



Additive Main Effects and Multiplicative Interactions (AMMI) Analysis of Growth of Half-sib Families of *Eucalyptus camaldulensis* Across Environments

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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, Thiyagadurgam, Karaikudi and Pulvayal after three years of planting during 2013. Additive main effects and multiplicative interactions (AMMI) analysis indicated that the 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 88.0% of the total genotype by environment interaction. The biplot technique was used to identify appropriate half-sib families to specific locations. Results showed that families 23, 7, 57 and 40 expressed high stability in performance across environments. Families 74, 92, 36, 88, 30 and 70 exhibited high yield in which environment potential. Family 36 and 74 showed low interaction with high growth performance and can be recommended for a wide range of environments. The families 30, 70 and 92 were having high productivity. Similarly the interaction with environment was also high. Hence, these families can be recommended for specific environments. The locations Marakkanam and Thiyagadurgam were found to be related and completely different from Karaikudi and Pulvayal. According to stability Pulvayal was found to be 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, Marakkanam.

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

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 (Genotype x Environment Interactions) (Johnson, 1997). When genotypes are evaluated in a single site, GEI effects cannot be estimated and get merged with genetic effects, causing an over estimation 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 extend. 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

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crop performance with changing environments, technically termed as genotype × environment (G × 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 widest range of environments, is one of the main objectives of breeding programs. Several methods have been applied to the evaluation of G × 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 yield, 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 locations in Tamil Nadu namely, Marakkanam, Karaikudi, Pulvayal and Thiyagadurgam planted during 2009 (Table 1). Of the 50 families used, seeds for 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 Karunyanagar, Coimbatore, 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.

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:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + \epsilon_{ger}$$

Where Y_{ger} = the observed yield of g^{th} genotype in e^{th} environment for r^{th} replicate; μ = the grand mean; α_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); g_n = 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:

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

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 mean volume of half sib families of *Eucalyptus camaldulensis* tested in four locations showed that 43.9 % of the total sum of squares was attributable to GEI effect 36.8% to genotype effect and only 19.3% to environmental effect (Table 2). The magnitude of GEI sum of squares was almost equal to genotype, indicating that there is substantial genotype contribution across environments. The GEI was about double the effect of environment. 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.

The analysis captured 56% of the discrimination at the first principal component axis (PCA 1) from 34.7% of the interaction degrees of freedom. It was also observed that the PCA 1 had sums of squares greater than that of environment. The second components captured 32% of the GEI sum of squares that amounts to a cumulative contribution to 88.0% 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 12 % of the GEI sum of

squares and was not significant and therefore did not help to predict valid observation.

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	Thiyagadurgam	11°48'23"N	79°05'19"E	374	Sandy loam
3	K	Karaikudi	10°00'51"N	78°46'19"E	251	Sandy clay loam
4	P	Pulvayal	10°22'27"N	78°42'21"E	374	Sandy clay loam

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 (Crossa *et al.*, 1990).

Table 2. Analysis of variance for the AMMI model

Source	df	Sum of squares	Mean of squares	F	F probability
Genotype	49	0.0021	0.0000436		
Environment	3	0.0011	0.000044		
Genotype X Environment	147	0.0025	0.000367		
IPCA1	51	0.0014	0.000028	**2.509	0.000
IPCA2	49	0.0008	0.000016	**2.777	0.000
IPCA3	47	0.0003	0.000006	****	1.000
Pooled error	600	0.007	0.00001		
Total	799	0.01277			

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

AMMI model 1 biplot positioned high potential environments viz., Marakkanam, Thiyagadurgam and Karaikudi in quadrant III and II, while the lower potential environment, Pulvayal was positioned in quadrant IV (Fig. 1). Pulvayal was observed to be poor environment and at the same time expressed low interactions score when compared to Thiyagadurgam and Marakkanam that scored high interaction scores (Table 3).

Table 3. Mean of growth yield together with first and second interaction principal components for different environments

Environment	Mean of yield	IPCA -1j*	IPCA -2j**
Marakkanam (M)	0.0144	-0.00035	0.03833
Thiyagadurgam (T)	0.0127	-0.05279	0.11245
Karaikudi (K)	0.0121	0.15666	-0.03713
Pulvayal (P)	0.0080	-0.10352	-0.11366

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

Thiyagadurgam was observed to be average environment and did not support any of the studied family. Marakkanam is 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, 30 and 92, 88 and 36 showed similar performance as they are close to each other. Families 30 and 92 are unstable families, however they are specifically adapted to high yielding environment, Marakkanam. Families, 62 and 66 are 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 family 74 was 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. Similarly, in the present study, family 74, 88 and 36 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 Marakkanam (M) and Thiyagadurgam (T) were the most discriminating environments as indicated by the longest distance between its marker and the origin.

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

Family	Volume		IPCA 1	IPCA 2	ASV	
	Mean	Rank			Value	Rank
1	0.0110	27	-0.0159	0.0098	0.036	16
2	0.0143	16	-0.0420	-0.0025	0.090	45
7	0.0135	18	-0.0072	-0.0103	0.019	4
8	0.0105	32	-0.0056	0.0236	0.026	7
10	0.0116	23	0.0151	-0.0383	0.050	27
12	0.0106	31	-0.0147	-0.0083	0.033	15
14	0.0157	7	-0.0118	0.0191	0.032	11
16	0.0100	36	-0.0245	0.0081	0.053	28
17	0.0145	15	-0.0170	0.0074	0.037	18
18	0.0129	19	-0.0296	-0.0225	0.068	35
23	0.0088	40	-0.0075	-0.0006	0.016	2
25	0.0147	10	0.0210	0.0155	0.048	26
27	0.0109	29	0.0031	-0.0178	0.019	5
28	0.0145	13	-0.0030	0.0317	0.032	13
30	0.0168	5	-0.0686	-0.0648	0.161	50
33	0.0095	39	-0.0018	-0.0404	0.041	20
34	0.0110	28	0.0125	0.0118	0.029	10
35	0.0147	11	-0.0381	-0.0170	0.084	43
36	0.0172	3	-0.0211	-0.0069	0.046	24
38	0.0078	45	0.0326	0.0064	0.070	37
39	0.0105	33	0.0022	0.0320	0.032	12
40	0.0108	30	0.0108	0.0080	0.025	6
44	0.0113	26	0.0121	-0.0309	0.040	19
46	0.0115	24	-0.0071	-0.0334	0.037	17
49	0.0114	25	0.0239	0.0492	0.071	39
53	0.0095	38	-0.0263	-0.0083	0.057	30
55	0.0127	20	-0.0024	0.0262	0.027	8
57	0.0137	17	0.0114	-0.0122	0.027	9
60	0.0104	35	0.0295	-0.0109	0.064	33
62	0.0074	46	-0.0006	-0.0175	0.018	3
66	0.0068	47	0.0065	-0.0071	0.016	1
67	0.0104	34	-0.0266	0.0125	0.059	32
70	0.0164	6	-0.0425	0.0207	0.094	46
71	0.0145	14	-0.0075	0.0428	0.046	22
73	0.0099	37	-0.0095	-0.0253	0.032	14
74	0.0185	1	0.0157	-0.0325	0.047	25
85	0.0087	41	0.0545	0.0067	0.117	48
88	0.0170	4	-0.0262	-0.0070	0.057	29
92	0.0174	2	-0.0673	0.0441	0.151	49
94	0.0064	48	0.0308	-0.0037	0.066	34
99	0.0082	44	0.0341	0.0016	0.073	40
105	0.0154	9	0.0249	0.0223	0.058	31
109	0.0121	22	0.0310	-0.0205	0.070	36
112	0.0125	21	0.0328	0.0027	0.071	38
115	0.0087	42	0.0094	0.0410	0.046	23
117	0.0048	50	0.0402	-0.0201	0.089	44
118	0.0146	12	0.0360	0.0046	0.078	42
121	0.0156	8	-0.0331	0.0281	0.077	41
136(ITC3)	0.0085	43	0.0475	-0.0163	0.103	47
137(ITC7)	0.0063	49	0.0200	-0.0010	0.043	21

IPCA = Interaction principal component analysis axis.

Table 5. Adaption of families for mean volume based on AMMI model

High mean & positive PCA	High mean & negative PCA	Low mean & positive PCA	Low mean & negative PCA
14, 36 and 74	30, 70, 92 and 121	23, 33, 62, 66, 73, 115 and 137	85, 117 and 136

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., 23, 7, 57 and 40 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, 49, 33, 85, 136, 70 and 121 were unstable as they are located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores.

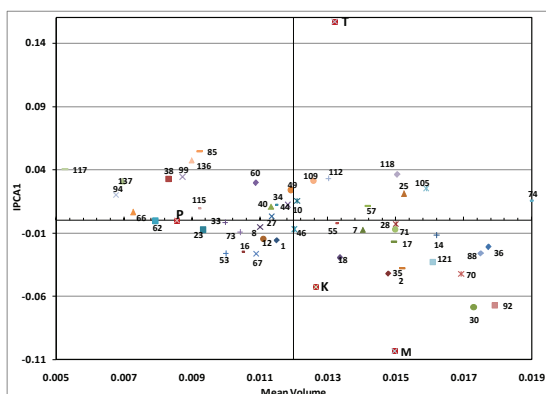


Fig.1. AMMI model 1 biplot of the 48 half sib families and 2 clones in 4 environments

Pulvayal and Karaikudi were observed to be closer and expected to support similar families. Further, Pulvayal is observed to highly stable 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.

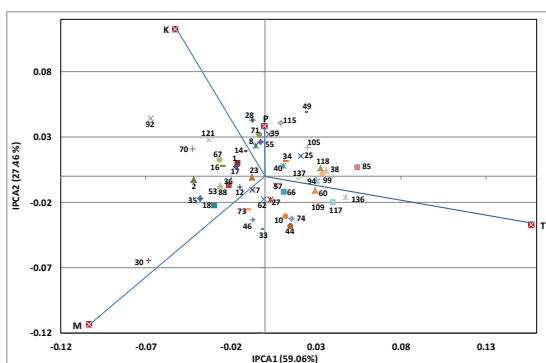


Fig.2. AMMI model 2 Biplot of 48 half sib families and 2 clones of growth yield for four environments using genotypic and environmental scores

AMMI adjusted mean volume based on untransformed data, AMMI stability values (ASV) and ranking of half-sib families based on the yield performance and ASV have been given in table 4. The half-sib family, 74, 92, 36 and 88 were observed to have high mean volume. The half-sib family, 66, 23, 62 and 7 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 4 have been classified into four levels of stability and yield performers and given in Table 5. The mean and PCA values were categorized into four classes viz., $> 0.015 \text{ m}^3$ (high mean), < 0.050 (Positive PCA) (14, 36 and 74) and $> 0.015 \text{ m}^3$ (high mean), > 0.075 (Negative PCA) (30, 70, 92 and 121) and $< 0.010 \text{ m}^3$ (Low mean), < 0.050 (Positive PCA) (23, 33, 62, 66, 73, 115 and 137) and $< 0.010 \text{ m}^3$ (Low mean), > 0.075 (Negative PCA) (85, 117 and 136). The commercial clones, 136 and 137 were observed to be poor in yield potential however; clone 137 was observed to have high stability. The half sib families, viz., 36 and 74 were found to have high yield along with high stability. Hence these clones can be grown across a wide range of environments without compromise on the yield. The family 30, 70 and 92 were although having high productivity however, the interaction with environment is high. Hence, these families can be recommended for specific environments.

References

- 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.
- Crossa, J., Vasal, S.K. and D.L. Beck. 1990. Combining ability estimates of CIMMYT's late yellow maize germplasm. *Maydic*, **35**: 279-185.
- Cruz, C. D., Regazzi, A. J. and P.C.S. Cameiro. 2004. Biometric Models Applied To Genetic Improvement. Viçosa: UFA, **3**:1.
- Finlay, K.W. and G.N. Wilkinson. 1963. The analysis of adaptation in a plant-breeding programme. *Aust. J. Agric. Res.*, **14**: 742-54.
- 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.
- Grondana, M. O., Crossa, J., Fox, P.N. and N.H. Pfeiffer. 1996. Analysis of variety yield traits using two dimensional separable ARIMA. *Process Biometric*, **52**:763-770.
- 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.
- 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.
- 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.

- 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.
- Purchase, J.L. 1997. Parametric analysis to describe G x E interaction and yield stability in winter wheat. PhD Thesis. Department of Agronomy, Faculty of Agriculture, University of the Orange Free State, Bloemfontein, South Africa.
- Shaw, D.V. and J. V. Hood. 1995. Maximising gain per effort by using clonal replicates in genetic tests. *Theoret. Appl. Genetics*, **71**: 392 – 399.
- Simmonds, N.W. 1991. Selection for local adaptation in a plant breeding programme. *Theoret. Appl. Genetics*, **82**: 363-369.
- 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.
- Vita, P.D., Mastrangelo, A.M., Matteua, L., Mazzucotelli, E., Virzi, N., Palumboc, M., Stortod, M.L., RizzabF. and L. Cattivelli. 2010. Genetic improvement effects on yield stability in durum wheat genotypes grown in Italy. *Field Crop Research*, **119**: 68-77.
- 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.
- Zobel, B. and J. Talbert. 1984. Applied Forest Tree Improvement. John Wiley & Sons. P: 505.