BLUP and Stability Analysis of Multi-Environment Trials in Lentil (*Lens culinaris* Medic) Genotypes under Rainfed Condition of Ethiopia

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Abstract

Twenty-five lentil genotypes including the check varieties were evaluated each over three seasons (2016 – 2018) at 8 locations (Akaki, Chefe Donsa, Dabat, Debre Zeit, Enewari, Hosanna, Kokate, Sinana) resulting in 11 environments in randomized completely block design with row column information. A factor analytic model was fitted to the pattern of genotype by environment (GxE) interaction using R ASReml package and predicted yield (t/ha^{-}) values for all genotypes under evaluation were obtained. The model adequately explained 90.6% of the GxE variance at an FA-2 of yield data. Environment and genotype evaluation based on GGE biplots has revealed a number of discriminative and representative environments while identifying ideal and high performing genotypes. Environment Db18LN was most discriminating followed by EN17LN, SN18LN and DZ16LP, whereas CD16LP and DZ16LP were found to be representative test site. Genotypes 6(DZ-2012-Ln-0218) was identified as high yielder and stable than other test genotypes and proposed for verification in the year 2020 for release as new variety and in the year 2021 it then registered with variety name "Furi" on the national catalogue of Ministry of Agriculture of the country.

Keywords: ASReml package, BLUP, Lentil yield stability, GGE Biplots, Factor Analytic

Introduction

Lentil (*Lens culinaris* Medic) is the important pulse crops in Ethiopia that is dominantly produced in the crop-livestock based farming systems of the central, north and northwest highlands of Ethiopia where vertisols are dominating. The crop can also grow in the lowland parts of the country provided that early maturing, resistant/tolerant to rust and low moisture stress varieties are developed.

Lentil has multiple uses in the country. The crop is good sources of dietary protein. It is also a rich source of essential vitamins, minerals, and important amino acids like lysine. The crop is also endowed with unique property in maintaining and improving soil fertility through symbiotic biological nitrogen fixation. Thus, it leaves substantial amount of residual nitrogen for subsequent crops and adds plenty of organic matter to maintain and improve soil health and fertility (Gaur *et al*., 2010). Hence, Ethiopian farmers usually grow the crop in rotation with cereals.

Besides being key components in the diets, lentil also attracts higher market prices than other staple crops, making them an important source of income for farmers. Despite the versatile uses of lentil in Ethiopia as stated above, the national average productivity of the crop in 2018/19 cropping season was 1.42 ton/ha (FOSTAT 2018; CSA 2019) as compared to its potential yield about 2.5 t/ha. Similarly, area under lentil production was 99,754 ha in 2018/19, but it was reduced to 87,444 ha in 2019/20 season, showing a 12.34% reduction in area coverage within a year (CSA 2020). Production and productivity follow the same trend of reduction as well. There are several factors accountable for this reduction and, for the significant yield gap between the achieved and the potential yield in the country. Even though, major diseases like rust and the newly emerged viral disease are recently causing major yield loss, however, the continuous varietal (genetic) and environmental variability are playing significant role in the stability of a given genotype/cultivar.

Regarding environmental variability, testing genotypes of annual crops for grain yield on a multi-locational or multi-year basis frequently shows GE interaction that complicates the selection or recommendation of materials. According to Annicchiarico (1997), it is possible to cope with genotype by year or genotype by location by year interaction effects only through selection for yield stability across environments defined as location by year combinations.

Kanouni, et al (2015) stated that GE analysis is important tool that help to identify superior varieties and their adaptation to and stability in diverse agro ecologies. In line to this fact, Padi, (2007) also observed that differential performance of chickpea under diverse environmental conditions decreases yield stability. Inefficiency in the GE analysis of variance may also result in wrong selection of genotypes for yield. There are many models for conducting GE whose applicability depends on the experimental data, the number of environments, and the accuracy of collected data and environmental information.

Earlier research work done in advancing GE by authors such as Gauch 1992; Imrie and Hacker 1993; Kang and Gauch 1996; Cooper and

Hammer 1996 have contributed significantly to the understanding and make use of the Biplot analysis as a tool. However, the way GE is measured and addressed between different users of different sectors varies. In this regard, Yan and Tinker (2006) stated that, biometricians and quantitative geneticists concentrate primarily on quantification of GE, while breeders and other practitioners are often concerned primarily with matching genotypes with environments.

The primary aim of a plant breeding in multi environment trials (MET) is selection either of potential new varieties or potential parents (Yan and Tinker, 2006). Selection requires definition of the trait(s) of interest and formation of an appropriate index based on these traits. Although it has been argued that environments (that is trials) can be regarded as traits in METs it is clear that this assumption may not be generally applicable, particularly for those METs which span several years of testing. Trial locations are usually chosen to represent a target ‘‘environment’’. The target environment could be an agro-ecological zone of commercial significance, or an environment classified by disease pressure or other biotic or abiotic factors. The trait of interest would therefore be the yield performance for the set of trials that align with the target environment (Yan and Tinker, 2006). In this study, we used average of grain yield ton per hectare of genotypes determined for individual environments using BLUPs fitted by factor analytic model in ASReml package, and biplot analysis implemented by GGE biplot with the aim to understand genotype by environment interaction in lentil, identification of best wide adaptable genotype across locations in the potential growing area of Ethiopia

Materials and Methods

Description of eco-location and genotypes

A study was undertaken by using germplasm of different genetic background to determine their level of GE in their biological yield responses. Twenty-five lentils advanced breeding genotypes including check varieties were evaluated each over three seasons between 2016 and 2018 at 8 locations resulting in 11 environments. The test genotypes were derived from series of trials called Preliminary Varity Trial (PVT) and National Varity Trial (NVT) tested at potential environments. Randomized complete block design with three 3 and 4 replications for PVT and NVT was used respectively. Each genotype was planted on four rows of 4m long in 20cm by 2cm inter and intra row spacing. Production was all under rain fed condition. The geographic information of testing sites is presented in Table 1.

Table 1. List of Test Environments, number of genotyped used, and their respective Geographic information

Test Site	Environment	No Genotypes	No Replication	Altitude (m.a.s.l)	Latitude (°N)	Longitude (°E)
Akaki	AK16LP	25	3	2207	8.87	38.85
Akaki	AK17LN	14	3	2207	8.87	38.85
Chefe Donsa	CD16LP	25	3	2450	8.96	39.1
Chefe Donsa	CD17LN	14	3	2450	8.96	39.1
Dabat	Db18LN	14	4	2557	12.97	37.77
Debre Zeit	DZ16LP	25	3	1910	8.73	39
Debre Zeit	DZ18LN	14	4	1910	8.73	39
Enewari	EN17LN	14	3	2667	9.88	39.15
Hosanna	HS18LN	14	4	2295	7.55	37.86
Kokate	KK18LN	14	4	2140	6.87	37.82
Sinana	SN18LN	14	4	2439	7.11	40.22

NB: PVT = Preliminary variety Trial, NVT = National Variety Trial, AK16LP=Lentil PVT at Akaki in 2016, AK17LN=Lentil NVT at Akaki in 2017, CD16LP=Lentil PVT at Chefe Donsa in 2016, CD17LN=Lentil NVT at Chefe Donsa in 2017, Db18LN=Lentil NVT at Dabat in 2018, DZ16LP=Lentil PVT at Debre Zeit in 2016, DZ18LN=Lentil NVT at Debre Zeit in 2018, EN17LN=Lentil NVT at Enewari in 2017, HS18LN=Lentil NVT at Hosanna in 2018, KK18LN=Lentil NVT at Kokate in 2018, SN18LN=Lentil NVT at Sinan in 2018

Table 2. List of genotypes over test years of 2016, 2017 and 2018 respectively

Code	Genotypes	Source	Remark
1	DENBI	MSI	Released variety
2	DERASH	MSI	Released variety
3	DZ-2012-Ln-0020	Introduction	Advanced line
4	DZ-2012-Ln-0050	Introduction	Advanced line
5	DZ-2012-Ln-0054	Introduction	Advanced line
6	DZ-2012-Ln-0218	Introduction	Advanced line
7	DZ-2012-Ln-0219	Introduction	Advanced line
8	DZ-2012-Ln-0228	Introduction	Advanced line
9	DZ-2012-Ln-0231	Introduction	Advanced line
10	DZ-2012-Ln-0232	Introduction	Advanced line
11	DZ-2012-Ln-0233	Introduction	Advanced line
12	DZ-2012-Ln-0234	Introduction	Advanced line
13	DZ-2012-Ln-0235	Introduction	Advanced line
14	DZ-2012-Ln-0236	Introduction	Advanced line
15	DZ-2012-Ln-0237	Introduction	Advanced line
16	DZ-2012-Ln-0238	Introduction	Advanced line
17	DZ-2012-Ln-0239	Introduction	Advanced line
18	DZ-2012-Ln-0240	Introduction	Advanced line
19	DZ-2012-Ln-0241	Introduction	Advanced line
20	DZ-2012-Ln-0242	Introduction	Advanced line
21	DZ-2012-Ln-0243	Introduction	Advanced line
22	DZ-2012-Ln-0244	Introduction	Advanced line
23	DZ-2012-Ln-0245	Introduction	Advanced line
24	DZ-2012-Ln-0255	Introduction	Advanced line
25	Check	Own gene pool	Local check

NB: MSI = Micro seed increase

Observations and data collection crop phenology traits

Days from sowing to the stages when 50% of the plants have started flowering was recorded from each plot as days to 50% flowering (DTF). Similarly, days from sowing to the stages when 90% of the pods mature was recorded from each plot as days to 90% maturity (DTM) and measurement of plant height in cent meter (PLH) was taken from five randomly selected plants from the ground to the tip using a ruler at maturity.

Grain Yield and Yield Component Traits

Hundred seed weight (HSW) of randomly selected hundred seeds weighed on a sensitive balance in gram was taken. Biomass yield (BMY) weight of all above ground plant part per plot was taken in gram and then converted to ton per hectare. Weight of seeds harvested from central two rows per plot in gram was taken and then converted to ton per hectare as grain yield (YLD). Grain harvest index (GHI) was also calculated as the ratio of grain yield to biological yield.

Statistical analysis

The genetic merit of each genotype for all traits was evaluated being combined over environments by best linear unbiased prediction (BLUP) using restricted maximum likelihood (REML) for variance component estimation in R. Pearson correlation was used to evaluate the association among traits. Factor analytic model was fitted using ASReml-R package and the predicted yield (tha^{-1}) values for all genotypes under evaluation were obtained base on procedures demonstrated by Kelly et.al. (2017). GGE biplot analysis was performed using R GGEBiplotGUI package of version 1.0.9 (Frutos et al 2014) using the BLUPs mean produced from factor analytic output. The GGE biplot methodology was used to analyse genotype performance for each environment, genotype stability, representative environment, and discriminating power of each environment.

Results and Discussion

Significant differences were observed among test genotypes for all of the characters under study indicated presence of considerable amount of variability in the tested genotypes. This variation could be exploited to improve yield (Table 3). High heritability was observed for all traits ranging over 85% for biomass yield t/ha to 98% for days to 50% flowering. Genotype DZ-2012-Ln-0245 get flowered early within 53 days, while genotype DZ-2012-Ln-0236 flowered lately within 68 days. The most early maturing genotype DZ-2012-Ln-0218 matured within 107 days, while late maturing genotype DZ-2012-Ln-0020 matured in 125 days. Variety Denbi was the tallest (36.24 cm) followed by genotype DZ-2012-Ln-0238 (36.27

cm). On the other hand, genotype DZ-2012-Ln-0243 (28.71 cm) was the shortest among all. Genotype DZ-2012-Ln-0228 had large seed size (3.7 cm) followed by DZ-2012-Ln-0243, and DZ-2012-Ln-0244 (3.6 cm). Local check on the other hand, had small seed size (2.1 cm). The highest grain harvest index (37%) was obtained from genotype DZ-2012-Ln-0218 which is now known by the variety name "Furi". Conversely, genotype DZ-2012-Ln-0235 had the smallest grain harvest index (16%). Variety Derash had the maximum biological yield (6.44 t/ha), while local check scored the minimum biological yield (3.99 t/ha). Genotype DZ-2012-Ln-0218 was found to be high performing in grain yield (2.33 t/ha), while genotype DZ-2012-Ln-0237 performed poorly in grain yield (0.86 t/ha).

Table 3. Mean values, and variance components viz of traits for different lentil genotypes across test Environments

Genotype	DTF	DTM	PLH	HSW	GHI	BMY	YLD
DENBI	57	111	36.42	2.4	0.33	5.76	2.13
DERASH	56	109	35.35	2.8	0.32	6.44	2.09
DZ-2012-Ln-0020	64	125	32.50	3.2	0.21	4.57	1.01
DZ-2012-Ln-0050	55	109	34.81	2.9	0.35	5.95	2.07
DZ-2012-Ln-0054	57	111	33.13	3.0	0.33	5.26	1.82
DZ-2012-Ln-0218	**55**	**107**	**35.47**	**2.9**	**0.37**	**6.30**	**2.33**
DZ-2012-Ln-0219	58	118	30.13	2.8	0.29	4.36	1.17
DZ-2012-Ln-0228	61	123	32.22	3.7	0.20	4.98	1.10
DZ-2012-Ln-0231	57	118	32.99	3.3	0.24	4.79	1.15
DZ-2012-Ln-0232	62	121	32.73	3.3	0.22	4.66	1.05
DZ-2012-Ln-0233	61	117	31.48	3.2	0.29	5.38	1.65
DZ-2012-Ln-0234	63	122	32.99	3.5	0.18	5.11	0.97
DZ-2012-Ln-0235	66	123	32.90	3.3	0.16	5.00	0.88
DZ-2012-Ln-0236	68	125	30.86	2.7	0.22	4.31	0.86
DZ-2012-Ln-0237	68	124	30.18	3.3	0.19	4.49	0.86
DZ-2012-Ln-0238	58	114	36.27	3.0	0.31	5.58	1.79
DZ-2012-Ln-0239	54	109	30.81	3.3	0.28	4.92	1.53
DZ-2012-Ln-0240	55	109	31.64	2.6	0.29	4.89	1.48
DZ-2012-Ln-0241	55	110	28.90	3.2	0.31	4.39	1.48
DZ-2012-Ln-0242	55	112	30.79	3.1	0.33	4.51	1.58
DZ-2012-Ln-0243	54	108	28.71	3.6	0.31	4.63	1.50
DZ-2012-Ln-0244	60	116	35.32	3.6	0.28	5.70	1.76
DZ-2012-Ln-0245	53	111	30.13	2.7	0.29	4.31	1.22
DZ-2012-Ln-0255	55	109	29.72	3.1	0.34	4.25	1.48
LOCAL CHECK	55	107	30.14	2.1	0.28	3.99	1.22
Grand mean	58	115	32.264	3.1	0.28	4.98	1.45
Heritability	98%	97%	89%	97%	92%	85%	96%
Genotype Variance	20.64	40.89	6.30	0.16	0.00	0.59	0.21
Residual Variance	5.40	10.47	9.52	0.10	0.00	1.15	0.12
LSD	2.83**	4.24**	2.73**	0.32**	0.07**	1.11**	0.41**
CV	3.97	2.82	9.57	10.37	22.74	21.57	23.76
No of Environments	**11**	**9**	**6**	**11**	**9**	**10**	**11**

NB: DTF= days to 50% flowering, DTM = days to90% maturity, HSW = hundred seed weight in gram, PLH = plant = height in cm, BMY= biomass yield ton per hectare, GHI = Grain harvest index, YLD: grain yield ton per hectare.

The estimates of correlation coefficients among the yield and its attributing traits are given in Table 4. Days to 50% flowering displayed positive and significant correlation between days to 90% maturity and hundred seed weight while days to 90% maturity was found positively and significantly correlated with days to 50% flowering and hundred seed weight. Plant height showed positive and significant correlation with biomass yield, grain harvest index, and grain yield. Hundred seed weight showed also positive and significant correlation with days to 50% flowering and days to 90% maturity. Biomass yield showed positive and significant correlation with plant height, grain harvest index, and grain yield. Grain harvest index showed positive and significant correlation with plant height, biomass yield, and grain yield (Table 4). In the current study, grain yield was positively and significantly correlated with plant height, biomass yield and grain harvest index. This indicates that these traits were positively associated to grain yield because of linkages of genes governing the characters at coupling phase and direct selection based on these traits may ultimately improve the seed yield. These results were in agreement with the findings of Hussan et al. (2018), Chowdhury et al. (2019) and Kishor et al. (2020).

Table 4. Phenotypic correlation coefficients among different yield and yield component traits in lentil genotypes

	DTF	DTM	PLH	HSW	BMY	GHI	YLD
DTF	**1**						
DTM	0.691**	**1**					
PLH	-0.086ns	-0.094ns	**1**				
HSW	0.389**	0.404**	0.044ns	**1**			
BMY	-0.138ns	-0.259*	0.697**	0.041ns	**1**		
GHI	-0.717**	-0.556**	0.342**	-0.439**	0.393**	**1**	
YLD	-0.490**	-0.487**	0.642**	-0.233*	0.831**	0.820**	**1**

NB: ** = significant at 1% and * = significant at 5% probability level, ns=non-significant

DTF= days to 50% flowering, DTM = days to90% maturity, HSW = hundred seed weight in gram, PLH = plant = height in cm, BMY= biomass yield ton per hectare, GHI = Grain harvest index, YLD: grain yield ton per hectare

A Multi-Environment Trial (MET) analysis was undertaken across the set of 11 environments using the raw data. FA models were found useful not only for adequately estimating/predicting genotype by environment (GxE) effects for balanced and unbalanced experiments, but also for estimating the covariance structure of GxE effects and conducting biplot analysis. Moreover, the correlated environments can be established based on the estimated GxE covariance structure, and help breeders choose genotypes based on BLUPs averaged across correlated environments. Accordingly, factor analytic model was fitted using ASReml-R package and the predicted yield (t/ha) values for all genotypes under evaluation were obtained base on procedures demonstrated by Kelly et.al. (2017).

A factor analytic model adequately explained 90.58% of the GxE variance at an FA-2 for yield. Table 5 presents a summary of the REML estimates of the total variance accounted for the effects for yield. These results demonstrate the complex nature of cross-over GxE interaction present for these data. The FA-2 model provides a satisfactory fit for most environments except KK18LNPE and EN17LNPE suggesting that these sites were generally not as well correlated with the other sites (environments). In addition, these sites had lower genotype variance than residual variance.

Table 5. Precent of Variations Explained by the Model in the Experiment

Environment	fac_1	fac_2	all	Genotype Variance	Residual Variance	Heritability	Mean yield t/ha
AK16LPPE	88.04	0.41	88.5	0.295	0.055	94%	1.06
AK17LNPE	83.44	16.6	100	0.110	0.342	49%	2.95
CD16LPPE	82.87	17.1	100	0.204	0.095	87%	1.78
CD17LNPE	73.66	23.8	97.5	0.158	0.126	79%	1.94
Db18LNPE	89.31	4.72	94	0.636	0.228	92%	1.95
DZ16LPPE	82.79	3.19	86	0.395	0.053	96%	1.34
DZ18LNPE	86.38	13.6	100	0.159	0.038	94%	0.90
EN17LNPE	66.48	33.5	100	0.043	0.131	50%	3.08
HS18LNPE	82.76	0.56	83.3	0.020	0.009	89%	0.72
KK18LNPE	59.8	40.2	100	0.006	0.016	61%	0.82
SN18LNPE	94.65	5.35	100	0.080	0.329	49%	1.75
Cumulative			90.58%				

NB: AK16LPPE=Lentil PVT at Akaki in 2016, AK17LN=Lentil NVT at Akaki in 2017, CD16LPPE=Lentil PVT at Chefe Donsa in 2016, CD17LNPE=Lentil NVT at Chefe Donsa in 2017, Db18LNPE=Lentil NVT at Dabat in 2018, DZ16LPPE=Lentil PVT at Debre Zeit in 2016, DZ18LNPE=Lentil NVT at Debre Zeit in 2018, EN17LNPE=Lentil NVT at Enewari in 2017, HS18LNPE=Lentil NVT at Hosanna in 2018, KK18LNPE=Lentil NVT at Kokate in 2018, SN18LNPE=Lentil NVT at Sinan in 2018, PVT = Preliminary variety Trial, NVT = National Variety Trial

Figure 1A presents the dendrogram using the REML estimate between environments correlation matrix as the similarity measure using the total effect. Two clusters were formed at a cut-off about 0.2 for the fitted value of yield data. The heatmap plot to provide further evidence that the clusters suggested from the dendrogram appear to describe the pattern of cross-over GxE (figure 1B).

A dendrogram classified the sites/Environments into two groups. The first group consisted of 6 environments (AK16LPPE, HS18LNPE, Db18LNPE, DZ18LNPE, KK18LNPE and DZ16LPPE). These environments had showed yield performance of low to medium magnitude. The second group of environments consisted of 5 environments such as AK17LNPE, CD16LPPE, CD17LNPE, EN17LNPE and SN18LNPE. Yield performance of genotypes in the second group was relatively higher indicating the suitability of these testing sites. Hence, they are the most representative of the overall lentil growing areas in the

country, which means breeders could have the opportunity to select a genotype with wider adaptability using those fewer testing sites. In addition, this has an important implication in reducing costs of conducting multi-location trails.

Furthermore, the heatmap graph illustrated in Fig. 2 classified the test environments into two major clusters in a similar manner with the dendrogram result. Accordingly, there was a strong and positive correlation among environments except for environment KK18LNPE, which showed weak and positive correlation with few other environments.

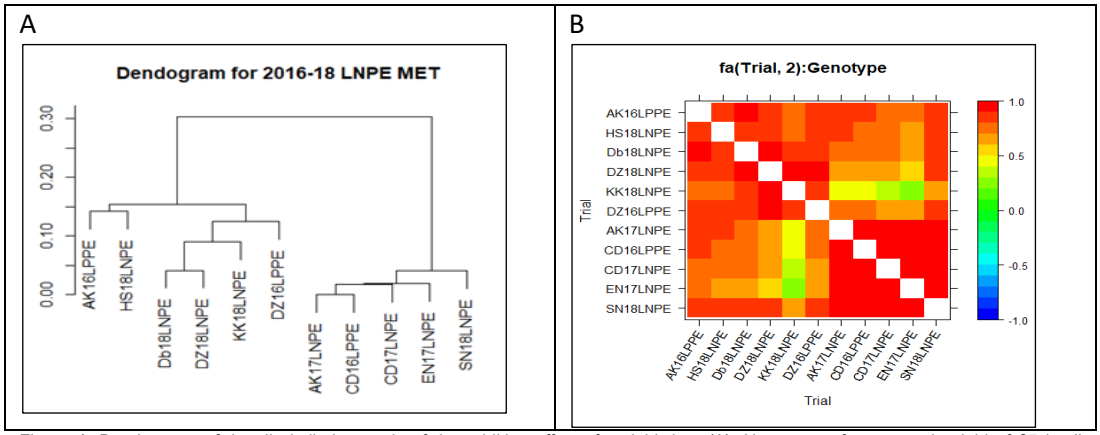

Figure 1. Dendrogram of the dissimilarity matrix of the additive effects for yield data (A). Heat map of mean grain yield of 25 lentil genotypes (t/ha) (B).

NB: AK16LPPE=Lentil PVT at Akaki in 2016, AK17LN=Lentil NVT at Akaki in 2017, CD16LPPE=Lentil PVT at Chefe Donsa in 2016, CD17LNPE=Lentil NVT at Chefe Donsa in 2017, Db18LNPE=Lentil NVT at Dabat in 2018, DZ16LPPE=Lentil PVT at Debre Zeit in 2016, DZ18LNPE=Lentil NVT at Debre Zeit in 2018, EN17LNPE=Lentil NVT at Enewari in 2017, HS18LNPE=Lentil NVT at Hosanna in 2018, KK18LNPE=Lentil NVT at Kokate in 2018, SN18LNPE=Lentil NVT at Sinan in 2018, PVT = Preliminary variety Trial, NVT = National Variety Trial

An interactive biplot implementation in R for modeling genotype-by-environment interaction in measuring the performance of trials (environments) in which 25 lentil genotypes were tested based on the suggestion given by Yan and Tinker (2006) and Frutos et al, (2014) are illustrated as follows using yield data of table 3.

Environment evaluation based on GGE Biplots

In evaluating relationships among test environments, the environment-vector view of the GGE biplot for the data in Table 6 was used. It is based on an environment-centered (centering = 2) GE table without any scaling (scaling = 0), and it is environment-metric preserving (SVP = 2) and its axes are drawn to scale (default feature of GGEBiplotGUI) (Frutos, et al, 2014). This biplot explained 96% of total variation of the environment-centered GE table. Assuming that it adequately approximates the environment centered two-way table in Figure 2.

Table 6. Mean yield (ton ha^{-1}) of 25 lentil genotypes tested at eleven environments in years between 2016 and 2018.

GID	Genotype	Environments										
		AK16LP	AK17LN	CD16LP	CD17LN	Db18LN	DZ16LP	DZ18LN	EN17LN	HS18LN	KK18LN	SN18LN
1	DENBI	2.19	3.33	2.07	2.46	2.76	2.38	1.44	3.88	0.90	0.95	1.81
2	DERASH	2.00	3.32	2.55	2.28	2.93	2.32	1.47	3.44	0.85	0.93	1.97
3	DZ-2012-Ln-0020	0.53	2.41	1.37	1.41	0.66	0.77	0.23	3.09	0.49	0.70	1.43
4	DZ-2012-Ln-0050	1.80	3.36	2.36	2.00	2.89	2.10	1.33	3.19	0.97	0.93	2.02
5	DZ-2012-Ln-0054	1.43	3.09	2.08	1.99	2.37	1.66	1.11	3.05	0.77	0.85	1.91
6	DZ-2012-Ln-0218	2.05	3.54	2.61	2.71	3.29	2.97	1.63	3.23	0.85	0.92	2.13
7	DZ-2012-Ln-0219	0.64	2.55	1.28	1.51	1.05	1.41	0.40	2.95	0.54	0.72	1.57
8	DZ-2012-Ln-0228	0.69	2.47	1.60	1.51	0.79	0.63	0.32	3.23	0.52	0.72	1.43
9	DZ-2012-Ln-0231	0.89	2.54	1.33	1.62	0.93	1.02	0.42	3.42	0.56	0.75	1.42
10	DZ-2012-Ln-0232	0.63	2.44	1.45	1.47	0.72	0.72	0.28	3.19	0.51	0.71	1.42
11	DZ-2012-Ln-0233	1.16	2.83	2.05	2.33	1.49	1.48	0.64	3.37	0.73	0.77	1.59
12	DZ-2012-Ln-0234	0.52	2.38	1.34	1.40	0.58	0.68	0.20	3.15	0.48	0.70	1.39
13	DZ-2012-Ln-0235	0.39	2.31	1.27	1.32	0.42	0.57	0.11	3.09	0.45	0.68	1.36
14	DZ-2012-Ln-0236	0.43	2.30	1.27	1.33	0.38	0.48	0.10	3.18	0.45	0.68	1.33
15	DZ-2012-Ln-0237	0.33	2.29	1.16	1.29	0.41	0.70	0.09	3.01	0.44	0.67	1.38
16	DZ-2012-Ln-0238	1.41	3.10	1.98	2.05	2.50	1.63	1.27	2.92	0.88	0.86	1.99
17	DZ-2012-Ln-0239	1.10	2.78	2.07	1.87	1.45	1.16	0.57	3.31	0.63	0.79	1.59
18	DZ-2012-Ln-0240	1.05	2.83	1.82	1.66	1.69	1.43	0.76	3.04	0.61	0.77	1.73
19	DZ-2012-Ln-0241	0.87	2.74	1.86	1.68	1.48	1.27	0.58	2.93	0.60	0.76	1.70
20	DZ-2012-Ln-0242	0.85	2.82	1.92	1.57	1.68	1.29	0.68	2.75	0.58	0.73	1.80
21	DZ-2012-Ln-0243	1.06	2.84	1.86	1.56	1.84	1.64	1.01	2.93	0.66	0.84	1.80
22	DZ-2012-Ln-0244	1.43	2.93	2.35	2.28	1.68	1.33	0.75	3.63	0.73	0.83	1.58
23	DZ-2012-Ln-0245	0.85	2.59	1.39	1.62	1.09	1.24	0.47	3.24	0.57	0.75	1.51
24	DZ-2012-Ln-0255	1.00	2.66	1.74	1.78	1.35	1.36	0.50	3.24	0.60	0.77	1.58
25	LOCAL CHECK	1.23	2.38	1.65	1.45	0.49	1.43	0.43	4.29	0.54	0.79	1.08

NB: AK16LP=Lentil PVT at Akaki in 2016, AK17LN=Lentil NVT at Akaki in 2017, CD16LP=Lentil PVT at Chefe Donsa in 2016, CD17LN=Lentil NVT at Chefe Donsa in 2017, Db18LN=Lentil NVT at Dabat in 2018, DZ16LP=Lentil PVT at Debre Zeit in 2016, DZ18LN=Lentil NVT at Debre Zeit in 2018, EN17LN=Lentil NVT at Enewari in 2017, HS18LN=Lentil NVT at Hosanna in 2018, KK18LN=Lentil NVT at Kokate in 2018, SN18LN=Lentil NVT at Sinan in 2018, PVT = Preliminary variety Trial, NVT = National Variety Trial

The lines that connect the test environments to the biplot origin are called environment vectors. According to Equation given by Kroonenberg, (1995) the cosine of the angle between the vectors of two environments approximates the correlation between them. The genotypes were represented on the biplots as the points derived from their scores for the first two components, and the environments as the vectors from the biplot origin to their points. The cosine of angle between a pair of environment vectors approximates correlation between them (Yan and Kang, 2003). An acute angle ($<90^o$) indicates a strong positive correlation; an angle close to 90^o indicates the environments are not correlated, whereas an obtuse angle close to 180^o represents a strong negative relationship (Kroonenberg, 1995). These graphic analyses were done using R GGEBiplotGUI package of version 1.0.9 as presented by Frutos et al (2014).

Accordingly, all the tested environments were displayed on the second and third quadrants of the GGE Biplot (Fig. 2). The largest angle formed between environments EN17LN and Db18LN; EN17LN and SN18LN were slightly larger than 90°, implying that the GE is moderately large. The remaining environments had angle less than 90° implying strong positive correlation among themselves. The presence of close associations among test environments suggests that the same information about the genotypes could be obtained from fewer test environments, and hence the potential to reduce testing cost. If two test environments are closely correlated consistently across years, one of them can be dropped without loss of much information about the genotypes (Yan and Tinker, 2006). Thus, some of the test environments such as Akaki (AK16LP, AK17LN), Chefe Donsa (CD16LP, CD17LN), Debre Zeit (DZ16LP, DZ18LN) and Dabat (Db18LN) can be dropped as they generate the same information about the genotype. On the other hand, the angles formed between EN17LN and KK18LN and also between EN17LN and DZ18LN close to 90^o and hence have no correlation.

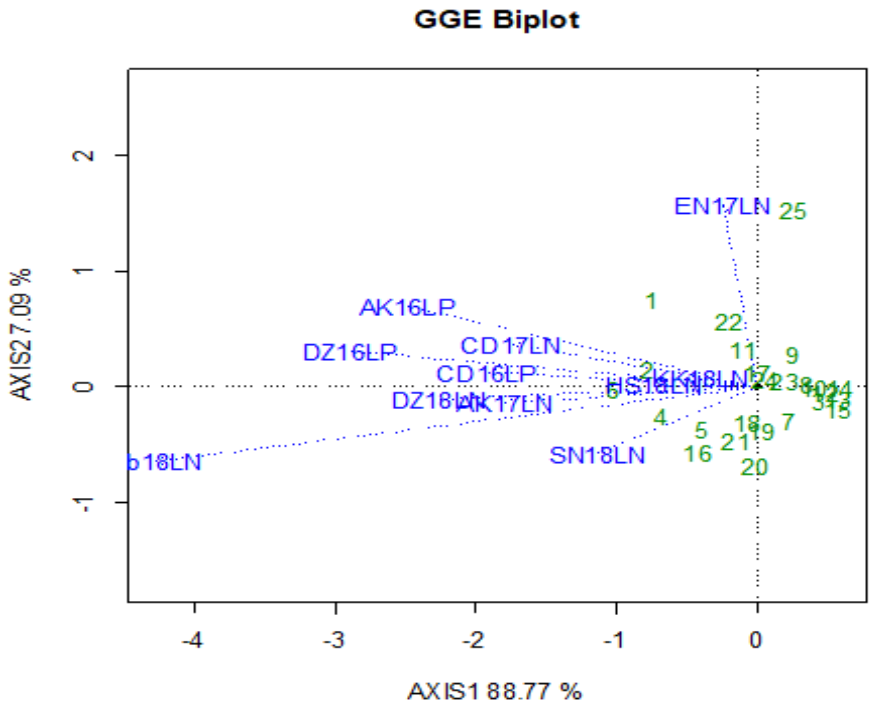

Figure 2. The environment-vector view of the GGE biplot to show similarities among test environments

The discriminating ability of test environments is shown in figure 3. The concentric circles on the biplot help to visualize the length of the environment vectors, which is proportional to the standard deviation within the respective environments and is a measure of the discriminating ability of the environments. Therefore, among the eleven environments, Db18LN was most discriminating (informative) followed by DZ16LP and AK16LP. KK18LN was least discriminating followed by HS18LN as these environments are located around the origin of the graph (Figure 3).

Regarding representativeness the test environments Yan and Tinker (2006) stated that the average environment represented by the small circle at the end of the arrow has the average coordinates of all test environments. The Average Environment Axis (AEA) is the line that passes through the average environment and the biplot origin. Accordingly, a test environment that has a smaller angle with the AEA is more representative of other test environments. Thus, CD16LP and DZ16LP are most representative whereas EN17LN and SN18LN least representative. Test environments that are both discriminating and representative like DZ16LP is good test environments for selecting generally adapted genotypes. Discriminating but non-representative test environments such as Db18LN are

useful for selecting adapted genotypes if the target specifically environments can be divided into mega-environments.

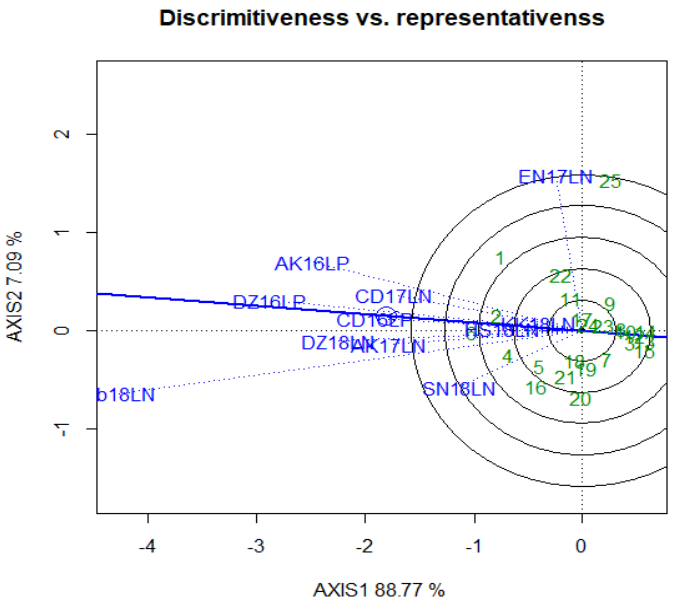

Figure 3. The discrimination and representativeness view of the GGE biplot

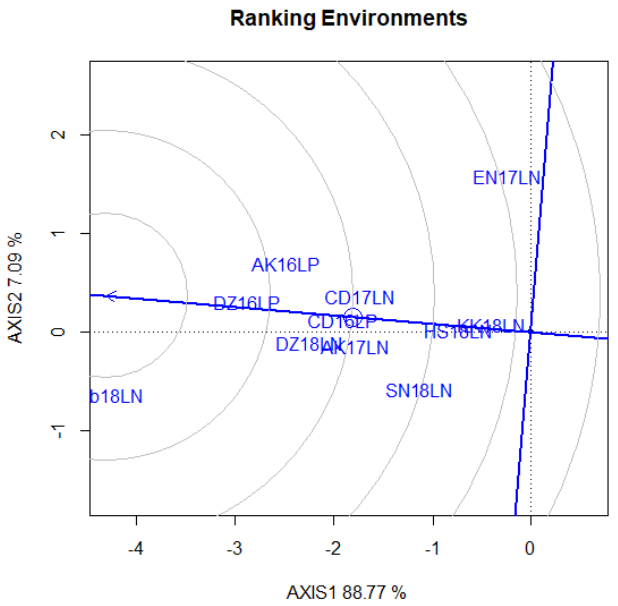

Figure 4. The discrimination and representativeness view of the GGE biplot to rank test environments relative to an ideal test environment.

Within a single mega-environment, the ideal test environment should be most discriminating (informative) and at the same time most representative of the target environment. Figure 4 defines an "ideal test environment", which is the center of the concentric circles. It is a point on the AEA with a distance to the biplot origin equal to the longest vector of all environments ("most informative"). DZ16LP is closest to this point and is, therefore, best, whereas KK18LN was the poorest for selecting cultivars adapted to the whole region.

Genotype evaluation based on GGE Biplots

To evaluate the mean performance and stability of the genotypes within a single mega-environment, the data should be genotype-metric preserving (SVP = 1) for appropriate genotype evaluations (Yan and Tinker, 2006). Accordingly, the single-arrowed line called Average Environment Coordinate (AEC) abscissa (or AEA) points to higher mean yield across environments. Thus, genotype 6 was fond to be the highest with the potential grain yield of 3.54 (t/ha^{-1}) at AK17lN, followed by 1 and 2 whereas genotype14 had the lowest mean yield. The AEC ordinate points to greater variability (poorer stability) in either direction. Thus, genotype 25 was highly unstable whereas 17 were highly stable. Genotype 25 was highly unstable because it had lower than expected yield in environments DZ18LNPE and AK16LPPE but higher than expected yield in AK17LNPE, and EN17LNPE environments (Figure 5).

Ranking genotypes relative to the Ideal Genotype

A genotype is said to an ideal if it had both high mean yield performance and high stability across environments. Figure 6 defines an "ideal" genotype (the center of the concentric circles) to be a point on the AEA ("absolutely stable") in the direction towards the pointing of the arrow and has a vector length equal to the longest vectors of the genotypes on AEA ("highest mean performance"). Therefore, genotypes located closer to the 'ideal genotype' are more desirable than others. Thus, genotype 1, 6 and 2 were more desirable than the other genotypes. However, genotypes 1 and 2 are released variety and thus no need of discussing about them. On the other hand, genotype 14 was the poorest genotype because it consistently performed poorly across environments.

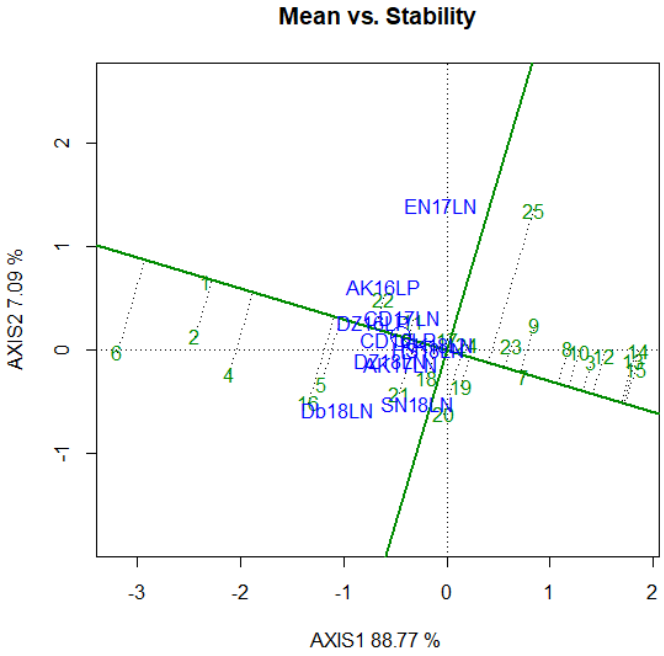

Figure 5. The average-environment coordination (AEC) views to show the mean performance and stability of the genotypes.

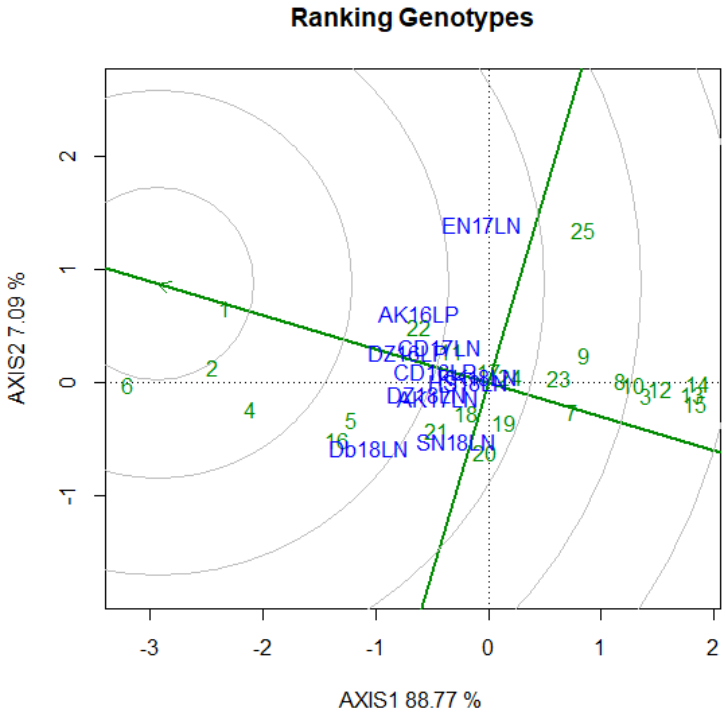

Figure 6. Ranking cultivars based on both mean performance and stability for experimental set A

Which-won-where?

One of the most attractive features of a GGE biplot is its ability to show the which-won-where pattern of a genotype by environment data set (Yan and Tinker, 2006). The polygon formed by connecting the markers of the genotypes that are farthest away from the biplot origin, such that all other genotypes are contained in the polygon. Figure 7 also contains a set of lines perpendicular to each side of the polygon. These perpendicular lines divide the biplot into several sectors. The winning genotype for each sector is the one located at the respective vertex. Genotypes located at the vertices of the polygon reveal the best or the poorest in one or other environment (Yan and Tinker 2006; Fructos *et al*, 2014).

Seven sectors were created with genotype's code number 6, 1, 25, 14, 20 and 16 as the vertex genotype. Environments EN17LN fell in the sector in which genotype 25 was the vertex cultivar. meaning that genotype 25 was the best cultivar for EN17LN site. The other ten environments fell in the sector in which genotype 6 was the vertex cultivar, which mean that genotype 6 was the best cultivar for these ten environments. No environments fell into sectors with genotype 14 and 20 as the vertices, indicating that these cultivars were not the paramount in any of the environments. In general, this result further verified the results depicted in the dendrogram (Fig. 1A).

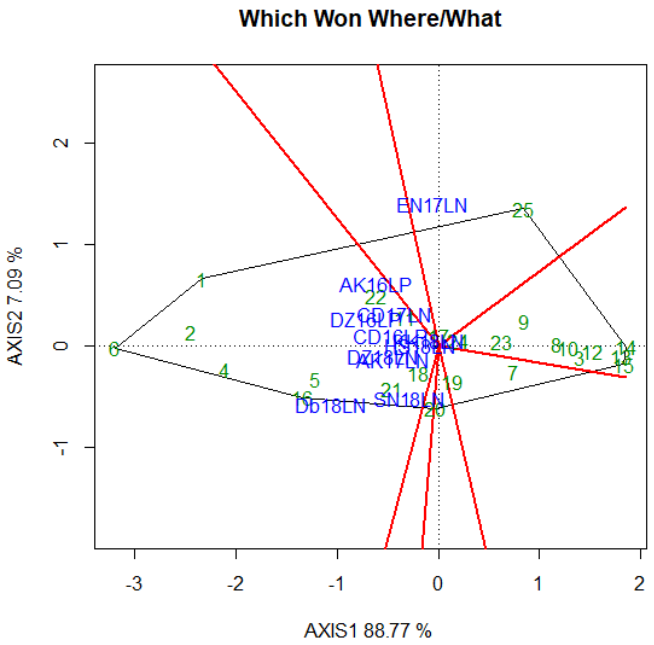

Figure 7. The which-won-where view of the GGE biplot.

Conclusions

A multi-environment trial (MET) analysis was undertaken across the sets of 11 environments for estimating the GxE effects with BLUPs by using factor analytic (FA) models, and thereby conducting GGE biplot analysis based on BLUPs of FA models. As a result, both informative and representative test environments were identified and also superior genotypes of high and stable performance were known within target environment. So, plant breeders can therefore, have such a more robust platform for evaluation of crop cultivars with greater confidence in selecting superior cultivars across a range of environments without minding about the limited amounts of seeds of test genotypes and size of experimental plots as unbalanced structure of test genotypes can easily be analyzed and BLUPs determined with FA model.

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