RESEARCH ARTICLE

STABILITY ANALYSIS OF BREAD WHEAT VARIETIES FOR NITROGEN USE EFFICIENCY CONTRIBUTING TRAITS IN *TARAI* PLAINS OF UTTARAKHAND

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Abstract: The AMMI model was employed to assess the phenotypic stability of twelve bread wheat varieties over six environments under three nitrogen doses for two consecutive years i.e. 2012-13 and 2013-14 in Pantnagar. For spike length, UP 2825 was overall stable performer whereas, QLD 11 and GW 445 were found to adapt in E_1. For E_3 two genotypes i.e. DBW 97 and HD 3112 showed adaptability. In case of trait, number of spikelets per spike, no genotype was found stable but GW 445 in E_2 showed higher value for this trait and was found well adapted to this environment and QLD 33 also had higher value with adaptability to E_3.

Keywords: Stability Analysis, AMMI Model, Nitrogen Utilization Efficiency

INTRODUCTION

Nitrogen (N) is one of the most important nutrient for cereals including wheat. Identification of N efficient wheat genotypes and their stability across environments by studying G × E interaction will help to reduce the economic burden upon farmers and also will decrease the environmental pollution due to excessive N application. Ortiz-Monasterio (1994) reported at low soil N levels there is better expression of uptake while at high N levels utilization is better expressed. It has also been reported that the efficiency components are inherited in a manner favourable for wheat selection (Gorny *et al.*, 2011). Various models for stability analysis have been employed in past but AMMI has proved to show better results for prediction of stability and adaptability of test varieties. By making use of basic interpretation of AMMI1 biplot graph which illustrates that if main effects have IPCA score close to zero, there is negligible interaction effects and when a genotype and an environment have the same sign on the IPCA axis, their interaction is positive; if different, their interaction is negative. The IPCA1 versus IPCA2 biplot (AMMI2 biplot), explain the magnitude of interaction of each genotype and environment. This method is more effective as it captures larger portion of G × E sum of square separating main and interaction effects. The goal of this study was to evaluate the G × E interaction using AMMI analysis for the traits contributing to nitrogen efficiency and singling out best stable genotypes across all the six environments as well as those adapted to specific ones.

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MATERIAL AND METHOD

The study involved twelve elite wheat genotypes *viz*., DBW 97, DPW 621-50, GW 445, HD 3104, HD 3112, HD 2932, HD 2967, UP 2672, UP 2825, QLD 11, QLD 33 and QLD 39. The experiment was planned as per factorial experimental design (two years × three nitrogen doses × twelve genotypes) in which twelve treatments were randomized in three replications under three N (nitrogen) levels each for two consecutive years (*rabi*, 2012-13 and *rabi*, 2013-2014) at N. E. Borlaug Crop Research Center, Pantnagar. Nitrogen was applied at three rates, N_0: control (120kg/ha- recommended dose), N_{100}: N was applied @ 100kg/ha i.e. below recommended dose, and N_{150}: N was applied @ 150kg/ha i.e. above recommended dose. 1/3rd of N was applied at the time of sowing as basal dose, and 1/3rd each was applied at 1st and 2nd irrigation as top dressing. Therefore, we got six environments i.e. E_1 (Y_1N_0), E_2 (Y_1N_{100}), E_3 (Y_1N_{150}), E_4 (Y_2N_0), E_5 (Y_2N_{100}) and E_6 (Y_2N_{150}). Morphological traits related to nitrogen use efficiency were observed and data was collected accordingly.

RESULT AND DISCUSSION

The pooled analysis of variance based on the AMMI model and per cent contribution of each component of source of variation to the total variation for all the characters have been depicted in Table 1 and Table 2, respectively. The mean sum of squares due to genotypes, environments and G × E interaction were highly significant for most of the characters. The G × E interaction was significant for various traits and it was further partitioned into three interaction PCA (IPCA) axes but only first two significant interactions (IPCA1 and IPCA2) were taken into account for the preparation of AMMI biplot graphs.

Table 1. Pooled ANOVA using AMMI model for different characters across the environments

Source of variation	Df	SL	SN
REP(ENV)	12	0.12	2.0207
ENV	5	9.92***	12.03**
GEN	11	5.12***	11.74***
ENV:GEN	55	0.44	3.56***
IPCA1	15	0.83	4.92***
IPCA2	13	0.51	5.08***
IPCA3	11	0.29	2.90
IPCA4	9	0.15	1.88
Residuals	7	0.08	0.99
Pooled Error	132	0.34	1.65

*****, **, *** = .1%, 1% and 5% respectively; ENV- Environment; REP- Replication; GEN- Genotype; PC1- Principal component 1; PC2- Principal component 2; PC3- Principal component 3, SL: spike length, SN: number of spikelets/spike.

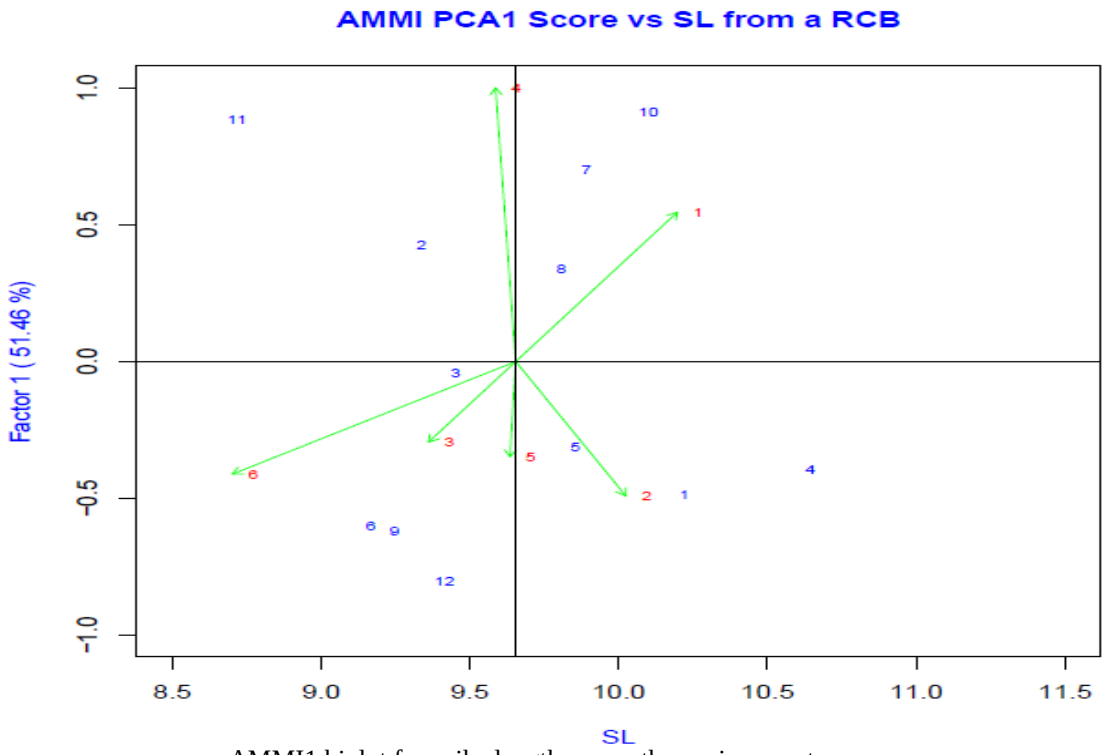
Table 2. Percent Contribution of different source of variation to the total variation

	SL	SN
ENV	28.07	9.59
GEN	31.88	20.59
ENV:GEN	13.74	31.19
IPCA1	51.46	37.71
IPCA2	27.34	33.76
IPCA1+ IPCA2	78.80	71.47

ENV- Environment; REP- Replication; GEN- Genotype; PC1- Principal component 1; PC2- Principal component 2; PC3- Principal component 3, SL: spike length, SN: number of spikelets/spike

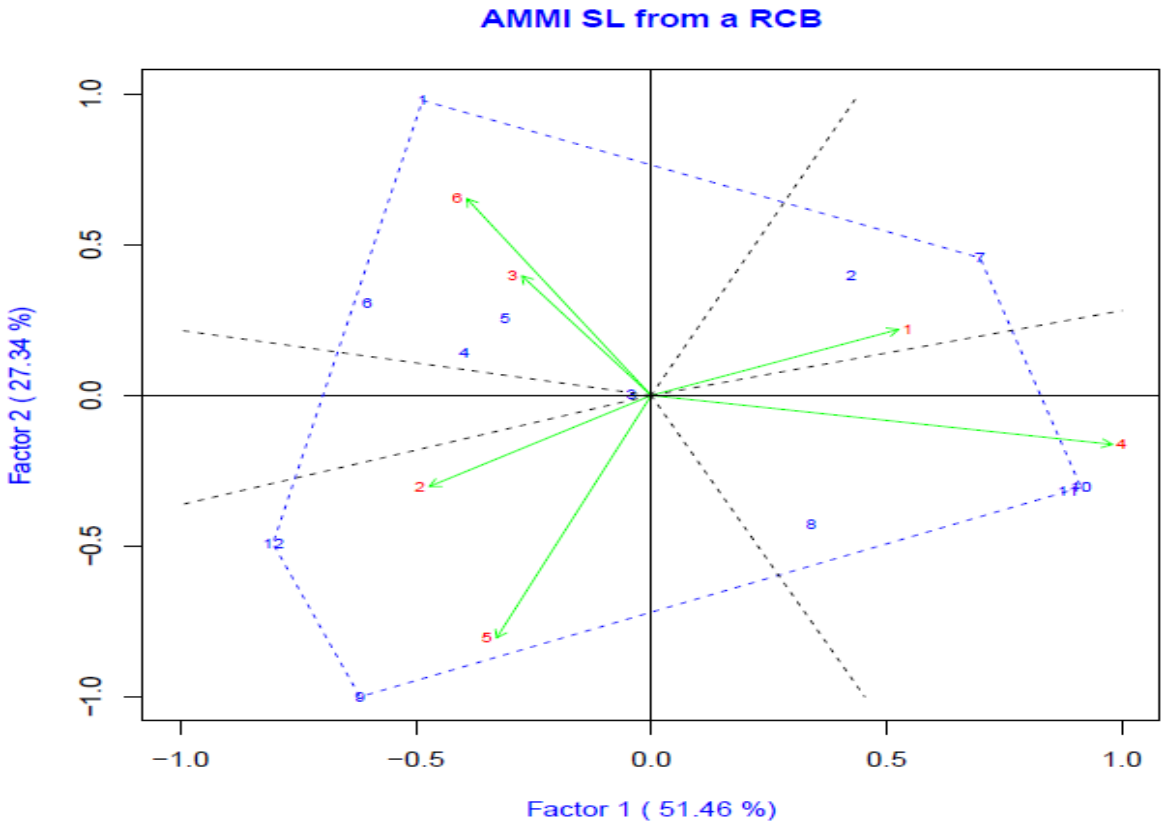
The pooled analysis of variance in AMMI model for spike length showed that environmental contribution to total variation was 28.07% while genotypic and G × E interaction effects shared 31.88% and 13.74% variation to the variation, respectively. The IPCA1 and IPCA2 of G × E interaction captured 51.46% and 27.34% of total interaction variation, respectively, and cumulative effect was 78.80% of the total interaction variation. The six genotypes on the right hand side of vertical line were having more spike length in which HD 3112 (10.65), QLD 33 (10.22) and UP 2672 (10.1) showed maximum spike length. In contrast, six genotypes were on left hand side of vertical line in which HD 2967, QLD 11, QLD 39 and HD 2932 had least value for this trait. Especially, HD 2967 (8.72) and QLD 39 (9.17) had the least value from the mean for spike length. Among the test environments, E_1 and E_2 occupied position on the right hand side of the midpoint of the main effect axis and seemed to be favorable environments in which E_1 displayed most favorable one. Regarding genotypes, UP 2825 was found most stable across all environments for spike length as it had no interaction or least affected by environmental factors. For number of spikelets per spike, pooled analysis of variance indicated that 9.59% of the total variation was due to environmental effects, 20.59% to genotypic effects and 31.19% to G × E interactions effects.

The IPCA1 of the G × E interactions effect captured 37.71% of the interaction variation while, 33.76% of the G × E interactions variation was due to IPCA2 component, cumulatively contributed to 71.47% of total interaction variation.



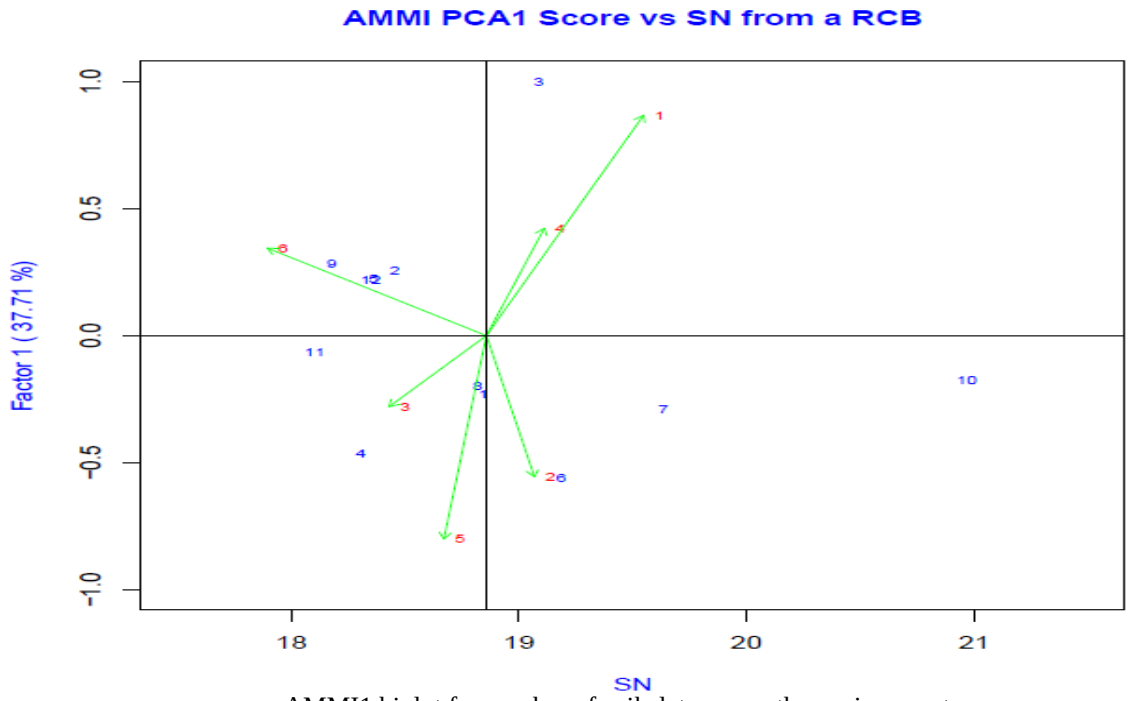
AMMI1 biplot for spike length across the environments

1 – 10: UP 2672, QLD 11, UP 2825, HD 3112, DBW 97, QLD 39, GW 445, HD 3104, HD 2932, QLD 33, HD 2967, DPW 621-50 respect; 1, 2,3,4,5,6: E_1, E_2, E_3, E_4, E_5, E_6 environments respect.



AMMI2 biplot for spike length across the environments

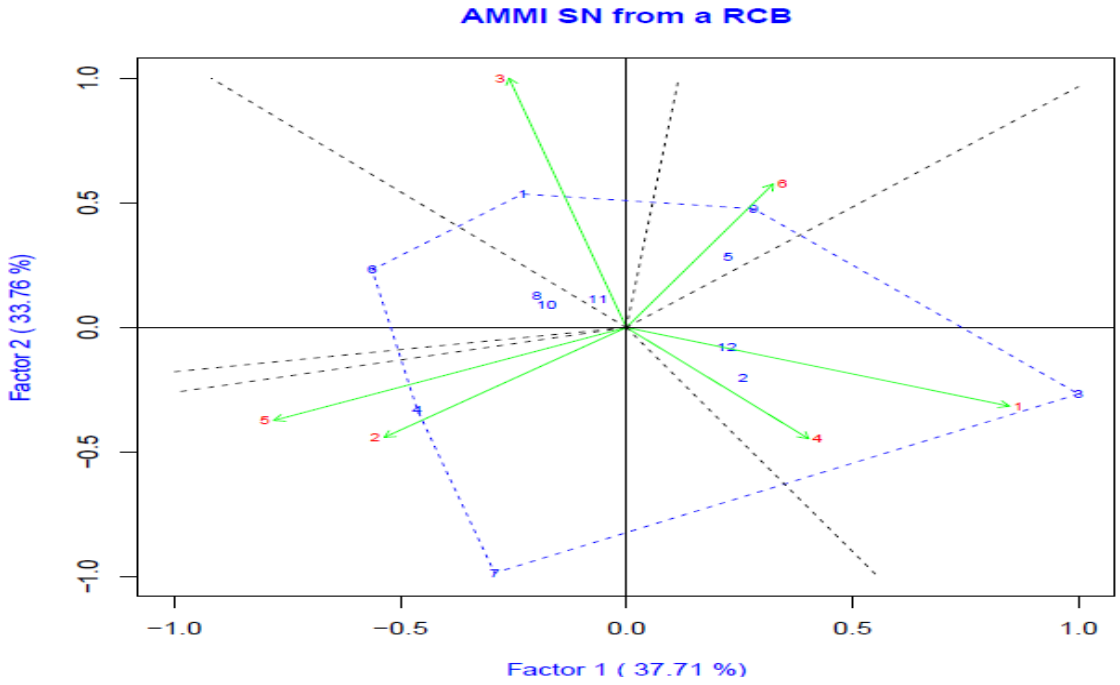
1 – 10: UP 2672, QLD 11, UP 2825, HD 3112, DBW 97, QLD 39, GW 445, HD 3104, HD 2932, QLD 33, HD 2967, DPW 621-50 respect; 1, 2,3,4,5,6: E_1, E_2, E_3, E_4, E_5, E_6 environments respect.



AMMI1 biplot for number of spikelets across the environments

1 – 10: UP 2672, QLD 11, UP 2825, HD 3112, DBW 97, QLD 39, GW 445, HD 3104, HD 2932, QLD 33, HD 2967, DPW 621-50 respect; 1, 2,3,4,5,6: E_1, E_2, E_3, E_4, E_5, E_6 environments respect.

In case of AMMI1 biplot analysis, relative variability due to genotypes was in lower magnitude than environmental effect variability as seen on AMMI1 biplot display. HD 2967 had lowest spikelet number (18.10) and with less IPCA1 score indicating more stability across the environments. The value for spikelet number in UP 2672 was closest to the mean but was having IPCA1 score quiet good therefore it was less stable across environments.



AMMI2 biplot for number of spikelets across the environments

1 – 10: UP 2672, QLD 11, UP 2825, HD 3112, DBW 97, QLD 39, GW 445, HD 3104, HD 2932, QLD 33, HD 2967, DPW 621-50 respect; 1, 2,3,4,5,6: E_1, E_2, E_3, E_4, E_5, E_6 environments respect.

In contrast, four genotypes were on right hand side of vertical line showing larger spikelet number with QLD 33 showing more value for this trait and stability across all environments. QLD 39 showed value for this trait as 19.19 but shows suitability for a particular environment. Among the test environments, E_5, E_6 and E_3 occupied left position to the vertical line and seemed unfavorable for consideration for this trait. E_4 being the most favorable environment as it gave stable genotype (Motamedi *et al*., 2013).

E_1 and E_4 had large scores on IPCA1 and lower IPCA2 score while E_2 showed almost similar scores of IPCA1 and IPCA2. E_6, E_5 and E_3 had large score on IPCA2 and lower score on IPCA1. In AMMI2 biplot, display positions of genotypes on the environmental vector showed that DBW 97 was well suited to E_6 whereas, HD 2967 was found well adapted to E_3 as it had very less IPCA1 and IPCA2 scores (Purchase and Hatting, 2000). DPW 621-50 was found adaptable to E_1 but had lesser score for IPCA2 but more IPCA1. QLD 33 was adapted to environment E_3 because of close acute angles between environment and genotypes but had lesser score for IPCA2 and more for IPCA1. HD 2932 was most desirable due to its higher spikelet number than other genotype adapted to E_6. In E_1, DPW 621-50 was found to show good response in having more value for spikelet number and classified as desirable with less interaction. Significant environmental main effect was seen for this trait. The G × E interaction effect was significantly high for number of spikes. For spike length, overall stable performer was UP 2825 whereas, QLD 11 and GW 445 were found to adapt in E_1. For E_3 two genotypes i.e. DBW 97 and HD 3112 (showed higher value for this trait) showed adaptability. For environment E_4, HD 2967 and QLD 33 and for E_6, DBW 97 and UP 2672 showed adaptability. In case of trait, number of spikelets per spike, no genotype was found stable enough but GW 445 in E_2 showed higher value for this trait and is well adapted to this environment similarly; QLD 33 also had higher value with adaptability to E_3. So, these genotypes could be considered best for such environment (Rad *et al.*, 2013 and Saleem *et al.*, 2015).

CONCLUSION

E_6 (environment under higher than recommended dose of nitrogen i.e. N_{150} for year, Y_2) showed least effect of GEI thus was quiet stable environment for the study. E_1 and E_4 (recommended dose applied during year Y_1, Y_2, respectively) showed highest GEI thus proved to be most diverse environments giving significant variability. UP 2825 was one of the best genotypes showing positive correlation of traits contributing nitrogen use efficiency. It was found to have stability for various characters such as spike length.

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