
HEIGHT GROWTH OF HALF-SIB FAMILIES OF EUCALYPTUS CAMALDULENSIS ACROSS ENVIRONMENTS USING ADDITIVE MAIN EFFECTS AND MULTIPLICATIVE INTERACTIONS (AMMI) ANALYSIS

Article Particulars

Received: 7.10.2017

Accepted: 25.10.2017

Published: 30.10.2017

**R. Chandrasekar****Smitha G. Nair****A. Nicodemus****A. Vinothkumar****V. Sivakumar**

Abstract

To determine the stability in yield and estimate the extend of genotype x environment interaction of half sib progenies of *Eucalyptus camaldulensis* across different locations, 48 half sib families and 2 clones were evaluated in a randomized block design (RBD) with 4 replications at four locations viz., Marakkanam, Thiyagathurgam, Karaikudi and Pulvayal after three years of planting during 2013. Additive main effects and multiplicative interactions (AMMI) analysis indicated that the height growth of half sib families were under the major effects of genotype x environment interactions. The first two principal component axes (PCA 1 and 2) were significant ($P \leq 0.01$) and cumulatively contributed to 84.31% of the total genotype by environment interaction. The biplot technique was used to identify appropriate half-sib families to specific locations. Results showed that the families, 74 and 118 were observed to be more stable as well as best performing family. The families, 36, 88, 74 and 118 showed low interaction with high growth performance and can be recommended for a wide range of environments. The families 30, 92 and 121 were although having high productivity, the interaction with environment was high. Hence, these families can be recommended for specific environments. Marakkanam and Thiyagathurgam were observed to be the favourable environment for most of the best performing families. According to stability Thiyagathurgam was found to be a

more stable environment and can be used for breeding programs. Families 30 and 92 are unstable families, however they are specifically adapted to high yielding environment, Pulvayal.

Keywords: Additive main effects and multiplicative interactions (AMMI), Biplot, Stability analysis, *Eucalyptus camaldulensis*

Introduction

The breeders conduct progeny trials in multiple locations in order to find out the superiority of the progenies across different locations. Multi-site tests are therefore necessary to provide information on the extent of GEI (Johnson, 1997). When genotypes are evaluated in a single site, GEI effects cannot be estimated and get merged with genetic effects, causing an overestimation of genetic parameters (Zobel and Talbert, 1984). In addition, performance of the individual within a family is completely linked to the unique environment of its specific position in the progeny test, and the confounding of genetic and environmental effects complicates individual selection and decreases the accuracy of the estimate of an individual's genetic potential (Shaw and Hood, 1985). At the same time, presence of environmental heterogeneity inflates the residual variance due to the confounding of tree-to-tree variation and decreases the benefits of using simple experimental designs (Grondona *et al.*, 1996).

The performance of the progenies varies across different locations depending on the soil and environmental factors. Half-sib progenies are segregating populations leading to variation in a greater extent. The superiority of a specific family for a particular location does not explain the genetic superiority. On the other hand, superiority of a specific family across different locations with minimum GEI could be attributed to genetic effect. At the same time, superiority of a family for a particular location with higher GEI reveals that the species should be bred for each such location. The selection process will be easy when the GEI is statistically insignificant. The genotypes better adapted to poor conditions express higher stability estimates than those adapted to better conditions (Simmonds, 1991). It is imperative to have clear understanding on the level of GEI and stability in growth performance of the varieties being tested for short-listing new varieties for a wide range of areas or a specific ecological region.

Crop genotypes grown in different environments would frequently encounter significant fluctuations in yield performance, particularly when the growing environments are distinctly different and the test genotypes differentially respond to changes in the growing environments or both. The fluctuation of crop performance with changing environments, technically termed as genotype \times environment ($G \times E$) interaction, potentially presents limitations on selection and recommendation of varieties for target set of environments, particularly when it is a "crossover" type or when rank order changes among the genotypes are involved (Navabi *et al.*, 2006).

Purchase (1997) revealed that, in most yield trials, the proportion of sum of squares due to differences among sites ranged from 80 to 90% and the variation due to genotype by environment interactions is often larger than that of the genotypes.

The additive main effect and multiplicative interaction (AMMI) method integrates analysis of variance (ANOVA) and principal component analysis (PCA) into a unified approach that can be used to analyse multi-location trials (Gauch and Zobel, 1996). AMMI produces bi-plot graphs, which display the variability of genotypes and genotype by environment interactions. Identifying genotypes with high yields and stability and at the same time adaptable to the wide range of environments, is one of the main objectives of breeding programs. Several methods have been applied to the evaluation of G x E interactions; however, the choice of the best method depends on the experimental design, number of environments available, required precision, and the type of desired information (Cruz *et al.*, 2004). Differences in genotype stability and adaptability to environment can be qualitatively assessed using the biplot graphical representation that scatters the genotypes according to their principal component values (Vita *et al.*, 2010). AMMI uniquely separates G, E, and GE as required for most agricultural research purposes, and also separates structural variation from noise as well as any other method for the purpose of gaining accuracy (Anandan *et al.*, 2009).

A study was conducted with the objectives of (i) determine genotypes with high yields, depending on the differential genotypic responses to environments (ii) interpret GEI obtained by AMMI analysis of growth yield in 48 half sib families and 2 clones of *Eucalyptus camaldulensis* over four environments.

Material and Methods

This study was carried out to determine the growth yield in 48 half sib families and 2 clones of *Eucalyptus camaldulensis* Dehnh. across four sites in Tamil Nadu namely, Marakkanam, Karaikudi, Pulvayal and Thiyagathurgam planted during 2009 (Table 1). Of the 50 families used, seeds of forty eight families including 74, 36, 88, 92, 30, 105, 17, 25, 121, 14, 70, 71, 35, 28, 2, 118, 57, 7, 18, 55, 34, 109, 46, 112, 49, 39, 44, 12, 1, 10, 8, 27, 73, 60, 16, 67, 40, 53, 33, 23, 115, 99, 62, 85, 38, 66, 94, and 117 were collected from Seed Orchards at Karunya nagar, Tamil Nadu. Two commercial clones namely, ITC 3 (136) and ITC 7 (137) were also included in the test for comparison. All experiments were arranged in accordance with a randomized block design (RBD) with 4 replications. The trees were planted at a spacing of 3x 2 meters. Ploughing was carried out once in a year. Total height and girth at breast height were recorded after three years of planting and single tree volume was calculated based on form factor method. Form factor was considered as 0.55.

Table 1 List of Field Trials Conducted Along with Soil and Climatic Conditions of the Trials

Environment		Site name	Latitude	Longitude	Altitude	Soil status
Number	Code					
1	M	Marakkanam	12°11'12"N	79°56'04"E	43	Sand
2	T	Thiyagathurgam	11°48'23"N	79°05'19"E	374	Sandy loam
3	K	Karaikudi	10°00'51"N	78°46'19"E	251	Sandyclayloam
4	P	Pulvayal	10°22'27"N	78°42'21"E	374	Sandy clay loam

CROP STAT software was applied to perform data analysis of AMMI on the yield obtained per plot across environments. The AMMI model equation according to Gauch and Zobel (1996) is:

$$Y_{ger} = \mu + a_g + \beta_e + \sum n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + \epsilon_{ger}$$

Where Y_{ger} = the observed yield of g^{th} genotype in e^{th} environment for r^{th} replicate; μ = the grand mean; a_g = the deviation of mean of the g^{th} genotype from the grand mean m ; β_e = the deviation of mean of the e^{th} environment from the grand mean m ; λ_n = the singular value for the n^{th} interaction principal component axis (PCA); γ_{gn} = the genotype eigenvector for n^{th} (PCA) axis; δ_{en} = the environment eigenvector values for the n^{th} PCA axis; ρ_{ge} = the residual effects; and ϵ_{ger} = the error term.

Furthermore, AMMI's stability value (ASV) was calculated in order to rank half-sib families in terms of stability using the formula suggested by Purchase (1997) as shown below:

$$\text{AMMI stability value (ASV)} = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA1score) \right]^2 + [IPCA2score]^2}$$

Where: SS = Sum of squares; IPCA1 = interaction principal component analysis axis 1; IPCA2 = interaction principal component analysis axis 2.

Results and Discussion

The AMMI analysis of variance carried out for height mean of half sib families of *Eucalyptus camaldulensis* tested in four locations showed that 22.98% of the total sum squares was attributable to GEI effect. The Genotype effect represented at 22.91% and environment effect expressed about 8.12% separately. The magnitude of genotype sum of squares was almost equal to GEI, indicating that there is substantial genotype contribution across environments. The contribution of environmental, genotype and their interaction vary across different species (Li *et al.*, 2017). The above results indicate that family selection, screening the families for different environments and genotype and environment matching are important stages of improvement.

Analysis of variance for the AMMI model					
Source	D.F.	Sum of squares	Mean of squares	F	F probability
Genotype	49	123.632	2.523		
Environment	3	43.832	14.611		

Genotype X Environment	147	124.027	0.844		
IPCA1	51	66.982	1.313	3.171498	0.000
IPCA2	49	37.587	0.767	1.852657	0.018
IPCA3	47	19.457	0.414		1.000
Pooled error	600	248.400	0.414		
Total	799	539.631			

** Significant at the 0.01 probability level; df =degree of freedom; F= tabulated frequency

The analysis was captured 54% of the discrimination at the first principal component axis (PCA 1). It was also observed that the PCA 1 had sums of squares greater than that of environment. The second components captured 30.30% of the GEI sum of squares that amounts to a cumulative contribution to 84.31% of the total GEI. The mean squares for the PCA 1 and PCA 2 were significant at $P < 0.01$ with a Hence, the interaction of the 48 half sib families and 2 clones with four environments was best predicted by the first two principal components of genotypes and environments with 100 degrees of freedom. Further, 3rd principal component captured only 15.68% of the GEI sum of squares and was not significant and therefore did not help to predict valid observation.

Earlier prediction assessment studies with AMMI also have shown that most accurate predictive model were made with first two interaction principal components (Verma *et al.*, 2015). On the other hand, a predictive AMMI model with significance in first four PCAs have been reported (Zahia *et al.*, 2010). In general, factors like type of crop, diversity of the germplasm and range of environmental conditions will affect the degree of complexity of the best predictive model (Cossa *et al.*, 1990).

AMMI model 1 biplot positioned high potential environments viz., Marakkanam and Thiyagathurgam in quadrant III and while the lower potential environment, Pulvayal and Karaikudi were positioned in quadrant II (Fig. 1). Pulvayal and Karaikudi were observed to be poor environment and at the same time expressed low interactions score when compared to Marakkanam and Thiyagathurgam that scored high interaction scores (Table 2). Marakkanam and Thiyagathurgam are observed to be the favourable environment for most of the best performing families. Further it was observed that the interaction effect was more in high yielding half sib families than the low yielding families.

Genotypes that are close to each other tend to have similar performance and those that are close to environment indicates their better adaptation to that particular environment. In the present study, 74, 118, 36, 88, 14, 30 and 92 showed similar performance as they are close to each other. Families 30 and 92 are unstable families. Family 66 is low yielding as well adapted to low yielding environments. The commercial clones studied also showed poor stability as well as growth performance when compared to most of the studies families. The families, 74 and 118 were observed to be more stable as well as best performing family. Finlay and Wilkinson (1963) stated that

the high yielding genotypes showing low interaction are adapted to a wide range of environments and genotypes with high interaction are suitable for specific environments. The families, 36, 88, 74 and 118 showed low interaction with high growth performance and can be recommended for a wide range of environments.

AMMI model 2 Biplot with first two components for 50 genotypes in 4 environments shown that Karaikudi (K) and Thiyagathurgam (T) were the most discriminating environment as indicated by the longest distance between its marker and the origin. However, due to their large IPCA scores, genotypic differences were narrow and were distributed closely at average environments. Genotypes with a smaller vector angle in between and have similar projection, designate their proximity in yield performance. Those genotypes that are clustered closer to the centre tend to be stable, and those plotted far apart are unstable in performance. Accordingly, families viz., 57, 74, 34, 36, 1, 88 and 7 were genotypes positioned closer to the origin of the biplot which indicates their stability in performance across environments. On the other hand, families viz., 30, 92, 2, 49, 38, 85, 136, 99, 117, 73, 33, and 112 were unstable as they are located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores. Karaikudi, Pulvayal and Thiyagathurgam were observed to be closer and expected to support similar families. Further, Karaikudi and Thiyagathurgam are observed to be unstable environment and can be used for breeding programs. Oliveira *et al.* (2014) has made similar recommendation based on AMMI stability parameters for conducting breeding trials for initial selection in yellow passion fruit.

AMMI adjusted mean based on untransformed data, AMMI stability values (ASV) and ranking of half-sib families based on the height growth and ASV have been given in table 3. The half-sib family, 36, 88, 14, 30 and 118 were observed to have maximum mean height. The half-sib family, 57, 7, 12, 74, 34 and 27 were shown ASV value close to zero, reflecting minimum GEI or stable yield over the environments. The stability ASV values and yield parameters given in table 3 have been classified into three levels of stability and yield performers and given in Table 4. The ASV values were categorized into three classes viz., < 0.500 (high stability), 0.500 to 0.800 (medium stability) and >0.800 (low stability). Similarly, the yield was also made into three classes viz., low (<7.50 cm), medium (7.50 to 8.20 cm) and high (> 8.20 cm). All the studied half sib families were classified into 9 groups. The commercial clones, 136 and 137 were observed to be poor in yield potential. The half sib families, viz., 74, 88 and 118 were found to have high yield along with high stability. The family 30, 92 and 121 were although having high productivity however, the interaction with environment is high. Hence, these families can be recommended for specific environments.

Environment	Mean of height	IPCA 1 *	IPCA 2 **
M	8.0386	8.039	0.55
T	8.1118	8.112	0.231
K	7.2519	7.252	-0.127
P	7.0506	7.051	-0.109

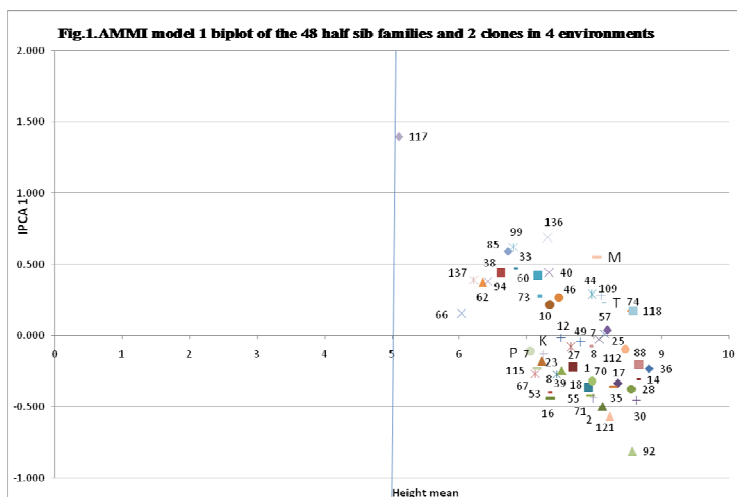


Table 2 Mean of Growth Yield together with First and Second Interaction Principal Components for Different Environments

* & ** are first and second interaction principal component environment, respectively

Fig1. AMMI Model 2 Biplot of 48 half sib Families and 2 Clones of Mean of Height for four Environments Using Genotypic and Environmental Scores

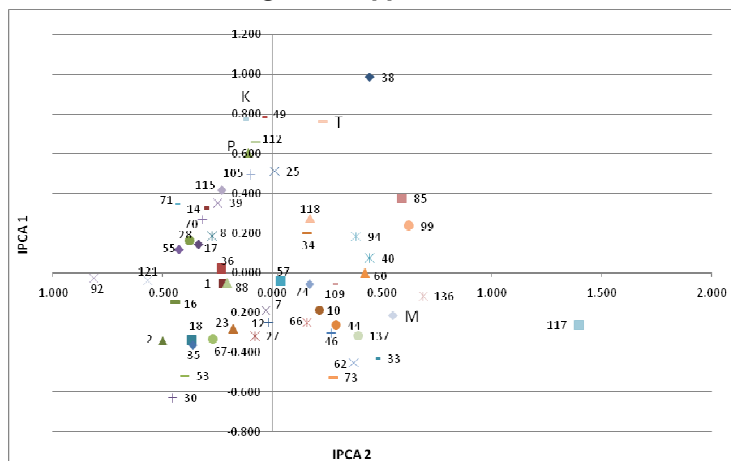


Table 3. AMMI adjusted mean of GBH based on untransformed data, AMMI stability values (ASV), and ranking orders of the genotypes tested across 4 environments.

Family	Height		IPCA 1	IPCA 2	ASV	
	Mean	Rank			Value	Rank
1	7.688	25	-0.222	-0.055	0.400	9
2	8.125	15	-0.497	-0.342	0.950	42
7	8.078	17	-0.027	-0.189	0.195	2
8	7.448	30	-0.272	0.186	0.520	16
10	7.339	32	0.216	-0.187	0.427	13

12	7.511	28	-0.016	-0.250	0.252	3
14	8.63	3	-0.306	0.327	0.636	25
16	7.354	31	-0.441	-0.146	0.799	37
17	8.356	10	-0.334	0.144	0.613	23
18	7.917	23	-0.365	-0.336	0.733	30
23	7.224	37	-0.177	-0.281	0.422	12
25	8.156	14	0.013	0.513	0.513	15
27	7.656	26	-0.078	-0.317	0.346	5
28	8.552	8	-0.376	0.162	0.690	27
30	8.63	4	-0.452	-0.627	1.021	44
33	6.806	42	0.473	-0.432	0.947	41
34	7.292	36	0.160	0.202	0.349	6
35	8.286	11	-0.360	-0.364	0.738	31
36	8.818	1	-0.230	0.022	0.411	10
38	6.615	45	0.444	0.986	1.264	48
39	7.516	27	-0.247	0.352	0.563	18
40	7.333	33	0.443	0.075	0.794	36
44	7.974	19	0.291	-0.262	0.580	20
46	7.478	29	0.268	-0.303	0.566	19
49	7.797	24	-0.044	0.784	0.788	35
53	7.317	34	-0.398	-0.518	0.879	40
55	7.943	21	-0.424	0.116	0.765	33
57	8.194	13	0.039	-0.041	0.081	1
60	7.161	38	0.422	0.001	0.752	32
62	6.344	47	0.372	-0.453	0.803	38
66	6.031	49	0.159	-0.249	0.376	8
67	7.125	41	-0.268	-0.333	0.582	21
70	7.972	20	-0.318	0.267	0.627	24
71	7.995	18	-0.439	0.347	0.856	39
73	7.161	39	0.278	-0.525	0.722	29
74	8.562	7	0.171	-0.057	0.311	4
85	6.728	44	0.591	0.377	1.118	45
88	8.667	2	-0.203	-0.050	0.366	7
92	8.568	6	-0.810	-0.028	1.444	49
94	6.422	46	0.382	0.184	0.705	28
99	6.797	43	0.622	0.237	1.133	46
105	8.464	9	-0.097	0.497	0.526	17
109	8.1	16	0.279	-0.055	0.501	14
112	7.932	22	-0.073	0.658	0.671	26
115	7.156	40	-0.229	0.417	0.583	22
117	5.105	50	1.396	-0.261	2.501	50
118	8.577	5	0.174	0.274	0.414	11
121	8.234	12	-0.565	-0.037	1.008	43
136	7.312	35	0.688	-0.117	1.232	47
137	6.217	48	0.391	-0.315	0.766	34

IPCA = Interaction principal component analysis axis.

Table 4. AMMI Stability Values of Height Mean

ASV	Height mean (cm)		
	<7.50 (Low)	7.50 to 8.20 (Medium)	> 8.20 (High)
<0.500(High stability)	10, 23, 34 and 66	1, 7, 12, 27, 36 and 57	74, 88, and 118
0.500 to 0. 800 (Medium stability)	8, 16, 40, 46, 53, 60, 62, 67, 73, 94, 115 and 137	18, 25, 39, 44, 49, 55, 70, 109 and 112	14, 17, 28, 35 and 105
>0.800(Low stability)	38, 85, 99, 117, 136 and 33	2 and 71	30, 92 and 121

References

1. Anandan, A., Eswaran, R., Sabesan, T. and M. Prakash. 2009. Additive main effect and multiplicative interactions analysis of yield performances in rice genotypes under coastal saline environments. *Advances in Biological Research*, 3(1-2):43-47.
2. Crossa, J., Vasal, S.K. and D.L. Beck. 1990. Combining ability estimates of CIMMYT's late yellow maize germplasm. *Maydic*, 35: 279-185.
3. Cruz, C. D., Regazzi, A. J. and P.C.S. Carneiro. 2004. Biometric Models Applied To Genetic Improvement. Viçosa: UFA, 3:1.
4. Finlay, K.W. and G.N. Wilkinson. 1963. The analysis of adaptation in a plant-breeding programme. *Aust.J.Agric. Res.*, 14: 742-54.
5. Gauch, H. G. and R.W. Zobel. 1996. AMMI analyses of yield trials. In: Genotype by Environment Interaction, Kang MS and Gauch HG (eds.). CRC, London. PP: 85-122.
6. Grondana, M. O., Crossa, J., Fox, P.N and N.H. Pfeiffer. 1996. Analysis of variety yield trait using two dimensional separable ARIMA. *Process Biometric*, 52:763-770.
7. Johnson, G. R. 1997. Site-to-site genetic correlation and their implications on breeding zone size and optimal number of progeny test sites for coast Douglas-fir. *Silvae Genet*, 46: 280-285.
8. Li, Y., Suontama, M., Burdon, R.D., Burdon and H. S. Dungey. 2017. Genotype by environment interactions in forest tree breeding: review of methodology and perspectives on research and application. *Tree Genetics & Genomes*, 13: 60.
9. Navabi, A., Yang, R. C., Helm, J. and D. M. Spawer. 2006. Can spring wheat growing mega environments in the northern great plain be dissected for representative locations or niche-adapted genotypes? *Crop Sci.*, 46: 1107-1116.
10. Oliveira, E.J.D., Freitas, J. P. X. D. and O. N. D. Jesus. 2014. AMMI analysis of the adaptability and yield stability of yellow passion fruit varieties. *Sci. Agric.* 71(2): 139-145.
11. Purchase, J.L. 1997. Parametric analysis to describe G x E interaction and yield stability I winter wheat. PhD Thesis. Department of Agronomy, Faculty of Agriculture, University of the Orange Free State, Bloemfontein, South Africa.

12. Shaw, D.V. and J. V. Hood. 1995. Maximising gain per effort by using clonal replicates in genetic tests. *Theor. Appl. Genetics*, 71: 392 – 399.
13. Simmonds, N.W. 1991. Selection for local adaptation in a plant breeding programme. *Theoret. Appl. Genetics*, 82: 363-369.
14. Verma, A., Chatrath, R., and I. Sharma. 2015. AMMI and GGE biplots for G 9E analysis of Wheat genotypes under rain fed conditions in central zone of India. *Journal of Applied and Natural Science*, 7: 656–661.
15. Vita, P.D., Mastrangelo, A.M., Matteua, L., Mazzucotelli, E., Virzi, N., Palumboc, M., Stortod, M.L., Rizzab, F. and L. Cattivelli. 2010. Genetic improvement effects on yield stability in durum wheat genotypes grown in Italy. *Field Crop Research*, 119: 68-77.
16. Zahia, K., Farrah, A. and B. Hamenna. 2010. Analysis of the genotype X environment interaction of barley grain yield (*Hordeum vulgare L.*) under semi arid conditions: *Adv. Environ. Biol.*, 4(1): 34-40.
17. Zobel, B. and J. Talbert. 1984. Applied Forest Tree Improvement. John Wiley & Sons. P: 505.