

Biplot Analysis of Multi-Environment Trials for Identification of Winter Wheat Mega-environments in Iran

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Abstract: The objective of this study was to explore the effect of genotype and genotype x location interaction on the grain yield, data of 20 winter wheat genotypes selected from Iran/ICARDA joint project grown in six locations via GGL (genotype plus genotype x location) biplot methodology. The GGL biplot graphically displays G plus GL of a MET in a way that facilitates visual genotype evaluation and mega-environment identification. The GGL biplots clearly identified yearly winning genotypes and their winning niches. Collective analysis of the yearly biplots suggests four winter wheat mega-environments in Iran. The first mega-environment contained location Ardebil where genotypes 135U8.01 and Manning/Sdv1//Dogu88 were the winners; the second and third mega-environments contained locations Shirvan, with genotype Kvz/Tm71/3/Maya"s"//Bb/Inia/4/Sefid and Zanjan with 'Azar-2', being the winners. The locations Kermanshah, Maragheh and Kordestan made up the fourth mega-environment where genotypes Unknown-11 and 'Sardari' were the winners. The results of this study indicate the possibility of improving progress from selections under diverse location conditions by applying the GGL biplot methodology.

Key words: Winter wheat • mega-environment • winner genotype • GGL biplot

INTRODUCTION

Investigation of mega-environments, which has been an important issue of much MET research, is a prerequisite for meaningful genotype evaluation and recommendation [1]. Mega-environments have been defined in different ways. Taking a global perspective of wheat breeding, CIMMYT defined a mega-environment as "a broad, not necessarily contiguous area, occurring in more than one country and frequently transcontinental, defined by similar biotic and abiotic stresses, cropping system requirements, consumer preferences and, for convenience, by volume of production"[2].

Usually yield of a genotype (or any other measure of genotype performance) in an location a mixed effect of genotype main effect (G), location main effect (L) and genotype x location interaction (GL). In normal MET, location (L) accounts for 80% of the total yield variation and G and GL each account for about 10% [3,4]. For the purpose of genotype evaluation, however, only G and GL are relevant [3]. Furthermore, both G and GL must be considered in genotype evaluation, thus the term GGL [4].

Yan [5] and Yan *et al.* [4] proposed a GGL biplot that allows visual examination of the GL interaction pattern of MET data. This GGL biplot was shown to effectively identify the GL interaction pattern of the data. It clearly shows which genotype won in which locations and thus facilitates mega-environment identification. A mega-environment is defined as a group of locations that consistently share the same best genotype(s). Another essential requirement for mega-environment differentiation is repeatability of the which-won-where pattern. Therefore, multi-site trials conducted over years are essential for addressing the mega-environment issue [1, 4, 5]. If the which-won-where patterns identified by a biplot are repeatable over years, different mega-environments (subregions) can be defined. By selecting superior genotypes for each mega-environment, both G and GL can be effectively exploited. The GGL biplot is still useful even in cases where the which-won-where patterns are not repeatable over years, which suggests that the tested environments belong to a single mega-environment. Ideal genotypes should have large first principle component (PC1) scores (higher average yield) and near zero PC2 scores (more stable). Similarly, ideal test

locations should have large PC1 scores (more discriminating of the genotypes) and near zero PC2 scores (more representative of an average location). Thus, the GGL biplot allows many important questions to be addressed effectively and graphically [6]. The objectives of this study were: (i) to use the GGL biplot technique to examine the possible existence of different mega-environments in Iran winter wheat growing regions and (ii) to address the question of "which won where pattern" in a MET dataset.

MATERIALS AND METHODS

Information for each year from 2003 to 2005 was taken from the database maintained at the Drayland Agricultural Research Institute (DARI) trials of Iran. These trials are sponsored by the Agricultural Research and Education Organization (AREO) of Iran. Each year 20 winter wheat genotypes currently grown in the six locations including Kermanshah (West of Iran), Maragheh (Western North of Iran), Shirvan (Eastern North of Iran), Zanjan (Centre of Iran), Kordestan (West of Iran) and Ardebil (Western north of Iran). The genotypes selected from the winter wheat improvement program based on Iran/ICARDA joint project. Experimental layout was a randomized complete block design with four replications in each environment. Sowing was done by an experimental drill in 1.2 m x 6 m plots, consisting of six rows with 20 cm between the rows. Seeding rate was 400 seeds m⁻² for each location. Fertilizer application was 41 kg N ha⁻¹ and 46 kg P₂O₅ ha⁻¹ at planting. Yield (kg ha⁻¹) was obtained by converting the grain yield obtained from plot to hectare. The GGL biplot method [4, 7] was used to study the genotype effect plus genotype by location Interaction effect of yield. This method has been described in detail by Yan and Rajcan [7].

RESULTS

Analysis of variance: Results of analysis of variance for the yearly data are presented in Table 1, which gives an overall picture of the relative magnitudes of the G, L and GL variance terms. Location was always the most important source of yield variation, accounting for 83% to 90% of the G+L+GL. GL was greater than G in all years. The large yield variation due to L, which is irrelevant to genotype evaluation and mega-environment investigation [3, 4, 8] justifies selection of site regression (SREG) as the appropriate model for analyzing the MET data. The large GL, relative to G, suggests the possible existence of different mega-environments. The PC1 and PC2 together, which make up a GGL biplot, explained from 76.6 to 84.0 % of the total interaction.

Winning genotypes and mega-environment identification

2003 Data: On each biplot, some corner or vertex genotypes, which are the most responsive ones, can be visually identified. These are either the best or the poorest genotypes at some or all locations; they can be used to identify possible mega-environments. The corner genotypes for the 2003 dataset were G8, G5, G4, G10, G19, G16 and G15 (Fig. 1). By connecting the markers of these corner genotypes a polygon is formed. By drawing perpendiculars to each side of the polygon passing through the origin, the locations are divided among several sectors, each with a different corner genotype [4]. In Fig. 1, the locations are divided between four sectors. The first sector contains location KN, with genotype G19 being the winner. The location KH make up the second sector with genotypes G10 and G4 being the winners. The location SN with G8, G15 and G16 and the location AL with G5 being the winners. Assuming that the biplot sufficiently approximates the variation of GGL, it can be mathematically proven that all sites in the same sector

Table 1: Genotype (G), Location (L) and genotype x location (GL) variance terms for yield of the Wheat Performance Trials, 2003 to 2005

Source	df	2003		2004		2005		Over all years	
		MS ⁺	Explained %	MS ⁺	Explained %	MS ⁺	Explained %	MS ⁺	Explained %
L	5	12670900**	85.93	22647300**	90.53	7689550**	81.76	9725000**	87.43
G	19	198147**	5.11	239145**	3.63	190548**	7.70	181327**	6.19
GL	95	69564**	8.96	76897**	5.84	52198**	10.54	37320**	6.37
PC1	23	156108**	54.33	201372**	63.40	143360**	66.49	107793**	69.93
PC2	21	68527**	21.78	45971**	13.22	28152**	11.92	23759**	14.07

⁺MS is mean squares. ** Significant at %1 level

Table 2: Yearly winning genotypes and their winning locations in Iran winter wheat performance trials, 2003 to 2005

Year	Winning genotype	Location groupings
2003	G4, G10	KH
	G5	AL
	G8, G15, G16	SN
	G19	KN
2004	G4, G14, G19	KH, KN, MH
	G2, G16,	SN
	G5, G12	AL
2005	G3, G19, G20	KH, ZN
	G5, G8	AL
	G14, G15	MH, KN
Overall years	G4	KH, MH
	G19	KN
	G16	SN
	G5, G8	AL

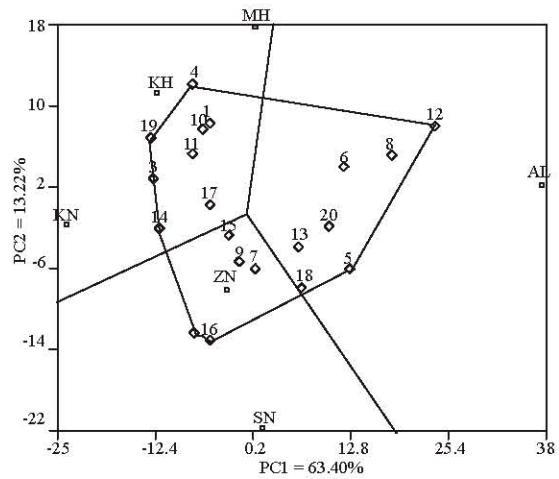


Fig. 2: Yearly GGL biplot for yield data of 2004 Iran winter wheat performance trial. The full names of genotypes and locations are presented in Fig. 1.

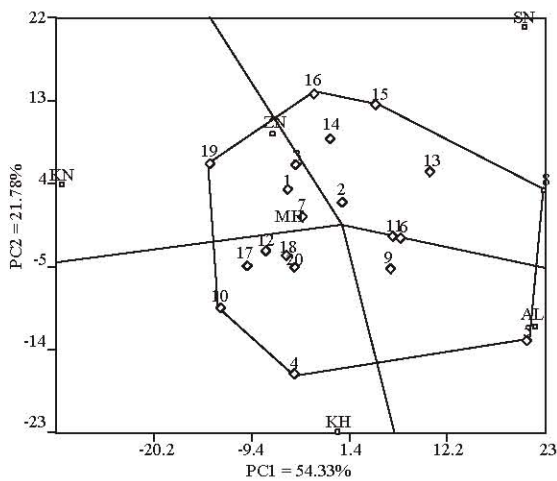


Fig. 1: Yearly GGL biplot for yield data of 2003 Iran winter wheat performance trial. The full genotype (Numbers) names are 1= Unknown-1, 2= Unknown-2, 3= Unknown-3, 4= Unknown-11, 5= 135U8.01, 6= 5294 Karaj 98-99, 7= 1-27-6149/Sabalan/84.40023, 8= Manning/Sdv1/Dogu88, 9= Recttal/TIA.2//TRK13, 10= Sardari/Ska/Aurifen, 11= Unknown-3, 12= Unknown-7, 13= Pf 82200/Sardari, 14= Ghafghaz// F9.10/Maya"s, 15= Khazar/3/ Jcam/ Emu"s"//Dove", 16= Kvz/ Tm71 /3/Maya"s"//Bb/Inia/4/Sefid, 17= Anza/ 3/Pi//Nar/Hys/4/Sefid, 18= Fengkang15/Sefid, 19= Sardari (National check), 20= Azar-2 (National check). The full locations (Letters) name are KH = Kermanshah, MH = Maragheh, SN= Shirvan, ZN = Zanjan, KN = Kordestan, AL= Ardebil

share the same winning genotype, which is the vertex genotype for that sector [4]. Vertex genotypes without any site in their sectors were not the highest yielding genotypes at any site; moreover, they were the poorest genotypes at some sites. Genotypes within the polygon, particularly those located near the plot origin, were less responsive than the vertex genotypes. If mega-environments are defined by different winning genotypes [4, 9], Fig. 1 suggests the existence of four mega-environments for winter wheat in Iran, namely the G8, G15 and G16-winning niche, G4 and G10-winning niche, G19-winning niche and G5-winning niche. However, such a subdivision can be regarded only as a suggestion insofar as it is based solely on 2003 year's data.

2004 Data: The vertex genotypes for the 2004 dataset were G2, G16, G14, G19, G4, G12 and G5 (Fig. 2). G3 was located at an intermediate point on the line connecting G14 and G19; therefore, it performed intermediately between G14 and G19 at all locations. In this year, three mega-environments defined for winter wheat in Iran, namely the G4, G14 and G19-winning niche, G5 and G12-winning niche and G2 and G16-winning niche. This subdivision can be recommended based solely on 2004 year's data.

2005 Data: In this year, the vertex genotypes were G3, G5, G8, G14, G15, G19 and G20 (Fig. 3). Like second year, mega-environments defined by different winning genotypes suggests the existence of three mega-environments for winter wheat in Iran, namely the G14 and

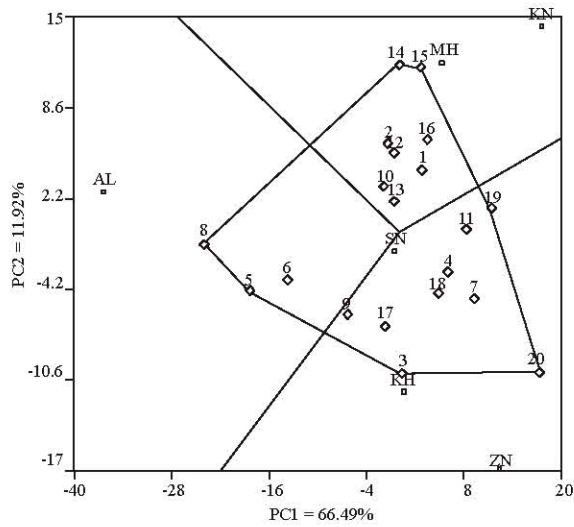


Fig. 3: Yearly GGL biplot for yield data of 2005 Iran winter wheat performance trial. The full names of genotypes and locations are presented in Fig. 1.

G15-winning niche, G3, G20 and G19-winning niche and G5 and G8-winning niche. However, such a subdivision can be suggested only based solely on third year's data.

2003-05 Data: Based on overall years biplot was conducted. In this biplot, corner genotypes were G4, G5, G8, G16 and G19 which are the most responsive ones. In this biplot, the locations fell into four sectors. Based overall years mega-environments are defined by different winning genotypes [4, 9]. Fig. 4 suggests the existence of four mega-environments for winter wheat in Iran, namely the G4-winning niche (Locations KH and MH), G19-winning niche (Location of KN), G16-winning niche (Location of SN) and G8 and G5 winning niche (Location AL). This is the first report of mega-environment identification based on winter wheat yield under rainfed condition in Iran.

Better locations for genotype evaluation: The better testing locations visually identified based on the GGL biplots for each of the three years are presented in Table 2. Among all six locations involved in the three years of testing, location AL was identified as a better location for genotype evaluation for three of the three years. Other locations that were identified as a better testing location included KH (three out of three years), KN (three out of three years), SN (two out of three years), KH (two out of three years). The location ZN was not identified as a good testing location in two of the years.

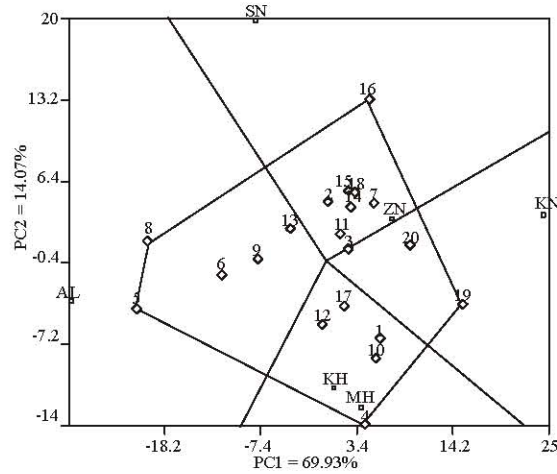


Fig. 4: GGL biplot based on the yield data of 20 winter wheat genotypes that were tested overall years. The full names of genotypes and locations are presented in Fig. 1.

Under limited resources and the need to conduct genotype evaluation in a limited number of locations, the better locations will be those with high values of the PC1 and small values of PC2 [4].

The locations KH, KN, AL, MH and SN were most discriminating as indicated by the longest distance between their marker and the origin (Fig. 4). However, due to their large first or secondary scores (PC1 or PC2). Genotypic differences observed at SN, KH and MH may not exactly reflect the genotypic differences in average yield over all sites, but genotypic differences at AL and KN should be highly consistent with those averaged over sites because they had a near-zero secondary effect score. At a site with a near-zero secondary effect score, the genotypes are essentially ranked according to their primary effect scores and the differences among genotypes are in proportion to the primary effect scores of the sites [4]. Thus, a genotype that yielded well at such a site has a large average yield. On the contrary, site ZN was neither discriminating (small primary effect score) nor representative (large secondary effect score); and therefore, genotypes had high yield at ZN did not necessarily give high average yield over sites. Analysis of multiple year data indicated that ZN represented a different mega-environment (Center of Iran) from the other winter wheat growing regions in Iran.

The Which-Won-Where Pattern: Visualization of the which-won-where pattern of MET data is important for studying the possible existence of different mega-

environments in a region [4, 6, 9]. The polygon view of a GGL biplot explicitly displays the which-won-where pattern and hence is a succinct summary of the GL pattern of a MET data set. The rays in Fig. 4 are lines that are perpendicular to the sides of the polygon or their extensions. Take Fig. 4 as an example, ray 1 is perpendicular to the side that connects genotypes G8 and G16 (the G8-G16 side); ray 2 is perpendicular to side G16-G19; similarly, ray 3 is perpendicular to side G19-G4 and ray 4 to side G4-G5. These four rays divide the biplot into four sectors and the locations fall into four of them (Fig. 4). An interesting feature of this view of a GGL biplot is that the vertex genotype for each sector had the highest yield in all locations that fall in the sector [4]. Thus, two locations KH and MH fall into the sector delineated by rays 3 and 4 and the vertex genotype for this sector is G4, suggesting that the highest-yielding genotype for these two locations in 2004 was 3295. Similarly, the location AL fall into the sector delineated by rays 1 and 4 and the vertex genotypes for this sector are G5 and G8, suggesting that the highest-yielding genotype for this location in all three years. A single location, KN, falls into the sector delineated by rays 2 and 3 and the vertex genotype for this sector is G19, suggesting that G19 was the highest-yielding genotype for KN in 2003 and 2005. SN is another single environment which falls into the sector delineated by rays 1 and 2 and the vertex genotype for this sector is G16, suggesting that G16 was the highest-yielding genotype for SN in 2003. The above statements on the which-won-where pattern based on the biplot can be largely, though not entirely, validated from the original data because only 84.0%, rather than 100%, of the GGL are explained by the biplot. Arguably, however, the pattern displayed by the biplot may be more robust than the individual data points in the raw data because the biplot is based on all data points. For example, the biplot indicate that genotype G16 was the highest yielding in SN (Fig. 4), whereas G8 was actually the highest yielding in SN. This is partially because G8 was, on the whole, poorer than G16 in location KN in all three years.

DISCUSSION

This analysis demonstrates that the GGL biplot is a useful tool for the analysis of yearly MET data. Based on a drawn-to-scale, two-dimensional GGL biplot, the similarities and differences among locations in their discrimination of the genotypes, the similarities and differences among the genotypes in their response to the

locations and the nature and magnitude of interaction between any genotype and any location can be readily visualized [4]. A single year data may indeed have limited value because of the year-to-year variation. Nevertheless, we believe biplot analysis of single year MET data is worthwhile and its reasons have been described in detail by Yan *et al.* [6]. Thus, although conclusions from a single year MET may not be decisive, they are valuable suggestions [6]. Even if the which-won-where pattern is proven to be unrepeatable over years, the researcher would still want to know the average yield and the stability of the cultivars based on each year's MET. Finally, although a biplot from a single year may not be very informative, biplots constructed from several years can be highly valuable [6]. Based on the genotype by site relations of Figs. 1-4, seems to be a single mega-environment, with ZN (Zanjan) as a unique test site. On the other hand, MH (Maragheh) always grouped together with at least one of the other sites, suggesting that it provided no unique information on the genotype performances. Consequently, suggested in future tests, Zanjan should always be used as a test site but Maragheh can be removed from the test sites. Analysis using the GGL biplot method revealed four winter wheat mega-environments in Iran under rainfed conditions: Center of Iran, west, western north and eastern north of Iran, which Zanjan, Shirvan and Ardebil are single mega-environments and the locations Maragheh, Kermanshah and Kordestan are another single mega-environment. Thus, for future breeding and genotype evaluation in Iran, different genotypes can be deployed for the four mega-environments to achieve optimal adaptation.

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