genotype T_6 (μ= 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 T_2, T_3 and T_4 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 T_5 and T_8 recorded b_i value of 0.75 and 0.58 with non-significant deviation from regression -0.21 and 1.44 respectively.

4.3.3.2 Number of branches plant^{-1}

The number of branches ranged from 4.29 (T_4) to 10.34 (T_8). The genotype T_1 (μ= 5.10, b_i = 1.10, S^2_{di}= -0.09), T_4 (μ= 4.29, b_i = 1.05, S^2_{di}= -0.03) and genotype T_5 (μ= 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 T_2, T_3 and T_6 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 T_7 (μ= 3.98, b_i = 0.78, S^2_{di}= 0.08).

4.3.3.3 Length of branches

Length of the branches ranged from 74.65 cm (T_8) to 22.96 cm (T_1). T_3 (b_i=1.05) was the genotype with near unit regression and non-significant deviation from regression, so T_3 was the stable genotype. T_8 was the genotype with more than unit regression and non-significant deviation from regression indicating high responsiveness towards the rich environment. The genotypes T_1 (b_i=0.62) and T_7 (b_i=0.29) showed less than unit regression with minimum non- significant deviation from regression. They were highly responsive in unfavourable environment.

4.3.3.4 Number of leaves plant[1]

The number of leaves varied from 145.03 (T_1) to T_3 (99.69). The genotype T_6 was identified as stable genotype with near unit regression (b_i=0.82) and non-significant deviation from regression. The genotype T_1 (b_i=0.58, S^2_{di}= -2.56) and T_7 (b_i=0.46, S^2_{di}= -2.03) were suitable for poor environment. They were performs under unfavourable environment.

4.3.3.5 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.

4.3.3.6 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.

4.3.3.7 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 T2, T4 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.

4.3.3.8 Dry fodder yield

The dry fodder yield ranged from 23.52g (T_3) to 34.25g (T_8). The genotype T_1 (μ=32.45, b_i=1.11, S^2_{di}= 0.22) was stable genotype with near unity regression coefficient and non-significant deviation from regression. The genotypes T_2 (μ=27.46, b_i=1.28, S^2_{di}= 0.05) T_4 (μ=31.23, b_i=1.27, S^2_{di} = -0.03) and T_8 (μ=34.25, b_i=1.93, S^2_{di} = 0.55) were identified as stable genotypes under favourable environment as they had more than one regression coefficient and non-significant deviation from regression. The genotype T_6 was identified as stable genotype under unfavourable environment due to the less than one regression coefficient and non-significant minimum deviation from regression.

4.3.3.9 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.

4.3.3.9 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

Fig 9. Comparison of green fodder yield with population mean of the eight hedge lucerne genotypes

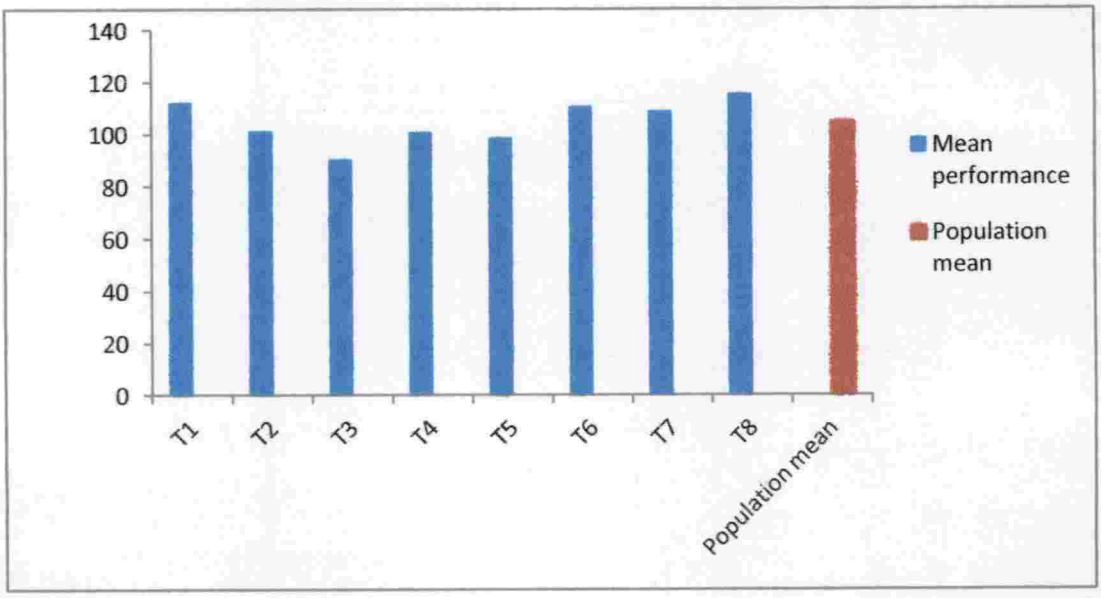


Fig 10. Comparison of dry fodder yield with population mean of the eight hedge lucerne genotypes

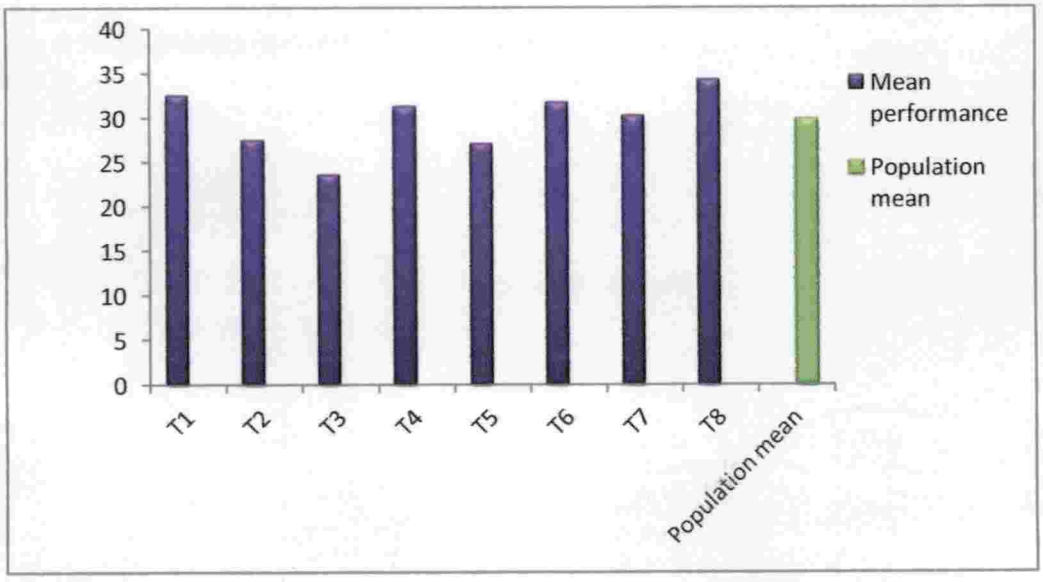


Fig 11. Comparison of dry matter production with population mean of the eight hedge lucerne genotypes

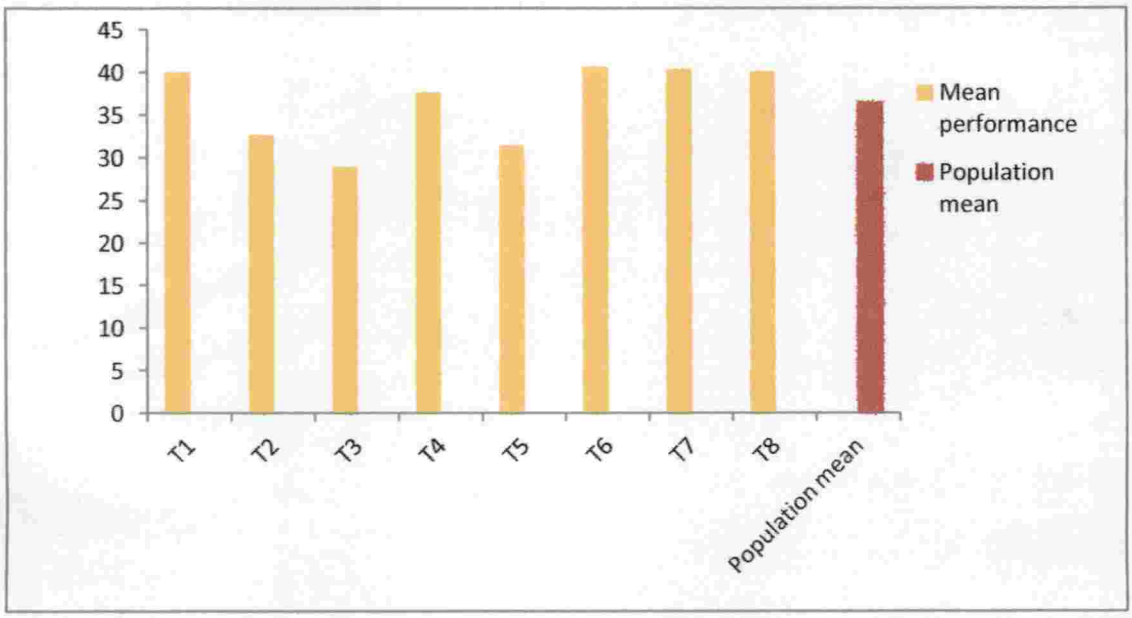


Fig12.Comparison of crude protein content with population mean of the eight hedge lucerne genotypes

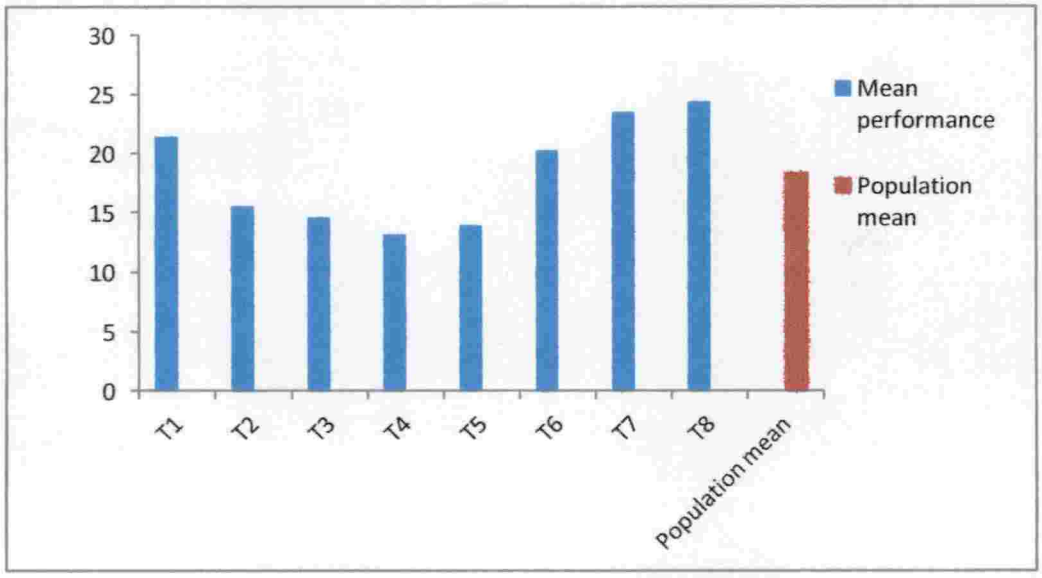
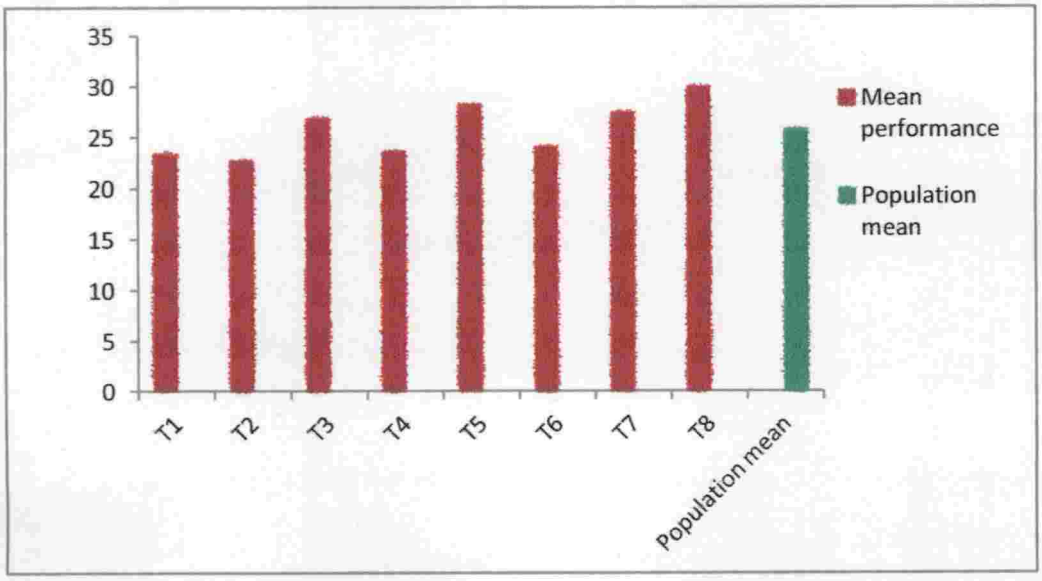


Fig 13. Comparison of crude fibre content with population mean of the eight hedge lucerne genotypes



deviation from regression and hence the genotype was suitable for poor environment.

4.3.3.10 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 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.

4.3.4 Identification of best genotypes for each location

Based on the ranking method, the best genotypes for each location were identified. The genotypes which had a score with mean value above mean ± SE (m) was assigned Rank 1. Those genotypes with score between mean ± SE (m) were assigned Rank 2 and the genotypes with score less than mean ± SE (m) were assigned Rank 3. The ranks of each genotype over four locations are described in Table 23. Based on the rank given to each genotype for the characters number of leaves plant^{-1}, green fodder yield, dry fodder yield, dry matter production, crude protein and crude fibre, the genotypes T_1, T_6 and T_8 were best suited for all locations (Table 23).

4.3.5 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.

Table 23. Ranking method for identifying best genotypes of hedge lucerne in each location

Table 23.1. .Location-I (COA, Vellayani)

Genotype	Number of leaves		Green fodder yield (g plant^{-1})		Dry fodder yield (g plant^{-1})		Dry matter production (g plant^{-1})		Crude protein content (%)		Crude fibre content (%)		Total of Rank
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	
T_1	146.23	1	116.55	1	34.31	1	41.96	1	23.61	1	24.52	3	8
T_2	113.12	3	103.09	3	28.60	3	34.02	3	16.93	3	24.64	3	18
T_3	104.89	3	96.04	3	25.99	3	32.65	3	16.16	3	28.49	2	17
T_4	128.20	2	105.84	2	32.81	1	40.21	1	14.16	3	24.25	3	12
T_5	136.53	1	96.35	3	27.18	2	33.67	3	14.99	3	29.55	1	13
T_6	142.74	1	113.34	1	31.94	2	43.08	1	21.66	2	25.06	3	10
T_7	111.00	3	112.21	1	30.36	2	40.48	1	24.44	1	28.64	1	9
T_8	146.12	1	119.57	1	35.89	1	43.04	1	25.46	1	30.99	1	6

Table 23. 2. Location-II (KVK, Kottarakkara)

Genotype	Number of leaves		Green fodder yield (g plant^{-1})		Dry fodder yield (g plant^{-1})		Dry matter production (g plant^{-1})		Crude protein content (%)		Crude fibre content (%)		Total of Rank
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	
T_1	147.45	1	110.69	1	31.97	1	40.19	1	21.17	1	22.71	3	8
T_2	143.87	1	101.99	2	27.25	2	32.30	3	16.02	3	22.25	3	14
T_3	99.37	3	88.89	3	22.84	3	27.25	3	14.54	3	26.66	1	16
T_4	124.68	2	97.42	2	31.11	1	36.12	2	13.14	3	23.44	3	13
T_5	144.09	1	103.91	2	28.05	2	31.17	3	14.15	3	28.52	1	12
T_6	143.26	1	109.93	1	32.23	1	41.12	1	19.93	2	24.03	3	9
T_7	114.81	2	108.36	1	30.16	1	42.69	1	23.06	1	27.64	1	7
T_8	144.99	1	112.99	1	33.12	1	38.87	1	24.46	1	29.58	1	6

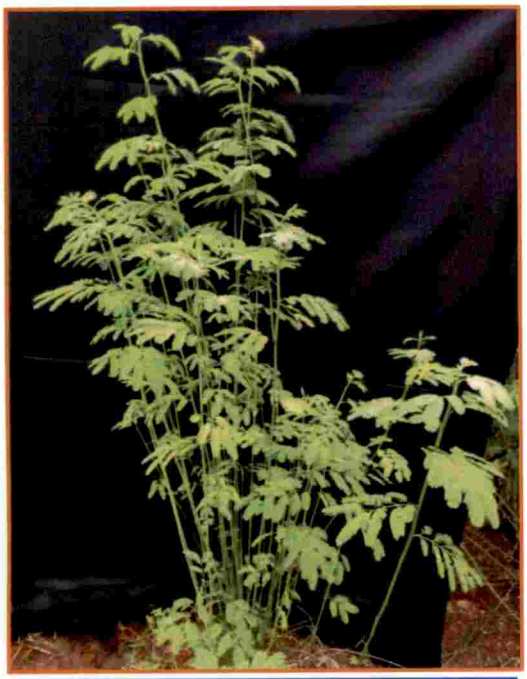
Table 23. 3. Location-III (Thrissur)

Genotype	Number of leaves		Green fodder yield (g plant^{-1})		Dry fodder yield (g plant^{-1})		Dry matter production (g plant^{-1})		Crude protein content (%)		Crude fibre content (%)		Total of Rank
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	
T_1	142.19	1	108.76	1	29.36	1	36.91	1	18.96	1	21.83	3	8
T_2	106.64	3	95.51	2	23.87	2	29.46	3	13.78	3	20.76	3	16
T_3	91.70	3	89.75	3	19.62	3	25.05	3	12.37	3	24.39	2	17
T_4	118.68	2	95.26	2	27.60	1	35.37	1	11.26	3	22.86	3	12
T_5	143.32	1	102.04	1	26.52	2	29.60	2	12.65	3	26.50	1	10
T_6	135.66	1	105.76	1	29.45	1	36.30	1	18.78	2	22.36	3	9
T_7	110.33	2	110.43	1	27.60	1	38.65	1	21.74	1	25.41	2	8
T_8	139.21	1	110.54	1	31.23	1	36.73	1	22.67	1	28.37	1	6

Table 23. 4. Location-IV (Ambalavayal)

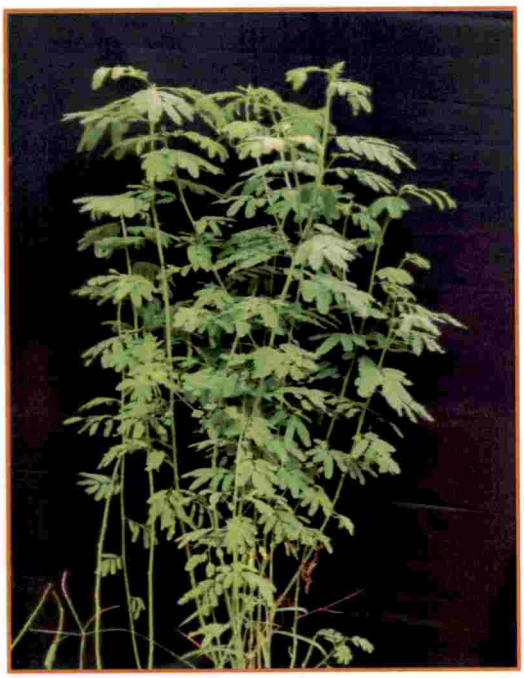
Genotype	Number of leaves		Green fodder yield (g plant^{-1})		Dry fodder yield (g plant^{-1})		Dry matter production (g plant^{-1})		Crude protein content (%)		Crude fibre content (%)		Total of Rank
	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	Mean	Rank	
T_1	144.26	1	113.39	1	34.18	1	40.64	1	21.82	1	24.35	3	8
T_2	115.03	3	104.52	2	30.12	2	34.69	2	15.31	3	23.23	3	15
T_3	102.81	3	94.37	3	25.62	3	30.64	3	15.32	3	27.78	2	17
T_4	127.89	2	104.70	2	33.41	1	38.64	1	13.95	3	23.79	3	12
T_5	135.43	1	95.11	3	26.36	3	31.06	3	13.88	3	28.28	1	14
T_6	142.49	1	112.17	1	33.48	1	41.99	1	20.69	2	24.79	3	9
T_7	112.54	3	112.20	1	32.67	2	39.48	1	24.71	1	27.97	2	10
T_8	143.00	1	118.56	1	36.75	1	41.53	1	24.98	1	31.52	1	6

Plate 3. Stable genotypes of Hedge lucerne over all locations



T_1 (IC 345276)

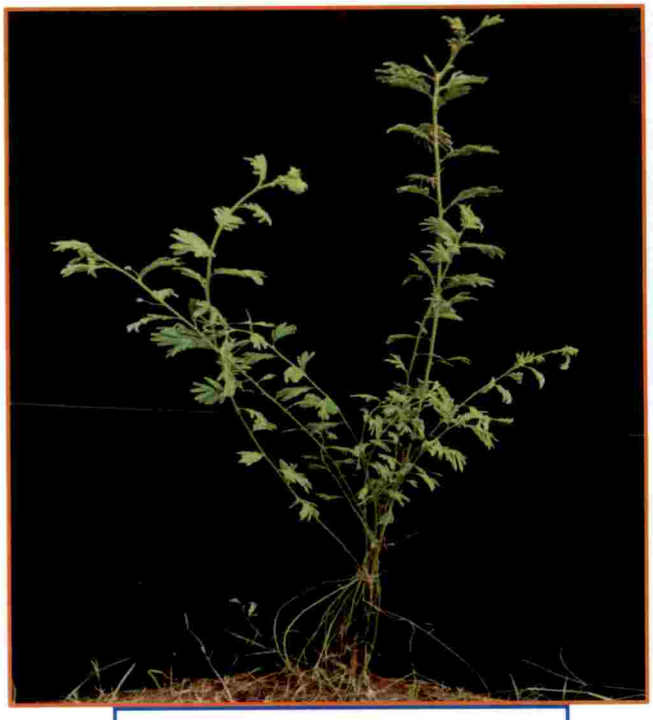
T_4 (IC 261839)



T_6 (IC 421199)

T_7 (TNDV 1)

Plate 4. Hedge lucerne suitable for favourable environments



T_2 (IC 343710)

T_8 (Thumburmuzhi local)

Plate 5. Hedge lucerne genotypes suitable for unfavourable environment

T_5 (IC 90934)

DISCUSSION

5. DISCUSSION

Hedge lucerne is a herbaceous perennial legume belonging to the family Fabaceae. No poisonous principle is observed in foliage. Hedge lucerne is preferred by cattle for its palatable green fodder and adequate amount of crude protein. The alarming gap between demand and supply in availability of fodder in Kerala necessities the production of high quality herbage devoid of anti-nutritional factors. However the genetic improvement achieved in hedge lucerne in terms of its productivity is very low.

The identification of superior genotypes remarks the success of crop improvement activities. Phenotypic stability and potential for high yield under favourable environment considered most in selecting superior genotypes. To analyze G x E interaction a number of parametric statistical procedures have been developed in which Eberhart and Russell model (1966) is the most widely used method. The nature of adaptation of genotypes can be studied from two main factors namely, regression coefficient (linear sensitivity) and the deviation from mean squares due to regression (non-linear sensitivity).

Based on the stability parameters the extent of deviation of yield and yield related characters over environments is studied to identify the best genotypes which are widely adapted. Multilocation testing of genotypes provides an opportunity for plant breeders to study the adaptability of genotypes to a particular environment and also to understand the stability of the genotypes over different environments. Thus information on Genotype x Environment interaction is of major importance to the plant breeders in identifying an improved stable genotype.

Realizing the importance of the stability analysis in performance of genotypes, in the present study eight genotypes of hedge lucerne were evaluated across four environments. The salient findings from this present study entitled "Genotype×Environment interaction in Hedge lucerne (*Desmanthus virgatus* (L.)

Willd.) for yield and quality" have been critically analyzed and discussed in light of available literature under the following subheads.

1. Pooled analysis of variance
2. Stability analysis for yield and its attributing traits

5.1. POOLED ANALYSIS OF VARIANCE

From the pooled analysis of variance, the genotypes showed significant differences for all the characters studied, which revealed the presence of genetic variability among the genotypes. Significant differences among the genotypes gave greater opportunity for selecting suitable genotypes with high mean value for all the characters of interest. Environments were highly significant for the characters *viz.,* 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 fodder yield (g), dry matter production (g), crude protein content (%) and crude fibre content (%/) suggesting the divergence among growing environments. The effect of genotype x environment were significant for all the characters studied, which indicated the differential response of genotypes to varying environment. Therefore, these genotypes must be evaluated over a wide range of environments where they are ultimately cultivated for commercial purposes. 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.

The joint regression analysis by stability analysis revealed that G x E interaction (linear) was highly significant for all the characters studied *viz.,* plant height (cm), number of branches plant^{-1}, length of branches plant^{-1}, number of leaves plant^{-1}, leaf to stem ratio, number of pods cluster^{-1}, green fodder yield , dry fodder yield, dry matter production , crude protein content and crude fibre content indicating that the genotypes had divergent linear response to the environmental changes for these characters. Comparable findings were reported by Saranya (2016) for the characters plant height, number of branches, number of leaves

plant^{-1} and total fresh weight in Neelamari, Preeti *et al.* (2016) for the characters plant height and dry matter yield in wheat, Mehraj (2017) for the traits plant height, fodder yield ha^{-1}, green fodder yield and leaf to stem ratio in oats.

5.2. STABILITY ANALYSIS FOR YIELD AND ITS ATTRIBUTING TRAITS

Several workers proposed different models for identifying stable genotypes which exhibit least interaction with environments. Finlay and Wilkinson (1963) developed a dynamic approach for interpretation of varying environments. They considered mean value of the genotype and their regression coefficient. But Eberhart and Russell improved this model by adding another stability parameter, *i.e.,* the deviation from regression and provided fresh approach to G x E interaction analysis. 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 poor environments (Eberhart and Rusell,1966).

5.2.1. Plant height (cm)

Two genotypes, T_1 and T_6 have recorded the highest mean value than population mean for the character plant height with The regression coefficient

near unity with non-significant deviation from regression, suggested that these two genotypes were stable for this character. The genotype T_2 had more than unity regression (1.41) and non-significant deviation from regression (0.56) and was found to be stable for favourable environments. The genotype T_5 was found to be stable for unfavourable environments with less than unity regression and non-significant deviation from regression. Similar results were observed by Sunil (2004) in turmeric, Panwar *et al.* (2011) in ocimum, Javia (2014) in okra, Saranya (2016) in neelamari, Preeti *et al.* (2016) in wheat, Patil *et al.* (2017) in oats also observed stability for the character plant height.

5.2.2. Number of branches plant^{-1}

Among the genotypes evaluated T_1 (5.10), T_4 (4.29) and T_5 (6.29) with regression near to unity and minimum deviation from regression was widely adapted with average stability. The genotypes T_3 (10.31) and T_6 (4.56) had regression coefficient greater than unity and non- significant deviation from regression, indicated that these genotypes were stable under favourable environments with predictable performance. Less than unity regression and non-significant deviation from regression was recorded for the genotype T_7 (3.98), which indicated the adaptability of the genotype under unfavourable environment. Similar findings were recorded by Ottai *et al.* (2006) in roselle, Abou *et al.* (2006) in white mustard, Saranya (2016) in neelamari and Patil *et al.* (2017) in okra.

5.2.3. Length of branches plant^{-1}

The genotype T_6 was considered as stable for the character length of branches plant^{-1} because of a regression coefficient near unity. The genotypes T_8 (b_i=1.21) recorded more than unit regression and non-significant deviation from regression, indicated that the genotype was suitable for favourable environment. The genotypes T_1 and T_7 reported less than unity regression for the character length of branches plant^{-1} with minimum non-significant deviation from regression, which suggested that these genotypes were suitable for unfavourable environments. 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.

5.2.4. Number of leaves plant^{-1}

The genotype T_6 which had the highest mean value (141.04), near unity regression (0.82) and minimum non- significant deviation from regression (1.41), was considered as a stable genotype. The genotypes T_1 and T_7 were stable under unfavourable environments. 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 and Mehraj *et al.* (2017) in oats.

5.2.5. Leaf to stem ratio

Among the genotypes T_4 (μ=0.76, b_i=1.09, S^2_{di}=0.0004) and T_7 (μ=0.84, b_i=1.18, S^2_{di}=0.0007) were considered as the stable genotypes because of the desirable mean, near unity regression and mean deviation from linearity, which can be suggested for wider environments. Whereas, the genotype T_6 (μ=0.88, b_i=1.56, S^2_{di}=0.000) was suitable for favourable environments due to greater than unit regression and non- significant deviation from linearity, while T_1 (μ=0.89, b_i=0.75, S^2_{di}=0.0005) genotype was suitable for unfavourable environments. These results were in accordance with the results of Nanavati (2016) in maize, and Mehraj *et al.* (2017) in oats.

5.2.6. *Number of pods cluster^{-1}*

The genotypes T_5 and T_7 recorded near unit regression (1.23 and 0.89) with non-significant S^2_{di} value (-0.003 and 0.015), indicated that the genotypes were stable across the environment. The genotypes T_1 and T_3 had higher than unity and minimum non-significant deviation from regression, which indicated that these genotypes were adaptable for favourable environments. The genotype T_8 was suitable for unfavourable environment and had regression coefficient of less than unity and non-significant deviation from regression. These findings are agreement with Ramesh *et al.* (2017) in pigeon pea.

5.2.7. Green fodder yield

The genotype had the high mean yield (112.35 g) than the population yield (104.93 g), near unit regression (1.12) and non-significant minimum deviation from regression (-0.62) was considered as stable genotype for the character green fodder yield. The genotype T_4 and T_8 genotypes performed well under favourable environment with regression coefficient of 1.74 and 1.52 respectively. The variable stability parameters were reported in green fodder yield by Nanavati (2016) in forage maize and Mehraj *et al.* (2017) in oats.

5.2.8. Dry fodder yield

The genotype T_1 (μ=32.45, b_i=1.11, S^2_{di}=0.22) possessed higher dry fodder yield than the population mean and were considered as highly adaptable genotypes having average stability and was expected to perform well in all the environment. The genotypes T_2, T_4 and T_8 had higher mean than population mean, more than unity regression with non-significant deviation from linearity, which suggested that these genotypes were stable under favourable environment and perform better under rich environment. The genotype T_6 (μ=31.77, b_i=0.77, S^2_{di}=0.42) were stable for unfavourable environment with high mean, less than unity regression and minimum deviation from regression. Similar findings for the variable stability parameters in dry fodder yield was noticed by Bikash *et al.* (2013) in pearl millet and Mehraj *et al.* (2017) in oats.

5.2.9. Dry matter production

The genotypes T_1, T_6 and T_8 had higher mean performance for dry matter production than the population mean. The genotype T_1 was stable with regression coefficient near unity (b_i=0.97) and non-significant deviation from regression (S^2_{di}=0.09). The genotypes T_6 (b_i=1.34) and T_8 (b_i=1.25) had regression coefficient greater than unity and minimum deviation from regression, which indicated that these genotypes were stable for favourable environment. The same findings for variation in stability parameters was observed by Preeti *et al.* (2016) in wheat.

5.2.10. Crude protein content

Two genotypes, T_4 and T_8 were stable for the character crude protein content in all the environment with regression coefficient of 0.97 and 0.91, with minimum deviation from regression of 0.01 and -0.06 respectively. The genotype T_1 (b_i=1.42) was stable under favourable environment. The genotype T_5 (b_i=0.69) had less than unity regression and non-significant deviation from regression (0.02) and was stable under unfavourable environment and 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.

5.2.11. Crude fibre content

Among the genotypes, T_1, T_5 and T_7 had near unity regression coefficient (0.97, 0.96 and 1.09) and minimum deviation from regression (0.098, 0.054 and -0.027) and their performances for the character crude fibre content can be predicted. They were well adapted for all the environments. The genotype T_2 (b_i=1.26, S^2_{di}=0.004) was found to be suitable for unfavourable environment. The genotype T_4 (b_i=0.45, S^2_{di}= -0.143) was suitable for poor environment for the trait crude fibre content.

Table 24. Comparison of hedge lucerne genotypes on the basis of mean performance and stability parameters

Sl. No.	Character	Stable	Favourable environment	Unfavourable environment	Population mean
1.	Plant height (cm)	T_1, T_6	T_2	T_5	97.49
2.	Number of branches	T_1, T_4, T_5	T_3, T_6	T_7	6.41
3.	Length of branches (cm)	T_6	T_8	T_1, T_8	45.75
4.	Number of leaves	T_6	-	T_1, T_7	128.20
5.	Leaf to stem ratio	T_4, T_7	T_6	T_1	0.81
6.	Number of pods	T_5, T_7	T_1, T_3	T_8	1.79
7.	Green fodder yield (g plant^{-1})	T_1	T_2, T_4, T_8	-	104.93
8.	Dry fodder yield (g plant^{-1})	T_1, T_8	T_2, T_4, T_8	T_6	29.74
9.	Dry matter production (g plant^{-1})	T_1	T_6, T_8	-	36.42
10.	Crude protein	T_4, T_8	T_1	T_6	18.34
11.	Crude fibre	T_1, T_7	T_2	T_5	25.77

SUMMARY

6. SUMMARY

The present study on "Genotype×Environment interaction in hedge lucerne (*Desmanthus virgatus* (L.) Willd.) for yield and quality" was carried out to identify stable genotypes of eight *Desmanthus virgatus* in varied environments with respect to yield and quality in four locations of Kerala *viz.,* College of Agriculture, Vellayani, College of Horticulture, Thrissur, Krishi Vigyan Kendra, Kottarakkara, Kollam and Regional Agricultural Research Station, Ambalavayal, Wayanad.

The eight genotypes of hedge lucerne *viz.,* 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) were evaluated in a Randomized Block Design (RBD) with four replications over four locations during 2017-2018. Eberhart and Russell model (1966) was used to analyze the stability and adaptability of yield and yield related characters of these genotypes. The present study showed significant mean squares due to genotypes for yield, quality and other component characters and this revealed the existence of high variability among the genotype studied. The mean squares due to Genotype x Environment interaction were significant for all the characters indicating the varying response of genotypes towards changing environment. Hence further analysis was done to assess the stability of genotypes.

In the stability analysis, the mean squares due to Environments + (Genotype x Environment) were significant for the characters *viz.,* plant height, number of branches plant^{-1}, number of leaves plant^{-1}, green fodder yield, dry fodder yield, dry matter production, dry matter production, crude protein content and crude fibre content strengthening the presence of G x E interaction for these characters. The sum of squares due to E + (G x E) was further partitioned into Environment (linear), Genotype x Environment (linear) and pooled deviation. Environment (linear) was significant for the characters such as, plant height, number of branches plant^{-1}, length of branches plant^{-1}, number of leaves plant^{-1}, leaf to stem ratio, number of pods plant^{-1}, green fodder yield, dry fodder yield,

dry matter production, crude protein content and crude fibre content. The mean squares due to Genotype x Environment (linear) was significant for the traits like, plant height, number of branches plant^{-1}, number of leaves plant^{-1}, leaf to stem ratio, green fodder yield and dry fodder yield. This indicated that the major component for differences in stability was due to both linear and non linear components.

The estimation of environmental indices for all the characters in all the four locations (Vellayani, Kottarakkara, Thrissur and Ambalavayal) revealed that Vellayani and Ambalavayal were most favourable or suitable environment for cultivation of hedge lucerne and Thrissur was the unfavourable environment for hedge lucerne cultivation.

The stability of the genotype was measured from the mean performance of a genotype along with two stability parameters *viz.*, regression coefficient (b_i) and deviation from regression coefficient (S^2_{di}).

The genotypes T_1 (IC 345276), T_4 (IC 261839), T_6 (IC 421199) and T_7 (TNDV 1) were identified as stable genotypes having regression coefficient near unity and non-significant deviation from regression with wider adaptability over environment for most of the characters. The genotype T_1 (IC 345276) was stable over all locations for different characters such as plant height, number of branches, green fodder yield, dry fodder yield, dry matter production and crude fibre. The genotype T_4 (IC 261839) was stable for the characters number of branches, leaf to stem ratio and crude protein across the locations. The genotype T_6 (IC 421199) was stable over locations for the characters *viz.*, plant height, length of branches and number of leaves, while the genotype T_7 (TNDV 1) was stable for leaf to stem ratio, number of pods and crude fibre.

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 such as leaf to stem ratio, green fodder yield, dry fodder yield and crude fibre. The genotype T_8 (Thumburmuzhi local) was

stable in favourable environment for length of branches, green fodder yield, dry fodder yield and dry matter production. The genotype T_5 (IC 90934) was found to be stable for the characters plant height and 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 i.e., College of Horticulture, Thrissur. The superior genotypes identified in the present study can be further promoted to farm trials before releasing them as a variety.

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7. REFERENCES

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GENOTYPE×ENVIRONMENT INTERACTION IN HEDGE LUCERNE (*Desmanthus virgatus* (L.) Willd.) FOR YIELD AND QUALITY

ARUN CHACKO

(2016-11-034)

Abstract of the thesis

Submitted in partial fulfilment of the

requirements for the degree of

MASTER OF SCIENCE IN AGRICULTURE

Faculty of Agriculture

Kerala Agricultural University

DEPARTMENT OF PLANT BREEDING AND GENETICS

COLLEGE OF AGRICULTURE

VELLAYANI, THIRUVANANTHAPURAM -695522

KERALA, INDIA

2018

ABSTRACT

The present work on "Genotype×Environment interaction in hedge lucerne (*Desmanthus virgatus* (L.) Willd.) for yield and quality" 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 2016-2018 with an objective to identify stable genotypes of *Desmanthus virgatus* in varied environments with respect to yield and quality.

The eight genotypes of hedge lucerne *viz.,* 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) were evaluated in a Randomized Block Design (RBD) with four replications over four locations during 2017-2018. 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, while COH, Thrissur was unfavourable for all the characters studied.

In the pooled analysis of variance for evaluation of hedge lucerne over locations, significant differences among the genotypes and environments were noticed for all the characters studied, suggesting that genotypes interacted significantly with environments.

Stability analysis revealed that the genotype T_1 (IC 345276) was stable over all locations for different characters such as plant height, number of branches, green fodder yield, dry fodder yield, dry matter production and crude fibre. The genotype T_4 (IC 261839) was stable for the characters number of branches, leaf to stem ratio and crude protein across the locations. The genotype T_6 (IC 421199) was stable over locations for the characters *viz.,* plant height, length of branches and number of leaves,

while the genotype T_7 (TNDV 1) was stable for leaf to stem ratio, number of pods and crude fibre.

The genotypes T_2 (IC 343710) and T_8 (Thumburmuzhi local) were identified as stable genotypes for favourable environments. The genotype T_2 (IC 343710) showed stable performance for the characters such as leaf to stem ratio, green fodder yield, dry fodder yield and crude fibre. The genotype T_8 (Thumburmuzhi local) was stable in favourable environment for length of branches, green fodder yield, dry fodder yield and dry matter production. The genotype T_5 (IC 90934) was found to be stable for the characters plant height and 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 i.e., College of Horticulture, Thrissur.