Review of Agronomy 1581330

The authors of „Estimation of genetic variances, heterotic effects, AMMI model and its components for yield stability of green super rice in multi-environmental conditions of Pakistan" presented several analyses on yield data of seven genotypes tested in eight locations and two years. The authors assumed a standard three-way additive model and a year-specific additive main effect and multiplicative interaction model to model genetic and non-genetic effects. Two of the seven genotypes are checks that refers also as baseline. Data and methods are (mostly) clearly described and the paper is well structured.

General comment

The authors had not provided a point-to-point response to my comments. The authors submitted a track-changes version that does not include all changes made. Only larger changes in text were marked. This makes it more difficult to see whether or where the authors had tried to account for my comments. My impression is, that most comments were not accounted for.

The paper listed six out of nine co-authors that were collecting data and reviewing manuscript. Collecting data is not a scientific work and thus these authors should be listed in acknowledgement. Acquiring the funding and other resources is also not a scientific contribution to the manuscript. If co-authors contributed significantly to the contest of the manuscript, they should be listed as co-authors. Please delete all authors listed for honor. You can use the acknowledgement to mention all persons helping in performing the experiments and creating the data.

Major comment

In an earlier version of the review I asked for additional information that a model assuming heterogeneous GxL variances (after accounting for year-by-location specific error variances) indeed resulted in a better model fit, e.g. in a smaller AIC. In case of a Finlay-Wilkinson regression there are just six degrees of freedom for the slope. I fear that even eight locations are not enough for the presented analysis. Note that the authors still stated that "homogeneity between error variance was processed". I have no idea what the author could had tested here.

The authors still fitted a two-way classification of environments in years and locations and a one-way classification into environments. I suggest to stick with the two years and eight locations and adjust stability measures according to this. Note that the authors performed a single-year analysis for AMMI and biplot analysis avoiding the problem above. In this case genotype and genotype-by-year effects are confounded. As the authors already have two-year data, they can (and should) avoid such confounding.

In Table 2 the authors listed nine environments. Please provide an overview of the available complete data and the reason why data were restricted to five or eight locations. I missed an explanation, why the authors now have eight locations available.

The authors claimed that "A genotype that has a constant high yield irrespective of environmental conditions is considered a "stable genotype" by most breeders." The authors had not provided a reference for this. I would argue that a stable genotype is a genotype that behaves like the average of genotypes showing high yield in high-yielding locations and low yield in low-yielding locations. The authors definition is in contrast to the formal definition used later on (Shukla´s stability, AMMI model) as both assumed small GEI, while the authors definition assumed GEI that counteracted

location effects. Please give a reference for your statement and use stability measures that accounted for your type of stability.

The authors listed a range of different stability measures that existed in literature. The authors missed correct use of lower and upper case letters here.

I wonder about the small trials with just 21 plots per trial. Have the authors tested more genotypes, but had reduced the data afterwards? Genotypes were highly selected in a previous two-year experiment. This raised the question to which population the tested one is (or should be) representative for (if it is representative at all). Note that the authors estimated a genetic variance that implies that genotypes were randomly drawn from a population of genotypes. I fear that at least the checks were not randomly drawn. Moreover, the checks may widely differ from lines and this the genetic variance does not explain the variance between lines but simply the variance between check and lines. Again, I fear that the selected seven genotypes are not representing a population and thus terms including the genetic variance are meaningless. Note that Figure 9 is unclear, as notations differ from figure to text and description is not informative, but I guess it shows that there are systematic differences between GSR lines and checks.

The three-way ANOVA model does not account for heterogeneous error variances (and potential other heterogeneity of variance components). In MET heterogeneous error variances are common.

The authors used an AMMI model including a general description of the AMMI model, but does not specify *n*. Note that the given model vary depending on *n*. Additionally, there are several font errors in the description. Here and in all other model, the authors do not clarify their assumptions on model terms (fixed random, variance-covariance structure). I suggest to fit three multiplicative interaction effects as the authors had assumed in their ANOVA analysis.

Biplot analysis based on mean performance of genotype *i* in environment *j*, but it is not specified, how the authors calculated theses means. This gets relevant in case the authors have at least one missing value in their data.

ASI and ASV where estimated per genotype, but this is not noted in equation in Material and Methods. Please clarify, which values were used in which equation.

H^2 is not defined

Table 3: What are the values presented? Please replace *** notation by simply showing the p-values.

The authors stated that they “Results revealed significant differences among the magnitude of genotypic variance and phenotypic variance.” Please specify the performed test, test statistics and which variance components were used. The authors later took ratios but have three genotype-by-environmental variances – not clear how they calculated ratios. More over, in Table 4, the authors presented Ve that was not defined in Material and Methods part. By the way, I am convinced that the authors are estimating interaction variances with environment and not as stated environmental variances.

From results section I can see that the authors performed by year analysis, but neither a model nor the fact itself is stated in M&M.

From discussion I can see that there are three years (2019-2021). I highly suggest to add all years available.

The authors claimed that “Multivariate stability models like AMMI, Shukla, Wricke's ecovalence, AMMI stability value and AMMI stability index and GGE biplots have been applied to trace the most

significant rice genotypes in terms of high mean yield and stability." What are most significant genotypes in terms of high yield and stability? Which test is performed to answer this question?

The authors concluded that "In our study, analysis of variance for the AMMI model showed that genotypes, locations, GL interaction and AMMI components 1 and 2 were significant. Thus, yield and PCs (1 and 2) contributions should be taken into account simultaneously to utilize the define effect of GL interactions and predict the genotypes more precisely." The significance of an effect within an analysis of variance does not provide more precise estimates of genotypes. To show that genotypes are estimated more precisely, the authors need some validation, e.g. some type of cross-validation.

In large parts the conclusion is a repetition of material and methods and results part (e.g. sentence 1, 3, 4). Other sentences cannot be concluded from the presented data and analysis (while I would agree with the statement in general). The section conclusion should include some concluding remarks. A summary is already given as abstract.

Minor comment

Use 2.1 × 0.9 m² or 2.1 m × 0.9 m (similar to other units)

Number till twelve should be written with letters, larger numbers with digits

Avoid a space between number and %.

Line 142 environmental variance is not a genetic component, additionally, Vp is still used twice – sorry for repeating my comments

The authors had not used index i throughout the equation and explanation. Please correct (Wricke). Furthermore, please change the order of Shukla and Wricke as the latter is used for the former.

Line 167 what are G × E interactions (add s here), as the authors have locations and years.

Line 158f the letters A and M in AMMI stands for additive main effect, thus the authors stated "The base of additive Main-effect and AMMI model" additive main effect and additive main effect and multiplicative interactions model.

All variables and non-digit indices should be printed in italics.

As the authors can see, most comments were even unchanged as their manuscript had not accounted for my comments.

There are typo errors in reference 39-