



Evaluation and identification of stable chickpea lines for yield contributing traits from an Association Mapping Panel

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ABSTRACT

An association mapping panel consisting of 380 genotypes of chickpea was evaluated for three different years viz. 2014-15, 2015-16, 2016-17 for yield contributing parameters viz., plant height, days to flowering, days to maturity, pod number per plant, seed number, 100 seed weight and plant yield. The AMMI analysis was performed mainly on seed weight and seed number which are the two most important yield contributing traits. The genotypes contributed 93.08 per cent of the total variance while the interaction effect was comparatively low with 4.1% for the two traits. AMMI analysis selected and identified genotypes IG5986, IG5982, ILC6025 and ICCV14307 as most desirable genotypes for seed weight and genotypes IG5893, ILC6891 and IG5856 for seed number. Identifying stable genotypes would help in strategic planning for yield improvement through component trait breeding.

1. Introduction

Protein calorie malnutrition is observed in infants and young children in developing countries and includes a range of pathological conditions arising due to lack of protein and calories in the diet (Haider M & Haider S. 1984). Malnutrition affects about 170 million people especially preschool children and nursing mothers of developing countries in Asia and Africa (Iqbal A et al.2006). The economic consequences represent losses of 11 percent of gross domestic product (GDP) every year in Africa and Asia (UNICEF data 2016). Legumes are food crops with high protein content and are therefore considered as an indispensable food source to fill in the protein gap experienced globally. Among pulse crops, Chickpea is one of the ancient pulse crops first domesticated in the Middle East approximately 7450 years ago (Maiti & Wesche-Ebeling, 2001). Chickpea is one of the world's most important legume

covering a global area of 13.98 Mha with the overall production of 13.7 Mt, comes second only after dry beans in world food legume production (FAOSTAT,2014). India is the world's biggest producer, with an annual production of around 9.8 Mt, representing 67% of total world chickpea production covering an area of 9.9 Mha (FAOSTAT,2014). Chickpea offers richest and cheapest benefits for human health. The seed is high in protein (20-30%) and dietary fibre, contains approximately 40% carbohydrates and only 3-6% oil (Gil et al., 1996). Furthermore, chickpea is a good source of essential minerals such as calcium, magnesium, potassium, phosphorus, iron, zinc and manganese, and has been recognised as one of the nutritionally best composed dry legumes for human consumption (Ibrikci et al., 2003). However, existing production in India is insufficient to meet increasing demand and on average India imports an average of 186,000 tonnes (\$US 74 million) p. a. (1998-2007). In

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order to mend the breach in global demand and increase chickpea production, identifying stable and adaptive genotypes in chickpea is a necessity.

To identify stable genotypes, the knowledge of GEI (Genotype Environment Interaction) is required for which AMMI (Additive Main Effects and Multiplicative Interaction) developed by Gauch (1988) is most preferred. AMMI analysis gives powerful information on the stability of a genotype to a general environment or to a particular environment, enabling mega environment delineation. It employs biplots for comprehension and study of the data.

Seed weight and seed number are two important component traits of chickpea that are known to have highest positive influence on seed yield per plant (Monpara et al., 2014, Srivastava et al. 2016, Tiwari et al., 2016). The effect of seed size on yield and yield components is significant for most of the traits and seed weight is an important yield determinant (Kuldeep et al., (2014), Akanksha et al., 2016, Mukesh et al., 2016, Tripti et al., 2016). Positive correlation between seed size, seed yield and seed weight has also been confirmed from the study by Bicer B.T. 2009 where larger seeded chickpea produced more seed yield. Therefore, the component traits viz., seed weight and seed number were used as the basis for identifying stable genotypes in the current study.

2. Materials and methods

Plant material

380 genotypes were incorporated in the study and used as an Association Mapping Panel. This panel was developed to map the QTLs for seed size and seed number. The genotypes consisted of Landraces from WANA (West Asia and North Africa) region obtained through ICARDA, training population and released varieties (genomic population) from IARI and ICRISAT and included 367 kabuli and 13 desi types.

The materials were grown at ICAR Indian Agricultural Research Institute Research farm, New Delhi (28° 382' N, 77° 802' E) receiving more than 400 mm annual rainfall and laid out in the field in Augmented Block Design (ABD) with 30 cm spacing between the rows and 10 cm spacing between plants. Trial was undertaken and data were recorded for 3 consecutive years viz. 2014-15, 2015-16, 2016-17 in 3 replications. Standard agronomic practices for chickpea were followed in all the years.

Statistical analysis

Genstat software (v.18.1) was used to analyse the data. ANOVA was studied for seed weight and seed number for its statistical significance. Cumulative analysis for the 3 years data was conducted after testing for the error variance of homogeneity. AMMI model was used for stability analysis as suggested by Zobel et al. (1988), Gauch (1992) and Purchase (1997). AMMI analysis is preferred as it gives estimate of total G x E interaction effect of each genotype and further partitions it into interaction effects due to individual environments.

3. Results

Pooled ANOVA for seed weight and seed number across the years was performed where different years were taken as random effects and genotypes were considered as fixed effects. The result shows Genotypes (G), Environmental (E) and interaction (GEI) effects being highly significant ($P < 0.01$) for seed weight and seed number thus indicating the prominence of all the three types of effects which is merely not random or due to chance (**Table 1**). Maximum variation was accounted by genotypic effect due to seed weight and seed number, contributing 93.08% and 91.13% respectively followed by G X E effects with 4.1 % and 3.33% for the two traits. The minimum variation was accounted by the environmental influence with 0.37 % and 0.06% for both the traits respectively.

Table 1. Pooled ANOVA for seed weight and seed number across the years

Source	d.f	Seed weight		Seed number	
		MSS	Variance (%)	MSS	Variance (%)
Genotypes	379	606.3**	93.08	103.1**	91.13
Environments	2	457.4**	0.37	13.5**	0.06
Rep within Env	6	31.7**		3.31**	
G X E	758	13.4**	4.1	1.88**	3.33
Error	2274	2.6		1.02	
Total	3419	72.2		12.5	

**Highly significant at $p < 0.01$

AMMI analysis

Genotype Environment signal (GEs) was calculated (Gauch, 2013) to deduce the appropriateness of the data to AMMI analysis. GE_N was calculated by subtracting GE_N (GE noise) from GEI. For calculating GE_N, error mean sum of square and degrees of freedom (df) for GE is required. Thus the first step included calculation of GE_N by multiplying the error mean sum of square with the degrees of freedom for GE ($2.6 \times 758 = 1970.8$ for both seed weight and seed number). Further, GE_N was computed ($10132 - 1970.8 = 8162.2$ for both seed weight and seed number). The reference here was that when SS due to GE_N is almost equal to SS due to GEI obtained in ANOVA, then GEI is said to be buried in the noise and thus considered signal poor. However, in this study, SS due to GE_N were far lesser than GEI sum of squares. Thus, the interaction was almost signal rich and not buried in the noise. This pronounced the usefulness of AMMI analysis in the study.

Ascertaining high yielding and stable genotypes

To understand main effects and interactions for seed weight and seed number, AMMI biplot was constructed (fig 1&2). AMMI biplot is a plot between the mean and the IPCA1 of GEI. The elucidation from the biplot is that if main effects have IPCA score nearing to zero, it indicates

negligible interaction between the genotype and the environment and when a genotype and an environment have the same sign on the IPCA axis, it shows positive interaction; negative interaction if different. In the figure, G369 was identified as the most stable genotype for seed weight with IPC1 score nearing zero (-0.009) and having a good mean seed weight of 37.33 g/100 seeds. G59 has the highest mean seed weight (49.1 g) with good stability (IPC1 score of 0.28). G60 and G61 have high mean seed weight (48.7 and 48.7 respectively) and with IPC1 score nearing zero (0.09 and 0.25). The most unstable genotype identified was G182 (IPC1 score of 0.78) and mean seed weight of 24.8 g.

For seed number per plant, genotype with the highest mean seed number was G182 (57.67) was less stable (IPCA1 score of -0.78). The most stable genotype was G57 with IPCA1 score close to zero (0.03) and mean seed number of 38.44. Further the most unstable genotype was identified to be G301 with mean seed number of 27.11. Genotypes G80 and G140 showed good stability (score of -0.28 and -0.37) with high seed number (50.44 and 53.56 respectively).

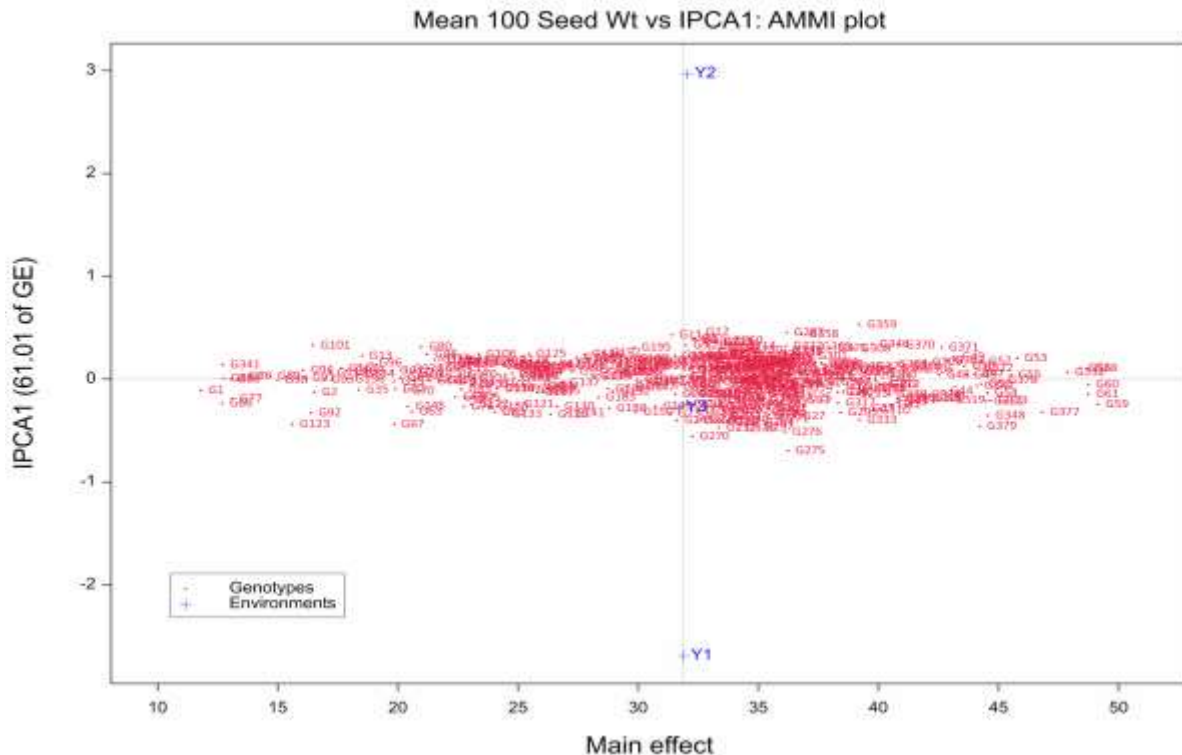


Figure 1. AMMI1 biplot for seed weight and seed number

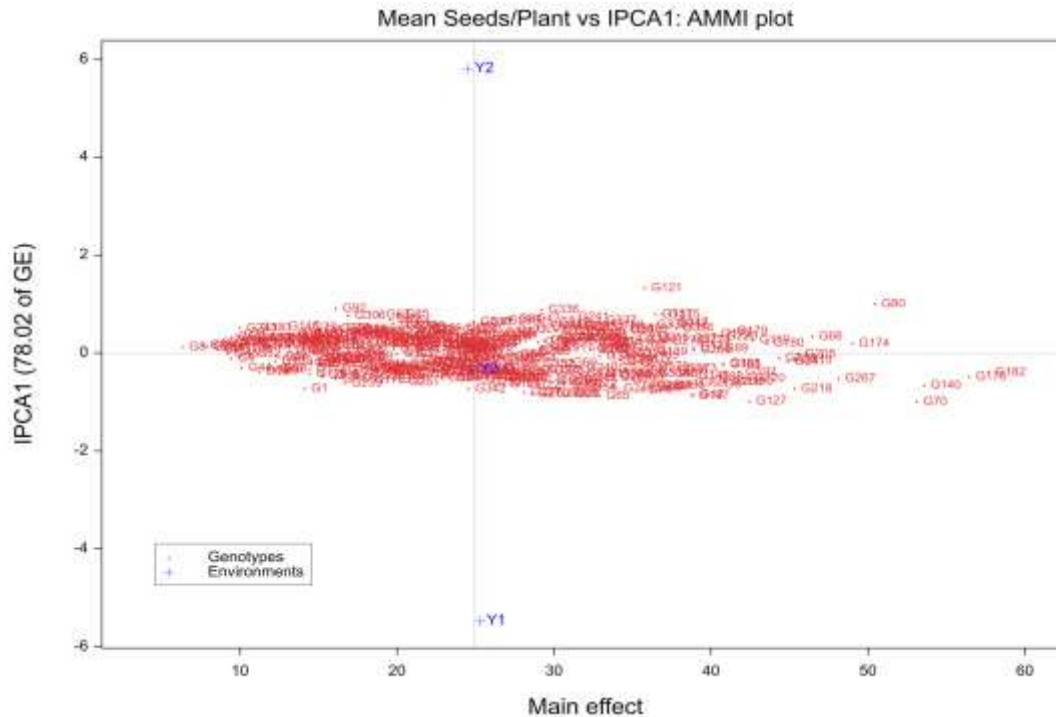


Figure 2. AMMI1 biplot for seed weight and seed number

Table 2. ANOVA for AMMI2 model for seed weight and seed number

**Highly significant at $p < 0.01$

Source	d.f	Seed weight			Seed number		
		MSS	%GE explained	% cumulative	MSS	%GE explained	% cumulative
Treatments	1139	211.5**			35.6**		
Genotypes	379	606.3**			103.1**		
Environments	2	457.4**			13.5**		
G X E	758	13.4**			1.8**		
IPCA1	380	24.4**	61.01	61.01	3.3**	78.02	78.02
IPCA2	378	2.3**	38.99	100	0.4**	21.98	100
Residual	0	0			0		
Error	2274	2.6			1.02		
Total	3419	72.2			12.5		

AMM2 biplot

This is a plot of IPCA1 vs IPCA2 and elucidates the magnitude of interaction of each of the genotype with the environment. In the biplot, for seed weight IPC1 accounted for 61.01% of the interaction and IPC2 accounted for 38.99%. Further, for seed number first component, IPC1 explained 78.02% of the genotype and environment interaction and IPC2 described 21.98%. For both the traits the first two interaction components explained 100 % of the G X E variation leaving no residue or noise (Table 2).

Scattered genotypes near the origin indicates minimum interaction of these genotypes with the environment. Distances from the origin are indicative of the amount of interaction that was exhibited by either genotypes over environments or environments over genotypes (Thangavel et al., 2011). From the biplot, G378, G34, G22, G85, G289, G312, G32 are scattered close to the origin indicating minimal interactions with the environment for seed weight (fig 3&4). Genotypes that are scattered far away from the origin viz. G275, G201, G2 shows prominent G X E interaction thus are less stable. For seed number, higher sensitivity to environment was shown by genotypes G70 and G267.

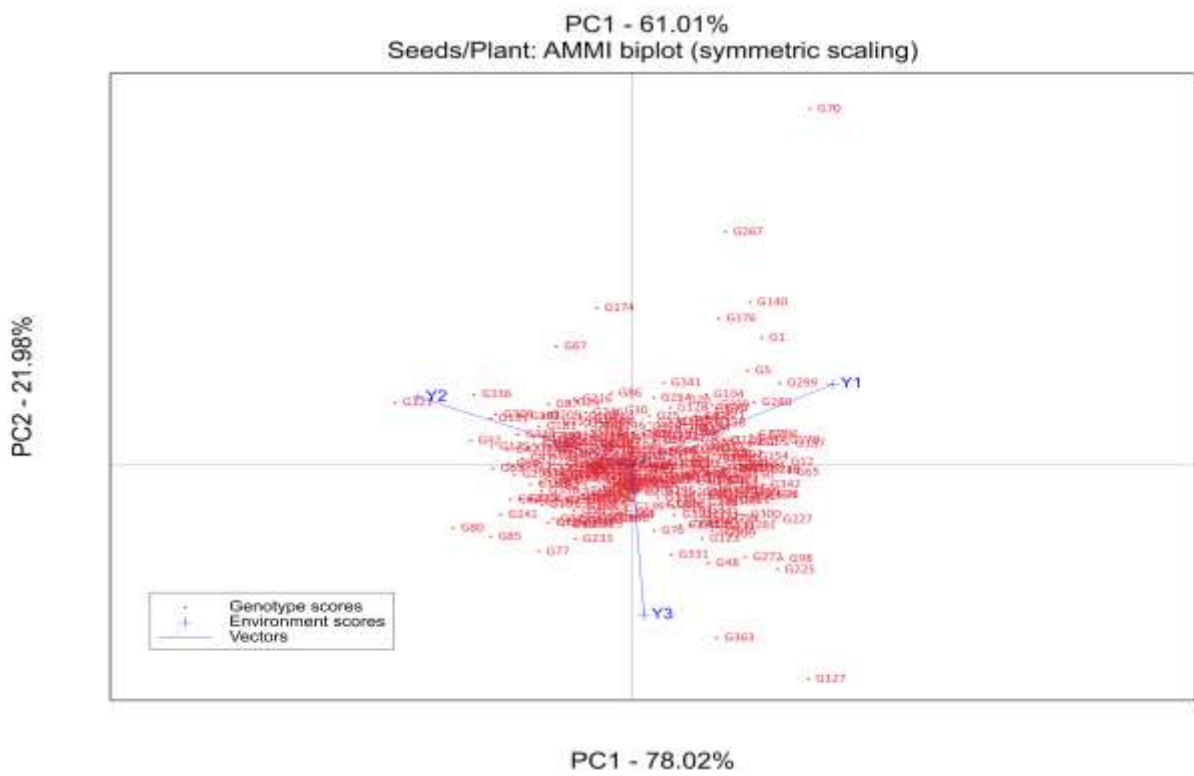
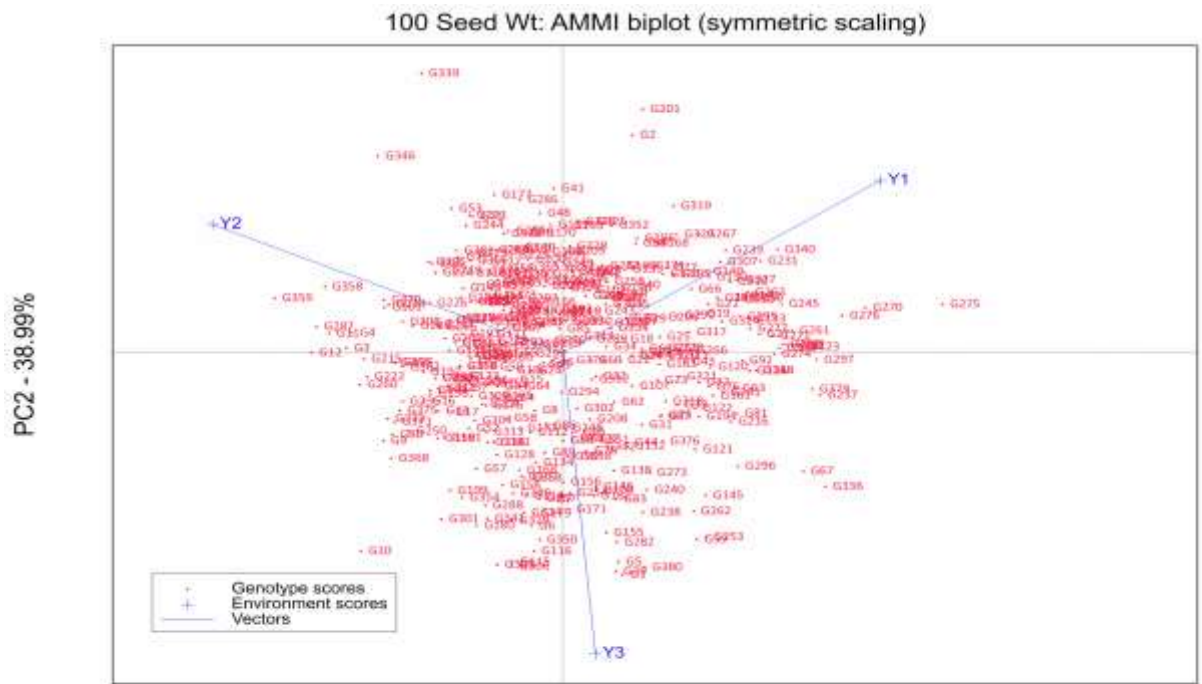


Figure 3 & 4. AMMI2 biplot of IPCA1 vs IPCA2

4. Discussion

The AMMI Analysis of variance showed that the genotype, environment and interaction effects are significant ($p < 0.01$) indicating difference in the genotypes behaviour in the environments. It justifies understanding the behaviour of the genotypes to rationalize the magnitude and extent of interaction with the environments (Gauch, 1992). Estimation of phenotypic stability in this study was thrived by the significance of GE interaction (Farshadfar and Sutka, 2006; Osiru et al., 2009). Selection for yield stability across environments defined as location year combinations would help cope with genotype-year or genotype-location year interaction effects (Annicchiarico, 1997). Many earlier reports on AMMI analysis have been made by Mukherjee et al., 2013, Akhter et al. 2014 in rice; Rad et al., 2013, in wheat, Shinde et al. (2002) and Pawar et al. (2012), Anuradha et al., 2016 in pearl millet, Sobaghpour et al 2012, Balapure et al., 2014, Kanouni et al., 2013 in chickpea. All these worker, observed significant G x E interaction for grain yield and stressed upon the usefulness of AMMI analysis for identifying and selection of promising stable genotypes for specific locations or environmental conditions. ANOVA revealed maximum variation explained by the genotypic effect similar to the studies shown by Akter et al., 2014 in rice and Anuradha et al., 2016 in pearl millet. Contradictory observation was made by Saboghpour et al., 2012, Balapure et al., 2016 and Kanouni et al., 2015 where largest contribution to total variation was by environmental effects and the genotype had little effect. The usefulness of the AMMI model is clear as they use overall fitting, impose no restrictions on the multiplicative terms and result in least square fit (Freeman, 1990). Gauch and Zobel (1996) emphasized the informativeness of AMMI1 with IPCA1 and AMMI2 with IPCA1 and IPCA2 biplots and the graphical representation of axes, either as IPCA1 or IPCA2 against main effects or IPCA1 against IPCA2. The first two IPCs, IPCA1 and IPCA2 could explain 100% of the interaction effect for seed weight and seed number per plant leaving no residue. This observation supported the findings of Gauch and Zobel which recommended that the most accurate model for AMMI can be predicted using the first two IPCAs. G369 and G57 were identified as the most stable genotypes for seed weight and seed number per plant deduced from their IPC scores from the biplot.

5. Conclusion

A genotype is best suited to a given environment when it presents high positive interactions with the specific environment making it invariably more suited to exploit the ecological and management conditions of the environment. The study of G X E interaction discerns the stability of a genotype to different environments and the above study clearly showed the convenience of AMMI model in deciphering the most stable and most unstable genotypes for different environments. It will further aide in developing environment wise adaptable genotypes depending on the extent of the genotype interaction with the environment. Less interactive genotypes for general adaptation and greater interacting genotypes for specific environments can be identified from this study.

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7. Compliance with ethical standards

Conflict of interest

The authors declared that they have no conflict of interest

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