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Evaluation of Black Cumin (*Nigella sativa* L.) Genotypes for Yield and Yield Related Parameters in Potential Growing Areas of Ethiopia

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ABSTRACT

Multi-environment trials were carried out at 3 locations in different black cumin growing zones of Ethiopia during June-December, 2017–2018 and 2018–2019 to select high yielding and adaptable genotypes for commercial production in Ethiopia. Ten advanced black cumin genotypes were evaluated with one standard check variety. The genotypes were arranged in Randomized Complete Block Design with three replications. The ANOVA revealed that the differences in seed yield among genotypes (G), environments (E) and genotype by environment interaction (GEI) were highly significant (p<0.01). Besides, significant (p<0.01) differences were obtained for days to 50% flowering, days to maturity, plant height, number of pod plant^{-1}, number of seeds pod^{-1}, seed yield plant^{-1}, and thousand seed weight. However, days to emergence, number of primary and secondary branches plant^{-1} were not significant (p>0.05). The highest seed yield was recorded from genotype 242840 (1102 kg ha^{-1}) followed by 242841(1038 kg ha^{-1}) and these genotypes had 35% and 26.39% yield advantage over the check variety-Aden respectively. Moreover, the two genotypes were better in oleoresin content among others. The partitioning of GE through GGE biplot analysis showed that PC1 and PC2 accounted for 47.09% and 18.18%, explaining 65.27% of the total variance. The GGE biplot ranked the genotypes for yield performance; the genotypes viz. 24840 and 24841 were among the five marker (winning) genotypes and showed their wider adaptability across the testing environments. Therefore, the genotypes were selected as potential candidate genotypes for on farm verification and possible release for commercial production in the testing environments and similar agro ecologies.

KEYWORDS: AMMI, GGE biplot, oleoresin content, stability, seed yield

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1. INTRODUCTION

Black cumin (*Nigella sativa* L.) is a member of Apiaceae (Umbelliferae), which is believed to be originated in Eastern Mediterranean, Southern Europe, West Asia, and Egypt, but is widely cultivated in Iran, Japan, China and Turkey (Atta, 2003; Kokdil et al., 2006; Cheikh-Rouhou et al., 2007, Shewaye, 2011). The Ethiopian black cumin varieties accumulate up to 50% thymol in their seed, a monocyclic phenolic compound that makes cumin valuable source for health care industry (Black et al., 2006, Merga et al., 2018). Its seed constituents have unique chemical properties with more than one hundred different chemical components (Bardideh et al., 2013). In Ethiopia, black cumin is one of the most important spice types which are mainly produced to flavor foods, preparation of oil for perfumes and medicinal purpose, source of income, crop diversification, and export purposes (Desalegn and Wubshet, 2018; Wubshet and Desalegn, 2019). It is also the second important cash crop which is exported to international markets next to ginger (Teshome and Anshiso, 2019). Ethiopia is a country with different and favorable agroecological zones for production of various spices, vegetables and crops (Dessie et al., 2019a; Dessie et al., 2019b). Many spice varieties particularly of black cumin, white cumin, pepper, paprika, turmeric, fenugreek, garlic, coriander, ginger, cardamom, and basil are grown in Ethiopia for consumption and commercial purposes (Tesfa et al., 2017), making it one of the top spice producer and consumer countries and ranking first and seventh in Africa and global stages, respectively (Anonymous, 2019).

In Ethiopia, black cumin is cultivated as a rain-fed crop in the highlands (1500 to 2500 m.a.s.l.) mainly in Amhara, Oromia and Southern Nations and Nationalities People's (SNNP) region often intercropped with cereals (Birhanu, 2015; Herms et al., 2015). It has similar ecological requirements as tef, chickpeas and lentil usually cultivated using residual moisture following the main rainy season (Girma et al., 2015). It requires well prepared land ploughed at least 3 times, (Ermias et al., 2015) followed by 2-3 harrowing and leveling (Ebrie et al, 2015).

Black cumin is propagated by seed. The sowing time varies as a function of the local environmental conditions (Mehmood et al., 2018). The recommended seed rate is 5–7.5 kg ha^{-1} (Girma, 2015 and 20 kg ha^{-1} (Roussis et al., 2017, Fekadu et al., 2021). Germination is promoted by darkness and high temperatures. A Maximum rate of germination was observed at 20°C with 20.7 seeds that corresponds to 41.40% (Abdullah, 2017).

Ethiopian annual production of black cumin seed was 18 thousand metric tons in the cropping year of 2015 (Anonymous, 2016). It is also the second important cash crop which is exported to international market next to ginger (Wubshet and Dessallegn, 2019). The national average productivity of black cumin was reported to be 0.79 t ha^{-1} (Habtewold et al., 2017); while Zigyalew (2020) reported 0.64 t ha^{-1}, which is well below the global average and some major producing countries including India (2.2 t ha^{-1}). However, high seed yield up to 1.7 t ha^{-1} at Adet, 1.8 t ha^{-1} at Woreta and 2.45 t ha^{-1} at Bale in Ethiopia were obtained (Adam, 2007, Getachew and Beriso, 2020). The low yields are mainly due to the low productivity of the varieties (Ermias et al., 2015) among other factors. Therefore, the objective of the present study was to identify high yielding, good quality black cumin genotypes and recommend the most promising ones for verification and release.

2. MATERIALS AND METHODS

2.1. Description of the study areas

Table 1: List of test locations and their description

Sites	AGZs	Altitude (masl)	Temperature (min/max)	Annual average rainfall	Soil types
Debre Zeit	Tepid to cool sub-moist highlands	1900	8.9°C 28.3°C/	851 mm	Alfisols/ Mollisols and Vertisols
Kulumsa	From cool highland to semi-arid	2200	10 oC 22oC/	840 mm	Luvisols
Sinana	Moist dega	2400	9.5oC 21.5oC/	1174 mm	Phaeozems and Cambisols

2.2. Plant materials and testing sites

Three hundred black cumin accessions were originally obtained from Ethiopian Biodiversity Institute (EBI) and evaluated under observation nursery at Kulumsa Agricultural Research Center (KARC) in 2015. The genotype with pedigree name (242825, 242839, 90506, 242221, 242840, 242226, 343835, 242222, 242841, 229806 and standard check Aden). Based on agronomic performance, yield data and quality, promising genotypes were selected and evaluated further in preliminary variety trial in 2016 for one year. Among which, ten genotypes which showed good agronomic performance, seed yield and quality were selected and advanced to multi-location variety trial. The genotypes

were evaluated along with one standard check variety, Aden in three representative growing areas (Kulumsa, Sinana and Debre Zeit Agricultural Research Centers) from 2017–2018 and 2018–2019.

2.3. Experimental design, agronomic practices and parameters measured

The treatments/genotypes were arranged in Randomized Complete Block Design (RCBD) replicated three times. Fine seed bed was preparation before sowing. The plot size was 3.6m^2; the seeds were sown at the rate of 15 kg ha^{-1} in each plot. Urea fertilizer was applied at the rate of 55 kg ha^{-1} in split; half at full emergence and half at flowering. The plots were made weed free using hand weeding as required. Data were collected on agronomic and yield parameters such as days 50% emergence (DE), days to 50% flowering (FD), days to 90 % maturity (MD), plant height (PH, cm), number of primary plant^{-1}(NB) and number of secondary branches per plant (NSB), number of pods plant^{-1} (NPP), number of seed pod^{-1} (NSP), seed yield plant^{-1} (SYPL), thousand seed weight (TSW, g) and seed yield (g plot^{-1}) and finally converted to kg ha^{-1}. The data for plant height, number primary and secondary braches plant^{-1}; number of pods plant^{-1} were taken from the average of ten randomly selected plants plot^{-1}. The rest data were taken from the whole plant bases.

Data for quality parameter, the oleoresin content (%) of the seed for each genotype was measured. Soxhlet extraction method was used (Dinagaran et al., 2016) to quantify the oleoresin content. The black cumin seed was grounded by using the electronic grinder (Panasonic, Japan, Model MJ-W176P) and the powder was packed in polyethylene bag to prevent it from contamination until the lab analysis was done. The oleoresin was extracted with organic solvents using n-hexane using Soxhlet apparatus for 2hrs at temperature of 40–45°C. The extracts were filtered and concentrated under a reduced pressure by rotary evaporator (model 4001 Rota vapor) and obtained crude extracts. The oil yield (%) was calculated as below.

$$\text{Oil yield} = \frac{\text{Yield of extract obtained (g)}}{\text{Weight of sample used (g)}} \times 100 \text{ --------- (1)}$$

2.4. Data analysis

Data for the agronomic and yield parameters were subjected to Analysis of Variance (ANOVA) using SAS Statistical Package Program (SAS, 2009). Before combining the data, Bartlett's test was used to determine the homogeneity of variances between environments to determine the validity of the combined ANOVA on the data and the data collected was homogenous. The significant differences among treatment means were compared using the Least Significant Difference Test (LSD) at 5% probability level. Besides, Additive main effects and multiplicative interaction (AMMI) model was used to test for the significance of genotype, and genotypes by environment interaction effects and GGE biplot analysis was computed to graphically depict the seed yield and adaptability of the genotypes across environments, using GGE Biplot GUI package in R (R Team, 2013).

3. RESULTS AND DISCUSSION

3.1. Analysis of variance for yield and yield components

The results from the analysis of variance for seed yield revealed that the differences between genotypes (G), environments (E) and genotype by environment interactions (GEI) were all highly (p<0.01) significant (Table 2). This

Table 2: AMMI analysis of variance for seed yield (t ha^{-1}) of 11 genotypes tested across three locations and two years (2017–2018 and 2018–2019)

Source of variations	Df	Sum^2	Mean^2	Sum of squares explained (%)		F value	Pr (>F)
				total	G×E		
Environment (E)	5	446.26	89.252	51.35	51.35	19.65	0.0002
Block/rep (B)	12	44.50	4.542			2.252	0.0013
Genotypes (G)	10	154.29	15.429	69.71	18.36	7.652	0.0002
GXE	50	254.87	5.097	100	30.29	2.528	0.0001
IPCA1	14	98.99	7.07	37.97	37.97		
IPCA2	12	67.59	5.63	63.90	25.92		
IPCA3	10	52.98	5.29	84.22	20.32		
IPCA4	8	26.89	3.36	94.54	10.32		
IPCA5	6	14.23	2.37	100	5.46		
Residuals	132	293.21	2.016				

E: environment; R: Replications; G: Genotype

was empirically reflected by the mean yield of genotypes across the environments as it ranged from 764 kg ha^{-1} (Aden**)** to 1102 kg ha^{-1} (genotype 242840). Similarly, the environmental index (location*year) (i.e., mean across genotypes) ranged from 755 kg ha^{-1} to 1068 kg ha^{-1} (Table 3). Significant GEI suggests that there were changes in the ranking orders of genotypes under varying environments. From the results, two genotypes (242840 and 242841) were superior in yield advantage and oleoresin content over the standard check (Aden) by 35%, 7.37% and 26.39%, 2.14% respectively (Table 3 and 5). Previously, Miheretu (2018) also reported highly significant differences among the genotypes for seed yield of black cumin evaluated at multi-locations (Ginir, Goro and Bale districts of south eastern Ethiopia). The effect of environments on genotypic performance of black cumin was reported by Gezahegn and Sintayehu (2016), and they reported that the locations viz. Oda Bultum and Habro (Western Hararge Zone, Ethiopia) were favorable environments while; the locations viz. Mechara (Eastern Hararge zone, Ethiopia) was unfavorable environment which was exhibited on seed yield performance of the genotypes.

The environment had the greatest effect with the environmental sum of squares (51.35%) than the genotypes (18.36%) and GEI (30.29%) effect. The AMMI analysis for the IPCA1 captured 37.97% and IPCA2 explained

Table 3: Mean seed yield (kg ha^{-1}) performance of eleven black cumin genotypes at three locations in 2017–2018 and 2018–2019

Sl. No.	Genotype	2017–2018			2018–2019			
		Kulumsa	Debreziet	Sinana	Kulumsa	Debreziet	Sinana	Combined mean
1.	242825	1238^{a}	950^{cde}	679^{bc}	739^{cde}	1112^{ab}	920	940^{cd}
2.	242839	954^{bc}	954^{cd}	781^{abc}	653^{efg}	1105^{ab}	939	898^{cde}
3.	90506	1271^{a}	1045^{bc}	738^{bc}	851^{bc}	814^{c}	768	914^{cde}
4.	242221	914^{cd}	1078^{bc}	594^{c}	703^{def}	1061^{b}	805	859de
5.	242840	1289^{a}	1021^{bc}	1012^{a}	1064^{a}	1337^{a}	889	1102^{a}
6.	242226	779^{d}	766de	820^{abc}	794^{cd}	1001^{bc}	817	829^{ef}
7.	242835	1164^{ab}	1201^{b}	893^{ab}	660^{efg}	1143^{ab}	700	960^{bc}
8.	242222	1235^{a}	1012^{bc}	614^{c}	603^{fg}	1256^{ab}	870	932^{cd}
9.	242841	1086^{abc}	1455^{a}	834^{abc}	978^{ab}	1135^{ab}	739	1038^{ab}
10.	229806	929^{bcd}	972^{bcd}	747^{bc}	723^{cdef}	1177^{ab}	707	876^{cde}
11.	Aden	887^{cd}	709^{e}	639^{c}	539^{g}	1097^{ab}	714	764^{f}
	Mean	1068	1015	759	755	1015	806	919
	LSD	249	242	242	139	267	278^{NS}	94
	CV (%)	13.71	14.10	18.73	10.89	14.10	20.25	15.62

NS: Non-significant at p>0.05; Means within a column having different letters are significantly different; LSD: Least significant difference; CV: Coefficient of variation

25.92%. The two IPC cumulatively captured 63.82% of the sum of square the GEI of black cumin genotypes, when the IPCA1 was plotted against IPCA2. Such a large sum and highly significant mean squares of environment indicated that the environments were diverse, with large differences among environmental means causing most of the variation in seed yield. This shows that the overpowering influence that environments can have on the yield performance of black cumin genotypes. The AMMI model with only two IPCA helps to make the best predictive assessment (Yan et al., 2000). The authors further explain that environments and genotypes having the same sign of IPCA-1 scores (i.e. anti-clock wise in the biplot, those falling in quadrats 1 and 3 or 2 and 4) interact positively while those having different signs of IPCA-1 scores interact negatively. Accordingly, the first two IPCA, explaining 69.71% of the total GEI sum of squares, will be used to depict the biplots described below.

3.2. Analysis of variance for other agronomic traits

The combined analysis of variance showed highly significant (p<0.01) differences among the test black cumin genotypes in days to 50% flowering, days to maturity, plant height, number of pod plant^{-1}, number of seed pod^{-1} and thousand seeds weight. However, the results for days to emergence, number of primary and secondary branches plant^{-1} were non-significant (p>0.05) (Table 4).

Table 4: Mean results of phenology, growth, yield and yield related traits of eleven black cumin genotypes over three environments and two years

Sl. No.	Genotype	ED	FD	MD	PH	NPB	NSB	NPPP	NSP	SYPL	TSW	Yield kg ha^{-1}
1.	242825	18.16	76.72^{bc}	135.59^{ab}	56.11^{cd}	5.97	16.05	17.40^{bc}	85.10^{bc}	1.95^{c}	2.02^{cd}	940^{cd}
2.	242839	18.46	75.81^{bc}	134.58^{bc}	55.40^{de}	5.74	16.62	16.22^{cd}	80.55^{cd}	2.18^{bc}	2.07^{bcd}	898^{cde}
3.	90506	18.12	77.01^{bc}	134.87^{b}	56.54^{cd}	5.87	16.67	16.84^{bcd}	80.66^{cd}	2.30^{b}	2.11^{bc}	914^{cde}
4.	242221	18.21	77.44^{abc}	134.72^{b}	56.53^{bcd}	5.85	17.81	17.84^{b}	79.40^{d}	2.21^{bc}	2.06^{bcd}	859de
5.	242840	19.22	75.51^{c}	135.77^{ab}	61.02^{a}	5.77	16.74	21.52^{a}	93.02^{a}	3.05^{a}	2.66^{a}	1102^{a}
6.	242226	17.92	71.26^{d}	132.67^{c}	53.49^{e}	5.30	15.54	15.93^{cd}	77.98^{d}	2.26^{b}	2.08^{bcd}	829^{ef}
7.	242835	18.38	79.01^{a}	136.45^{ab}	57.17^{bcd}	6.16	16.19	16.73^{bcd}	86.27^{b}	2.12^{bc}	2.07^{bcd}	960^{bc}
8.	242222	18.37	77.49^{ab}	135.37^{ab}	55.95^{cd}	5.81	16.17	17.09^{bcd}	78.53^{d}	2.09^{bc}	2.04^{bcd}	932^{cd}
9.	242841	18.36	77.59^{ab}	137.08^{a}	60.94^{a}	5.98	17.06	21.08^{a}	93.31^{a}	3.08^{a}	2.59^{a}	1038^{ab}
10.	229806	18.62	79.24^{a}	134.87^{b}	57.58^{bc}	5.76	16.99	15.66d	85.06^{bc}	2.30^{b}	2.16^{b}	876^{cde}
11.	Aden	18.01	79.05^{a}	136.27^{ab}	58.45^{b}	5.41	15.92	15.91^{cd}	78.03^{d}	2.06^{bc}	1.95^{d}	764^{f}
	Mean	18.35	76.92	135.49	57.21	5.78	16.52	17.47	83.45	2.32	2.16	919
	LSD	0.7NS	1.97	1.97	2.06	0.57^{NS}	2.35^{NS}	1.62	4.70	0.30	0.14	94
	CV (%)	6.02	3.90	2.20	5.44	15.00	21.80	14.07	8.53	19.88	9.94	15.62

The mean capsule (pod) number plant^{-1}, plant height, primary branch plant^{-1}, number of seed pod^{-1}, seed yield plant^{-1} and thousand seed weight was ranged from 21.52–15.66, 61.02–53.49, 5.98–5.41, 93.31–79.40, 3.08–1.95 and 2.59–1.95, respectively (Table 4). The highest mean plant height (61.02 cm) followed by 60.94 cm was recorded from the genotypes 242840 and 242841 respectively (Table 4). Likewise, the highest number of capsules (pods) plant^{-1} (21.52) was recorded from genotype 242840 followed by genotype 242841(21.08); while the lowest value (15.910 was obtained from the check variety-Aden. Similarly, the highest mean thousand seed weight (2.66 g) was also recorded from the genotype 242840 followed by genotype 242841 (2.59 g); while the lowest thousand seed weight (1.95 g) was recorded from Aden variety. Similar findings were reported by Miheretu (2016); Girma et al. (2016) and Getachew and Beriso (2020), who indicated that black cumin seed yield is significant with plant height, number of capsules plant^{-1}, number of primary branches plant^{-1}, and number of seeds capsule^{-1}. Other researcher's Ermias et al. (2015); Miheretu, (2018) reported the existence of significant differences among black cumin genotypes for phenological and growth parameters including days to 50% flowering, days to 90% maturity, plant height, number of primary and secondary branches, yield components (number of capsules and number of seeds capsule^{-1}) and seed yield.

3.3. Mean oleoresin content of the genotypes

Differences among black cumin genotypes for oleoresins content (yield) were obtained over locations. The highest oleoresin content was recorded in Sinana from genotype 242840 (55.67%) followed by 242841 (46.58%) (Table 5). The lowest oleoresin content (31.17%) was obtained in Sinana as well from genotype 242835. Nevertheless, the mean values over locations showed that the highest oleoresin content was obtained from genotypes 242840 (43.24%) and 24841 (41.13%). Oleoresin content is affected both by

Table 5: Mean oleoresin contents (%) of the black cumin genotypes over the three locations

S1. No.	Genotypes	Sinana	Debre Zeit	Kulumsa	Mean	Oleoresin yield advantage (%)
1.	242825	33.16	37.89	39.13	36.73	-8.79
2.	242839	35.81	34.77	40.83	37.14	-7.77
3.	90506	42.53	32.49	40.65	38.56	-4.25
4.	242221	40.06	36.99	41.70	39.58	-1.71
5.	242840	55.67	35.40	38.64	43.24	7.62
6.	242226	35.69	39.01	28.72	34.47	-14.40
7.	242835	31.17	37.30	38.53	35.67	-11.42
8.	242222	35.66	40.85	46.63	41.05	2.14
9.	242841	46.58	38.02	38.78	41.13	2.14
10.	229806	42.17	37.34	37.60	39.04	-3.05
11.	Aden	39.65	40.88	40.27	40.27	-

genotypes and environments (Tuncturk et al., 2005; Ozel et al., 2009; Matthaus and Ozcan, 2011). The present results showed that genotypes viz. 242840 and 242841 were superior to the released variety- Aden with an advantage of percent oleoresin content 7.37% and 2.14% respectively (Table 5). Ermias et al. (2015) reported percent oleoresin content of 24.79 to 28.4% for three previously released varieties and local check in the mid and high land areas of Kaffa zone, southwest Ethiopia. The commercial black cumin varieties viz. Gemmachis and Soressa had oleoresin of 28.4% and 23.8%, respectively (Anonymous, 2016). Edris et al. (2016) reported oleoresin of black cumin seed that varies from 10.2 to 23.7%. These differences may be due to the genetic factors, seasonal variations, genetic× environment interaction effects and/ or combination of two or more factors.

3.4. The which-won-where view of the genotypes on the GGE biplot

The GGE biplot analysis identified the winning genotypes and their interaction patterns, which are helpful in estimating the possible existence of different mega environments. In this biplot, a polygon was connecting the vertex genotypes with straight lines, and the rest of the genotypes were placed inside the polygon. The vertex genotypes were 242840, 242841, 242226, Aden and 242222 having the farthest distance from the origin (Figure 1). These genotypes are considered as the best or poorest in some or all environments which could be more responsive to environmental changes and are considered as specially adapted genotypes. The genotypes fell into five sections and tested environments fell into two sections. The first section included three environments DZ18, KU19 and SN18 and three genotypes 242841, 242835 and 90506, and the vertex genotype of this section was 242841, a high-yielding genotype, and did well in the majority of the environments. Hence, this was considered as a genotype adapted to wider environments. The second section contained three genotypes 242226 (vertex genotype), 242221 and 229806, which were placed farthest from the origin and from all of the environments and, these genotypes were the poorest genotype in all environments. The third section contained genotype 242839 and variety- Aden as vertex genotype, which gave the worst performance, as they did not perform in any of the six environments. On the other hand, the genotype located near the origin responded less than the vertex genotypes. Two genotypes (42222 and 242825.) were placed in the fourth section and the vertex genotype was genotype 42222, which did not adapt to any of the environments. The last section contained only one genotype (242840), which was also the vertex genotype for this section and the three environments SN19, DZ19 and KU18 fell in this section. The vertex genotype (242840) in this section was the best genotype in those environments. Environments within the same section have the same winning genotype, and environments in different sections have different winning genotypes. Therefore, 242835 and 90506 appeared to be near the origin of the biplot, performing moderately on average, and these genotypes were less responsive to environments than the vertex genotypes. Vertex genotypes were the most reactive genotypes because they are the furthest from the origin in their direction. In this study, the portioning of GE through GGE biplot analysis showed that PC1 and PC2 accounted for 47.09% and 18.18% of the GGE sum of squares, respectively, and explained 65.27% of the total variance.

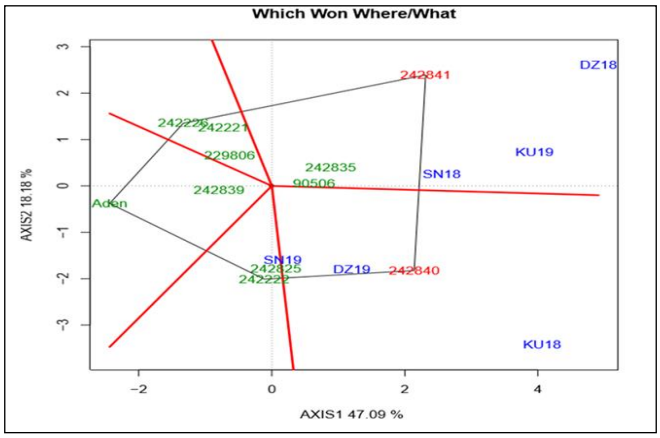

Figure 1: The which-won-where view of the genotypes on the GGE biplot

3.5. Mean ranking and stability of genotypes across environments

Mean yield and stability performance over environments of each genotype was examined using the method of average environmental coordinates (test) (AEC). The result showed that genotypes 242835 and 90506 ranked first and second in stability (wider adaptability) followed by 229806 and 242839 (Figure 2). In contract, genotypes 24840 and 24841 had the highest yield potential among the tested genotypes including the check-variety (Aden); however were less stable. The biplot analysis also identified genotypes which yielded higher than the average yield to the right of the vertical line; and genotypes with lower than the average yield to the left of that line. Therefore, genotypes 242226, 242221, 229806, Aden, 242839, 42222 and 242825 yielded lower than the average; while genotypes 242841, 242835, 90506, and 242840 yielded higher than the average. Several researchers used this stability analysis and found useful to identify high yielding and stable genotypes for different types of crops (Desalegn et al., 2004; Kalic et al., 2010; Kadi et al., 2010). Stability is not the only parameter for selection, because the most stable genotypes would not necessarily give the best yield performance (Mohammadi et al., 2010), hence there is a need for approaches that

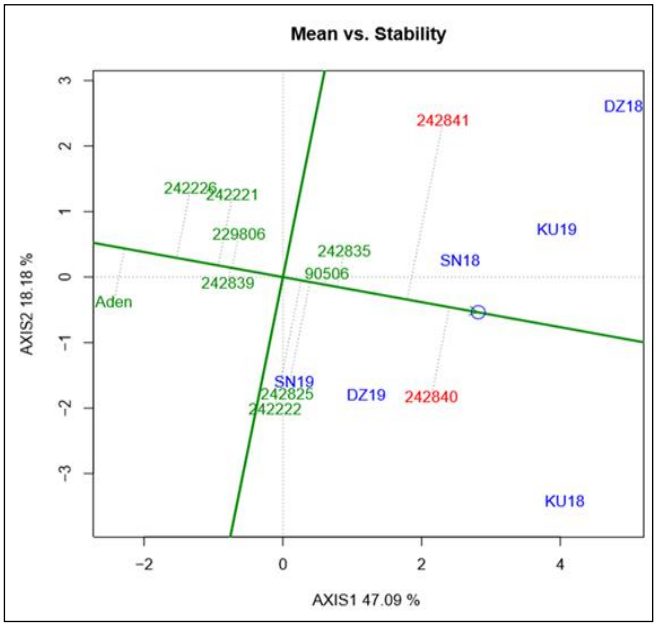

Figure 2: Mean ranking and stability of genotypes across environments

incorporate both mean yield and stability in a single index, that is why various authors introduced different selection criteria for simultaneous selection of yield and stability: rank-sum, modified rank-sum and the statistics yield stability (Farshadfar, 2008; Atta et al., 2009)

3.6. Evaluation of genotypes relative to an ideal genotype

An ideal genotype (most stable and high mean yield) should be placed on the nearest to the center of concentric circles (Figure 3). Such an ideal genotype is defined by having the greatest vector length of the high yielding genotypes and with zero GEI, as represented by an arrow pointing to it. Although such an ideal genotype may not exist in reality, it can be used as a reference for genotype evaluation. As a result, a negligible distance between genotype and the virtual ideal genotype, represent an ideal genotype. Therefore, genotype 242840 was closest to the concentric center. In addition, following to genotypes 242835, 90506, and 242841, located on the next consecutive concentric circle, may be regarded as desirable genotypes.

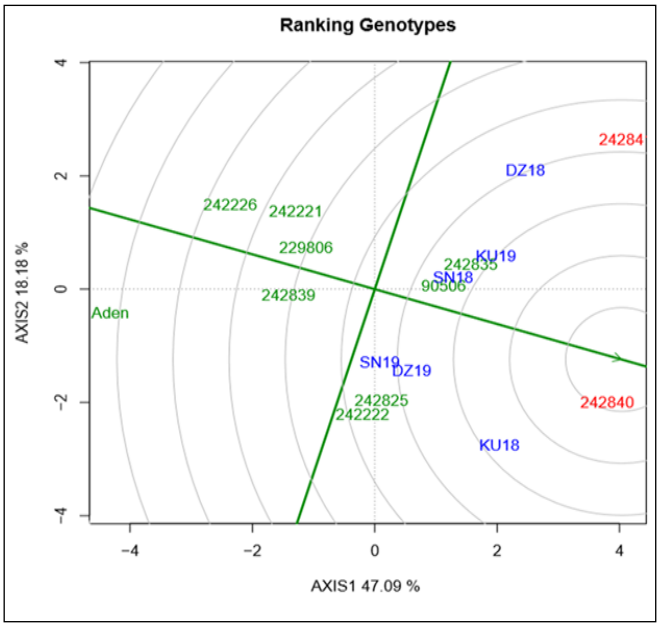

Figure 3: Evaluation of genotypes relative to an ideal genotype

4. CONCLUSION

Genotypes 242840 and 242841 showed the highest mean seed yield potential in all environments. Moreover, the genotypes showed the highest seed quality among the others. "Mean vs stability" view of GGE biplot, 242840 was the highest yielding genotype; while 242841 was the second-highest yielding genotype. As a result, genotypes 242840 and 242841 had 35 and 26.39% yield advantages over the check variety-Aden respectively. Therefore, the overall results suggested that, both genotypes could be designated as potential candidate varieties for release.

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