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RESEARCH ARTICLE

Higher Order AMMI (HO-AMMI) analysis: A novel stability model to study genotype-location interactions

B. C. Ajay*, R. Abdul Fiyaz[1], S. K. Bera, Narendra Kumar, K. Gangadhar, Praveen Kona, Kirti Rani and T. Radhakrishnan

Abstract

Additive main effects and multiplicative interaction (AMMI) model is most widely used to analyze genotype x environment interactions (GEI) wherein interaction effects of location is masked by year effect. Hence, presently available models are not able to estimate interaction effects of genotype x location (GLI) and genotype x year (GYI) separately. Moreover, genotype ranking differs as number of years of evaluation vary making selection of genotype for target location difficult. In the present study, a novel stability model i.e., Higher-order-AMMI (HO-AMMI) analysis which can calculate GLI without the confounding effect of GYI and GLYI has been proposed. GEI of AMMI model and all 2-way interactions of HO-AMMI model follow χ^2 distribution, whereas 3-way interaction (GLYI) of HO-AMMI follow noncentral χ^2 distribution. With increase in number of years of evaluation contribution of GLI towards total variation increased whereas in AMMI model contribution of GEI towards total variation decreased. Variation explained by multiplicative components is higher in HO-AMMI compared to AMMI model. Genotypes were ranked using GL, GY and GL+GY+GLY interactions of HO-AMMI and GEI of AMMI for stability and yield and compared their ranks with field ranking. Correlation and linear regression analysis have indicated high association of GLI (HO-AMMI) with field ranking with high R^2 values. Further, HO-AMMI model was able to remove the confounding effect of GYI and GLYI on GLI for accurate identification of genotype for target location irrespective of number of years of evaluation. Hence, HO-AMMI model can be used under multi-environment trials(MET) for selecting genotypes efficiently.

Keywords: AMMI, Genotype environment interactions (GEI), HO-AMMI, multi-environment trials (MET), stability

Introduction

Observed phenotype is attributed to genotype (G), environmental (E), and genotype x environment interaction (GEI). Genotype performing well in one environment may not perform in another. For trials with non-significant GEI, means across environments are sufficient indicators. However, when GEI are large, means obscure subgroups of settings where genotypes perform differently (Fox et al. 1977). A genotype chosen for one environment/location may not function well in another. Plant breeders generally examine genotypic performance across environments/locations (METs) to uncover GEI and quantify them to identify adaptive genotype. Most METs compare genotypes across locations (L) and years (Y). Hence, GE term in ANOVA can be divided into different interactions (I), location x year (LY), genotype x location (GL), genotype x year (GY), and genotype x location x years (GLY). Y=u+G+L+Y+GY+GL+GLY

When GL is significant, locations are divided into homogeneous regions that minimise GE within the regions to exploit specialised adaptability. However, when GY and GLY terms predominate, representative location should be used to estimate genotypic responses (Fox et al. 1997). Additive main effects and multiplicative interaction (AMMI) model is a prominent multiplicative model for studying GE interactions which is fit in two stages, at first stage, the model's main effects are calculated using additive two-way ANOVA with least squares and in second stage model's multiplicative terms are estimated by applying the singular value decomposition (SVD) on the ANOVA residuals (Gauch 1988).

ICAR-Directorate of Groundnut Research, PB No. 5, Junagadh 362 001, India ; [1]ICAR-Indian Institute of Rice Research, Hyderabad 500 030, India

Corresponding Author: B. C. Ajay, ICAR-Directorate of Groundnut Research, PB No. 5, Junagadh 362 001, India, E-Mail: ajaygpb@yahoo.co.in

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Currently available AMMI models only compute GEI using combinations of location and year as environment and do not partition GEI into GLI, GYI, and GLYI. The current study aimed to offer a unique stability model called "Higher-Order Additive Main Effects and Multiplicative Interaction (HO-AMMI)" that can decompose GEI into GYI, GLI and GLYI and compute IPCAs for GLI alone without GYI and GLYI confounding effects. We compare the findings of HO-AMMI and AMMI models to rank genotypes.

Materials and methods

Higher Order-Additive Main effects and Multiplicative Interaction (HO-AMMI)

HO-AMMI model computes all possible two-way and three-way interactions such as GLI, GYI, GLYI separately to calculate stability values without the confounding effects of other interactions. IPCAs estimated using GLI could be used to identify genotypes for target location precisely. Higher-Order AMMI model equation can be written as:

$$X_{ijk}= m+Y_i+L_j+G_k+YL_{ij}+GY_{ik}+GL_{jk}+GLY_{ijk}+e_{ijk}$$

Where,

X_{ijk} – Yield in i^{th} year, j^{th} location and k^{th}genotype
m – General mean
Y_i – random main effect of i^{th} year
L_j – fixed main effect of j^{th} location
G_k – fixed main effect of k^{th}genotype
YL_{ij} – random interaction effect of i^{th} year and j^{th} location
GY_{ik} – random interaction effect of k^{th}genotype and i^{th} year
GL_{ik} – random interaction effect of k^{th}genotype and j^{th} location
GLY_{ijk} – random interaction effect of k^{th}genotype, ini^{th} year and j^{th} location
e_{ijk} - average error associated with the response of the k^{th} genotype in i^{th} year and j^{th} location

In HO-AMMI model, all two-way (GYI, GLI and LYI) and three-way (GLYI) interactions were computed separately following "factor analytic model" suggested by Gollob (1968) and Gauch (1988) using SVD. HO-AMMI model involving SVD can be represented as,

$$X_{ijk}= m+Y_i+L_j+G_k+\Sigma^t_{n=1}\lambda_{n(ki)}\alpha_{kn}\gamma_{in}+\Sigma^t_{n=1}\lambda_{n(kj)}\alpha_{kn}\gamma_{jn}+\Sigma^t_{n=1}\lambda_{n(ij)}\alpha_{jn}\gamma_{in}+\Sigma^t_{n=1}S_nU_{kn}V_{ijn}+e_{ijk}$$

Where,

$\lambda_{n(ki)}$ – singular value of n^{th} multiplicative component for k^{th} genotype in i^{th} year
$\lambda_{n(kj)}$ – singular value of n^{th} multiplicative component for k^{th} genotype in j^{th} location
$\lambda_{n(ij)}$ – singular value of n^{th} multiplicative component for i^{th} year in j^{th} location
S_n - singular value of n^{th} multiplicative component for k^{th} genotype in i^{th} year and j^{th} location
α_{kn} - n^{th} singular vector for k^{th} genotypes
α_{jn} - n^{th} singular vector for j^{th} location
γ_{in} –n^{th} singular vector for i^{th} year
γ_{jn} - n^{th} singular vector for j^{th} location
U_{kn} – combined n^{th} singular vector for k^{th} genotypes
V_{ijn} - combined n^{th} singular vector for i^{th} year in j^{th} location

Simulated data and comparison of models

To compare AMMI and HO-AMMI models, four distinct trials' yields of peanut were simulated. Each of four tests had 20 locations. Experiments-1 and 2 evaluated 10 genotypes over 2 and 3 years, whereas experiments-3 and 4 evaluated 20 genotypes over 2 and 3 years, respectively. The HO-AMMI analysis was performed in R (R core team 2018) using the packages 'MASS' and AMMI model using package 'agricolae'. Modified AMMI stability Index (MASI) was calculated as stated by Ajay 1 et al. (2018a) using the package 'ammistability' (Ajay 2 et al. 2018b). Then, for both AMMI and HO-AMMI models, SSI was determined using genotype ranking based on MASI and pod yield. We used spearman's rank correlation to compare SSI and field ranks. AMMI and HO-AMMI models were correlated with field ranking using 'performanceAnalytics' package, linear regression plots were created to find the model with high R^2. Efficiency of GLI and GEI models was compared using RMSE values.

Field ranking

To arrive at field ranking for genotypes, every location and year in an experiment were considered as separate environments. For example, in the experiment-1, 20 location and 2 years were considered as 40 environments and genotypes were ranked for all environments separately. Number of times genotype received rank '1' over 40 environments was computed. Similarly, number of times genotype receiving ranks '2' to '10' were computed. The overall genotype ranking was calculated using Garrett and Woodworth's (1971) ranking formula. Garrett's Table-converts percent position to scores for each genotype. Then, for each genotype, the scores of all ranks were summed up, and mean score was computed for ranking genotypes.

Results and discussion

AMMI and HO-AMMI

AMMI ANOVA for four different experiments is given in Supplementary Table S1. In this model sources of variation were grouped into main effects G, E and GEI. All three sources of variation significantly influenced pod yield among four experimental data sets. Environment had maximum variation followed by GEI whereas G had least influence. In experiment-1 and 2, nine IPCAs were significant whereas ten IPCAs were significant in experiment-3 and 4 explaining 100% variation in GE sum of squares.

Unlike AMMI model, which computes G, E and GEI effects, the HO-AMMI model computes direct G, L, and Y effects, as well as multiplicative effects of all possible interactions (GLI, GYI, LYI, GLYI). In all four tests, G, L, Y, LYI, GLI, GYI, and GLYI had significant effects on pod yield (Supplementary Table S2). Location explained maximum variation ranging from 54.6 to 62.2% across all four tests, followed by LYI, GLI, GLYI, G and GYI. LYI (IPCA1$_{LY}$) and GYI (IPCA1$_{GY}$) had one interaction principal component which was significant in experiments 1–3 but non-significant in experiment-4. All four GLI's had nine significant IPCAs explaining 100% of GLI sum of squares. The percentage contribution of IPCA1-9$_{GY}$ to GLI was the same in experiment 1 and 2 and 3 and 4, even though the genotypic mean was different (Supplementary Tables S3 to S6) indicating that regardless of years of evaluation, GLI will provide reliable information regarding genotype performance over a wide range of locations. GLYI had ten significant IPCAs in experiments-1 and 2, and eleven significant IPCAs in experiments-3 and 4. In HO-AMMI model GLI, GYI, or LYI, interaction components are organized in decreasing order of variation and follow χ^2 distribution (Gollob 1968). GLYI has noncentral χ^2 distribution (Gollob 1968) and are not ordered in descending order. In this study, IPCA1$_{GLY}$ explained least variation with non-significant sum of squares. IPCA2$_{GLY}$ explained maximum variation followed by IPCA3$_{GLY}$. Because IPCA1$_{GLY}$ was negative and non-significant, it was excluded from common variance (Lorenzo-Seva 2013).

Model comparison

Estimation of interactions inside GEI is different between HO-AMMI and AMMI. In experiment-1 and 2, HO-AMMI divided GEI (22.4 and 21.05%) into GLI (13.73 and 15.1%), GYI (0.4 and 0.3%), and GLYI (8.27 and 6.07%). In Experimet-3 and 4 GEI (22.1 and 21.24%) too was divided into GLI (13.69 and 15.1%), GYI (0.39 and 0.29%), and GLYI (8.14 and 5.95%). This shows that HO-AMMI was able to extract GYI and GLYI from GLI. As previously reported, G and GL variances were confounded with GY and GLY variances (Holland and Nyquist 2010; Arief et al. 2015). HO-AMMI model eliminates confounding effects of GY and GYL while estimating GL variation.

In AMMI model, G explained variation increased with a number of years evaluation, whereas GEI decreased. In HO-AMMI model, more years of evaluation increased GLI contribution and decreased LYI and GLYI contribution. In AMMI model, G effect increased with number of genotypes, E effect reduced and GEI remained unchanged. In HO-AMMI model with increase in number of genotypes G effect grew, and location and year main effects declined. Variation in GEI and GLI interaction effects over years also indicated that genotypes should be examined in as many years as possible to increase the accuracy of interaction effects in both models. Arief et al. (2019) found that number of years of evaluation impacts the accuracy of GY and GYL calculations and present results are also in confirmation with Holland and Nyquist (2010) and Arief et al. (2015). HO-AMMI model has larger percent variation explained by multiplicative components than AMMI model.

Comparison of genotype ranking

The ranking of genotypes based on SSI for interactions such as GLI, GYI, GLYI and GLI+GYI+GLYI of HO-AMMI; GEI of AMMI model and field ranking were studied (Supplementary Table S7). There were clear differences in genotype ranking between different interactions of HO-AMMI, AMMI and field ranking among all four experimental data sets. Experiments-1 and 2 have similar sets of genotypes and locations but differ in the number of years of evaluation and similarly with respect to experiments-3 and 4. Ranking of genotypes on the basis of GLI and GYI was same between experiments-1 and 2 and between experiments3 and 4 whereas ranking of genotypes based on GLI+GYI+GLYI, field rank and AMMI differed between different years of testing. This indicates that when AMMI is applied ranking of genotypes vary with different years of evaluation which makes selection of genotypes cumbersome. But GLI interaction evaluated by HO-AMMI provides accurate ranking of genotypes irrespective of number of years of evaluation as confounding effects of GYI and GLYI have been removed. This further corroborates the observations made by earlier reports that V_G and V_{GL} were confounded by V_{GY} and V_{GYL} (Holland and Nyquist 2010; Ariefet al. 2015).

Association among different rankings

Correlations between field ranking and interaction components of AMMI (GEI) and HO-AMMI models (GLI, GYI, GLYI, GLI+GYI+GLYI) are depicted in Fig.1. In experiment 1, HO-AMMI and AMMI GLI were significantly correlated with field rating. In experiment 2, GLI, GYI, and AMMI ranked highly with field ranking, while GLI ranked highly with GLI+GYI+GLYI and AMMI ranking. In experiments 3 and 4, field ranking was associated with GLI, GYI, GLYI, GLI+GYI+GLYI. In all four tests, field rank correlated with GLI more than GYI, GLYI, GLI+GYI+GLYI, and AMMI. Fig. 2 shows the scatter plots of linear regression between field ranking using GL and AMMI. GLI had greater R^2 values than AMMI with field rank. RMSE values for GLI and GEI of HO-AMMI models for all four experiments are shown in Fig. 3. All four trials had low RMSE for GLI. HO-AMMI GLI has a good correlation, R^2 value and low RMSE value compared to AMMI GEI, indicating that HO-AMMI GLI accurately predicts genotype ranking.

Biplots comparison of HO-AMMI and AMMI models

When environment consists of both locations and years selection of genotypes for particular location becomes difficult in AMMI model as GLI effect is masked by GYI and GLYI interaction effects. Confounding effect of year is overcome in HO-AMMI model whereas GEI is partitioned into GLI, GYI and GLYI. Biplots for HO-AMMI were generated based on GLI as they had high R^2 values with field ranking compared to other models. Biplots of GLI from HO-AMMI model was compared with AMMI model. Figs. 4a and 4b

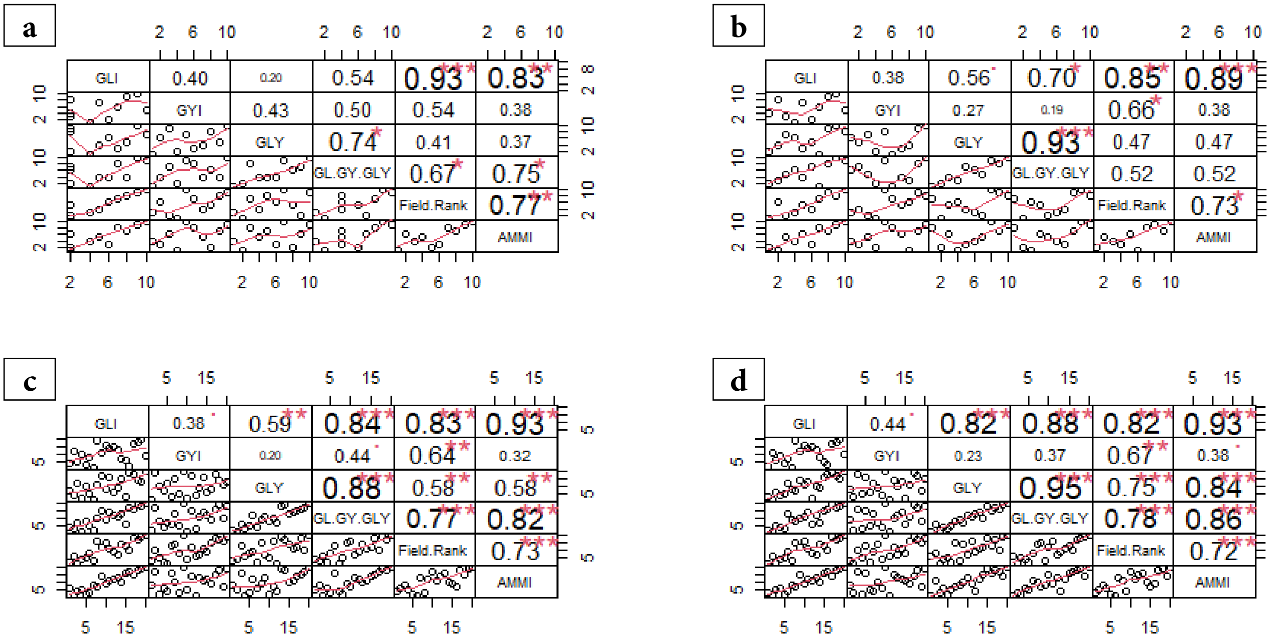

Fig.1. Linear regression analysis (R^2) performed between GL, GY, GLY, GL+GY+GLY interactions of HO-AMMI and GEI interaction of AMMI with field ranking in experiments-1 (a), 2 (b), 3 (c) and 4 (d).

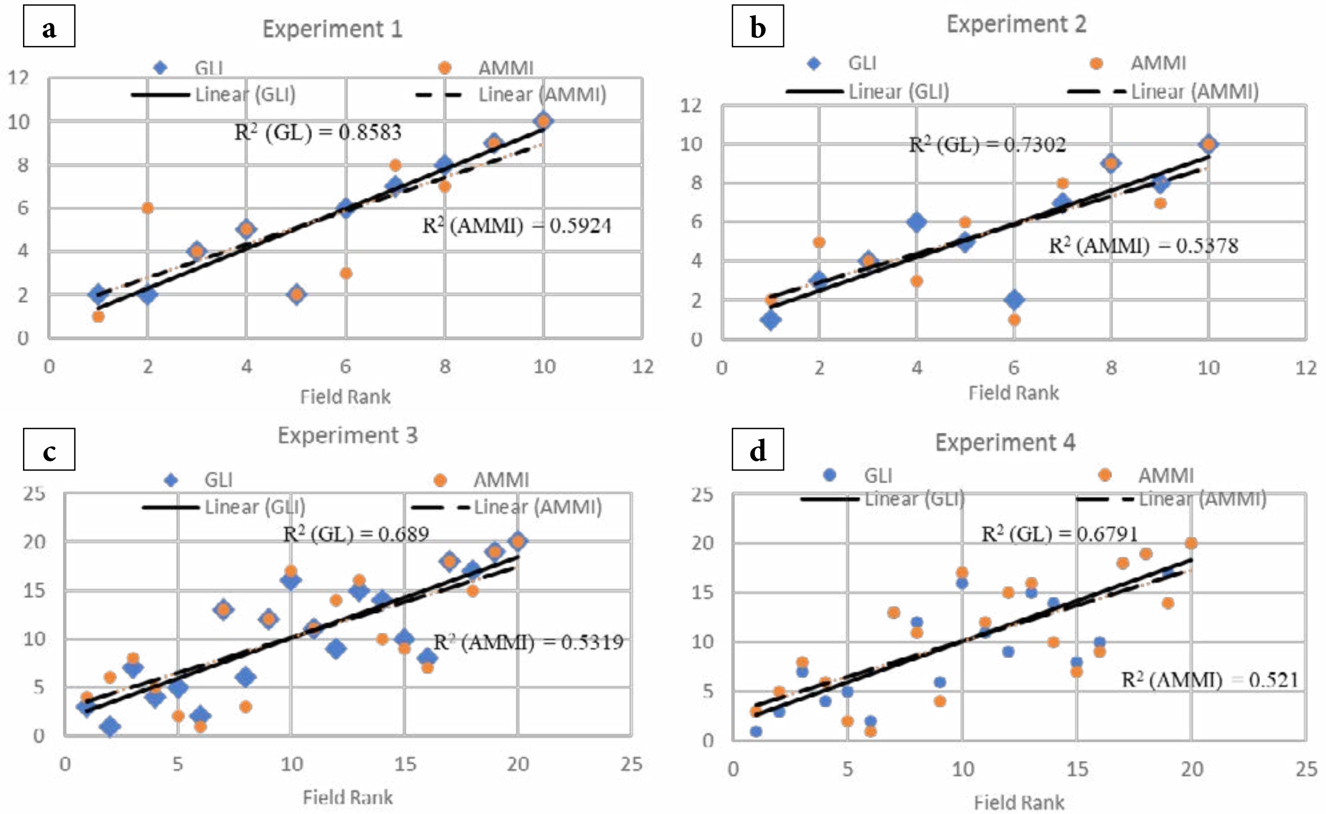

Fig. 2. Linear regression of genotype x location interaction (GLI) from HO-AMMI model and AMMI model with field rank under different experimental conditions

represent GLI based HO-AMMI model for experiments 1 and 2, respectively. Distribution of genotype points in both the experiments revealed that the genotypes 1 and 10 are close to the origin with minimal GL effect whereas remaining eight genotypes are scattered away from the origin and are affected by GLI effect. The genotype 2 had positive interaction with location E13 hence, exhibited specific adaptation to that environment. Genotype, 10 displayed positive interaction with locations E8, E12, E19 and E20. Similarly, location specific genotypes could be identified for experiments 3 and 4.

Fig. 4c and 4d represents AMMI model for experiment-1 and 2, respectively. Genotype, 10 is close to the origin with minimal GEI effect in both the experiments and remaining genotypes were sensitive to environment. In experiment 1 genotypes, 4, 5 and 7 had specific adaptation with environments E6Y2, E1Y1 and E7Y2. In experiment 2 genotypes, 4 and 7 were adapted to environments E6Y2, E6Y3, E1Y1 and E7Y2; genotype, 3 adapted to E7Y1, E12Y2 and E2Y1; genotype-1 with E14Y3, E15Y3 and E15Y1. Similar such interpretations could be drawn for experiments 3 and 4 as well.

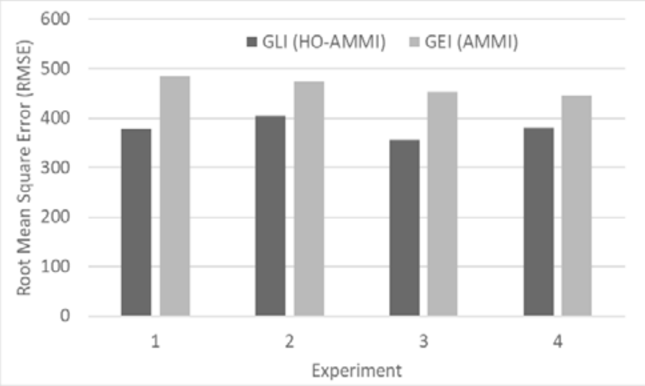

Fig. 3. Root Mean Square Error (RMSE) for GLI from HO-AMMI and GEI from AMMI model under different experiments.

Association and distribution of genotypes with locations was same in HO-AMMI model irrespective of number of years of evaluation, whereas in AMMI model though genotypic distribution was almost same distribution of environments varied. In AMMI model total number of environments is a product of number of locations and number of years of evaluation. Therefore, a trial with 20 locations and 2 years will have 40 environments and number of environments increases with the increase in locations and years, whereas in HO-AMMI model irrespective of number of years of evaluation GLI biplot will produce similar results. Also, selection of genotypes for target location is easy in HO-AMMI model as GLI biplot is based on genotypes and locations only without the year effect, whereas in AMMI model year effect is masking the location effect making genotypic selection difficult. HO-AMMI model was able to provide accurate ranking of genotypes for a location without confounding effect of GYI and GLYI. Also, GLI biplots from HO-AMMI model depicted very clear picture about the association of genotype with target location which was missing in AMMI models. Hence, HO-AMMI model would help the breeder to identify high yielding genotype for a target location without the confounding effect of years.

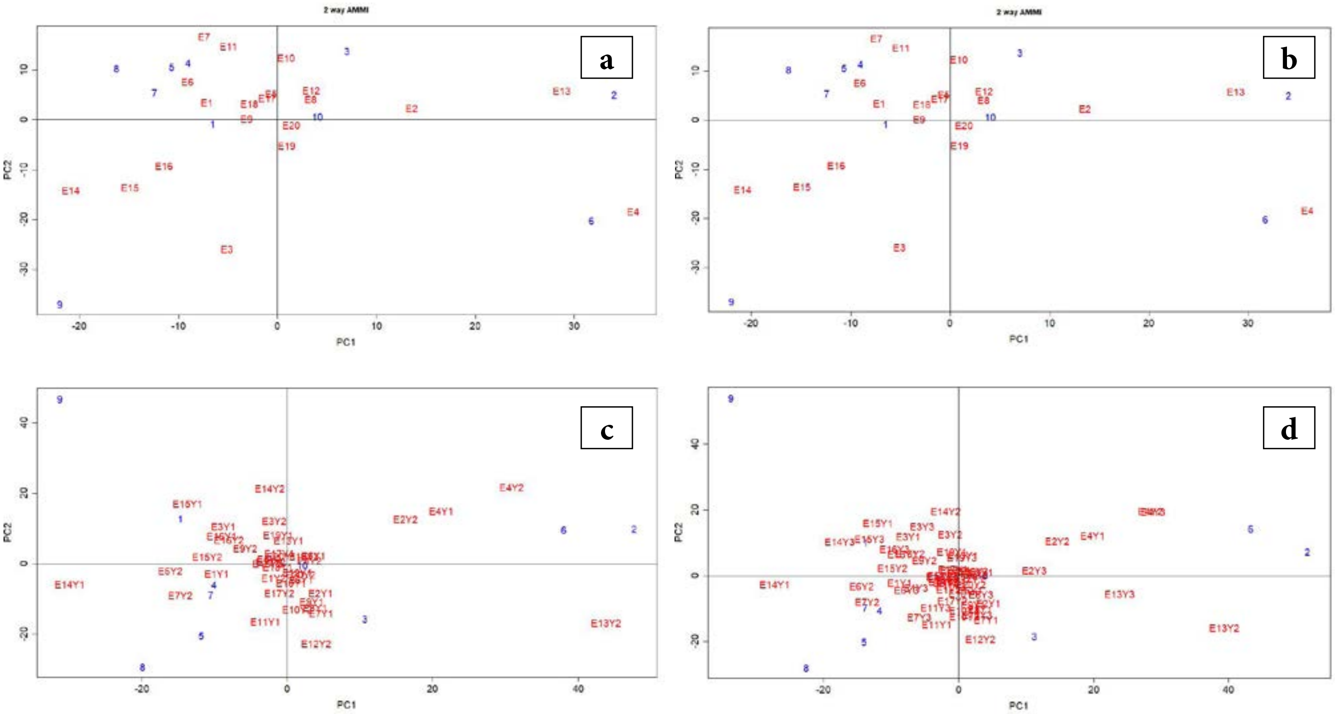

Fig. 4. (a) Biplot showing the effect of primary and secondary interaction principal components (PC1 and PC2), respectively for genotype x location interaction (GLI) for HO-AMMI and genotype x environment interaction for AMMI model under experiments 1 and 2: a) HO-AMMI experiment 1, b) HO-AMMI experiment 2, c) AMMI experiment 1 and d) AMMI experiment 2

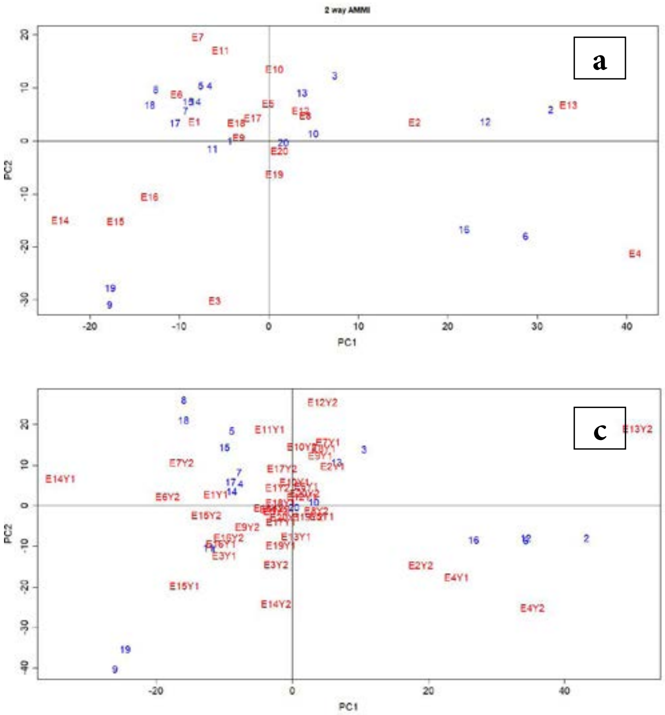

Fig. 4. (b) Biplot showing the effect of primary and secondary interaction principal components (PC1 and PC2), respectively for genotype x location interaction (GLI) for HO-AMMI and genotype x environment interaction for AMMI model under experiment 3 and 4: a) HO-AMMI experiment 3, b) HO-AMMI experiment 4, c) AMMI experiment 3 and d) AMMI experiment 4

Authors' contributions

Conceptualization of research (BCA, SKB, TR); Designing of the experiments (BCA, RAF); Contribution of experimental materials (BCA, NK, PK); Execution of field/lab experiments and data collection (GK, KR); Analysis of data and interpretation (BCA, RAF); Preparation of manuscript (BCA, SKB).

Supplementary materials

Supplementary Tables S1 to Supplementary Table S7 having analysed data are presented.

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Supplementary Table S1. AMMI analysis of variance for studying genotype-environment-interactions (GEI) under different combinations of genotype, location, and year

	Experiment-1			Experiment-2			Experiment-3			Experiment-4		
	Df	MSS	GEI SS%	Df	MSS	GEI SS%	Df	MSS	GEI SS%	Df	MSS	GEI SS%
Environment(E)	39	23532482**	73.19	59	25529364**	75.74	39	40270269**	70.57	59	43687365**	72.87
Genotype(G)	9	803185**	0.58	9	1370809**	0.62	19	4096885**	3.50	19	6992618**	3.76
Rep(E)	80	52401	0.33	120	45568	0.27	80	89656	0.32	120	77967	0.26
G*E	351	800638**	22.41	531	762875**	20.37	741	667166**	22.21	1121	637536**	20.20
IPCA1	47	2140297**	35.80	67	2226431**	36.82	57	3052948**	35.2	77	3355380**	36.15
IPCA2	45	1160549**	18.58	65	1154583**	18.53	55	1637548**	18.22	75	1725544**	18.11
IPCA3	43	832427**	12.74	63	869859.3**	13.53	53	1190451**	12.76	73	1326417**	13.55
IPCA4	41	713853**	10.41	61	673566**	10.14	51	991896**	10.23	71	1016062**	10.09
IPCA5	39	554526**	7.70	59	531312**	7.74	49	764772**	7.58	69	784367**	7.57
IPCA6	37	434503**	5.72	57	366817**	5.16	47	626832**	5.96	67	590757**	5.54
IPCA7	35	304589**	3.79	55	261755**	3.55	45	435330**	3.96	65	393624**	3.58
IPCA8	33	262829**	3.09	53	200749**	2.63	43	350276**	3.05	63	291948**	2.57
IPCA9	31	196967**	2.17	51	150720**	1.9	41	257790**	2.14	61	217117**	1.85
IPCA10							39	114102**	0.90	59	118716**	0.98
Error	720	60853	3.49	1080	55228	3.00	1520	49684	3.39	2280	45089	2.91

Supplementary Table S2. Higher-order-AMMI (HO-AMMI) analysis of variance for studying genotype-location-year-interactions (GLYI) under different combinations of genotype, location, and year

	Experiment-1			Experiment-2			Experiment-3			Experiment-4		
	Df	MSS	GEI SS%	Df	MSS	GEI SS%	Df	MSS	GEI SS%	Df	MSS	GEI SS%
Locations(L)	19	37343416**	56.58	19	56014655**	62.23	19	63904102**	54.56	19	95855164**	59.83
Year (Y)	1	684401**	0.05	2	342214**	0.04	1	1171875**	0.05	2	585961**	0.04
Genotype(G)	9	803185**	0.58	9	1204808**	0.63	19	4096885**	3.50	19	6145797**	3.84
Rep(L)	40	44322^{ns}	0.14	40	66476^{ns}	0.16	40	75833^{ns}	0.14	40	113741**	0.15
Rep(Y)	2	34576^{ns}	0.01	4	17288^{ns}	0.00	2	59284^{ns}	0.01	4	29642^{ns}	0.00
L*Y	19	10924078**	16.55	38	5462039**	12.14	19	18694247**	15.96	38	9347123**	11.67
IPCA1$_{LY}$	19	10924078**	100.00	20	10377874**	100.00	19	18694247**	100	20	887976**	100
G*Y	9	563296**	0.40	18	281648**	0.30	19	459987**	0.39	38	229994**	0.29
IPCA1$_{GY}$	9	563296**	100.00	10	506967**	100	19	459987**	100	20	21849^{ns}	100
G*L	171	1006924**	13.73	171	1510360**	15.10	361	843646**	13.69	361	1265446**	15.01
IPCA1$_{GL}$	27	2523819**	39.58	27	3785694**	39.58	37	3198276**	38.86	37	1599143**	38.86
IPCA2$_{GL}$	25	1342395**	19.49	25	2013502**	19.49	35	1656693**	19.04	35	828283**	19.04
IPCA3$_{GL}$	23	1144595**	15.29	23	1716842**	15.29	33	1408822**	15.27	33	704423**	15.27
IPCA4$_{GL}$	21	717635**	8.75	21	1076531**	8.75	31	916865**	9.33	31	458436**	9.33
IPCA5$_{GL}$	19	708893**	7.82	19	1063238**	7.82	29	802700**	7.64	29	401309**	7.64
IPCA6$_{GL}$	17	504433**	4.98	17	756696**	4.98	27	582705**	5.17	27	291370**	5.17
IPCA7$_{GL}$	15	215538**	1.88	15	323306**	1.88	25	232581**	1.91	25	116273**	1.91
IPCA8$_{GL}$	13	197469**	1.49	13	296202**	1.49	23	202447**	1.53	23	101240**	1.53
IPCA9$_{GL}$	11	112776*	0.72	11	169102**	0.72	21	139029**	0.96	21	69497**	0.96
G*L*Y	171	606844**	8.27	342	303422**	6.07	361	501589**	8.14	722	250795**	5.95
IPCA1$_{GLY}$	27	-2011298^{ns}	-52.33	46	-1180546^{ns}	-52.33	37	-2499260^{ns}	-51.07	56	-1651302^{ns}	-39.50
IPCA2$_{GLY}$	25	2851395**	68.69	44	1620117**	68.70	35	3537050**	68.37	54	2292552**	54.84
IPCA3$_{GLY}$	23	1470736**	32.60	42	805401**	32.60	33	1765898**	32.18	52	1120658**	26.81
IPCA4$_{GLY}$	21	862380**	17.45	40	452743**	17.45	31	955832**	16.36	50	592606**	14.18
IPCA5$_{GLY}$	19	453818**	8.31	38	226916**	8.31	29	512740**	8.21	48	309791**	7.41
IPCA6$_{GLY}$	17	346842**	5.68	36	163786**	5.68	27	378443**	5.64	46	222132**	5.31
IPCA7$_{GLY}$	15	620377**	8.97	34	273692**	8.97	25	662159**	9.14	44	376218**	9.00
IPCA8$_{GLY}$	13	298952**	3.75	32	121443**	3.74	23	297149**	3.77	42	162719**	3.89
IPCA9$_{GLY}$	11	400493**	4.25	30	146857**	4.25	21	333451**	3.87	40	175069**	4.19
IPCA10$_{GLY}$	9	304149**	2.64	28	97761**	2.64	19	239200**	2.51	38	119599**	2.86
IPCA11$_{GLY}$	--	--	--	--	--	--	17	107119**	1.01	36	50584	0.18
Error	758	60903	3.68	1156	49445	3.34	1558	51053	3.57	2356	41803	3.24

Supplementary Table S3. Mean pod yield (kg/ha) of 10 peanut cultivars grown in 20 hypothetical locations over two years under experiment-1

Location	Groundnut Cultivar									
	1	2	3	4	5	6	7	8	9	10
E1	2360	1619	1733	2022	1958	1713	1955	2234	1884	1755
E2	1497	1423	1594	1887	1555	1375	1411	1663	1026	1598
E3	2635	2708	2526	2576	2130	1724	2989	2863	2159	2297
E4	1463	1256	2195	1575	2490	2430	1695	2004	1387	1702
E5	3552	4837	3712	3338	3897	4690	3648	3589	2922	3983
E6	2833	2433	2218	2200	3384	1996	2889	3015	3982	2739
E7	2266	1451	1267	1710	2125	1418	1788	1808	2744	1899
E8	1487	1283	1792	1997	1618	1335	2099	1285	2536	1699
E9	1218	824	1317	844	954	747	915	936	915	1047
E10	1396	1281	1529	1370	1296	904	1300	1137	1421	1215
E11	1400	1299	1142	1067	1262	1194	1426	792	1478	1167
E12	3827	4771	3789	3748	3923	3823	3452	3579	3729	3748
E13	1655	1242	1724	1366	1309	1613	1443	1424	1478	1514
E14	2124	1428	1595	1751	1713	2811	2044	2348	2979	1787
E15	2285	3673	2473	1605	1767	3327	1620	1145	2439	2495
E16	3039	3757	3135	2767	3277	2207	3356	2708	3287	2936
E17	2763	1934	2268	2567	2595	1738	2334	2082	2213	2256
E18	2883	2775	3084	2603	3651	1946	2620	2957	2556	2842
E19	2245	2705	2230	2282	2480	2643	3153	2724	2232	2516
E20	1645	2528	2249	2162	2611	2123	2850	2566	2673	2579
Mean	2229	2261	2178	2072	2300	2088	2249	2143	2302	2189

Supplementary Table S4. Mean pod yield (kg/ha) of 10 peanut cultivars grown in 20 hypothetical locations over three years under experiment-2

Location	Groundnut Cultivar									
	1	2	3	4	5	6	7	8	9	10
E1	2518	1727	1848	2156	2088	1827	2085	2382	2009	1872
E2	4083	5090	4041	3998	4185	4078	3682	3817	3977	3998
E3	2266	1523	1701	1868	1828	2998	2181	2505	3178	1906
E4	2438	3918	2638	1712	1885	3549	1728	1221	2602	2662
E5	3241	4007	3344	2951	3495	2354	3580	2888	3506	3132
E6	2947	2063	2419	2738	2768	1854	2490	2221	2361	2406
E7	3075	2960	3289	2777	3894	2076	2794	3154	2727	3032
E8	2395	2885	2379	2434	2645	2819	3363	2905	2380	2684
E9	1755	2696	2399	2306	2785	2264	3040	2737	2851	2751
E10	1596	1518	1700	2013	1659	1467	1506	1774	1094	1705
E11	2811	2889	2694	2748	2272	1839	3188	3054	2303	2450
E12	1560	1340	2341	1680	2656	2592	1808	2138	1479	1816
E13	3788	5159	3959	3560	4157	5003	3891	3828	3117	4249
E14	3022	2596	2366	2347	3609	2129	3081	3216	4248	2921
E15	2417	1547	1351	1824	2267	1512	1907	1929	2927	2025
E16	1586	1368	1912	2130	1726	1424	2239	1371	2705	1813
E17	1300	879	1404	901	1018	797	976	999	976	1117
E18	1489	1367	1631	1461	1383	964	1387	1213	1515	1296
E19	1493	1386	1218	1138	1347	1274	1521	845	1576	1245
E20	1766	1325	1839	1457	1396	1721	1539	1518	1577	1615
Mean	2377	2412	2324	2210	2453	2227	2399	2286	2456	2335

Supplementary Table S6: Mean pod yield (kg/ha) of 20 peanut cultivars grown in 20 hypothetical locations over three years under the experiment-4

Location	Groundnut Cultivar																			
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
E1	2518	4083	2266	2438	3241	2947	3075	2395	1755	1596	2811	1560	3788	3022	2417	1586	1300	1489	1493	1766
E2	1727	5090	1523	3918	4007	2063	2960	2885	2696	1518	2889	1340	5159	2596	1547	1368	879	1367	1386	1325
E3	1848	4041	1701	2638	3344	2419	3289	2379	2399	1700	2694	2341	3959	2366	1351	1912	1404	1631	1218	1839
E4	2156	3998	1868	1712	2951	2738	2777	2434	2306	2013	2748	1680	3560	2347	1824	2130	901	1461	1138	1457
E5	2088	4185	1828	1885	3495	2768	3894	2645	2785	1659	2272	2656	4157	3609	2267	1726	1018	1383	1347	1396
E6	1827	4078	2998	3549	2354	1854	2076	2819	2264	1467	1839	2592	5003	2129	1512	1424	797	964	1274	1721
E7	2085	3682	2181	1728	3580	2490	2794	3363	3040	1506	3188	1808	3891	3081	1907	2239	976	1387	1521	1539
E8	2382	3817	2505	1221	2888	2221	3154	2905	2737	1774	3054	2138	3828	3216	1929	1371	999	1213	845	1518
E9	2009	3977	3178	2602	3506	2361	2727	2380	2851	1094	2303	1479	3117	4248	2927	2705	976	1515	1576	1577
E10	1872	3998	1906	2662	3132	2406	3032	2684	2751	1705	2450	1816	4249	2921	2025	1813	1117	1296	1245	1615
E11	2140	3470	1926	2072	2755	2505	2614	2036	1491	1357	2389	1326	3220	2569	2054	1348	1105	1266	1269	1501
E12	1468	4326	1295	3330	3406	1754	2516	2452	2292	1291	2455	1139	4385	2206	1315	1163	747	1162	1178	1126
E13	1571	3435	1446	2242	2842	2056	2796	2022	2039	1445	2290	1990	3365	2011	1148	1625	1194	1387	1036	1563
E14	1833	3398	1587	1455	2508	2327	2360	2069	1960	1711	2336	1428	3026	1995	1551	1810	766	1242	968	1239
E15	1775	3557	1554	1602	2971	2353	3310	2248	2367	1410	1931	2258	3534	3068	1927	1467	865	1175	1145	1187
E16	1553	3467	2549	3017	2001	1576	1764	2396	1925	1247	1563	2204	4252	1810	1285	1210	677	819	1083	1463
E17	1773	3130	1853	1469	3043	2117	2375	2858	2583	1280	2710	1537	3307	2619	1621	1903	829	1179	1293	1308
E18	2025	3245	2129	1038	2455	1888	2681	2469	2327	1508	2596	1817	3254	2733	1640	1165	849	1031	718	1291
E19	1708	3381	2701	2212	2980	2007	2318	2023	2424	930	1958	1258	2649	3611	2488	2299	830	1288	1340	1340
E20	1591	3398	1620	2263	2662	2045	2577	2281	2338	1449	2083	1543	3611	2483	1721	1541	949	1102	1059	1373
Mean	1898	3788	2031	2253	3006	2245	2754	2487	2367	1483	2428	1796	3766	2732	1823	1690	959	1268	1206	1457

Supplementary Table S5: Mean pod yield (kg/ha) of 20 peanut cultivars grown in 20 hypothetical locations over two years under the experiment-3

Location	Groundnut Cultivar																			
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
E1	2360	1619	1733	2022	1958	1713	1955	2234	1884	1755	2006	1377	1473	1718	1664	1456	1662	1898	1601	1492
E2	1497	1423	1594	1887	1555	1375	1411	1663	1026	1598	1272	1210	1355	1604	1322	1169	1200	1414	872	1358
E3	2635	2708	2526	2576	2130	1724	2989	2863	2159	2297	2240	2302	2147	2190	1811	1465	2541	2434	1835	1952
E4	1463	1256	2195	1575	2490	2430	1695	2004	1387	1702	1243	1068	1865	1339	2117	2066	1441	1704	1179	1447
E5	3552	4837	3712	3338	3897	4690	3648	3589	2922	3983	3019	4111	3155	2837	3313	3987	3101	3051	2484	3386
E6	2833	2433	2218	2200	3384	1996	2889	3015	3982	2739	2408	2068	1885	1870	2876	1697	2455	2562	3385	2328
E7	2266	1451	1267	1710	2125	1418	1788	1808	2744	1899	1926	1233	1077	1454	1806	1205	1520	1537	2333	1614
E8	1487	1283	1792	1997	1618	1335	2099	1285	2536	1699	1264	1090	1523	1697	1376	1135	1784	1092	2155	1445
E9	1218	824	1317	844	954	747	915	936	915	1047	1036	701	1119	718	811	635	778	796	778	890
E10	1396	1281	1529	1370	1296	904	1300	1137	1421	1215	1187	1089	1300	1164	1102	768	1105	966	1207	1033
E11	1400	1299	1142	1067	1262	1194	1426	792	1478	1167	1190	1104	971	907	1073	1015	1212	673	1256	992
E12	3827	4771	3789	3748	3923	3823	3452	3579	3729	3748	3253	4056	3221	3186	3335	3250	2934	3042	3169	3186
E13	1655	1242	1724	1366	1309	1613	1443	1424	1478	1514	1407	1056	1465	1161	1113	1371	1226	1210	1257	1287
E14	2124	1428	1595	1751	1713	2811	2044	2348	2979	1787	1806	1214	1356	1488	1457	2389	1738	1996	2532	1519
E15	2285	3673	2473	1605	1767	3327	1620	1145	2439	2495	1943	3122	2102	1364	1502	2828	1377	973	2073	2121
E16	3039	3757	3135	2767	3277	2207	3356	2708	3287	2936	2583	3193	2664	2352	2785	1876	2853	2302	2794	2496
E17	2763	1934	2268	2567	2595	1738	2334	2082	2213	2256	2348	1644	1928	2182	2206	1478	1984	1770	1882	1917
E18	2883	2775	3084	2603	3651	1946	2620	2957	2556	2842	2450	2359	2621	2212	3103	1654	2227	2514	2173	2416
E19	2245	2705	2230	2282	2480	2643	3153	2724	2232	2516	1908	2299	1895	1940	2108	2246	2680	2315	1897	2139
E20	1645	2528	2249	2162	2611	2123	2850	2566	2673	2579	1398	2148	1912	1838	2219	1804	2422	2181	2272	2192
Mean	2229	2261	2178	2072	2300	2088	2249	2143	2302	2189	1894	1922	1852	1761	1955	1775	1912	1821	1957	1861

Supplementary Table S7. Ranking of genotypes using GLI, GYI, GLYI, GLI+GYI+GLYI interactions of HO-AMMI model; GEI interaction of AMMI model and field ranking under four different experiments

Genotype	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
	Experiment-1																			
GL	3	7	5	8	1	10	6	9	4	2										
GY	3	6	7	9	4	5	2	10	1	8										
GLY	9	3	4	5	2	7	6	10	1	8										
GL+GY+GLY	7	8	4	4	2	9	4	10	1	6										
Field Rank	2	7	4	8	1	10	6	9	3	5										
AMMI	6	8	5	7	1	10	3	9	4	2										
	Experiment-2																			
GL	3	7	5	8	1	10	6	9	4	2										
GY	3	6	7	9	4	5	2	10	1	8										
GLY	7	1	3	9	2	8	5	10	6	4										
GL+GY+GLY	5	1	4	8	2	9	7	10	6	3										
Field Rank	2	7	5	9	1	10	4	8	3	6										
AMMI	5	8	6	7	2	10	3	9	4	1										
	Experiment-3																			
GL	1	13	4	6	3	16	5	12	7	2	9	18	10	17	11	20	14	19	15	8
GY	4	13	10	8	5	2	3	15	1	12	11	18	16	17	14	9	7	20	6	19
GLY	7	9	2	5	12	19	10	6	1	4	17	14	8	18	16	20	15	13	3	11
GL+GY+GLY	4	11	1	5	7	17	8	12	2	3	15	19	9	16	14	20	13	18	6	10
Field Rank	2	7	4	8	1	10	5	9	3	6	12	17	15	18	11	20	14	19	13	16
AMMI	6	13	5	3	4	17	2	12	8	1	14	18	9	15	11	20	10	19	16	7
	Experiment-4																			
GL	1	13	4	6	3	16	5	12	7	2	9	18	10	17	11	20	14	19	1	13
GY	2	13	9	7	6	3	4	15	1	11	12	18	16	17	14	10	8	20	2	13
GLY	3	10	4	12	6	18	5	2	8	1	14	17	11	19	13	20	9	15	3	10
GL+GY+GLY	2	12	4	13	5	16	3	6	9	1	10	17	11	19	14	20	7	18	2	12
Field Rank	1	7	4	9	2	10	5	8	3	6	12	17	16	19	11	20	14	18	1	7
AMMI	3	13	6	4	5	17	2	11	8	1	15	18	9	14	12	20	10	19	3	13