

Stability analysis of malt barley varieties in the highlands of Arsi and West Arsi Zones of Ethiopia

Adane Choferie¹, Shimeles Gezahegn¹, Workeneh Mekasa³, Amberber Haile¹,
Tesfahun Alemu²

¹Kulumsa Agricultural Research center, P.O.box 489, Assela, Ethiopia

²Holetta Agricultural Research center, P.O.Box 31, Holetta, Ethiopia

³Ambo Agricultural Research center, P.o.box 37, Ambo Ethiopia

Abstract: The experiment was conducted from 2015/16 to 2018/19 cropping season at Kofele and Bekoji. The experiment was laid using RCBD with three replications. The ANOVA showed significant difference among genotypes and high genotype x environment interaction for most traits. The mean separation test showed that genotype MN BRITE named Iftu after official release provide the maximum grain yield as compared to the two standard checks (Bekoji-I and Bahati) and other candidate genotypes. Besides, this genotype has an extract and protein content within the range of the malt factories' requirements. Therefore, this genotype was verified and officially released in the 2019/20 cropping season for wider production in Arsi, West Arsi, Central Showa and similar agro ecologies of Ethiopia.

Keywords: Analysis of variance, Barley, GGEbiplot, Malt barley, Malt quality and Stability analysis.

I. INTRODUCTION

In Ethiopia barley is the fifth important cereal crop that cover about 7.39% of the total area cultivated (CSA, 2020). The total area covered by barley reach around 1 million hectare and the average national productivity reach about 2.5t/ha (CSA, 2020). Barley grown from the low land to the highland areas of the countries with various agro-ecological conditions that makes Ethiopia to be one of the centers of diversity for the crop.

Malt barley is one of the important cash crops in the highlands of Ethiopia. The total household actively engaged in barley production during the 2019/20 cropping season was 3.9 million (CSA 2020). But out of the total production an estimated 90% is food barley and only 10% is malting barley (Alemu et al., 2014). In contrary the country allotted foreign currency for importing jumped from 124 thousand USD to 40 million from 1997 to 2014. With this trend the projection jumped to 420 million by 2025 (Tarekegn, 2015). This increase associated with the expansion of the capacity of the already existed breweries and the establishment of new breweries like DIAGO and Hinken and maltsters like Sufflet Malt and Bort Malt.

Barley is mainly cultivated in the high potential areas of the country ranging from 2300-3000 m.a.s.l with evenly distributed rainfall condition (500 -800mm) with a pH 5.5 to 7.3. Even if the country has the best environmental condition for malt barley production still now the country fulfills its demand by importing from abroad. About 40% of the malt barley requirement in the country was imported from abroad that cost the country foreign exchange. With the increasing demand of malt barley in the country and the expansion of breweries and maltsters the demand for raw malt barley is increasing every year. On the other hand, as malt barley is the industrial crop it needs to satisfy the quality standards required by the malt factories and the breweries. That requires a well-designed breeding program to develop malt barley

varieties that satisfy the demand from the breweries and malt factories. This in mind the national barley breeding program every year conducts a yield trial to identify malt barley varieties that meet the quality standards.

Even if the area covered by barley is about 1 million ha (CSA, 2020) the area allocated to malt barley is only about 150,000 ha that indicating the future potential that can be exploited for the malt barley production. In addition the malt import increased from 130,000 tons to 211,000 tons of malt (221,000 tons of malt barley) in 2010. This showed in one side the potential Ethiopia has for malt barley production and market potential, in other way the necessity of working hard to fulfill the demand and make the country benefited.

The national barley improvement program works to develop malt barley varieties that satisfy the quality requirements by the breweries and the malt factories. For malt barley plumb seed, high extract (>80%), low protein (8-11.5%), high friability (>70%) are the major criteria (AMF, 2016). One of the important criteria besides the quality traits in malt barley breeding is the yield capacity, disease resistance and stability across the environments. The stability and yielding capacity across location can be studied using the GGEbiplot analysis (Yan, 2001, Yan and Hunt, 2001 and Yan and Tinker, 2006). The GGEbiplot technique is the visual presentation of the multi environments trial (MET) experiments to investigate the stability and productivity of the tested genotypes (Yan, 2001).

The GGEbiplot analysis help to understand the stability and the yielding ability of the genotypes using the biplot based on the G + GE model. The analysis helps to visualize the performance of the genotypes and understand which variety perform well where that helps to identify the best genotype for specific mega environment (Yan and Hunt (2001)).

Therefore, this experiment was conducted with the objective of identifying high yielding, disease resistance (scald and net blotch) and stable across high potential areas of barley growing environments with the desired malt quality parameters.

II. MATERIALS AND METHODS

Genetic materials and experimental condition: The trial comprises 12 genotypes with 10 candidate varieties and two checks (Bahati and Bekoji I). The experiment laid in Randomized complete block design with three replications with a plot size of 1.2m x 2.5 with between row spacing of 0.2m. The trial was conducted at Bekoji and Kofele from 2016 to 2018 cropping season. Both locations are potential malt barley producing areas in the region. All the cultural practices such as weed management and fertilizer applications were done according to the recommendation for each site.

Data collected: The agronomic data Days to heading, days to maturity, plant height, diseases (scald, net blotch and leaf rust), 1000-kernel weight, hectoliter weight, lodging, and grain yield/ha were recorded from each experimental unit (plot). From the same plot the malt quality traits grain protein, friability and malt extract were estimated using the Tango NIR infrared analyzer at malt barley laboratory, Holetta Agricultural Research Center.

Data analysis:

The collected data was analyzed according to the model for RCBD over locations and years as follow.

$$Y_{ijly} = \mu + Y_y + L_l + (R/YL)_{jyl} + G_i + GL_{il} + GY_{iy} + GLY_{ily} + e_{ijrly}$$

Where, μ is the grand mean, Y_y the year effect, L_l the location effect, $(R/YL)_{jyl}$ the replication within year and location effect, G_i the genotype effect, GL_{il} the genotype x location interaction effect, GY_{iy} the genotype x year interaction effect, GLY_{ily} is the GenotypexLocationxYear interaction effect and e_{ijrly} is the error term. The analysis of variance and adjusted mean was estimated using R software v. 5.6 (R Core Team, 2019).

GGEbiplot analysis: To understand the stability and the performance of the tested entries over years and locations the GGEbiplot model (Yan et al. 2000, 2007; Yan and Hunt 2001; Yan and Kang 2003) was employed using the GGEbiplotGUI package of R (Frutos et al. 2014). In the analysis the G + GE model was employed to partition the genotype and genotype x environment interaction effect. Based on this analysis the highly performing and stable malt barley genotypes were selected for the variety verification trial for the high potential malt barley growing areas in the country.

III. RESULTS AND DISCUSSIONS

The analysis of variance for yield in individual location in each years revealed that there was significant variation among the tested genotypes except for Kofele in 2017 experiment (Tables 1). The maximum yield was consistently obtained from MN BRITE in the two locations and all the years. Whereas the minimum yield in both the locations and years was obtained from FEG192-69.

The Combined analysis of variance showed highly significant difference among the tested genotypes for all traits except malt extract and friability (Tables 2 and 3). Among the genotypes, MN BRITE gave a 10.5 and 17.4% yield advantages over the standard checks Bekoji I and Bahati respectively. The MN BRITE (the candidate variety) gave a grain yield of 5712.8kg/ha whereas the best standard check (Bekoji-I recorded 5158.6kg/ha. Similarly the same genotype has acceptable malt extract value required by the malt industry comparable to the standard check (Bekoji I). The extract value is within the range of the Assela Malt factory. Similarly the protein content is within the acceptable range that is from 8.5 to 11.5%. There was also significant genotype by environment interaction indicating the importance of identifying a stable variety across the test environments or a specific genotype for a specific environment (Tables 2).

TABLE I: Mean seed yield (kg/ha) of 12 malt barley genotypes tested under National Variety Trial in the years 2016, 2017 and 2018

Genotype	2016		2017		2018		Mean
	Bekoji	Kofele	Bekoji	Kofele	Bekoji	Kofele	
Bahati	4842.6	5057.5	5161.5	4219.6	5747.3	4939.7	4994.7
Bekoji I	5006.5	5221.4	5325.4	4383.4	5911.1	5103.6	5158.6
Burton	4874.9	5089.8	5193.8	4251.9	5779.6	4972	5027
FEG192-69	4048.2	4263.1	4367.1	3425.2	4952.9	4145.3	4200.3
FEG 192-42	4786.4	5001.3	5105.2	4163.3	5691	4883.5	4938.4
FEG192-16	4604.7	4819.6	4923.6	3981.7	5509.4	4701.8	4756.8
GEN2 -036	4902.1	5117	5221	4279.1	5806.8	4999.2	5054.2
Hol 211	4797.7	5012.6	5116.6	4174.7	5702.4	4894.8	4949.8
M-135	5365.9	5580.8	5684.7	4742.8	6270.5	5462.9	5517.9
M-145	5040	5254.9	5358.9	4416.9	5944.6	5137.1	5192.1
MN BRITE	5560.8	5775.6	5879.6	4937.7	6465.4	5657.8	5712.8
STARSO 620B	4493.8	4708.7	4812.7	3870.8	5398.5	4590.9	4645.9
Mean	4860.3	5075.2	5179.2	4237.2	5764.9	4957.4	5012.4
Minimum	4048.2	4263.1	4367.1	3425.2	4952.9	4145.3	4200.3
Maximum	5560.8	5775.6	5879.6	4937.7	6465.4	5657.8	5712.8
LSD 0.05%	1101	871.3	892.5	NS	1437	1429.5	447.6
CV %	15.4	11.6	11.6	16.8	16.6	19.5	15.5

TABLE II: Combined analysis of variance of the evaluated traits among the tested genotypes.

Source	DF	DHE	DMA	SC	NB	PLH	TKW	HLW	GYLD
Geno	11	104.5***	59.30***	3.55***	7.56***	1400.51***	79.96***	167.55***	1372976***
Env	4	959.4***	984.64***	23.27***	15.66***	1007.72***	2063.28***	4277.2***	11668155***
Env:Rep	10	8.5	5.47	2.20	0.58	76.26	7.70	16.95	1262714
Geno:Env	44	24.0***	13.52***	1.13**	1.59***	76.61***	14.11***	31.29***	749975.1**
Residuals	110	5.5	6.70	0.54	0.32	16.39	4.40	6.03	410412.4

NB: Geno.-Genotypes, Env.- Environment, Rep.-Replication, DHE – Days to heading, DMA – Days to maturity, PLH- plant height, HLW – hectoliter weight, SC- scald, NB – net blotch, TKW – 1000 kernel weight, GYLD – Grain yield kg/ha

TABLE III: The mean performance of the genotype evaluated at Bekoji and Kofele over 2016 to 2018 cropping seasons

Entry	Genotype	DHE	DMA	PLH	HLW	SC	NB	TKW	GYLD	Extract	Friability	Protein
G11	Bahati	86ab	148.1bc	106.1bcde	64.2b	2.8ab	1.6a	57.1c	4994.7abc	79.7ab	62a	11a
G12	Bekoji I	89.7b	145.9abc	111.4def	63.1b	2.2a	2.2a	54bc	5158.6abc	80ab	75a	11a
G1	Burton	83.7ab	143.2a	86.5a	62.9b	4.1b	1.2a	48.7ab	5027abc	82b	76a	11a
G4	FEG 192 -69	89.7b	150.1c	122.4f	62.8b	2.3a	2a	50.8abc	4200.3d	82.2b	65a	11a
G3	FEG 192-42	84.1ab	147.8abc	113.9ef	56.5a	2.3a	2a	45.3a	4938.4abcd	76.2a	66a	12a
G2	FEG192-16	88.7b	145ab	115.1ef	60.2ab	2.7ab	4.3b	55bc	4756.8bcd	79.4ab	50a	12a
G5	GEN2 -036	88.4b	146abc	111.1cde	64.2b	2.7ab	2.1a	54.3bc	5054.2abc	80.5b	71a	12a
G6	Hol 211	85.7ab	145.8abc	108cde	63.3b	2.7ab	2.4a	55.7bc	4949.8abcd	80ab	78a	12a
G7	M 135	85.5ab	147.9bc	100.3bc	60.5ab	1.8a	1.5a	52.2abc	5517.9ab	81.3b	67a	11a
G8	M 145	85.7ab	144.1ab	101.5bcd	61.8b	2.9ab	1.7a	52.4bc	5192.1abc	79.6ab	73a	11a
G9	MN BRITE	81.5a	144.7ab	95.8ab	63b	2.5a	1.6a	55.8bc	5712.8a	79.1ab	70a	9a
G10	STARSO 620B	89b	147.7abc	110.8cde	64.2b	2.8ab	2.2a	54.5bc	4645.9cd	80.7b	75a	11a

NB Abbreviations are as given in Table II.

GGEbiplot and stability analysis

The GGEbiplot analysis of the experiment showed that genotype G9 performed best at Bekoji in 2018, whereas the standard check Bekoji I (G12) performed better at kofele in 2016 and 2018 cropping seasons. The candidate varieties G6, G8, G10 did not perform well in any of the environments (Fig.1). The mean and stability analysis of the GGEbiplots (Fig.2) showed that candidate variety G9 (MN BBRITE) recorded the highest average mean yield than the other candidate varieties and the standard checks. According to Yan and Tinker (2006) the line with arrow shows the performance of the genotypes whereas the second perpendicular line indicates the stability of the genotypes across environments. From this aspect G7 and G5 are the most stable genotypes whereas G4 and G8 are the most unstable genotypes from this experiment (Fig. 2). The standard check Bekoji I (G12) is more stable than MN BRITE but its poor performing based on its yielding ability. Therefore, we can deduce from fig. 2 that candidate variety G9 (MN BRITE) is high yielder and relatively stable genotypes in this experiment.

The ranking of the tested genotypes in relation to the ideal genotype showed candidate variety G9 (MN BBRITE) is more close to the ideal genotype (Fig.3). Whereas candidate variety G10 is far from the concentric circle. In the graph the genotype lied in the center of the concentric circle considered the most ideal genotype whereas a genotype located far from the center considered as poor performing and do not satisfy the characteristics of an ideal genotype (Yan 2001; Yan and Hut 2001 and Yan and Tinker 2006)). In this graph the standard check is far from the center of the concentric circle indicating its poor performance as compared to the best candidate variety G9 (MN BRITE).

According to Yan (2001) the GGEbiplot figure of which won where/what showed which genotypes are best to which environment. Based on this assumption G9 (MN BRITE) preform best at Bekoji, and Kofele in 2017 and 2018 cropping season and the same genotype considered as the best performer in these locations than other genotypes (Fig.4). The standard check variety (G12) performed better at kofele in 2016 cropping season. But it is not the best performing one than others in this group since G8 is the best in this condition.

Generally the result of the combined mean separation and GGEbiplot analysis showed the candidate variety G9 (MN BRITE) is the highest yielding among the tested genotypes and relatively stable. The highest average yield (57.1Qt/ha) was recorded from this candidate which is a 10.7% yield advantage over the standard check (Bekoji I). Therefore, the candidate variety (MN BRITE) which has a yield advantage and stable performance across the test environments was verified and evaluated in 2019/20 cropping season by national variety release technical committee both at Kofele, Bekoji and Holeta research fields and at two farmers' fields at each of the above three locations by farmers' management condition and released for wider production.

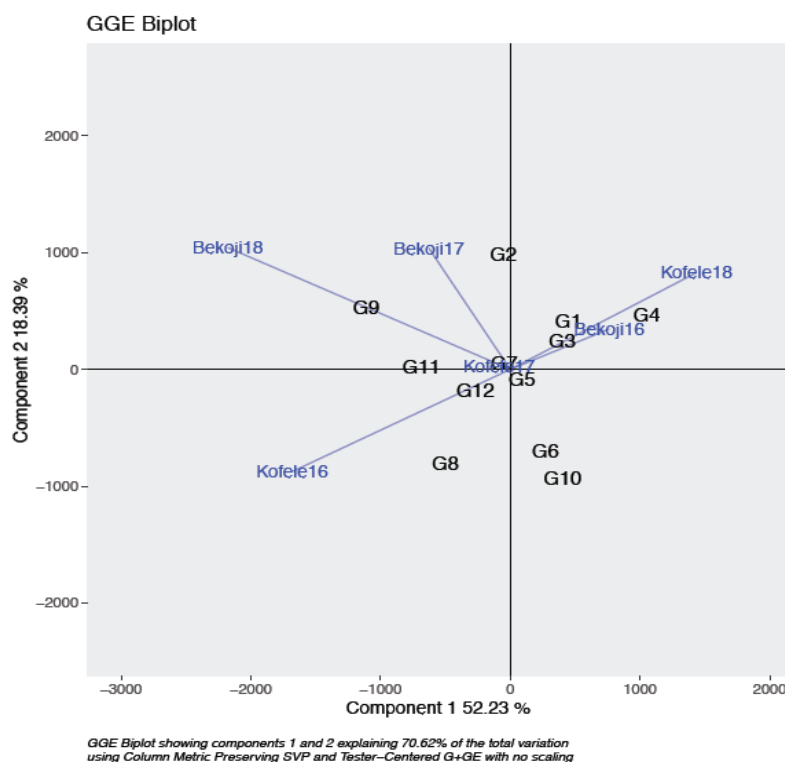


Fig. 1: The GGEBiplot analysis of the tested genotypes evaluated at Bekoji and kofele from 2016 to 2018 cropping season.

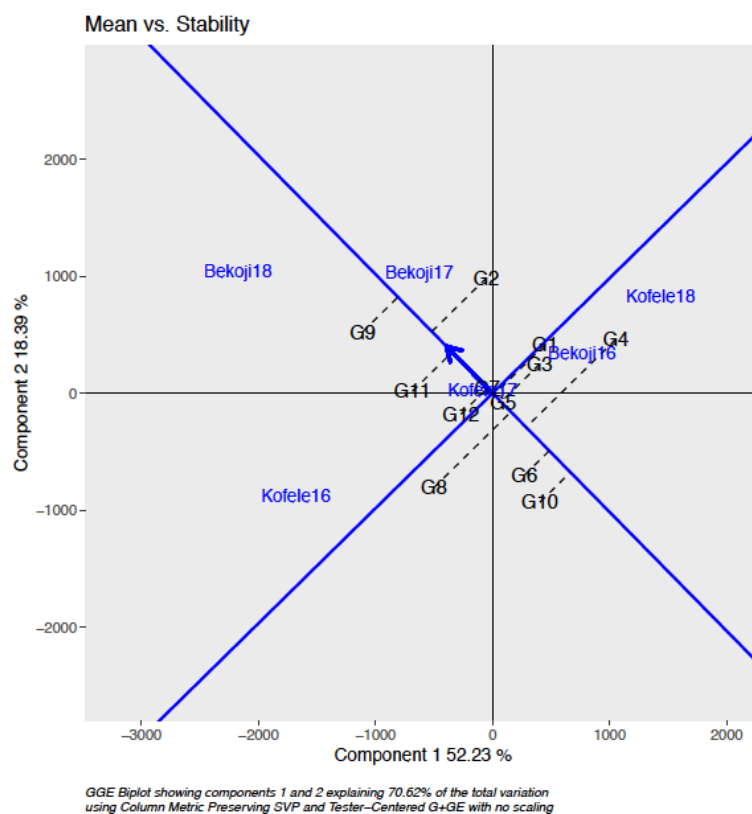


Fig. 2: The GGEBiplot for mean and stability of the genotypes the line with arrow showed the yield capacity of the genotypes and the second line showed the stability of the genotypes evaluated at Bekoji and Kofele from 2016 to 2018 cropping season.

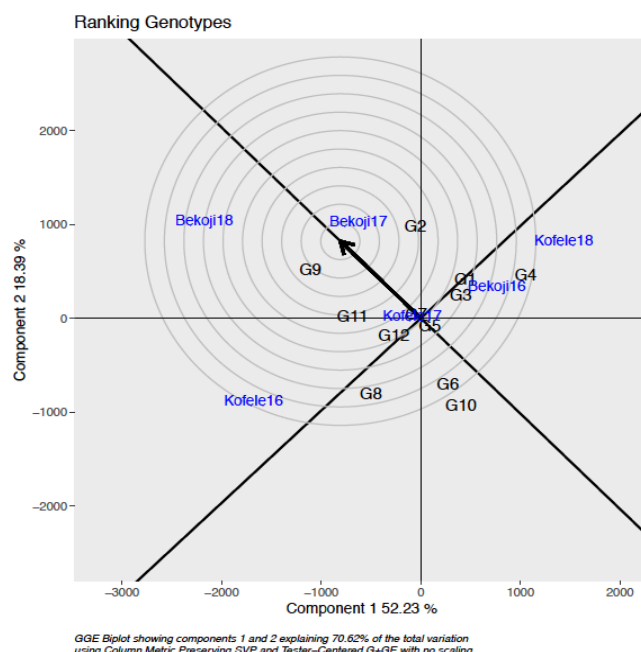


Fig.3: The GEEBiplot figure showing the ranking of the genotype in relation to the ideal genotypes for the genotypes tested at Bekoji and Kofele from 2016 to 2018 cropping season.

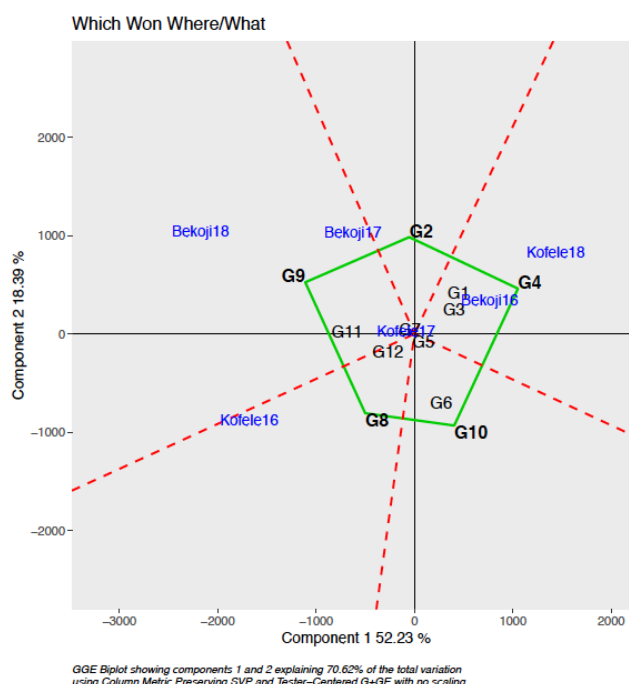


Fig. 4: The GGEBiplot showing which genotypes win where/what for genotypes evaluated at Bekoji and Kofele from 2016 to 2018 cropping season.

IV. CONCLUSION

In this experiment malt barley genotypes including standard check varieties under production were evaluated from 2016 to 2018 cropping season at Bekoji and Kofele under the national variety trial. The result showed highly significant difference among the genotypes for the recorded traits except for extract and friability. In addition highly significant genotype by environment interaction was observed for grain yield among tested genotypes.

The mean performance for grain yield showed that genotype MN Brite was better than standard checks (Bekoji I and Bahati) and all other tested genotypes across the test locations and years. This same genotype showed good stability across the environments and years. Similarly this genotype recorded the required quality standard for the malt barley with an average mean malt extract of 80% and within the range of protein content set by the malt factory. Therefore, these genotype was proposed for variety verification trial in 2019/20 cropping season. Variety release technical committee was assigned to evaluate the performance of this candidate variety along with checks at research sites and two farmers' fields at each of Bekoji, Holeta and Kofele and approved as variety for wider production. The barley research team of Kulumsa agricultural research center finally named this variety Iftu.

REFERENCES

- [1] Alemu, D., Kelemu, K. and Lakew, B. 2014. Trends and prospects of malting barleyvalue chains in Ethiopia. Addis Ababa, Ethiopia.
- [2] Assela Malt Factory (AMF). 2016. 2015/2016 Disclosure Journal. December, 2016. Assela, Ethiopia.
- [3] CSA (central statistical agency). 2020. Agricultural sample survey: area and production of major crops, Meher season. Vol. I. Addis Ababa, Ethiopia.
- [4] Frutos et al. 2014 Frutos, E., Galindo, M.P., Leiva, V.(2014) An interactive biplot implementation in R for modeling genotype-by-environment interaction. Stoch. Environ. Res. Risk Assess. 28:1629-1641
- [5] R Core Team, 2019 R Core Team (2019). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <https://www.R-project.org/>.
- [6] Tarekegn Garomas (2015). The Role of Smallholder Farmers in the Import Substitution and Industrialization of Ethiopia: The Case of Malt Barley Producers in Arsi and Bale Areas, Ethiopia. (MSC Thesis). Indira Gandhi National Open University (IGNOU) St. Mary's University (SMU), Addis Ababa, Ethiopia
- [7] Yan, 2001, Yan W (2001) GGEbiplot—a Windows application for graphical analysis of multi-environment trial data and other types of two-way data. Agron J 93:1111–1118
- [8] Yan, W. et Tinker, N. A. 2006. Biplot analysis of multi-environment trial data: Principles and applications. Can. J. Plant Sci. 86: 623–645.
- [9] Yan W, Hunt LA, Sheng Q, Szlavniks Z (2000) Cultivar evaluation and mega-environment investigation based on GGE biplot. Crop Sci 40:597–605
- [10] Yan W, Kang MS, Ma B-L, Woods S, Cornelius PL (2007) GGE biplot vs. AMMI analysis of genotype-by-environment data. Crop Sci 47:643–653
- [11] Yan and Hunt2001; Biplot Analysis of Multi-environment Trial Data 289
- [12] Yan W, Kang MS (2003) GGE biplot analysis: a graphical tool for breeders, geneticists, and agronomists. CRC Press, Boca Raton, FL