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Research paper

Genotype × Environment interaction studies in lentil under Afghanistan environments

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Lentil (*Lens culinaris Medik. culinaris)* is an important pulse crop causative to nutrition and food security of people in Afghanistan. Genotype by environment interaction (GEI) is one of the major factors restraining the efficiency of any breeding program. This study consisted of two lentil yield trials conducted in alpha design with two or three replicates at three locations for two years (2014-2015 and 2015-2016). Genotypic differences were significant (P<0.05) in all the environments. Genotype × location interactions were found significant (P<0.01) in each year for LIEN-LS and LIEN-SS trials. There were significant genotype × year interactions of crossover type. For LIEN-LS genetic materials, Herat and Mazar formed a mega-environment based on responses in 2015 and 2016. High yielding genotypes with specific adaptation to Mazar and Herat environment were LG16 (FLIP2012-21L) in 2015 and LG24 (FLIP2013-3L) in 2016, whereas LG30 (FLIP2013-20L) was identified as high yielding with specific adaptation to Nangarhar environment during both the years. The high yielding genotypes in 2015 were LG32 (FLIP2013-29L) at Herat, LG16 (FLIP2012-21L) at Mazar and LG30 (FLIP2013-20L) at Nangarhar from LIEN-LS. In 2016, LG12 (FLIP2013-16L) at Herat, LG5 (FLIP2013-3L) at Mazar and LG1 (FLIP2013-20L) at Nangarhar were identified as high yielding genotypes. In 2015-16, SG12 (FLIP 2013-51L) at Herat, SG2 (FLIP2013-59L) at Mazar and SG6 (FLIP2013-66L) at Nangarhar were the top yielding genotypes from LIEN-SS. The identified genotypes from LIEN-LS and LIEN-SS at the two locations (Mazar and Nangarhar) may be used for up-scaling lentil production to support food security in Afghanistan as well as for generating new genotypes using crossing-selection-evaluation cycle.

Key words: lentil, genotypes × environment interaction, adaptation, Afghanistan, GGE bi-plot

INTRODUCTION

Lentil (*Lens culinaris* Medikus subsp. *culinaris*) is an important pulse crop contributing to food security of people in Asia and Africa. Lentil production in the world is 4.8 million tonnes from 4.5 million hectares with an average yield of 1.07 t/ha in 2014 (FAO, 2016). Based on production worldwide, lentil ranks sixth among the major pulses and consisted 6% of total dry pulse production. Canada, India, Turkey, Australia, Nepal, Bangladesh, and USA are top lentil-growing countries. Afghanistan grows pulses on about 70 thousand hectare area with chickpea, lentil and mungbean as major crops with no independent record of production. To meet its domestic requirement, it imports ~1500 to 2000 tonnes of lentil every year. In neighboring countries with similar agro-ecology like Iran and Pakistan, lentils grown on relatively much larger scale estimated at 17457 ha and 12952 ha (FAO, 2016). Although domesticated in the Fertile Crescent in the Mediterranean environments, it has spread globally in successful cultivation in sub-tropical, temperate, and non-tropical dry environments including South Asia, Sub-Saharan Africa and North Africa, Europe, Latin America, North America and Oceania. Since its seed contains high levels of protein (up to 33%), macronutrients (Fe and Zn), and vitamins (β-Carotene, thiamin, niacin, folic acid) (Bhatty, 1988; Savage, 1988), it provides nutritional security for the people in the developing countries where poor consumers cannot afford costly animal products. Lentil straw is used as animal feed (Erskine el al., 1990a), and serves as an additional source of income. Lentil is often grown on marginal lands. Since its cultivation improves soil health by enriching soil carbon, nitrogen and organic matter status, it provides sustainability to cereal based cropping systems (Sarker et al., 2009; Ryan et al., 2012; Christiansen et al., 2015). A number of field studies on lentil have been conducted at ICARDA including adaptation and rationalization of testing sites using international nursery trials (Sarker et al., 2010) and using on-farm trials (Sarker et al., 2007), effect of climatic variable for predicting lentil yields (Sarker et al., 2003), and modeling spatial variability in the fields to improving the breeding progress (Sarker et al., 2001, 2015).To meet the protein requirement of population in Afghanistan, high yielding lentil varieties with wide and specific adaptation are needed for fitting into various cropping systems. Genotype-environment interaction (GEI) is an important component of phenotypic variation, and must be accounted and interpreted while identifying genotypes in response to the environments. Several techniques have been described in literature for estimation of GEI (Kemptorne, 1952; Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Linet et al., 1986; Gauch and Zobel, 1988; Delacy et al., 1996a, b). To detect the presence of GEI, and quantify and identify any patterns in it, yield trials are conducted at several locations over years. Past studies have reported significant GEI in lentil (Sarker et al., 2010; Sabaghnia at al., 2008, 2012; Abo-Hegazy et al., 2012). Sarker et al. (2010) examined the yield response of lentil genotypes evaluated at 111 environments covering 16 countries over seven years. The primary purpose was to rationalize testing sites based on genotypic responses and climatic variables, and to identify high yielding stable lentil lines. Formation of mega-environments and identification of genotype with specific adaptation are often presented using a graphical tool called GGE-biplot (Yan et al., 2000; Yan, 2011; Imtiaz et al., 2013; Sayar and Han, 2016).In Iran environments, GEI analysis was carried out to examine its nature in lentil by Sabaghnia et al. (2008, 2012). Abo-Hegazy et al. (2012) applied a number of standard procedures for stability analysis of lentil genotypes evaluated at two locations over three years in Egypt, and found insignificant correlation between yield and stability, indicating the possibility of combining high yield and stability in lentil varieties. Although several GEI studies have been presented in lentil for environments in many countries, but such studies are not available for lentil growing environments in Afghanistan. International Center for Agricultural Research in the Dry Areas (ICARDA), with the world mandate for lentil improvement, develops new varieties following selection-recombination-selection-evaluation cycle and has been conducting lentil trials in Afghanistan environments. Two Lentil International Elite Nurseries, one (LIEN-SS) comprising small seeded elite lines and another (LIEN-LS) comprising large seeded elite lines were evaluated in at three locations over two years (i) to examine genotypic variation in lentil, (ii) to detect genotypes × environment interaction and (iii) to identify stable high yielding genotypes with specific and wide adaptation to agro-ecologies of Afghanistan.

MATERIALS AND METHODS

Environments and Genetic Material

A total of 72 lentil genotypes were tested in two trials during 2015 and out of which 30 genotypes were tested in 2016 during the winter season at three locations in Afghanistan: Herat (39° 11 N, 68° 131 E, 964 m asl, average annual precipitation 205 mm, soil type was loam), Mazar (36° 39 25.4 N, 66° 57 39.9 E, 398 m asl, average annual precipitation 282 mm and soil type was clay loam)and Nangarhar (34° 25 N, 70° 27 E, 552 m asl, average annual precipitation 225.5 mm and soil type was loam to sandy loam). Each of the two trials, Lentil International Elite Nursery - Large Seed (LIEN-LS) and Lentil International Elite Nursery - Small Seed (LIEN-SS), were conducted at the same three locations: Herat, Mazar and Nangarhar.

Experimental Design

During 2014-15, both trials, LIEN-LS and LIEN-SS, each comprising 36 elite lines, were evaluated in simple lattice design at three locations. During 2015-16, the two yield trials each comprising 14 selected genotypes with one local check were conducted in randomized complete block design (RCBD) with three replicates (Table 1). The numbers of genotypes common between the years of each trial were 14. The plot sizes were 2.25m^2 with 0.25m row to row distance, 3m row length and 2 rows per plot in 2015, and 4.8m^2 with 4 rows, each 4 m long and 30cm row to row distance in 2016. Trials were planted between 09 November and 27 January, and crop was harvested between 24 May and 4 June. The crop was managed following the standard agronomic practices recommended by the Afghanistan Research Institute of Agriculture (ARIA). Grain yield was estimated from 2.25m² plot area for all the trials in 2015 and 1.8m² plot area in 2016. The plot yield was converted to tonne per hectare for statistical analysis.

Statistical Analysis

The dataset from each individual year-location combination was analyzed by fitting the mixed model where block effects were assumed random in case of lattice design, and the analysis of variance (ANOVA) model was fitted for data from RCBD. Since our interest lied in evaluating and comparing the specific genotypes obtained from materials already screened at ICARDA research station at Aleppo in Syria, their effects were assumed as fixed. For each trial type, *i.e.* large seeded and small seeded materials, analysis was carried out on combined data over all the locations each year and also combined over the years and locations. The combined analyses provided information on genotype × location interaction (GLI) and genotype × year interaction within locations (GYIwL). Since the locations represented repeatable diverse environments, their effects as well as GLI were assumed fixed. When combining data over the years, the year effects and GYIwL were assumed random. Furthermore, the datasets combined over years were based on common genotypes and in RCBD (*i.e.* for LIEN-LS we ignored incomplete blocks only when combining over the years). To describe further an insight of the statistical analysis models, let Yield, Rep, Blk, Geno, Loc and Year represent vectors containing plot-wise values for the yield (response), replicates, blocks within replicates, genotypes, locations and years, respectively. These models were fitted using the REML (restricted maximum likelihood) procedure with VCOMPONENTS directive in GenStat software (VSN Inc. 2015) given in the following. Data from a single simple lattice design (*i.e.* a given location and year combination):

VCOMPONENTS [Fixed=Geno] Rep + Rep.Blk ; constraints=positive

Data from simple lattices combined over locations for a given year:
VCOMPONENTS [Fixed=Geno+ Loc + Geno. Loc] Loc.Rep + Loc.Rep.Blk ; constraints=positive

Data from RCBDs combined over locations for a given year:
VCOMPONENTS [Fixed=Geno+ Loc + Geno. Loc] Loc.Rep ; constraints=positive

Data from RCBDs combined over locations and years:
VCOMPONENTS [Fixed=Geno+ Loc + Geno. Loc] Year.Loc + Geno.Year.Loc+ Year.Loc.Rep; constraints=positive

Genotype plus genotype × environment interaction (GGE) bi-plot (Yan 2011) presentation was carried out to identify genotypes for specific adaptation to the location. GGE bi-plots are graphical presentation of genotypes and environments, and are used to compare environments for their genotypic differentiation, formation of mega-environments and identifying genotypes adapted specifically to an environment. These plots are obtained from an approximation of a GGE matrix into sum of products of vectors for genotypes and environments (and hence the bi-plots), and displaying them on an often two- dimensional plot where genotypes are represented by points and environments by vectors. The exterior most points (genotypes) are connected as the sides of a polygon and perpendiculars are drawn from the center onto the polygon sides. If the region formed by the perpendiculars on the neighboring sides of the polygon contains a set of environments, then these environments form a mega-environment. GenStat software environment (VSN Inc., 2015) was used to fit the models and the GGE bi-plots..

RESULTS AND DISCUSSION

Genotypic Variability at Individual Environments

For each location of the trials, Table 1 summarizes experimental information in terms of mean and field heterogeneity measured by the plot-error coefficient of variation (CV). The statistical significance of genotypic effect is given as P-value, the probability of observing large value of the test statistics or extreme data when the genotype effect is absent. Genotypic differences at individual environments (location – year combination) were found statistically significant (P <0.001 – 0.044) covering both the trials (12 data sets). The overall mean at an environment varied from 0.27– 1.33 t/ha for LIEN-LS and 0.27 – 1.34 t/ha for LIEN-SS. The CV varied from 20 - 40% in fields of LIEN-LS trial and 19 – 40% for the LIEN-SS trial. The environments where the CV was very high (>30%), the mean yield was found very low, 0.27 – 0.77 t/ha (5 environments). Thus there is a need to look into field plot and data analysis techniques to reduce the experimental error.

Table 1. Lentil trial name, location, number of genotypes, experimental design, location mean grain yield, coefficient of variation (CV), and significance (P-value) for genotypic effect.

Trial name†	Year	Location Name	Experimental designs	No of genotypes	overall means	CV (%)	P-Value
LIEN-LS	2015	Herat	Simple lattice	36	0.27	31.58	0.032
		Mazar	Simple lattice	36	1.19	19.80	<0.001
		Nangarhar	Simple lattice	36	1.14	24.07	<0.001
	2016	Herat	RCBD	15	0.27	39.99	0.001
		Mazar	RCBD	15	1.33	22.81	0.006
		Nangarhar	RCBD	15	0.70	35.4	0.041
LIEN-SS	2015	Herat	Simple lattice	36	0.32	22.38	<0.001
		Mazar	Simple lattice	36	0.72	26.52	<0.001
		Nanagarhar	Simple lattice	36	1.14	35.35	0.044
	2016	Herat	RCBD	15	0.27	39.99	0.001
		Mazar	RCBD	15	1.34	18.99	0.028
		Nangarhar	RCBD	15	0.77	37.44	0.007

†LIEN -LS =Lentil International Elite Nursery Large Seed -2015. LIEN-SS =Lentil International Elite Nursery Small Seed -2015. RCBD = Randomized complete block designs (with three replicates).
CV= coefficient of variation. P-value = Probability of observing the extreme data in the absence of genotypes effects.

Genotype × Environment Interaction

Table 2 presents results on genotype × location interaction (GLI) for each year and genotype × year interaction within locations (GYIwL) in terms of significance and estimates of variance components. Year-wise data analysis showed that genotype × location interactions (GLI) were significant (P<0.002) in both the trials in both years (Table 2A). For the cases with significant GLI, the genotypic variation (G) averaged over locations was also found significant (P<0.008). Combined over the locations and the years, genotype × year interaction within locations (GYIwL) was found significant (P<0.001) for LIEN-LS (Table 2B). The GLI was found significant in LIEN-SS trials only (P=0.003) and G was found insignificant in each of the trials. This is reflecting a strong crossover type interaction due to the year in LIEN-LS. Therefore, the specific adaptation to the locations was examined year-wise only for LIEN-LS and combined over years for LIEN-SS using GGE bi-plot procedure. Based on a two-year multi-location trial in ten lentil genotypes in Iran, Sabaghnia et al. (2012) also found significant genotype × location ×year interaction.

In another study with eleven genotypes and 20 environments arising from seven locations over three years, Dehghani et al. (2008) found significant GEI. In this case instead of partitioning the interaction into location and year, univariate stability indices were used to evaluate genotypes and used coefficient of variation (CV) and stability variance as parameters for stability analysis. Erskine et al. (1990) and Summer field et al. (1985) also reported significance of G × L in most of the trials because of diverse genotypes and a wide range of environments characterized due to temperature, photoperiod and rainfall patterns, the most influential determinants of adaptation in lentil. Abo-Hegazy et al. (2013) reported significant GEI while testing 24 lentil genotypes in two environments in Egypt. Similarly, the performance of genotypes in different environments and G×E interaction in lentil was reported (Hamdi and Rabeia, 1991; Hamdi et al., 1995; Selim, 2000; Hamdi et al., 2002). Studies conducted in Afghanistan, Akbarzai et al. (2017) in wheat and Mohammadi et al. (2017) in chickpea reported significant GEI in three multi-location and two-year trials.

Identification of Specifically Adapted and High Yielding Genotypes

The GGE represents genotype main effect (G) plus genotype × environment interaction (GE), the main sources of variation for cultivar evaluation in a multi environment trials (Yan et al., 2007). A GGE biplot exhibits genotypes and environments as points and vectors to approximate GGE obtained from the multi-environment dataset (Yan et al., 2000). GGE bi-plots for LIEN-LS trial are given in Figure 1 for 2015 and Figure 2 for 2016. The two dimensions of bi-plot representation explained 98% of the variation in GGE and results in formation of a mega-environment comprising Herat and Mazar locations (Figure 1). Nangarhar stands in a separate sector. Mazar was found the most genotype-discriminating location while Herat was the least. Thus in case rationalization of locations for lentil evaluation is carried out; Mazar would be a preferred location over Herat.

Table 2. Significance of lentil genotype, genotype × location interaction and error variance from year-wise combined data over locations and years, and genotype × year interaction within location.

A: Year wise significance of genotype main effect and genotype × location interaction and error variance

Sources of interest	LIEN-LS		LIEN-SS	
	2015	2016	2015	2016
p-values				
Genotype (G)	<0.001	0.003	0.008	<0.001
G×Location interaction	<0.001	<0.001	0.002	0.001
Estimated variance				
Error	0.0469±0.00767	0.0538±0.00806	0.0678±0.01108	0.0539±0.00836

Model: Fixed terms are Location (L), Genotype (G) and G×L interaction (GLI). Random terms are Replication (R) within L, and in addition incomplete blocks within R within L for CIEN-W (2014-15) where simple lattice design was used.

B: Significance of genotype main effect and genotype × location interaction and genotype × year interaction within location variance components

Sources of interest	LIEN-LS	LIEN-SS
p-value		
Genotype	0.94	0.105
G×L Interaction	0.113	0.003
GYI (L)	<0.001	>0.999
Estimated variance		
GYI(L)	0.10129±0.02808	0+/-0(bound)
Error	0.102±0.0115	0.102+/-0.0115

Model used: Fixed terms are Location (L), Genotype (G) and G×L interaction. Random terms are Year (Y) within L, G×Y interaction within L, Replication (R) within Y and L. The number of common genotypes between the two years for combined analyses over locations and years were 14 for LIEN -LS and LIEN-SSTrials.

Let the genotypes of LIEN-LS be coded as LG1 to LG36. The winner for the mega-environment (Herat and Mazar) was LG16 (FLIP2012-21L), at vertex of the polygon on the extreme right side along the first principal component axis, and is specifically adapted to Mazar. Genotype LG30 (FLIP2013-20L) was specifically adapted to Nangarhar environment. The representation of GGE based on 2016 data on 15 genotypes (LG1…LG15), as the same as of 2015, showed that the two locations (Herat and Mazar) represent a mega-environment (Figure 2). Thus this mega-environment is repeatable over the years and can be used for rationalizing the testing location for lentil yield trials in Afghanistan. Mazar and Nangarhar were the two most genotype-discriminating locations, like that of Figure 1. The winners for the mega-environment (Herat and Mazar) was LG24 (FLIP2013-3L) and for Nangarhar was LG30 (FLIP2013-20L). Based on 2015 and 2016 data, the GGE biplot showed that Herat and Mazar formed one mega-environment in LIEN-SS trial too (Figure 3). SG30 (FLIP2013-59L) and SG5 (FLIP2012-95L) were the winner genotypes and specific adapted to Herat and Mazar. SG31 (FLIP2013-66L) was specific adapted to Nangarhar. Identification of a desirable genotype with stable grain yield through GGE biplot is similar to those found in stability study of other crops as Fan et al., 2007 identified 4 hybrid genotypes of maize (*Zea mays L.)* out of 13 which were tested at 10 locations in China; Dehghani et al. (2006) reported two stable genotypes of barley (*Hordeum vulgare L.)* and three mega environments based on 19 genotypes at 10 Iranian environments; Kaya et al. (2006) tested 25 genotypes at 9 environments in Turkey and reported two mega environments and identified stable and specific adapted genotypes while used GGE biplotsin Wheat (*Triticum aestivum* L.); Samonte et al. (2005) reported three mega environments using AMMI and SERG GGE Biplot analysis for stability and adaption in rice *(oryza sative* L.); and Sabaghnia et al. (2008) reported three mega environments in Iran while tested 11 lentil lines at 7 environments. GGE biplots for identification of high yielding and stably adapted genotypes in Afghanistan were used in wheat (Akbarzai et al., 2017) and in chickpea (Mohammadi et al., 2017).

Table 3 lists top ten genotypes with high mean (adjusted mean in case of simple lattice designs) yields in each trial and each year where GEI was found statistically significant (P<0.01). The highest yielding genotype in LIEN-LS, 2015 was LG32 (FLIP2013-29L) at Herat (yield 0.45 t/ha), LG16 (FLIP2012-21L) at Mazar (2.49 t/ha)and LG30 (FLIP2013-20L) at Nangarhar (2.14 t/ha). When compared to the average over all the genotypes at a location, these top genotypes, yielded additional 0.18 t/ha (LG32), 1.3 t/ha (LG16) and 1 t/ha (LG30), respectively at the location where they were the best. In 2016,LG29 (FLIP2013-16L) was the highest yielding genotype at Herat (yield 0.45 t/ha), followed byLG22 (FLIP2012-27L) andLG17 (FLIP2012-22L),with mean value 0.43 t/ha and 0.42 t/ha. LG24 (FLIP2013-3L) was the top yielding genotype at Mazar (yield 1.95 t/ha) followed by LG29 (FLIP2013-16L) with yield 1.74t/ha. LG30

Table 3. Lentilmean grain yields (t/ha) of top ten high yielding genotypes at specific locations in Afghanistan, 2015 – 2016 for the two trials.

LIEN-LS (2015)[$]

Rank	GCode[@]	Genotype name	Herat (t/ha)	GCode	Genotype name	Mazar (t/ha)	GCode	Genotype name	Nangarhar (t/ha)
1	LG32	FLIP2013-29L	0.45	LG16	FLIP2012-21L	2.49	LG30	FLIP2013-20L	2.14
2	LG17	FLIP2012-22L	0.41	LG14	FLIP2012-19L	2.08	LG22	FLIP2012-27L	2.10
3	LG36	LOCAL CHECK	0.39	LG15	FLIP2012-20L	2.07	LG32	FLIP2013-29L	2.07
4	LG29	FLIP2013-16L	0.37	LG17	FLIP2012-22L	1.85	LG4	FLIP2012-4L	1.79
5	LG13	FLIP2012-18L	0.36	LG7	FLIP2012-8L	1.58	LG24	FLIP2013-3L	1.65
6	LG7	FLIP2012-8L	0.35	LG13	FLIP2012-18L	1.56	LG18	FLI2012-23L	1.59
7	LG14	FLIP2012-19L	0.34	LG21	FLIP2012-26L	1.53	LG35	FLIP1997-6L(CHCK 2	1.57
8	LG27	FLIP2013-14L	0.33	LG24	FLIP2013-3L	1.52	LG20	FLIP2012-25L	1.57
9	LG24	FLIP2013-3L	0.32	LG11	FLIP2012-13L	1.49	LG21	FLIP2012-26L	1.41
10	LG4	FLIP2012-4L	0.31	LG12	FLIP2012-14L	1.35	LG28	FLIP2013-15L	1.39
	SE		0.06			0.23			0.19
	LSD5%		0.18			0.50			0.56
	Mean (36 genotypes)		0.27			1.19			1.14

LIEN-LS (2016)

Rank	GCode	Genotype name	Herat (t/ha)	GCode	Genotype name	Mazar (t/ha)	GCode	Genotype name	Nangarhar (t/ha)
1	LG29	FLIP2013-16L	0.45	LG24	FLIP2013-3L	1.95	LG30	FLIP2013-20L	1.25
2	LG22	FLIP2012-27L	0.43	LG29	FLIP2013-16L	1.74	LG14	FLIP2012-19L	0.87
3	LG17	FLIP2012-22L	0.42	LG32	FLIP2013-29L	1.70	LG31	FLIP2013-24L	0.84
4	LG18	FLIP2012-23L	0.35	LG12	FLIP 2012-14L	1.47	LG4	FLIP2012-4L	0.79
5	LG32	FLIP2013-29L	0.32	LG13	FLIP 2012-18L	1.34	LG12	FLIP 2012-14L	0.79
6	LG12	FLIP 2012-14L	0.28	LG30	FLIP2013-20L	1.31	LG29	FLIP2013-16L	0.74
7	LG31	FLIP2013-24L	0.27	LG11	FLIP2012-13L	1.31	LG24	FLIP2013-3L	0.69
8	LG30	FLIP2013-20L	0.24	LG16	FLIP2012-21L	1.28	LG18	FLIP2012-23L	0.69
9	LG24	FLIP2013-3L	0.22	LG4	FLIP2012-4L	1.16	LG13	FLIP 2012-18L	0.66
10	LG4	FLIP2012-4L	0.18	LG31	FLIP2013-24L	1.12	LG32	FLIP2013-29L	0.65
	SE		0.06			0.18			0.14
	LSD5%		0.51			0.41			0.34
	Mean (15 genotypes)		0.27			1.33			0.70

LIEN-SS (2015 and 2016)

Rank	SGCode (1-36)	Genotype name	Herat (t/ha)	SGcode	Genotype name	Mazar (t/ha)	SGcode	Genotype name	Nangarhar (t/ha)
1	SG26	FLIP 2013-51L	0.47	SG30	FLIP2013-59L	1.47	SG31	FLIP2013-66L	1.57
2	SG30	FLIP2013-59L	0.43	SG5	FLIP2012-95L	1.47	SG23	FLIP2013-47L	1.45
3	SG22	FLIP2013-45L	0.40	SG21	FLIP2013-41L	1.36	SG9	FLIP2012-164L	1.31
4	SG31	FLIP2013-66L	0.38	SG2	FLIP2012-48L	1.28	SG18	FLIP2012-231L	1.25
5	SG21	FLIP2013-41L	0.34	SG18	FLIP2012-231L	1.26	SG33	FLIP2013-69L	1.20
6	SG6	FLIP 2012-97L	0.33	SG23	FLIP2013-47L	1.23	SG21	FLIP2013-41L	1.17
7	SG5	FLIP2012-95L	0.32	SG26	FLIP 2013-51L	1.15	SG10	FLIP2012-169L	1.10
8	SG9	FLIP2012-164L	0.30	SG22	FLIP2013-45L	1.10	SG32	FLIP2013-68L	1.09
9	SG23	FLIP2013-47L	0.28	SG32	FLIP2013-68L	1.07	SG30	FLIP2013-59L	1.07
10	SG2	FLIP2012-48L	0.26	SG6	FLIP 2012-97L	1.00	SG22	FLIP2013-45L	1.06
	SE		0.06	SG30		0.25			0.37
	LSD5%		0.17	SG5		0.51			0.59
	Mean (36genotypes		0.30			1.13			1.12

For estimating means combined over year within each location in LIEN-SS, Genotype effects fixed and Year, Year x Geno interaction, Replicate effects within year random. [$]For LIEN -LS trial, the mean yields are adjusted for lattice blocks. [@]GCode= Genotype codes are G1…G36, where the same code over different trial-types or years for the same trial type generally stand for different genotypes. LC= Local check. SE= standard error. LSD5%= Least significant difference at 5% level of significance. LIEN -LS = Lentil International Elite Nursery Large Seed -2015. LIEN-SS = Lentil International Elite Nursery Small Seed -2015.

(FLIP2013-20L) was the top yielding genotype at Nangarhar (yield 1.25 t/ha) followed LG14 (FLIP2012-19L) at 0.87 t/ha. These top genotypes yielded additional 0.18 t/ha, 0.62 t/ha and 0.55t/ha over the respective location average, where found best. The assessment of the common 14 genotypes from LIEN-SS combined over two years gave the locations means of 0.30 t/ha at Herat, 1.12 t/ha at Mazar and 1.11 t/ha at Nangarhar. The top yielding genotypes for LIEN-SS at Herat was SG26 (FLIP 2013-51L) with yield of 0.46 t/ha (0.16 t/ha additional over Herat location mean), SG30 (FLIP2013-59L) at Mazar (1.47 t/ha which is 0.16 t/ha addition over the location mean) and SG31 (FLIP2013-66L) at Nangarhar (1.59 t/ha which is 0.45 t/ha additional over the location mean).

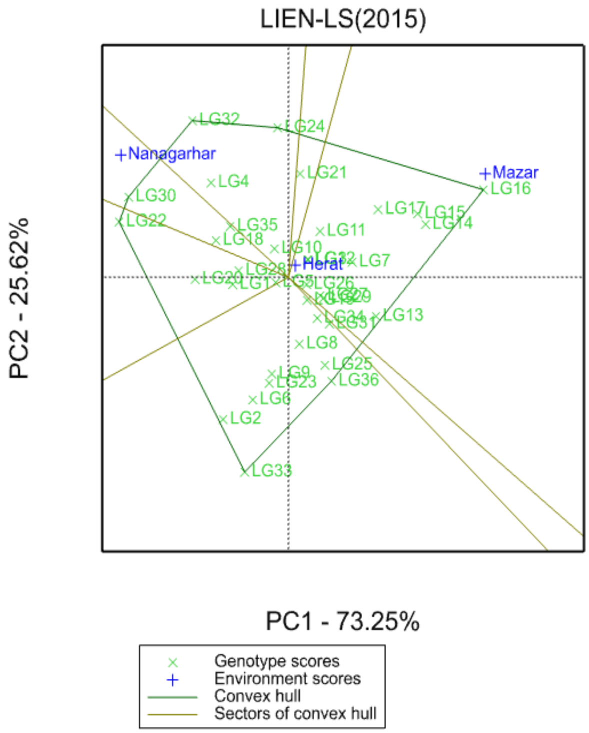

Figure 1. Genotype main effect plus genotype × environment interaction (GGE) biplot (scatter plot) for Lentil genotypes (LG1…LG36) and environments (Herat, Mazar, Nangarhar) for grain yield in 2015 under the trial LIEN-LS.

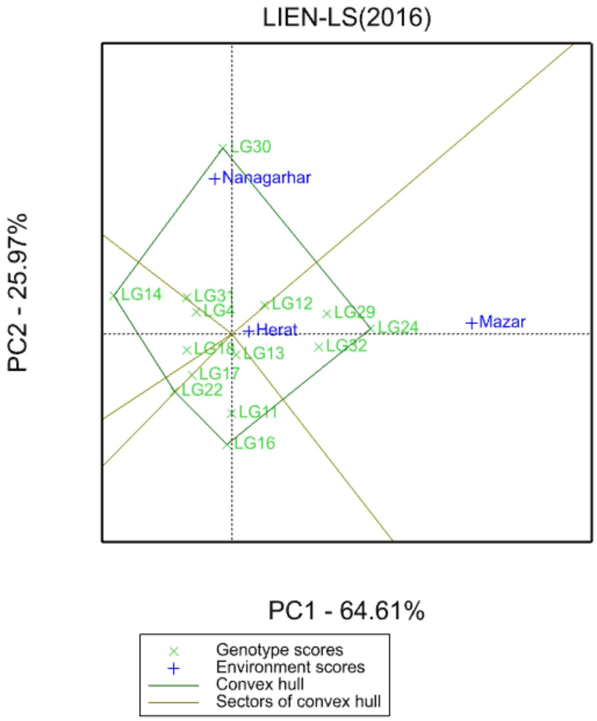

Figure 2. Genotype main effect plus genotype × environment interaction (GGE) biplot (scatter plot) for Lentilgenotypes (LG1…LG15) and environments (Herat, Mazar and Nangarhar) for grain yield in 2016 under the trial LIEN-LS.

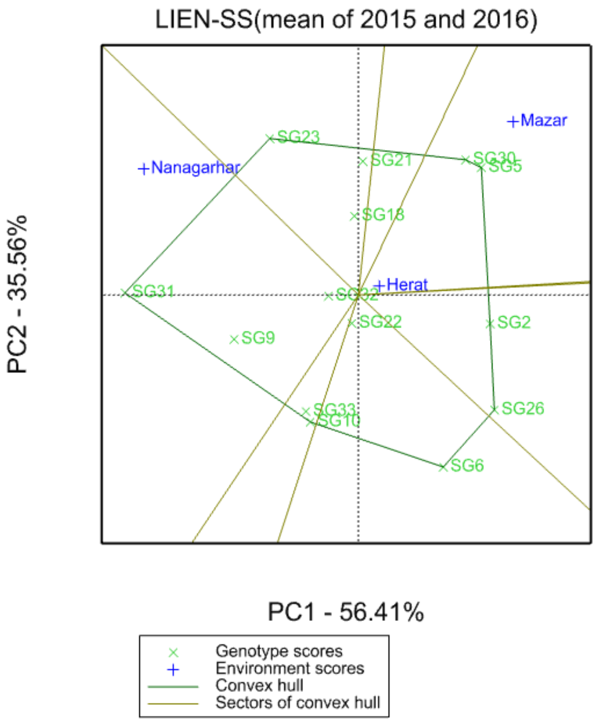

Figure 3. Genotype main effect plus genotype × environment interaction (GGE) biplot (scatter plot) for lentil genotypes (SG1…SG15) and environments (Herat, Mazar and Nangarhar) for grain yield in 2016 under the trial LIEN-SS.

CONCLUSION

This study presents the findings of two lentil trials conducted at three locations in Afghanistan for two years (2015 and 2016). Genotypic differences were statistically significant (P<0.05) in all the environments. Genotype x location interaction was found significant (P<0.01) in each of the two years for LIEN-LS and LIEN-SS trials. There was strong genotype x year interaction of crossover type. For LIEN-LS genetic materials, Herat and Mazar formed a mega-environment based on responses in 2015 as well in 2016. The specifically adapted genotypes were LG16 (FLIP2012-21L) in 2015 and LG24 (FLIP2013-3L) in 2016 at Mazar and Herat, LG30 (FLIP2013-20L) at Nangarhar. In 2015-16, the SG12 (FLIP 2013-51L) at Herat, SG2 (FLIP2013-59L) at Mazar and SG6 (FLIP2013-66L) at Nangarhar were top yielding genotypes from LIEN-SS. The identified genotypes from LIEN-LS and LIEN-SS at the two locations (Mazar and Nangarhar) may be used for up-scaling the production to support food security in Afghanistan as well as for generating new genotypes using crossing, selection and evaluation.

AUTHOR CONTRIBUTIONS

Darya Khan Akbarzia, Suhilla Nisar and Lina Mohammdi were carried out the experiment and collect data for analysis including writing the full manuscript.

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COMPETING INTERESTS

The authors declare that they have no conflicts of interest associated with the publication of this article.

ETHICS APPROVAL

Not applicable.

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