Reny Herawati <reny.herawati@unib.ac.id>

Submission Confirmation

1 pesan

Annals of Agricultural Science <em@editorialmanager.com> 5 Juli 2021 12.46
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Kepada: Reny Herawati <reny.herawati@unib.ac.id>

Dear Reny,

We have received your article "Comparative Study for Stability and Adaptability through Different Models to Developing Hight Yield Inbred Line derived from Landraces Rice Varieties" for consideration for publication in Annals of Agricultural Sciences.

Your manuscript will be given a reference number once an editor has been assigned.

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Kind regards,

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Annals of Agricultural Sciences

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Reny Herawati <reny.herawati@unib.ac.id>

A manuscript number has been assigned: AOAS-D-21-00348

1 pesan

Annals of Agricultural Science <em@editorialmanager.com> 8 Agustus 2021 20.54
Balas Ke: Annals of Agricultural Science <annals_agrsci@agr.asu.edu.eg>
Kepada: Reny Herawati <reny.herawati@unib.ac.id>

Ms. Ref. No.: AOAS-D-21-00348
Title: Comparative Study on the Stability and Adaptability of Different Models to Develop a High-Yield Inbred Line from Landrace Rice Varieties
Annals of Agricultural Sciences

Dear Reny,

Your submission "Comparative Study on the Stability and Adaptability of Different Models to Develop a High-Yield Inbred Line from Landrace Rice Varieties" has been assigned manuscript number AOAS-D-21-00348.

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Thank you for submitting your work to Annals of Agricultural Sciences.

Kind regards,

Ali Ali, Ph.D.
Editor in Chief
Annals of Agricultural Sciences

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Reny Herawati <reny.herawati@unib.ac.id>

Editor handles AOAS-D-21-00348

1 pesan

Annals of Agricultural Science <em@editorialmanager.com> 8 Agustus 2021 20.54
Balas Ke: Annals of Agricultural Science <annals_agrsci@agr.asu.edu.eg>
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Ms. Ref. No.: AOAS-D-21-00348
Title: Comparative Study on the Stability and Adaptability of Different Models to Develop a High-Yield Inbred Line from Landrace Rice Varieties
Annals of Agricultural Sciences

Dear Reny,

Your submission "Comparative Study on the Stability and Adaptability of Different Models to Develop a High-Yield Inbred Line from Landrace Rice Varieties" will be handled by Associate Editor Hany Samir Osman, Ph.D..

You may check on the progress of your paper by logging on to the Editorial Manager as an author.

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Thank you for submitting your work to this journal.

Kind regards,

Editorial Manager
Annals of Agricultural Sciences

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Reny Herawati <reny.herawati@unib.ac.id>

Your Submission

3 pesan

Annals of Agricultural Science <em@editorialmanager.com> 30 Agustus 2021 17.22
Balas Ke: Annals of Agricultural Science <annals_agrsci@agr.asu.edu.eg>
Kepada: Reny Herawati <reny.herawati@unib.ac.id>

Ms. Ref. No.: AOAS-D-21-00348
Title: Comparative Study on the Stability and Adaptability of Different Models to Develop a High-Yield Inbred Line from Landrace Rice Varieties
Annals of Agricultural Sciences

Dear Reny,

The reviewers have commented on your above paper. They indicated that it is not acceptable for publication in its present form.

However, if you feel that you can suitably address the reviewers' comments (included below), I invite you to revise and resubmit your manuscript.

Please carefully address the issues raised in the comments.

If you are submitting a revised manuscript, please also:

a) outline each change made (point by point) as raised in the reviewer comments

AND/OR

b) provide a suitable rebuttal to each reviewer comment not addressed

To submit your revision, please do the following:

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I look forward to receiving your revised manuscript.

Yours sincerely,

Ali Ali, Ph.D.
Editor in Chief
Annals of Agricultural Sciences

Reviewers' comments:

Reviewer #1: 1.The Materials and Methods is too lenghty since the most common methodolgies were use. So citing refrences is sufficient.
2. Justification of using specific non-parametric metholdology is needed, since there aare better non parametric methodolgies like Fox's stability function (Fox et al. 1990), superiority index (Lin and Binns, 1988), Huehn's stability

statistics (Huehn, 1979), and Thennarasu (1995) statistics etc are there.
3. Number of genotypes are limited.
4. Colour code of the heat map needs to be specified.
5. Ressults and discussions are too lengthy, needs a better connvergence among in writing.

Reviewer #2: In this study, the authors carried out a comparative study on the stability and adaptability of different models to develop a high-yield inbred line from landrace rice varieties. Overall, the authors have done a good job, and there are no major issues with the experimentations. However, some minor problems must be solved before further consideration.

1. Please start the abstract from background, problems, and objectives. Do not directly start it from methodology.
2. Would you please define the undefined abbreviations in the abstract?
3. Please provide relevant references for the first 8 lines of the introduction.
4. In the methodology, the authors are requested to mention the genotype sources.
5. Why were only two replications carried out?
6. In Table 4, the 3rd last column, it should be 1000.
7. Overall, the results are well presented; however, the discussion lacks recent reports.
8. There are some typing and formatting errors in the text. Please carefully proofread the entire text.
9. Would you please use the continued line numbering?
10. In table 8, define the meaning of asterisks as a footnote.
11. Figure 2-5 was not entirely explained in the results. The authors must explain the meaning of PC1 and PC2. What does their % reflect?
12. At the end of the conclusion, please add some future perspectives and explain how these genotypes can develop future varieties.

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Reny Herawati <reny.herawati@unib.ac.id> 31 Agustus 2021 07.07
Kepada: Annals of Agricultural Science <annals_agrsci@agr.asu.edu.eg>

Dear editor,

We will revise the manuscript according to the reviewer's suggestion as soon as possible

Thank you for the response

Best regards,

Reny Herawati et al

[Kutipan teks disembunyikan]

Reny Herawati <reny.herawati@unib.ac.id> 5 September 2021 21.58
Kepada: Annals of Agricultural Science <annals_agrsci@agr.asu.edu.eg>

Dear Mr. Ali Ali, Ph.D.
Editor in Chief
Annals of Agricultural Sciences,

Thank you for your e-mail dated on August 30, 2021, informing us of the editorial decision on our manuscript “Comparative Study on the Stability and Adaptability of Different Models to Develop a High-Yield Inbred Line from Landrace Rice Varieties”, AOAS-D-21-00348”.

We would like to express our appreciation to you and the anonymous reviewers for the time and effort that had been spent in processing our paper. We confirm that the paper has been appropriately revised in accordance with your comment and the comments made by the reviewers, and the revised manuscript has been uploaded to the Editorial Manager.

Once again, sincere thanks for the time and effort in further processing our revised manuscript.

Sincerely,
Reny Herawati et al

Pada tanggal Sen, 30 Agu 2021 pukul 17.22 Annals of Agricultural Science <em@editorialmanager.com> menulis:
[Kutipan teks disembunyikan]

Round 1:

Response to Reviewer 1 (Comments)

Reviewer #1:

1.The Materials and Methods is too lenghty since the most common methodolgies were use. So citing refrences is sufficient.

Rebuttal to reviewer comment:
Material and methods compiled based on guide for author of AOAS: “Provide sufficient details to allow the work to be reproduced by an independent researcher”.

2. Justification of using specific non-parametric metholdology is needed, since there aare better non parametric methodolgies like Fox's stability function (Fox et al. 1990), superiority index (Lin and Binns, 1988), Huehn's stability statistics (Huehn, 1979), and Thennarasu (1995) statistics etc are there.

According to the reviewer’s suggestion, we have revised:
“The nonparametric methods have some advantages over the parametric stability methods. These methods reduce the bias caused by outliers and no assumptions are needed about the distribution of the observed and easy to use and interpret and the additions or deletions of one or few genotypes don’t cause much variation of results (Huehn, 1990; Mortazavian and Azizi-Nia, 2014; Goksoy et al., 2019). The nonparametric approach is based on the phenotype rank in each test environment with a stable genotype. The concept of nonparametric stability, as related to phenotype rank in each environment, refers to a homeostatic G × E interaction theory. This involves the stability of a genotype in all environments (Huehn, 1990). Nassar and Huehn (1987) stated that nonparametric analyses are unbiased and need not consider the type of data distribution. Furthermore, Yue et al. (1997) found that nonparametric stability analysis serves as an alternative to the parametric approach, although it cannot explain the adaptability of the lines. However, for these reasons, the nonparametric method is usually utilized, as reported by Huehn (1990). (line number 67-80)

3. Number of genotypes are limited.

Rebuttal to reviewer comment:
Multi-environment trials play a key role in selecting the best varieties/genotypes to be used in diverse environments. We focused on superior genotypes from selection based on desirable morphological characters and high yields. It is costly if there are many genotypes to be tested in a multilocation trial.

4. Colour code of the heat map needs to be specified.

According to the reviewer’s suggestion, we have revised:
Adding information on the Fig. 1..”Data described according to the mean yield of the genotypes in five environments. High values are indicated in brown and low values in white” (line number 237-238)

The GxE heat-map described according to the mean yield of the genotypes in five environments is shown high values in brown and low values in white (Fig 1) (line numbers 249-250)

5. Ressults and discussions are too lengthy, needs a better connvergence among in writing.

Rebuttal to reviewer comment::
Our research compares 3 stability and adaptability models, namely parametric, non-parametric, and GGE biplot. Therefore, it seems quite long because it is presented in a comprehensive and in-depth manner

Response to Reviewer 1 (Comments)

Reviewer #2: In this study, the authors carried out a comparative study on the stability and adaptability of different models to develop a high-yield inbred line from landrace rice varieties. Overall, the authors have done a good job, and there are no major issues with the experimentations. However, some minor problems must be solved before further consideration.

1. Please start the abstract from background, problems, and objectives. Do not directly start it from methodology.

Rebuttal to reviewer comment:
Abstract compiled based on guide for author of AOAS : “The abstract should state briefly the purpose of the research, the principal results and major conclusions”.

According to the reviewer’s suggestion, we have revised:
The objective of this study was to estimate yield potential, adaptability, and stability of superior lines resulting from inbred landraces based on parametric and nonparametric stability tests, and a genotype main effect plus G×E interaction (GGE) biplot. (line numbers 6-8)

2. Would you please define the undefined abbreviations in the abstract?

According to the reviewer’s suggestion, we have revised:
define the undefined abbreviations of GGE “genotype main effect plus G×E interaction (GGE)” (line number 8)
Revised: define the undefined abbreviations of TOP “The genotype occurred in the top third of the ranks” (line number 15)

3. Please provide relevant references for the first 8 lines of the introduction.

According to the reviewer’s suggestion, we have revised:

Adding reference “Khairullah et al., 2021”(line number 38)

4. In the methodology, the authors are requested to mention the genotype sources.

Rebuttal to reviewer comment: the genotypes source available already (line numbers 96-99)

5. Why were only two replications carried out?

Rebuttal to reviewer comment:
Because the number of seeds obtained from the selection was very limited to be tested in several places, so only 2 replications were used in this experiment

6. In Table 4, the 3rd last column, it should be 1000.

According to the reviewer’s suggestion, we have revised:…000 should be 1000

7. Overall, the results are well presented; however, the discussion lacks recent reports.

Rebuttal to reviewer comment:
We use references from the first source who found the analytical formula so that it seems old, but the total references used are more than 50% from the journals of the last 6 years

8. There are some typing and formatting errors in the text. Please carefully proofread the entire text.

According to the reviewer’s suggestion, we have revised

9. Would you please use the continued line numbering?

According to the reviewer’s suggestion, we have revised

10. In table 8, define the meaning of asterisks as a footnote.

According to the reviewer’s suggestion, we have revised: *, **:significant at 0.05 and 0.01 (line number 350)

11. Figure 2-5 was not entirely explained in the results. The authors must explain the meaning of PC1 and PC2. What does their % reflect?

According to the reviewer’s suggestion, we have revised:

The contribution of diversity explaining the indicators used to observe the relationship between genotypes and environment trials was 100%. However, by conducting biplot analysis, which reduced all the indicators into two-side dimensions, the information that could be explained was about 88%. Two principal components (PC1 and PC2) were used to construct the GGE-biplot graph, explaining 53% and 35.1% (Fig 3, 4, and 5), It meant that biplot analysis has already represented enough information on the relationship among those two indicators. (line numbers 419-425)

12. At the end of the conclusion, please add some future perspectives and explain how these genotypes can develop future varieties.

According to the reviewer’s suggestion, we have revised:

Furthermore, this study is expected to be able to solve the problem of providing superior varieties originating from breeding programs through the developing of landraces varieties for high yield, wide adaptation, stability, and resistance to biotic and abiotic stress (line numbers 544-547)

Comparative Study on the Stability and Adaptability of Different Models to Develop a High-Yield Inbred Line from Landrace Rice Varieties

ABSTRACT

The objective of this study was to estimate yield potential, adaptability, and stability of superior lines resulting from inbred landraces based on parametric and nonparametric stability tests, and a genotype main effect plus G×E interaction (GGE) biplot. Fourteen inbred lines from Bengkulu landrace rice varieties were evaluated in five environments from January 2019 to November 2020. The experiment was conducted using a complete randomized block design with two replications. The results showed that the highest yield grouping based on the G × E heat-map, genotypes G13(BKL4-B1-268-10), G10(BKL2-B3-264-6), G7(BKL1-B3-261-3), and G5(BKL1-B1-259-1), was found in Sungai Serut. There was a strong positive correlation (r = 1.00) between the mean yield (Y_i) and YSi, S^2_{di} and Di, and W_i^2 and StabVar. Meanwhile, The genotype occurred in the top third of the ranks (TOP) had a positive correlation of 0.78, indicating a suitable stability parameter to identify high-yield genotypes. Biplot GGE analysis showed that two sectors provide a suitable environment for the genotype tested. The first sector, genotypes G7(BKL1-B3-261-3), G10(BKL2-B3-264-6), and G13(BKL4-B1-268-10), was well adapted to Sawah Dendam, Aur Gading, Desa Semarang, and Sungai Serut, and the second sector, comprising genotypes G6(BKL1-B2-260-2) and G5(BKL1-B1-259-1), was well adapted to Talang Benih. There were four consistently stable lines based on parametric and nonparametric stability analyses: G10(BKL2-B3-264-6), G7(BKL1-B3-261-3), G13(BKL4-B1-268-10), and G5(BKL1-B1-259-1). The GGE approach methods showed consistent stability, and lines G13(BKL4-B1-268-10), G10(BKL2-B3-264-6), G5(BKL1-B1-259-1), G7(BKL1-B3-261-3), and G6(BKL1-B2-260-2) had high-yield potential, wide adaptability, and stability, and are recommended for further testing as candidates for new varieties.

Comment [R1]: Reviewer2 comments:
Please start the abstract from backgrour
problems, and objectives. Do not directly
start it from methodology.

Rebuttal to reviewer comment:
Abstract compiled based on guide for author
AOAS : “The abstract should state briefly th
purpose of the research, the principal results
and major conclusions”.

Comment [R2]: Revised number 2 (suggest
by reviewer 2) : define the undefined
abbreviations of GGE

Comment [R3]: Revised number 1 (sugges
by reviewer 2): Start from objectives

Comment [R4]: Revised number 2 (suggest
by reviewer 2) : define the undefined
abbreviations of TOP

Keywords: inbred line; landraces; parametric stability; nonparametric stability; GGE biplot

1. Introduction

Rice cultivation in Indonesia is an essential part of the national economy. It is spread out at an altitude of relatively 0 to 450 m above sea level. Therefore, it is necessary to provide varieties suitable for site-specific agroecosystems. Bengkulu Province is in the southern part of Sumatra, Indonesia, where the cultivation of local rice varieties is still quite extensive, with various types contributing significantly to rice production. Local varieties (landraces) have the advantage that they are more resistant to biotic or abiotic stress, but generally have long maturity, greater height, and poor grain yield (Khairullah et al., 2021). However, efforts to enhance production can be realized through plant breeding programs. A breeding program with one cycle of recurrent selection and pedigree has been carried out since 2010 by crossing landrace varieties Sriwijaya and Bugis with drought-tolerant lines IR148 and IR7858-1 (Herawati et al., 2017), and several progeny lines have been identified on a molecular level as being resistant to drought (Herawati et al., 2021). Furthermore, this study is expected to solve the problem of providing superior varieties originating from breeding programs through the development of landrace varieties for high yield, wide adaptation, stability, and resistance to biotic and abiotic stress.

Comment [R5]: Revised number 3 (suggest
by reviewer 2)

The success of these studies depends on two factors: the accuracy of the estimated results related to the experiment and the ability to estimate the new environment (Fasahat et al., 2014). Recommendations for developing new high-yielding varieties include reliable and accurate predictions of yield (Alam et al., 2015; Ikmal et al., 2020). Multilocation experiments are important to obtain genotypes that are adapted to a specific location or tend to be stable under various environmental conditions (Gauch, 2006; Ponnuswamy et al., 2018).

Multilocation trials are important in plant breeding and other studies carried out in the field of agronomy. A combination of agronomy and plant breeding is needed to improve plant characteristics and stability testing before releasing new varieties. This information can be obtained from several experiments. A single stability analysis method may not be sufficiently representative to determine the performance of genotypes across environments because it will give different results, which sometimes lead to wrong decisions about genotype stability. Breeders generally use several methods to determine genotype adaptation and stability and to interpret genotype stability for variety release recommendations. Using several stability methods helps them make the right decision about the stability of a genotype by comparing statistical relationships between them (Shukla et al., 2015; Goksoy et al., 2019).

Parametric and nonparametric approaches are used to analyze the stability of genotypes. Several previous studies have investigated the adaptability and stability of plant genotypes (Abdipour et al., 2017; Goksoy et al., 2019; Subasi and Basalma, 2021). The nonparametric methods have some advantages over the parametric stability methods. These methods reduce the bias caused by outliers and no assumptions are needed about the distribution of the observed and easy to use and interpret and the additions or deletions of one or few genotypes don't cause much variation of results (Huehn, 1990; Mortazavian and Azizi-Nia, 2014; Goksoy et al., 2019). The nonparametric approach is based on the phenotype rank in each test environment with a stable genotype. The concept of nonparametric stability, as related to phenotype rank in each environment, refers to a homeostatic G × E interaction theory. This involves the stability of a genotype in all environments (Huehn, 1990). Nassar and Huehn (1987) stated that nonparametric analyses are unbiased and need not consider the type of data distribution. Furthermore, Yue et al. (1997) found that nonparametric stability analysis serves as an alternative to the parametric approach, although it cannot explain the adaptability of the lines. However, for these reasons, the nonparametric method is usually utilized, as reported by Huehn (1990).

Comment [R6]: Revised number 2 (suggest
by reviewer1)

The analysis of mega-environments uses GGE biplot to study the stability of a genotype (Akter et al., 2015; Balakrishnan et al., 2016; Shahriari et al., 2018). It is an interactive analysis technique consisting of the main effect of the genotype (G) and the G × E interaction (Yan and Kang, 2003). GGE is constructed using two main components, namely PC1 and PC2, derived from single value decomposition with data obtained through multilocation experiments. Biplots are multi-dimensional; however, the two dimensions PC1 and PC2 are the most common. This study aimed to obtain information on yield potential, adaptability, and stability of superior lines resulting from inbred landraces with superior varieties. These lines are recommended to be widely adapted to the environment of rainfed lowland irrigated rice and dry land as candidates for new varieties.

2. Materials and Methods

Comment [R7]: The question no.1 of review
1: The Materials and Methods is too
lenghty

Rebuttal to reviewer comment:
Material and methods compiled based on gu
for author of AOAS: Provide sufficient detai
to allow the work to be reproduced by an
independent researcher.

The experiment was conducted from January 2019 to November 2020, in five environments in Bengkulu Province, namely Aur Gading (North Bengkulu), Talang Benih (Rejang Lebong), Sawah Dendam, Sungai Serut, and Desa Semarang. Environmental characteristics are presented in Table 1. The genotypes used were 14 superior inbred lines from Bengkulu local rice varieties (Sriwijaya and Bugis) with superior drought-tolerant lines (IR7858-1 and IR148) and two checks: Inpago 12 and Rindang 2 (Table 2).

Comment [R8]: The genotype source
The question no.4 by reviewer 2

Rebuttal to reviewer comment:
the genotypes source available already

Table 1
Characteristics of 5 environments trial in Bengkulu Province

Environment	Year	Soil Type	Altitude (m)	Rainfall (mm)	Temperature (º C)		Irrigation Type
					Min	Max	
Sungai Serut (SS)	2019	Ultisol	60	101	26	36	semi technical
Desa Semarang (DS)	2019	Ultisol	50	112	26	35	semi technical
Talang Benih (TB)	2019	Andosol	300	118	24	34	Technical
Sawah Dendam (SD)	2020	Ultisol	50	277	25	35	Technical
Aur Gading (AG)	2020	Ultisol	100	215	26	36	Rainfed

Table 2
Genotype, accession number, and pedigree

No.	Genotype	Accesion number	Pedigree
1	G1	BKL3-RS1-1-253-18	Sriwijaya x IR148
2	G2	BKL4-RS1-1-256-21	Sriwijaya x IR7858-1
3	G3	BKL4-RS1-2-257-22	Sriwijaya x IR7858-1
4	G4	BKL4-RS1-3-258-23	Sriwijaya x IR7858-1
5	G5	BKL1-B1-259-1	Bugis x IR7858-1
6	G6	BKL1-B2-260-2	Bugis x IR7858-1
7	G7	BKL1-B3-261-3	Bugis x IR7858-1
8	G8	BKL2-B1-262-4	Bugis x IR148
9	G9	BKL2-B2-263-5	Bugis x IR148
10	G10	BKL2-B3-264-6	Bugis x IR148
11	G11	BKL3-B1-265-7	Sriwijaya x IR148
12	G12	BKL3-B3-267-9	Sriwijaya x IR148
13	G13	BKL4-B1-268-10	Sriwijaya x IR7858-1
14	G14	BKL4-B3-270-12	Sriwijaya x IR7858-1
15	Inpago 12	Check Variety	-
16	Rindang 2	Check Variety	-

Comment [R9]: Number of genotypes ar
limited (Question number 3 by reviewer1)

Rebuttal to reviewer comment:
Multi-environment trials play a key role in selecting the best varieties/genotypes to be used in diverse environments. We focused o
superior genotypes from selection based on desirable morphological characters and high yields.

The study was carried out using a completely randomized block design with two replications. The experimental plot was 5 m × 5 m in size. Twenty kg of manure was spread and mixed with the soil in the first fertilization. Planting was performed with a spacing of 20 cm × 20 cm, and each plot was fertilized with 400 g urea, 200 g SP-36, and 200 g KCl a week after planting,

Comment [R10]: Why two replications? (Question number 5 by reviewer2)

Rebuttal to reviewer comment:
Because the number of seeds obtained from selection was very limited to be tested in several places, so only 2 replications were us in this experiment

The variables observed were plant height, number of productive tillers, panicle length, number of filled grains/panicles, percentage of empty grains, 1000-grain weight, grain weight per hill, and grain weight per plot. Harvesting was carried out using physiological ripening criteria marked by 80% yellowish panicles in one plot. Furthermore, the grain was dried until it reached a moisture content of ±14%. The grain yield per hectare was derived from the conversion of grain weight per plot.

The yield component variables were analyzed using combined variance analysis and the least significant difference test at a 5% level, according to Steel and Torrie (1980). The estimation of yield adaptability and stability is based on the coefficient of variance (CVi) (Francis and Kannenberg, 1978) and regression (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966) as follows:

$$b_i = 1 + \frac{\sum_i (x_{ij} - \bar{x}_i - \bar{x}_j + \bar{x}_{..})(\bar{x}_j - \bar{X})}{\sum_j (\bar{x}_j - \bar{X})^2}$$

$$\boldsymbol{S^2_{di} = \frac{1}{E-2}\left[\sum_i (x_{ij} - \bar{x}_i - \bar{x}_j + \bar{X}) - (b_i - 1)^2 \sum_i (\bar{x}_j - \bar{X})^2\right],}$$

where x_{ij} is the grain yield of genotype I in environment j; $\bar{x}_i$ is the average yield of inbred line I and $\bar{x}_j$ is the average performance of the environment j, and $\bar{X}$ is the grand mean. The genotypes would be more adapted to favorable environmental conditions if $b_i > 1$. The genotypes would be adapted to unfavorable growing conditions if $b_i < 1$, and if $b_i = 1$, those genotypes would have an average adaptation to all environments. Genotypes with $S^2_{di} = 0$ would be most stable, whereas a $S^2_{di} > 0$ would indicate lower stability across all environments.

Wricke's ecovalence (W_i^2) and Shukla's stability variance (σ2) were measured as follows:

$$W_i^2 = \sum (x_{ij} - \bar{x}_i - \bar{x}_j + \bar{X})^2$$

where x_{ij} is the observed yield response, $\bar{x}_i$ and $\bar{x}_j$ correspond to the previous notations, and $\bar{X}$ is the grand mean. Genotype stability occurs when $W_i^2 = 0$. The stability parameter uses stability variance (σ_i^2), which was obtained from the following equation:

$$\sigma_i^2 = \left[\frac{P}{(p-2)(q-1)}\right] \text{x } (x_{ij} - \bar{x}_i - \bar{x}_j + \bar{x}_{..})^2 - \frac{SSGE}{(p-2)(q-1)}$$

The sum of square the genotype-environment interaction was determined as follows:

$$SSGE = \sum_i Wi = \sum_i^p \sum_i^q (x_{ij} - \bar{x}_i - \bar{x}_j + \bar{x}_{..})^2$$

Nonparametric stability parameters include Kang's yield and stability index (YS$_i$). (Kang) and Nassar and Huehn (1987) proposed four nonparametric stability statistics, $S_i^{(1)}$, $S_i^{(2)}$, $Si^{(3)}$, and $S_i^{(6)}$, which are based on yield ranks of genotypes in each environment and are estimated as follows:

$$\boldsymbol{S_i^{(1)}} = \mathbf{2}\sum_{j}^{n-1}\frac{\sum_{j'=j+1}^{n}\left|r_{ij}-r'_{ij}\right|}{[N(n-1)]} \qquad \boldsymbol{S_i^{(2)}} = \frac{\sum_{j=1}^{n}(r_{ij}-\bar{r}_i)^2}{(N-1)} \qquad \boldsymbol{S_i^{(3)}} = \frac{\sum_{j=1}^{n}(r_{ij}-\bar{r}_i)^2}{\bar{r}_i}$$

$$\boldsymbol{S_i^{(6)}} = \frac{\sum_{j=1}^{n}\left|r_{ij}-\bar{r}_i\right|}{\bar{r}_i}$$

In the above equation, $\boldsymbol{r_{ij}}$ is the rank of the i^{th} genotype in the j^{th} environment, $\boldsymbol{\bar{r}_i}$ is the mean rank across all environments for each genotype, and N is the number of environments. The genotype with the lowest value would be the most stable across environments.

Thennarasu (1995) proposed four nonparametric stability parameters based on adjusted ranks of genotypes within each test environment. The formulas to compute these statistics are shown below:

$$NP^{(1)} = \frac{1}{N}\sum_{j=1}^{n}\left|r'_{ij} - M_{di}\right| \qquad NP^{(2)} = \frac{1}{N}\left[\sum_{j=1}^{n}\frac{\left|r'_{ij}-M'_{di}\right|}{Mdi}\right]$$

$$NP^{(3)} = \frac{\sqrt{\frac{\sum(r'_{ij}-\overline{r'}_i)^2}{N}}}{\bar{r}_i} \qquad NP^{(4)} = \frac{2}{N(N-1)}\left[\sum_{j=1}^{n-1}\sum_{j=j+1}^{n}\left|r'_{ij} - r'_{ij'}\right|/\bar{r}_i\right]$$

where r'_{ij} is the rank of i^{th} genotype in the j^{th} environment based on adjusted data, $\overline{r'}_i$ is the mean ranks for adjusted data, M'_{di} the median ranks for adjusted data, while $\bar{r}_i$ and Mdi are obtained from the original data. The relationships among the stability using Spearman's rank correlation and the stability analyses were based on the main components of the GGE biplot and analyzed using PBSTAT-GE software (www.pbstat.com).

3. Results and Discussion

Comment [R11]: The question no.5 of reviewer 1: Ressults and discussions are too lengthy

Rebuttal to reviewer comment:
Our research compares 3 stability and adaptability models, namely parametric, non-parametric, and GGE biplot. Therefo it seems quite long because it is present in a comprehensive and in-depth manne

3.1. Agronomic performance of inbred lines

This study evaluated the yield performance and stability of 14 inbred lines from landrace varieties compared to two superior varieties (Inpago 12 and Rindang 2) under different irrigation types in Bengkulu, Indonesia. The combined analysis of variance indicated wide variability in the lines under testing (Table 3), which suggests that the lines interacted differentially regarding yield component performance; therefore, further general adaptability and stability analysis across lines should be followed before their selection for release as new varieties.

Table 3
Mean square of combined analysis of variance across environment of yield component of 14 inbred lines

Source of variance	Df	Panicle length	Number of Productive Tiller per hill	Filled grain per panicle	Unfilled grain per panicle (%)	1000-grain Weight (g)	Grain weight per hill (g)	Yield (tonnes/ha)

Environment (E)	4	38.21**	359.49**	18,356.66**	524.74**	50.88**	9,464.23**	324.66**
Replication/R	5	0.24	2.06	92.26	35.44**	1.30*	21.90	2.04**
Genotype (G)	15	8.92**	49.11**	839.64**	235.55**	12.24**	444.43**	31.46**
GxE	60	2.80**	13.96**	1,156.62**	74.51**	1.88**	372.63**	11.96**
Residuals	75	0.39	1.10	53.53	7.77	0.44	15.27	0.57

*, ** Significant at the 0.05 and 0.01 probability levels, respectively

Yield response is a combination of yield components, namely panicle length, number of productive tillers, number of filled grains, 1000-grain weight, and grain weight per hill (Table 4). The appearance of the agronomic characteristics showed that the panicle length of 24.85–27.04 cm was significantly different from that of Rindang 2. The number of productive tillers ranged from 9.68–15.22, which was significantly different from that of Rindang except for G1(BKL3-RS1-1-253-18), while G7(BKL1-B3-261-3) surpassed Inpago 12 check varieties. The number of filled grains per panicle and percentage of empty grains ranged from 112.99–151.57, and 14.65–25.75, respectively. The 1000-grain weight was quite low, relatively, at 26.45–28.52. In contrast, the weight of filled grains per hill ranged from 22.46 g in G1(BKL3-RS1-1-253-18) to 42.82 g I G11(BKL3-B1-265-7), as shown in Table 4.

Tabel 4

Agronomic performance of genotypes tested in different location yield trials.

Genotype	Panicle length	Number of Productive Tiller per hill	Filled grain per panicle	Unfilled grain per panicle (%)	1000-grain Weight (g)	Grain weight per hill (g)	Grain yield (tonnes/ha)
1	27.04^{a}	9.68^{gh}	120.22^{efg}	25.75^{bc}	27.01^{defg}	22.46^{i}	5.97^{h}
2	25.51^{cde}	10.17^{g}	112.99^{h}	23.46^{cd}	27.22^{cdef}	24.98^{hi}	6.07^{gh}
3	26.36^{b}	10.09^{g}	119.73^{fg}	22.38^{de}	27.86^{b}	28.53^{fg}	6.73^{fg}
4	25.97^{bc}	10.39^{fg}	118.33^{fgh}	19.11^{fg}	26.91^{defg}	31.30^{ef}	7.28^{ef}
5	24.85^{f}	13.59^{d}	129.27^{bc}	15.65^{hi}	27.35^{bcde}	38.69^{bc}	10.31^{b}
6	25.01^{ef}	13.53^{d}	126.87^{bcd}	14.94^{i}	26.45^{g}	37.25^{cd}	9.06^{c}
7	26.00^{bc}	15.63^{a}	129.49^{bc}	17.47^{gh}	26.52^{g}	41.87^{ab}	10.20^{b}
8	25.62^{cd}	13.74^{cd}	121.42^{defg}	22.45^{de}	27.63^{bc}	35.44^{cd}	8.07^{d}
9	26.04^{bc}	15.43^{ab}	123.72^{cdef}	19.81^{fg}	27.50^{bcd}	42.37^{a}	8.76^{c}
10	25.23^{def}	13.78^{cd}	126.41^{bcde}	14.65^{i}	28.52^{a}	41.50^{ab}	10.47^{ab}
11	25.90^{bc}	15.22^{ab}	115.09^{gh}	18.30^{fg}	27.18^{cdef}	42.82^{a}	8.02^{d}
12	25.83^{bc}	11.85^{e}	131.48^{b}	20.43^{ef}	26.58^{g}	34.50^{de}	6.89^{f}
13	25.93^{bc}	13.07^{d}	151.57^{a}	18.63^{fg}	26.69^{fg}	42.27^{a}	11.14^{a}
14	25.87^{bc}	11.14^{ef}	130.34^{b}	23.65^{cd}	27.01^{defg}	35.32^{cd}	7.74^{de}
pago 12	22.71^{g}	14.62^{bc}	120.36^{defg}	27.44^{b}	23.29^{h}	34.69^{de}	7.87^{de}
indang 2	26.32^{b}	9.07^{h}	116.77^{gh}	32.66^{a}	26.87^{efg}	26.25^{gh}	5.13^{i}

Comment [R12]: Revised number 6 (sugges
by reviewer 2)…000 should be 1000

LSD 5%	0.55	0.93	6.52	2.48	0.59	3.48	0.67
CV	2.43	8.34	5.87	13.24	2.46	11.16	9.29

Numbers in one column followed by the same letter show no significant difference based on the LSD test at 5%; CV = coefficient of variance

All genotypes tested in Aur Gading had a mean yield of 4.52 tons/ha, while G9(BKL2-B2-263-5) had the highest value of 6.41 tons/ha (Table 5). However, this was the lowest compared to other environments. The irrigation system relies only on rainfall, and farmers usually cultivate this grain once a year. This is encouraging because some of the genotypes tested in this environment were above the average yield of the Rindang 2, the check variety. Therefore, this line can be considered a potential line for cultivation as upland rice or under rainfed systems. It differs from the Sungai Serut and Talang Benih environments supported by a technical irrigation system, with a mean grain yield of 12.65 tons/ha and 9.82 tons/ha. The highest yield grouping comprised G13(BKL4-B1-268-10), G10(BKL2-B3-264-6), G7(BKL1-B3-261-3), and G5(BKL1-B1-259-1), and was found in the Sungai Serut.

Table 5
Means of grain yield (tonnes/ha) in 5 environments of 14 genotypes

Genotype	Grain yield (tonnes/ha)					Mean
	Aur Gading (AG)	Desa Semarang (DS)	Sawah Dendam (SD)	Sungai Serut (SS)	Talang Benih (TB)	
G1	3.18	4.76	4.58	5.57	11.52	5.92
G10	4.97	9.55	11.82	14.85	11.18	10.47
G11	3.85	5.50	6.60	17.37	6.79	8.02
G12	4.15	4.48	4.48	15.96	5.40	6.89
G13	4.57	11.38	12.22	15.24	12.29	11.14
G14	3.85	6.34	6.25	15.73	6.56	7.74
G2	3.28	4.34	4.69	8.84	9.14	6.06
G3	5.21	4.14	4.36	9.01	10.93	6.73
G4	4.39	4.32	5.09	7.51	15.10	7.28
G5	5.19	8.14	10.16	13.11	14.96	10.31
G6	4.93	5.93	7.18	13.52	13.76	9.06
G7	4.37	7.47	10.33	16.31	12.52	10.20
G8	4.55	5.93	7.26	15.21	7.39	8.07
G9	6.41	5.84	7.43	16.84	7.26	8.76
Inpago 12	5.07	7.36	7.82	12.07	7.05	7.87
Rindang 2	4.37	4.30	6.40	5.29	5.29	5.13
Mean	4.52	6.23	7.29	12.65	9.82	8.10
LSD 0.05	1.12	0.80	0.56	0.56	2.49	0.57
CV (%)	14.10	7.33	4.22	2.52	14.48	9.40

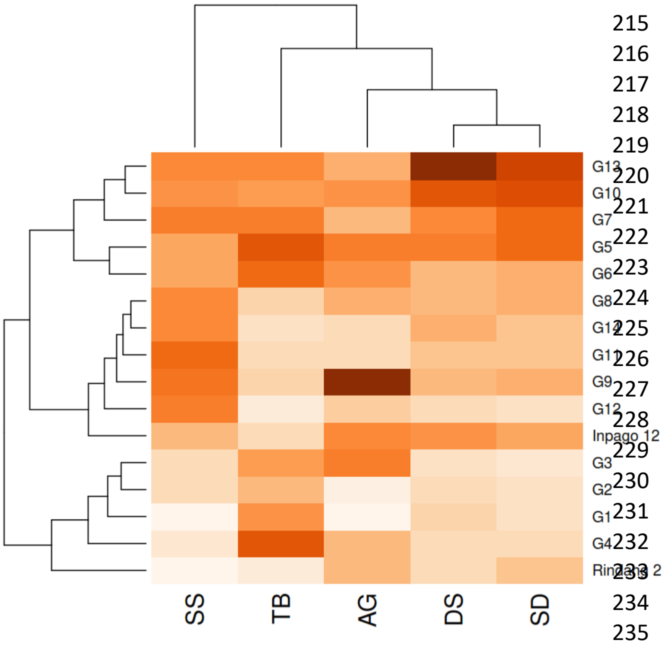

Fig 1. GxE Heat-map genotypes tested at five environments (AG = Aur Gading; DS = Desa Semarang; SD = Sawah Dendam; SS = Sungai Serut; TB = Talang Benih). Data described according to the mean yield of the genotypes in five environments. High values are indicated in brown and low values in white.

Some of the lines had a yield potential of over 5 tons/ha, and some genotypes even exceeded the check varieties, namely Inpago 12 and Rindang 2. Furthermore, G10(BKL2-B3-264-6), G13(BKL4-B1-268-10), G5(BKL1-B1-259-1), and G7(BKL1-B3-261-3) had a potential yield of more than 10 tons/ha, thereby exceeding the check varieties of 7 tons/ha and 5 tons/ha, as shown in Table 5. These lines have agronomic characteristics of new varieties, namely the number of productive tillers > 13, the number of filled grains > 126 grains / panicle, and the percentage of empty grains < 19% per panicle according to SES IRRI (2013) (Table 4).

The GxE heat-map described according to the mean yield of the genotypes in five environments is shown high values in brown and low values in white (Fig 1). The highest-yielding group was comprised of genotype G13(BKL4-B1-268-10), G10(BKL2-B3-264-6), G7(BKL1-B3-261-3), and G5(BKL1-B1-259-1), with the highest yields being found in Sungai Serut. Furthermore, the moderate-yield group contained G8(BKL2-B1-262-4), G14(BKL4-B3-270-12), G11(BKL3-B1-265-7), G9(BKL2-B2-263-5), G12(BKL3-B3-267-9), and Inpago 12 in Sungai Serut (SS). Meanwhile, the low-yield group comprised G3(BKL4-RS1-2-257-22), G2(BKL4-RS1-1-256-21), G1(BKL3-RS1-1-253-18), and G4(BKL4-RS1-3-258-23) in Talang Benih (TB). The highest grain yield of 12.65 tons/ha was discovered in Sungai Serut, followed by 9.82 tons/ha, 7.23 tons/ha, 6.23 tons/ha, and 4.52 tons/ha in TB, Sawah Dendam, Desa Semarang, and Aur Gading, respectively, as shown in Table 5.

3.2. Parametric Stability Analysis

Comment [R13]: Revised number 4 (sugge by reviewer1)… Colour code of the heat ma needs to be specified

Comment [R14]: idem

The parametric stability analysis showed that G10(BKL2-B3-264-6), G13(BKL4-B1-268-10), G5(BKL1-B1-259-1), G7(BKL1-B3-261-3), and Inpago 12 had variance coefficient (CVi) values of 34.61%, 35.49%, 37.68%, and 32.64% and environmental variance ($S_i^{(2)}$) values of 3.13, 5.48, 4.51, 1.74, respectively, as shown in Table 6. These genotypes are stable because the two values are relatively close to 0. Based on the variance coefficient and environmental variance values, they are classified as genotypes with static stability (Becker and Leon, 1988). Genotypes G10(BKL2-B3-264-6), G13(BKL4-B1-268-10), G5(BKL1-B1-259-1), and G7(BKL1-B3-261-3) had b_i values of 1.02, 1.05, 1.06, and 1.42, and grain productivity of 10.47, 11.14, 10.31, 10.2 tons/ha over the total mean, respectively, as shown in Table 4. According to Finlay and Wilkinson (1963), a genotype with a regression coefficient (b_i) of 1 and a mean yield greater than the total mean is regarded as stable, with high adaptability to all environments.

Table 6
Parametric stability analysis: coefficient of variability, environmental variability, regression coefficient and regression deviation, and stability in 14 genotypes, and 2 checks in 5 environments

Genotype	Y_i (tonHa^{-1})	CV_i	bi	P_b_i	S^2d_i	P_s^2d_i	W_i^2	D_i	StabVar (σ^2)
G1	5.97	53.89	0.51**	0.006	9.96***	0.000	40.34	8.45	22.2
G10	10.47	34.61	1.02 ns	0.899	3.11***	0.000	10.19	7.12	4.97
G11	8.02	66.73	1.51**	0.004	7.19***	0.000	32.86	7.94	17.93
G12	6.89	73.88	1.35*	0.044	9.50***	0.000	34.41	8.36	18.81
G13	11.14	35.49	1.06 ns	0.744	5.46***	0.000	17.36	7.6	9.06
G14	7.74	59.36	1.28 ns	0.106	5.65***	0.000	21.04	7.64	11.17
G2	6.07	44.88	0.79 ns	0.231	1.11***	0.004	5.93	6.69	2.53
G3	6.73	45.48	0.73 ns	0.125	4.94***	0.000	18.57	7.5	9.76
G4	7.28	62.65	0.79 ns	0.230	18.97***	0.000	59.53	9.92	33.16
G5	10.31	37.68	1.06 ns	0.707	4.50***	0.000	14.53	7.41	7.45
G6	9.06	46.92	1.24 ns	0.161	2.90***	0.000	11.95	7.08	5.97
G7	10.2	45	1.42*	0.017	0.48 ns	0.053	9.48	6.55	4.56
G8	8.06	51.51	1.20 ns	0.258	3.37***	0.000	12.52	7.18	6.3
G9	8.76	52.13	1.21 ns	0.227	7.70***	0.000	25.74	8.03	13.86
Inpago 12	7.87	32.64	0.71 ns	0.094	1.74***	0.000	9.56	6.83	4.61
Rindang 2	5.13	16.7	0.11***	0.000	0.54*	0.040	34.93	6.56	19.11

Y: overall mean of yield. LSD 0.05: 0.17; CVi: coefficient of variability (Francis and Kannenberg); b: coefficient of regression to index the environment (Finlay and Wilkinson; Eberhart and Russel). Stable (a=0.05): 0.9 - 1.1 P_bi : P-value for b with null hypothesis b=1; s^2d: deviation of regression (Eberhart and Russel); P_s^2di: P-value for s^2d with null hypothesis s=0; W_i^2 : Wricke ecovalence; Di: Hanson's parameter stability; StabVar : Shukla *stability variance* (σ^2)

Wricke (1962) developed the ecovalence method (W_i^2), which measures the contribution of each genotype to the total square of the genotype × environment interactions. A genotype is considered stable assuming it has a low ecovalence value. The analysis showed that the stable genotypes were G10(BKL2-B3-264-6), G2(BKL4-RS1-1-256-21), G7(BKL1-B3-261-3), and Inpago 12, with low ecovalence values of 10.19, 5.93, 9.48, and 9.56, respectively (Table 6).

The stability evaluation method applied by Hanson (1970) was used to investigate the total genotype in a few environments concerning D_i parameters. Stable genotypes such as G2(BKL4-RS1-1-256-21), G7(BKL1-B3-261-3), Inpago 12, and Rindang 2 had low D_i values of 6.69, 6.65, 6.83, and 6.56, respectively (Table 6).

The stability parameter designed by Shukla (1972) is based on the concept that genotypes with the smallest StabVar (σ2) are the most stable. G10(BKL2-B3-264-6) (4.97), G2(BKL4-RS1-1-256-21) (2.53), G7(BKL1-B3-261-3) (4.56), and Inpago 12 (4.61) (Table 4) were the most stable lines, while G4(BKL4-RS1-3-258-23) and G1(BKL3-RS1-1-253-18) were the most unstable. The results obtained using both methods (CVi and σ2) showed that G10(BKL2-B3-264-6) and G7(BKL1-B3-261-3) were the most stable lines.

3.3. Nonparametric stability analysis

The nonparametric stability method is based on the ratio of the genotype rank to each environment. A genotype is stable assuming it ranks the same in several environments (Kang, 1988; Nassar and Huehn, 1987; Fox et al., 1990; Huehn, 1990). The Kang yield and stability index (YS_i) combined the genotype yield and Shukla stability variance into one statistical test. Kang and Pham (1991) stated that rank-sum is another nonparametric stability statistic regarded as yield, and Shukla (1972) stability variance was used as the selection criteria. This analysis realized a score of 1 for yield and stability, thereby permitting the identification of stable genotypes. Furthermore, the genotypes with the maximum and minimum yields were both assigned to rank 1. Ranks based on yield and stability variance were attached to each genotype. The genotype with the minimum rank-sum was the most desirable one. Moreover, when a genotype has a YS_i > mean, then YSinya is selected. The genotypes with (+), namely G10(BKL2-B3-264-6), G13(BKL4-B1-268-10), G5(BKL1-B1-259-1), G6(BKL1-B2-260-2), G7(BKL1-B3-261-3), G8(BKL2-B1-262-4), and G9(BKL2-B2-263-5), were selected based on YS_i, as shown in Table 7.

The two stability methods designed by Nassar and Huehn (1987) are S1 and S2. Moreover, both methods are based on the ranking of the genotypes in the number of environments. Genotypes with slight changes in rank are more stable (Becker and Leon, 1988). The variance of S1 and S2 (Zi (1) as well as Zi (2)) is smaller than the value of Table Z (Tables Chi-sq Zi (1), Zi (2)), which implies that the genotype is stable. The sums of Zi (1) = 16.63 and Zi (2) = 8.73 are smaller than the Chi-sq Sum Zi (1) table. However, when Zi (2) = 26.29, it indicates that the stability ratings of the tested genotypes were insignificantly different. Fox et al. (1990) suggested a nonparametric superiority measure for general adaptability using graded ranks from cultivars. The ranking was carried out at each location. In addition, the number of sites where the genotypes occurred in the upper, middle, and lower third of the rankings is calculated. Those that occur mostly in the upper third are considered widely adapted cultivars. Based on Fox et al. (1990), those discovered in the top three ranked environments tested were identified as properly adapted genotypes. Following this method, G5(BKL1-B1-259-1), G10(BKL2-B3-264-6), G13(BKL4-B1-268-10), G7(BKL1-B3-261-3), and G9(BKL2-B2-263-5) were properly adapted to these environments, unlike the others, as shown in Table 7. Genotypes with small NPi (1), NPi (2), NPi (3), and NPi (4) values are considered to be more stable. Based on these values, G2(BKL4-RS1-1-256-21), G5(BKL1-B1-259-1), G11(BKL3-B1-265-7), G8(BKL2-B1-262-4), and Inpago 12 were more stable than the others, as shown in Table 7.

Table 7

The result of the analysis non-parametric stability

Genotype	YSi	Si(1)	Zi(1)	Si(2)	Zi(2)	Si(3)	Si(6)	TOP	NPi(1)	NPi(2)	NPi(3)	NPi(4)
G1	-9	6.20	0.35	27.80	0.37	5.15	1.21	0	3.40	0.26	0.39	0.51
G10	10 +	6.20	0.35	24.70	0.10	6.42	2.33	2	3.60	0.72	0.93	1.29
G11	0	5.40	0.00	25.70	0.17	10.52	1.83	1	2.80	0.28	0.49	0.59
G12	-6	7.90	2.95	41.25	3.43	7.00	1.31	0	5.10	0.43	0.50	0.68
G13	11 +	7.40	1.92	35.30	1.69	8.00	3.00	2	4.40	0.88	1.33	1.85
G14	-2	4.80	0.12	15.00	0.34	7.40	1.80	0	3.00	0.27	0.35	0.48
G2	-8	3.60	1.29	8.50	1.39	1.63	0.59	0	2.20	0.17	0.20	0.28
G3	-7	6.80	0.97	31.30	0.87	13.04	2.15	1	4.20	0.35	0.46	0.63
G4	-4	6.80	0.97	35.30	1.69	11.80	2.00	1	4.00	0.33	0.53	0.68
G5	9 +	4.60	0.22	13.30	0.54	9.36	2.55	3	2.80	0.93	0.74	1.05
G6	6 +	6.40	0.52	26.00	0.19	3.21	1.27	1	3.80	0.54	0.69	0.97
G7	8 +	5.80	0.10	22.50	0.01	8.20	2.29	2	3.60	0.90	0.87	1.18
G8	1 +	2.80	2.78	5.00	2.27	0.75	0.50	0	1.60	0.20	0.25	0.35
G9	5 +	7.20	1.57	34.80	1.58	12.90	2.97	2	4.70	0.78	0.91	1.24
Inpago 12	-1	4.80	0.12	14.50	0.39	7.73	2.22	0	2.80	0.56	0.46	0.65
Rindang 2	-10	7.20	1.57	36.70	2.05	2.67	0.96	0	4.40	0.29	0.40	0.53

YS: Kang's yield and stability index; '+': selected genotypes having YSi> mean of 8.10; Si(1), Si(2), Si(3), Si(6): Nassar and Huehn's nonparametric stability parameters; SumZi(1) : 16.63; SumZi(2) : 17.61; Chi-sqtabelZi(1), Zi(2): 8.73; Chi-sqtabelSumZi(1), SumZi(2): 26.29; TOP: Fox's TOP - Number of sites at which the genotype occurred in the top third of the ranks; NPi(1), NPi(2), NPi(3), NPi(4): Thennarasu's nonparametric stability parameters

Table 8

Spearman correlation between stability parameters

	Yi	CVi	bi	s2di	Wi2	Di	StabVar	YSi	Si(1)	Si(2)	Si(3)	Si(6)	TOP	NPi(1)	NPi(2)	NPi(3)
Yi																
CVi	0.25															
bi	0.59*	0.24														
s2di	0.14	0.76**	0.01													
Wi2	0.46	0.54*	0.40	0.76**												
Di	0.14	0.76**	0.01	1.00**	0.76**											
StabVar	0.46	0.54*	0.40	0.76**	1.00**	0.76**										
YSi	1.00**	0.25	0.59*	0.14	0.46	0.14	0.46									
Si(1)	0.10	0.11	0.19	0.38	0.57*	0.38	0.57*	0.10								
Si(2)	0.24	0.20	0.30	0.44	0.70**	0.44	0.70**	0.24	0.97**							
Si(3)	-0.22	0.20	0.01	0.42	0.25	0.42	0.25	-0.22	0.29	0.28						
Si(6)	-0.68**	-0.27	-0.36	0.12	-0.13	0.12	-0.13	-0.68**	0.27	0.15	0.73**					
TOP	0.78**	0.22	0.46	0.00	0.19	0.00	0.19	0.78**	-0.15	-0.06	-0.59*	-0.82**				
NPi(1)	0.08	0.09	0.15	0.33	0.51*	0.33	0.51*	0.08	0.98**	0.93**	0.32	0.30	-0.20			
NPi(2)	-0.72**	-0.40	-0.27	-0.15	-0.25	-0.15	-0.25	-0.72**	0.30	0.16	0.50*	0.86**	-0.81**	0.36		
NPi(3)	-0.76**	-0.19	-0.36	0.09	-0.06	0.09	-0.06	-0.76**	0.48	0.36	0.50*	0.84**	-0.88**	0.50	0.88**	
NPi(4)	-0.75**	-0.26	-0.36	0.03	-0.13	0.03	-0.13	-0.75**	0.48	0.35	0.46	0.84**	-0.83**	0.51*	0.92**	0.99**

**, **:significant at 0.05 and 0.01*

Comment [R15]: Revised number 10 (suggested by reviewer 2) : define the meaning of asterisks as a footnote

Parametric and nonparametric methods have their advantages and disadvantages; each method describes a particular way of looking at the GE interaction phenomenon. Each of these approaches complements the other for interpreting GE interactions, so it was finally determined that a clear picture of the interaction as a genotype was differentially sensitive to the environment (Dehghani et al., 2016). Correlation analysis is beneficial for breeders in interpreting the results of both methods.

3.4. Correlation of the relationship between stability parameters

The regression coefficient b_i was correlated with Y_i (0.59), and all stability parameters were tested. YS_i was negatively correlated with Si (6) (−0.68), NPi (2) (−0.72), NPi (3) (−0.76), and NPi (4) (−0.75). There was a strong and positive correlation (r = 1.00) between the mean yield (Y_i) and YS_i, S^2_{di}, and D_i, as well as W21 and Stabvar, while TOP had a positive correlation of 0.78 (Table 8).

The Spearman correlation analysis of the stability parameters indicated that Y_i, YS_i, TOP, and b_i had a positive correlation, as shown in Table 8. This is consistent with studies carried out by Becker and Leon (1988) and Mut et al. (2010), which found a correlation between Y_i and the TOP stability parameter. Selection to improve yield is expected to change grain yield stability by increasing the TOP parameter (Abdipour et al., 2017; Goksoy et al., 2019). It was directed toward the development of site-specific genotypes by optimizing environmental conditions. Genotypes tend to produce poor yields when planted in a less optimal environment and will produce high yields when planted in an optimal environment. The regression coefficient b_i was correlated with Y_i and all the tested stability parameters. YS_i was negatively correlated with $S_i^{(6)}$, NPi (2), NPi (3), and NPi (4). Similarly, there was a strong and positive correlation (r = 1.00) between the mean results and YS_i, S^2_{di}, and D_i, as well as W21 and Stabvar. Furthermore, TOP had a positive correlation of 0.78, indicating a stability parameter suitable for identifying high-yield genotypes (Mut et al., 2010; Abdipour et al., 2017).

The principal component analysis correlating the genotype with the yield and stability parameters is shown in Fig 2. Genotypes that are close to the stability parameter are considered “stable” or “good.” The results of the biplot analysis showed that G13(BKL4-B1-268-10), G10(BKL2-B3-264-6), G5(BKL1-B1-259-1), G7(BKL1-B3-261-3), and G9(BKL2-B2-263-5) had the highest stable yields based on the TOP stability parameters and were strongly correlated with YS_i and b_i (Fig 2, Table 8). This makes sense because TOP is calculated based on the number of locations where the genotypes had the highest yield rank.

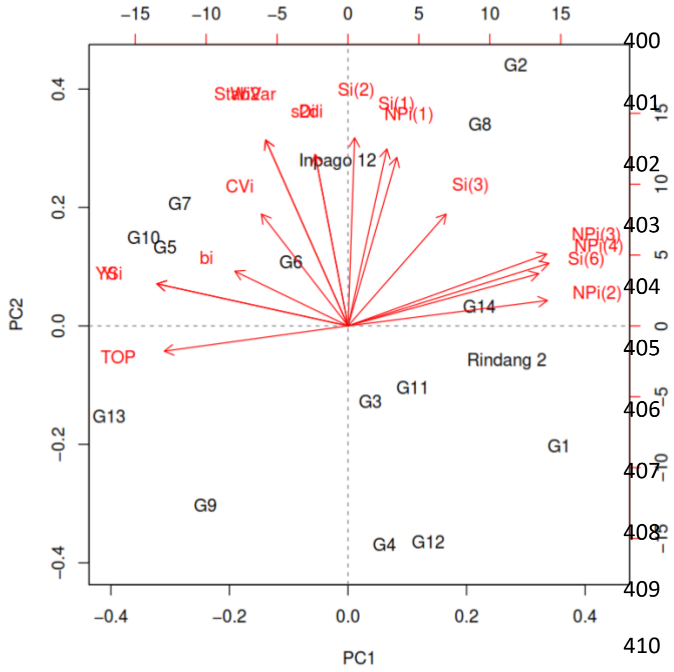

Fig 2. Mapping of stability parameters of 14 genotype base on PCA biplot

3.5. GGE biplot analysis

Biplot analysis was used to interpret the AMMI model, as indicated by AMMI1 and AMMI2. The AMMI1 biplot is a plot of the main effect (yield) and the score for the first principal component (PC1). In contrast, the AMMI2 biplot is a plot of the first (PC1) and the second (PC2) principal component scores. The results of the AMMI variance analysis showed that the interaction with the main component 1 (PC1) was significant at a probability level of less than 1% (Table 9). The effective breakdown of the genotype × environment interaction into four main components showed three essential components. The contribution of diversity explaining the indicators used to observe the relationship between genotypes and environment trials was 100%. However, by conducting biplot analysis, which reduced all the indicators into two-side dimensions, the information that could be explained was about 88%. Two principal components (PC1 and PC2) were used to construct the GGE-biplot graph, explaining 53% and 35.1% (Fig 3, 4, and 5), It meant that biplot analysis has already represented enough information on the relationship among those two indicators.

Comment [R16]: Revised number 11 (suggested by reviewer 2)

Table 9

Analysis of variance of AMMI model

Source of variance	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Environment (E)	4	1296.28	324.07	158.27	0.00
Replication/E	5	10.24	2.05	3.53	0.01
Genotype (G)	15	454.38	30.29	2.53**	0.01

GxE	60	717.73	11.96	20.61**	0.00
PC1	18	497.07	27.62	47.58**	0.00
PC2	16	117.91	7.37	12.70**	0.00
PC3	14	93.29	6.66	11.48**	0.00
PC4	12	10.17	0.85	1.46*	0.16
Residuals	73	42.37	0.58		

*, ** Significant at the 0.05 and 0.01 probability levels, respectively

GGE biplot graphs are better than the AMMI in the mega-environmental analysis for evaluating genotypes. The GGE biplot is more descriptive on G + GE and comprises the productive part of the biplot properties. GGE biplots have been used to analyze mega-environments (Kebede and Getahun, 2017; Zulqarnain et al., 2017), for genotype evaluation (Islam et al.) and evaluation of environmental trials (Tekdal and Kendal) and to analyze heterotic patterns (Kannababu et al., 2017), and their applications are becoming popular in quantitative analysis and plant breeding. The polygon visualization in the GGE biplot is practical and elegant. This method divides the environment into several groups and predicts the ideal genotype (Yan and Kang, 2003).

The analysis of discriminativeness and the representativeness of the environments produced genotype rankings relatively close to the mean. In Desa Semarang and Sawah Dendam, G13(BKL4-B1-268-10) had the highest yield, followed by G10(BKL2-B3-264-6), G5(BKL1-B1-259-1), G7(BKL1-B3-261-3), and G6(BKL1-B2-260-2), as shown in Fig 3.

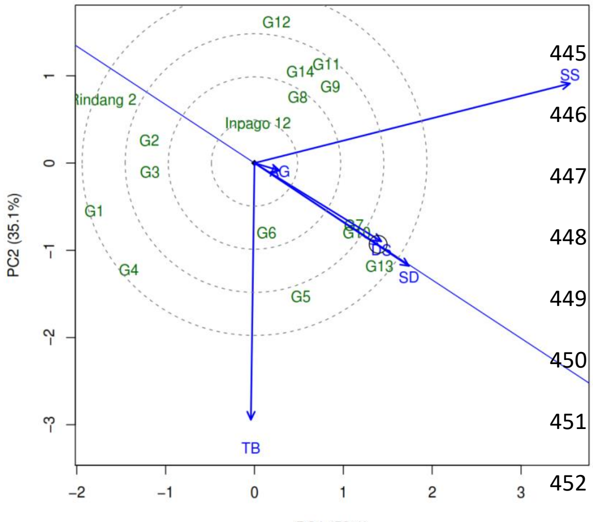

Fig 3. Biplot showing the discriminating ability and the representativeness of environments from 14 genotypes and five environment trials

These results were consistent when analyzed based on the highest mean grain yield ratings tested in the five environments (Fig 4). The genotype determined using the biplot in respect to the most extended vector was combined with G × E = 0 and represented by dots and arrows. It was a stable and high-yield genotype. Fortunately, G13(BKL4-B1-268-10), G10(BKL2-B3-264-6), and G7(BKL1-B3-261-3) were ideally stable because their projections in AEA were close to zero. However, those close to the ideal genotype were G5(BKL1-B1-259-1) and G6(BKL1-B2-260-2). The deficient yield genotypes were Rindang 2, G1(BKL3-RS1-1-253-18), G2(BKL4-RS1-1-256-21), G3(BKL4-RS1-2-257-22), and G12(BKL3-B3-267-9), because it was located far from the ideal ones.

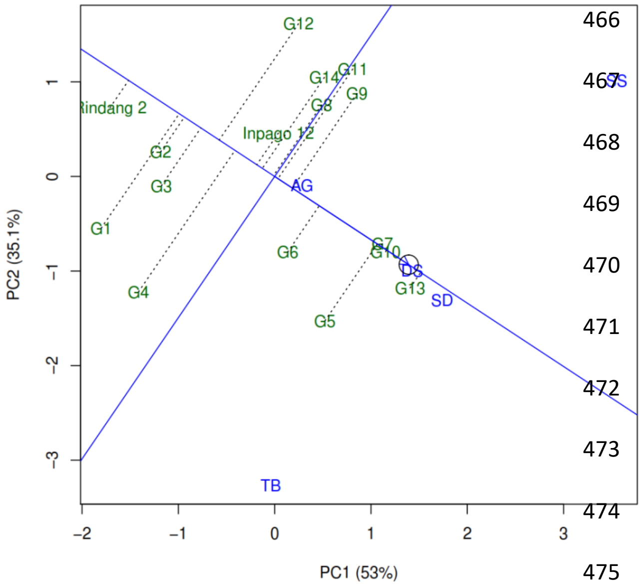

Fig 4. Mean versus stability biplot for grain yield showing the stability and performance of each genotype

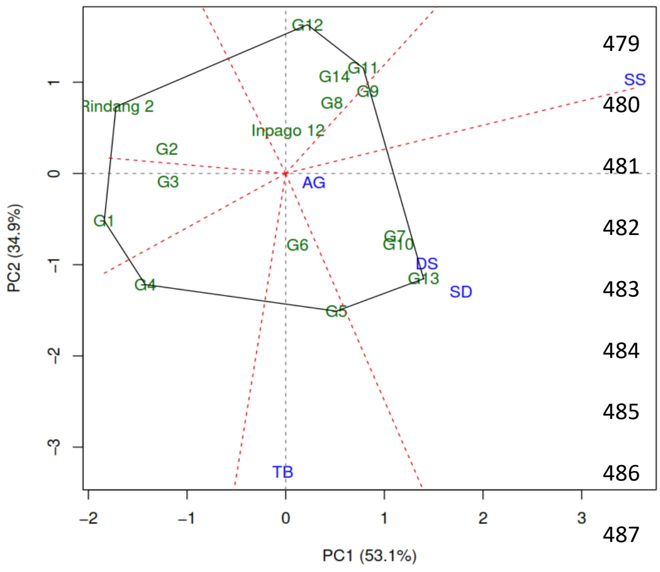

Fig 5. GGE biplot with mega-environment sectors: which won where biplot for grain yield showing identification of winning genotypes and their related mega-environments

The polygon is drawn from the position of the point farthest to the axis (0, 0), which then forms an angle. Therefore, all genotypes are present in the polygon. Subsequently, a perpendicular line is drawn from the axis (0, 0) to each side of the polygon, dividing the location into sectors, with each having a different genotype angle. Apparently, in each sector, the genotype suited at the top of the polygon was identified as the best in all the locations (Yan and Kang, 2003). Seven genotypes were located at the top of the polygon: G5(BKL1-B1-259-1), G13(BKL4-B1-268-10), G11(BKL3-B1-265-7), G12(BKL3-B3-267-9), Rindang 2, G1(BKL3-RS1-1-253-18), and G4(BKL4-RS1-3-258-23) (Fig 5). The genotypes were spread across seven sectors, but only two provided a suitable environment for the genotypes to be tested. The first sector, which comprises G7(BKL1-B3-261-3), G10(BKL2-B3-264-6), and G13(BKL4-B1-268-10), is appropriately adapted to the Sungai Serut, Aur Gading, Semarang Village, and Sawah Dendam environments. The second sector included G6(BKL1-B2-260-2) and G5(BKL1-B1-259-1), which were precisely adapted to the environment in TB.

Stability analysis using several methods can help breeders make decisions quickly and comprehensively to obtain stable superior genotypes. It can be done by comparing the results of the statistical relationship between them (Shukla et al., 2015; Goksoy et al., 2019). We compared the results of several methods to determine the yield stability of the lines (Table 10).

Table 10

A summary of the stability analysis using a parametric, nonparametric, and GGE biplot to determine the yield stability of the inbred lines

Methods	Parameters	Stability	Stability Lines
Parametric stability			
Regression	bi	b=1	**G10**, **G13, G5, G7**
	bi and S2di	b=1; S2di=0	**G10, G5, G6, G7**, G8
Variace	Wi2	Low	**G10**, G2, **G7**, Inpago 12
	σ2	Low	G10, G2, **G7**, Inpago 12
	Di	Low	G2, **G7**, Inpago 12, Rindang 2
	CVi	Low	**G10, G13, G5, G7**, Inpago 12
Nonparametric stability			
	Ysi	YSi> mean	**G10, G13, G5, G6**, **G7**, G8, G9
	Si(3), Si(6)	Zi< Chi-sq-table	all genotipe
	Si(1), Si(2)	Zi< Chi-sq-table	all genotipe
	NPi(1), NPi(2), NPi(3), NPi(4)	Low	G2, **G5**, G8, G11, Inpago 12
	TOP	The top third of the ranks	**G13, G10, G5, G7**, G9
GGE biplot			
	discrimitiveness vs. representativeness		**G13, G10, G5, G7, G6**
	mean vs. stability		**G13, G10, G5, G7, G6**
	which−won−where		**G13, G10, G5, G7, G6**

Bold letters indicated the stable genotype frequency of each parameter

Based on parametric stability analysis as well as the results of nonparametric analysis, the genotypes that had high frequency were G10 (BKL2-B3-264-6), G7 (BKL1-B3-261-3), G13 (BKL4-B1-268-10), and G5 (BKL1-B1-259-1); meanwhile, the biplot GGE analysis showed that there was an additional stable genotype, G6(BKL1-B2-260-2) (Table 10). Overall, the results of this study indicated that there were four consistently stable lines based on parametric and nonparametric stability analyses: G10(BKL2-B3-264-6), G7(BKL1-B3-261-3), G13(BKL4-B1-268-10), and G5(BKL1-B1-259-1). The GGE approach methods showed consistent stability, with lines G13(BKL4-B1-268-10), G10(BKL2-B3-264-6), G5(BKL1-B1-259-1), G7(BKL1-B3-261-3), and G6(BKL1-B2-260-2) showing high-yield potential, wide adaptation, and stability, and these should be tested more widely as candidates for new varieties.

4. Conclusion

Landrace varieties are a source of germplasm that can be developed into new superior varieties that are resistant to biotic or abiotic stress through plant breeding programs. Multilocation trials are essential in plant breeding as well as in other studies carried out in the field of agronomy. A combination of agronomy and plant breeding is needed to improve plant characteristics and stability tests before releasing new varieties. A single stability analysis method may not be sufficiently representative to determine the stability performance of genotypes across environments. In this study, we evaluated 14 inbred lines in five environmental trials. Stability analysis uses a parametric approach, nonparametric approach, and GGE biplot. This study indicated that there were four consistently stable lines based on parametric and nonparametric stability analyses: G10(BKL2-B3-264-6), G7(BKL1-B3-261-3), G13(BKL4-B1-268-10), and G5(BKL1-B1-259-1). The GGE approach methods showed consistent stability, and lines G13(BKL4-B1-268-10), G10(BKL2-B3-264-6), G5(BKL1-B1-259-1), G7(BKL1-B3-261-3), and G6(BKL1-B2-260-2) showed high-yield potential, wide adaptation, and stability, and are recommended to be tested more widely as candidates for new varieties. Genotypes G7(BKL1-B3-261-3), G10(BKL2-B3-264-6), and G13(BKL4-B1-268-10) were more adapted to the Sungai Serut, Aur Gading, Semarang Village, and Sawah Dendam environments, while G6(BKL1-B2-260-2), and G5(BKL1-B1-259-1) were properly adapted to the environment in Talang Benih. Furthermore, this study is expected to be able to solve the problem of providing superior varieties originating from breeding programs through the developing of landraces varieties for high yield, wide adaptation, stability, and resistance to biotic and abiotic stress.

Comment [R17]: Revised number 12 (suggested by reviewer 2)

Declaration of Competing Interest

All authors declare that they have no conflict of interest

Acknowledgments

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CRediT authorship contribution statement

Reny Herawati: Suggested the main idea of research, experimental design, data analysis, writing the original draf and editing paper. Angelita Puji Lestari, Nurmegawati: investigation and supervising the research work in the the field, reviewing and editing of the paper. Dwi Wahyuni Ganefianti: data interpretation, reviewing, and editing of draft paper. Atra Romeida: project administration, reviewing and editing of the paper.

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Reny Herawati <reny.herawati@unib.ac.id>

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Kepada: Reny Herawati <reny.herawati@unib.ac.id>

Ms. Ref. No.: AOAS-D-21-00348R1
Title: Comparative Study on the Stability and Adaptability of Different Models to Develop a High-Yield Inbred Line from Landrace Rice Varieties
Annals of Agricultural Sciences

Dear Reny,

The reviewers have commented on your above paper. They indicated that it is not acceptable for publication in its present form.

However, if you feel that you can suitably address the reviewers' comments (included below), I invite you to revise and resubmit your manuscript.

Please carefully address the issues raised in the comments.

If you are submitting a revised manuscript, please also:

a) outline each change made (point by point) as raised in the reviewer comments

AND/OR

b) provide a suitable rebuttal to each reviewer comment not addressed

To submit your revision, please do the following:

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I look forward to receiving your revised manuscript.

Yours sincerely,

Ali Ali, Ph.D.
Editor in Chief
Annals of Agricultural Sciences

Reviewers' comments:

Reviewer #2: The authors have addressed most of the comments. However, minor points must be addressed before publication.

1. The authors should carefully check the journal publication records and listen to the reviewer's comments. A

background and problem statements should be added at the start of the abstract. This is the standard style for any publication, and one cannot directly start it from objectives. Before objectives, it is crucial to justify the importance of the study. Would you please incorporate this suggestion in the abstract?
2. It is highly recommended that at least 3-6 replications must be carried for any project. The authors should take of this fact in the future.

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Reny Herawati <reny.herawati@unib.ac.id> 28 November 2021 13.18
Kepada: Annals of Agricultural Science <support@elsevier.com>

Dear Ali Ali, Ph.D.
Editor in Chief
Annals of Agricultural Sciences,

Thank you for your e-mail dated on November 28, 2021, informing us of the editorial decision on our manuscript “Comparative Study on the Stability and Adaptability of Different Models to Develop a High-Yield Inbred Line from Landrace Rice Varieties”, AOAS-D-21-00348R1”.

We would like to express our appreciation to you and anonymous reviewer#2 for the time and effort that had been spent in processing our paper. We confirm that the paper has been appropriately revised in accordance with your comment and the comments made by reviewer#2 (for minor points must be addressed before publication), and the revised manuscript has been uploaded to the Editorial Manager.

Once again, sincere thanks for the time and effort in further processing our revised manuscript.

Sincerely,
Reny Herawati et al

[Kutipan teks disembunyikan]

Round 2:

Response to Reviewer 2 (Comments)

Reviewer #2:
1. The authors should carefully check the journal publication records and listen to the reviewer's comments. A background and problem statements should be added at the start of the abstract. This is the standard style for any publication, and one cannot directly start it from objectives. Before objectives, it is crucial to justify the importance of the study. Would you please incorporate this suggestion in the abstract?
2. It is highly recommended that at least 3-6 replications must be carried for any project. The authors should take of this fact in the future.

Replies to Reviewer #2

Comment 1: First of all, we deeply appreciate your helpful comments. We have added sentences a background and problem statements in the **abstract**. This was stated on the **Abstract** sections highlighted with red color. In addition, we have added the statements on page 1, lines 6-10.

A B S T R A C T

Multilocation trials are important in plant breeding carried out in the field of agronomy. A combination of agronomy and plant breeding is needed to improve plant characteristics and stability testing before releasing new varieties. A single stability analysis method may not be sufficiently representative to determine the performance of genotypes across environments, which sometimes lead to wrong decisions about genotype stability. The objective of this study was to estimate yield potential, adaptability, and stability of superior lines resulting from inbred landraces based on parametric and nonparametric, and a genotype main effect G×E interaction (GGE) biplot. Fourteen inbred lines from Bengkulu landrace rice varieties were evaluated in five environments from January 2019 to November 2020. The experiment was conducted using a complete randomized block design with two replications. The results showed that the highest yield grouping based on the G×E heat-map, genotypes G13(BKL4-B1-268-10), G10(BKL2-B3-264-6), G7(BKL1-B3-261-3), and G5(BKL1-B1-259-1), was found in Sungai Serut. There was a strong positive correlation (r=1.00) between the mean yield (Y_i) and YSi, S^2_{di} and Di, and W_i^2 and StabVar. Meanwhile, The genotype occurred in the top third of the ranks (TOP) had a positive correlation of 0.78, indicating a suitable stability parameter to identify high-yield genotypes. There were four consistently stable lines based on parametric and nonparametric stability analyses: G10(BKL2-B3-264-6), G7(BKL1-B3-261-3), G13(BKL4-B1-268-10), and G5(BKL1-B1-259-1). The GGE approach methods showed consistent stability, and lines G13(BKL4-B1-268-10), G10(BKL2-B3-264-6), G5(BKL1-B1-259-1), G7(BKL1-B3-261-3), and G6(BKL1-B2-260-2) had high-yield potential, wide adaptability, and stability, and are recommended for further testing as candidates for new varieties.

Comment 2: Thank you for your valuable comment. As the reviewer suggested, we have revised and added sentences in the **conclusion** as highly recommended in the widely trials. This was stated on the **conclusion** sections highlighted with red color. Those was stated on page 18, lines 540-542.

Conclusion

Landrace varieties are a source of germplasm that can be developed into new superior varieties that are resistant to biotic or abiotic stress through plant breeding programs. Multilocation trials are essential in plant breeding as well as in other studies carried out in the field of agronomy. A combination of agronomy and plant breeding is needed to improve plant characteristics and stability tests before releasing new varieties. A single stability analysis method may not be sufficiently representative to determine the stability performance of genotypes across environments. In this study, we evaluated 14 inbred lines in five environmental trials. Stability analysis uses a parametric approach, nonparametric approach, and GGE biplot. This study indicated that there were four consistently stable lines based on parametric and nonparametric stability analyses: G10(BKL2-B3-264-6), G7(BKL1-B3-261-3), G13(BKL4-B1-268-10), and G5(BKL1-B1-259-1). The GGE approach methods showed consistent stability, and lines G13(BKL4-B1-268-10), G10(BKL2-B3-264-6), G5(BKL1-B1-259-1), G7(BKL1-B3-261-3), and G6(BKL1-B2-260-2) showed high-yield potential, wide adaptation, and stability, and it is recommended to be tested more widely at least 3-6 replications must be carried out for each trial in order to obtain a representative as a candidate for new varieties. Genotypes G7(BKL1-B3-261-3), G10(BKL2-B3-264-6), and G13(BKL4-B1-268-10) were more adapted to the Sungai Serut, Aur Gading, Semarang Village, and Sawah Dendam environments, while G6(BKL1-B2-260-2), and G5(BKL1-B1-259-1) were properly adapted to the environment in Talang Benih. Furthermore, this study is expected to be able to solve the problem of providing superior varieties originating from breeding programs through the developing of landraces varieties for high yield, wide adaptation, stability, and resistance to biotic and abiotic stress.

Comparative Study on the Stability and Adaptability of Different Models to Develop a High-Yield Inbred Line from Landrace Rice Varieties

A B S T R A C T

Multilocation trials are important in plant breeding carried out in the field of agronomy. A combination of agronomy and plant breeding is needed to improve plant characteristics and stability testing before releasing new varieties. A single stability analysis method may not be sufficiently representative to determine the performance of genotypes across environments, which sometimes lead to wrong decisions about genotype stability. The objective of this study was to estimate yield potential, adaptability, and stability of superior lines resulting from inbred landraces based on parametric and nonparametric, and a genotype main effect G×E interaction (GGE) biplot. Fourteen inbred lines from Bengkulu landrace rice varieties were evaluated in five environments from January 2019 to November 2020. The experiment was conducted using a complete randomized block design with two replications. The results showed that the highest yield grouping based on the G×E heat-map, genotypes G13(BKL4-B1-268-10), G10(BKL2-B3-264-6), G7(BKL1-B3-261-3), and G5(BKL1-B1-259-1), was found in Sungai Serut. There was a strong positive correlation (r=1.00) between the mean yield (Y_i) and YSi, S^2_{di} and Di, and W_i^2 and StabVar. Meanwhile, The genotype occurred in the top third of the ranks (TOP) had a positive correlation of 0.78, indicating a suitable stability parameter to identify high-yield genotypes. There were four consistently stable lines based on parametric and nonparametric stability analyses: G10(BKL2-B3-264-6), G7(BKL1-B3-261-3), G13(BKL4-B1-268-10), and G5(BKL1-B1-259-1). The GGE approach methods showed consistent stability, and lines G13(BKL4-B1-268-10), G10(BKL2-B3-264-6), G5(BKL1-B1-259-1), G7(BKL1-B3-261-3), and G6(BKL1-B2-260-2) had high-yield potential, wide adaptability, and stability, and are recommended for further testing as candidates for new varieties.

Comment [R1]: Revised comment 1; We ha added sentences a background and problem statements in the abstract.

Keywords: inbred line; landraces; parametric stability; nonparametric stability; GGE biplot

1. Introduction

Rice cultivation in Indonesia is an essential part of the national economy. It is spread out at an altitude of relatively 0 to 450 m above sea level. Therefore, it is necessary to provide varieties suitable for site-specific agroecosystems. Bengkulu Province is in the southern part of Sumatra, Indonesia, where the cultivation of local rice varieties is still quite extensive, with various types contributing significantly to rice production. Local varieties (landraces) have the advantage that they are more resistant to biotic or abiotic stress, but generally have long maturity, greater height, and poor grain yield (Khairullah et al., 2021). However, efforts to enhance production can be realized through plant breeding programs. A breeding program with one cycle of recurrent selection and pedigree has been carried out since 2010 by crossing landrace varieties Sriwijaya and Bugis with drought-tolerant lines IR148 and IR7858-1 (Herawati et al., 2017), and several progeny lines have been identified on a molecular level as being resistant to drought (Herawati et al., 2021). Furthermore, this study is expected to solve the problem of providing superior varieties originating from breeding programs through the development of landrace varieties for high yield, wide adaptation, stability, and resistance to biotic and abiotic stress.

The success of these studies depends on two factors: the accuracy of the estimated results related to the experiment and the ability to estimate the new environment (Fasahat et al., 2014). Recommendations for developing new high-yielding varieties include reliable and accurate predictions of yield (Alam et al., 2015; Ikmal et al., 2020). Multilocation experiments are important to obtain genotypes that are adapted to a specific location or tend to be stable under various environmental conditions (Gauch, 2006; Ponnuswamy et al., 2018).

Multilocation trials are important in plant breeding and other studies carried out in the field of agronomy. A combination of agronomy and plant breeding is needed to improve plant characteristics and stability testing before releasing new varieties. This information can be obtained from several experiments. A single stability analysis method may not be sufficiently representative to determine the performance of genotypes across environments because it will give different results, which sometimes lead to wrong decisions about genotype stability. Breeders generally use several methods to determine genotype adaptation and stability and to interpret genotype stability for variety release recommendations. Using several stability methods helps them make the right decision about the stability of a genotype by comparing statistical relationships between them (Shukla et al., 2015; Goksoy et al., 2019).

Parametric and nonparametric approaches are used to analyze the stability of genotypes. Several previous studies have investigated the adaptability and stability of plant genotypes (Abdipour et al., 2017; Goksoy et al., 2019; Subasi and Basalma, 2021). The nonparametric methods have some advantages over the parametric stability methods. These methods reduce the bias caused by outliers and no assumptions are needed about the distribution of the observed and easy to use and interpret and the additions or deletions of one or few genotypes don’t cause much variation of results (Huehn, 1990; Mortazavian and Azizi-Nia, 2014; Goksoy et al., 2019). The nonparametric approach is based on the phenotype rank in each test environment with a stable genotype. The concept of nonparametric stability, as related to phenotype rank in each environment, refers to a homeostatic G × E interaction theory. This involves the stability of a genotype in all environments (Huehn, 1990). Nassar and Huehn (1987) stated that nonparametric analyses are unbiased and need not consider the type of data distribution. Furthermore, Yue et al. (1997) found that nonparametric stability analysis serves as an alternative to the parametric approach, although it cannot explain the adaptability of the lines. However, for these reasons, the nonparametric method is usually utilized, as reported by Huehn (1990).

The analysis of mega-environments uses GGE biplot to study the stability of a genotype (Akter et al., 2015; Balakrishnan et al., 2016; Shahriari et al., 2018). It is an interactive analysis technique consisting of the main effect of the genotype (G) and the G × E interaction (Yan and Kang, 2003). GGE is constructed using two main components, namely PC1 and PC2, derived from single value decomposition with data obtained through multilocation experiments. Biplots are multi-dimensional; however, the two dimensions PC1 and PC2 are the most common. This study aimed to obtain information on yield potential, adaptability, and stability of superior lines resulting from inbred landraces with superior varieties. These lines are recommended to be widely adapted to the environment of rainfed lowland irrigated rice and dry land as candidates for new varieties.

2. Materials and Methods

The experiment was conducted from January 2019 to November 2020, in five environments in Bengkulu Province, namely Aur Gading (North Bengkulu), Talang Benih (Rejang Lebong), Sawah Dendam, Sungai Serut, and Desa Semarang. Environmental characteristics are presented in Table 1. The genotypes used were 14 superior inbred lines from Bengkulu local rice varieties (Sriwijaya and Bugis) with superior drought-tolerant lines (IR7858-1 and IR148) and two checks: Inpago 12 and Rindang 2 (Table 2).

Table 1

Characteristics of 5 environments trial in Bengkulu Province

Environment	Year	Soil Type	Altitude (m)	Rainfall (mm)	Temperature (º C)		Irrigation Type
					Min	Max	
Sungai Serut (SS)	2019	Ultisol	60	101	26	36	semi technical
Desa Semarang (DS)	2019	Ultisol	50	112	26	35	semi technical
Talang Benih (TB)	2019	Andosol	300	118	24	34	Technical
Sawah Dendam (SD)	2020	Ultisol	50	277	25	35	Technical
Aur Gading (AG)	2020	Ultisol	100	215	26	36	Rainfed

Table 2

Genotype, accession number, and pedigree

No.	Genotype	Accesion number	Pedigree
1	G1	BKL3-RS1-1-253-18	Sriwijaya x IR148
2	G2	BKL4-RS1-1-256-21	Sriwijaya x IR7858-1
3	G3	BKL4-RS1-2-257-22	Sriwijaya x IR7858-1
4	G4	BKL4-RS1-3-258-23	Sriwijaya x IR7858-1
5	G5	BKL1-B1-259-1	Bugis x IR7858-1
6	G6	BKL1-B2-260-2	Bugis x IR7858-1
7	G7	BKL1-B3-261-3	Bugis x IR7858-1
8	G8	BKL2-B1-262-4	Bugis x IR148
9	G9	BKL2-B2-263-5	Bugis x IR148
10	G10	BKL2-B3-264-6	Bugis x IR148
11	G11	BKL3-B1-265-7	Sriwijaya x IR148
12	G12	BKL3-B3-267-9	Sriwijaya x IR148
13	G13	BKL4-B1-268-10	Sriwijaya x IR7858-1
14	G14	BKL4-B3-270-12	Sriwijaya x IR7858-1
15	Inpago 12	Check Variety	-
16	Rindang 2	Check Variety	-

The study was carried out using a completely randomized block design with two replications. The experimental plot was 5 m × 5 m in size. Twenty kg of manure was spread and mixed with the soil in the first fertilization. Planting was performed with a spacing of 20 cm × 20 cm, and each plot was fertilized with 400 g urea, 200 g SP-36, and 200 g KCl a week after planting,

The variables observed were plant height, number of productive tillers, panicle length, number of filled grains/panicles, percentage of empty grains, 1000-grain weight, grain weight per hill, and grain weight per plot. Harvesting was carried out using physiological ripening criteria marked by 80% yellowish panicles in one plot. Furthermore, the grain was dried until it reached a moisture content of ±14%. The grain yield per hectare was derived from the conversion of grain weight per plot.

The yield component variables were analyzed using combined variance analysis and the least significant difference test at a 5% level, according to Steel and Torrie (1980). The estimation of yield adaptability and stability is based on the coefficient of variance (CVi) (Francis and Kannenberg, 1978) and regression (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966) as follows:

$$b_i = 1 + \frac{\sum_i (x_{ij} - \bar{x}_i - \bar{x}_j + \bar{x}_{..})(\bar{x}_j - \bar{X})}{\sum_j (\bar{x}_j - \bar{X})^2}$$

$$\boldsymbol{S^2_{di} = \frac{1}{E-2} [\sum_i (x_{ij} - \bar{x}_i - \bar{x}_j + \bar{X}) - (b_i - 1)^2 \sum_i (\bar{x}_j - \bar{X})^2]},$$

where x_{ij} is the grain yield of genotype I in environment j; $\bar{x}_i$ is the average yield of inbred line I and $\bar{x}_j$ is the average performance of the environment j, and $\bar{X}$ is the grand mean. The genotypes would be more adapted to favorable environmental conditions if $b_i > 1$. The genotypes would be adapted to unfavorable growing conditions if $b_i < 1$, and if $b_i = 1$, those genotypes would have an average adaptation to all environments. Genotypes with $S^2_{di} = 0$ would be most stable, whereas a $S^2_{di} > 0$ would indicate lower stability across all environments.

Wricke’s ecovalence (W_i^2) and Shukla’s stability variance (σ2) were measured as follows:

$$W_i^2 = \sum (x_{ij} - \bar{x}_i - \bar{x}_j + \bar{X})^2$$

where x_{ij} is the observed yield response, $\bar{x}_i$ and $\bar{x}_j$ correspond to the previous notations, and $\bar{X}$ is the grand mean. Genotype stability occurs when $W_i^2 = 0$. The stability parameter uses stability variance (σ_i^2), which was obtained from the following equation:

$$\sigma_i^2 = \left[\frac{P}{(p-2)(q-1)}\right] \mathrm{x}\, (x_{ij} - \bar{x}_i - \bar{x}_j + \bar{x}_{..})^2 - \frac{SSGE}{(p-2)(q-1)}$$

The sum of square the genotype-environment interaction was determined as follows:

$$SSGE = \sum_i Wi = \sum_i^p \sum_i^q (x_{ij} - \bar{x}_i - \bar{x}_j + \bar{x}_{..})^2$$

Nonparametric stability parameters include Kang's yield and stability index (YS_i). (Kang) and Nassar and Huehn (1987) proposed four nonparametric stability statistics, $S_i^{(1)}$, $S_i^{(2)}$, $Si^{(3)}$, and $S_i^{(6)}$, which are based on yield ranks of genotypes in each environment and are estimated as follows:

$$\boldsymbol{S_i^{(1)} = 2\sum_j^{n-1}\frac{\sum_{j'=j+1}^{n}|r_{ij}-r'_{ij}|}{[N(n-1)]}} \qquad \boldsymbol{S_i^{(2)} = \frac{\sum_{j=1}^{n}(r_{ij}-\bar{r}_i)^2}{(N-1)}} \qquad \boldsymbol{S_i^{(3)} = \frac{\sum_{j=1}^{n}(r_{ij}-\bar{r}_i)^2}{\bar{r}_i}}$$

$$\boldsymbol{S_i^{(6)}} = \frac{\boldsymbol{\sum_{j=1}^{n}}|r_{ij} - \bar{r}_i|}{\boldsymbol{\bar{r}_i}}$$

In the above equation, $\boldsymbol{r_{ij}}$ is the rank of the i^{th} genotype in the j^{th} environment, $\boldsymbol{\bar{r}_i}$ is the mean rank across all environments for each genotype, and N is the number of environments. The genotype with the lowest value would be the most stable across environments.

Thennarasu (1995) proposed four nonparametric stability parameters based on adjusted ranks of genotypes within each test environment. The formulas to compute these statistics are shown below:

$$NP^{(1)} = \frac{1}{N}\sum_{j=1}^{n}|r'_{ij} - M_{di}| \qquad NP^{(2)} = \frac{1}{N}\left[\sum_{j=1}^{n}\frac{|r'_{ij}-M'_{di}|}{Mdi}\right]$$

$$NP^{(3)} = \frac{\sqrt{\frac{\sum(r'_{ij}-\overline{r'}_i)^2}{N}}}{\bar{r}_i} \qquad NP^{(4)} = \frac{2}{N(N-1)}\left[\sum_{j=1}^{n-1}\sum_{j=j+1}^{n}|r'_{ij} - r'_{ij'}|/\bar{r}_i\right]$$

where r'_{ij} is the rank of i^{th} genotype in the j^{th} environment based on adjusted data, $\overline{r'}_i$ is the mean ranks for adjusted data, M'_{di} the median ranks for adjusted data, while $\bar{r}_i$ and Mdi are obtained from the original data. The relationships among the stability using Spearman's rank correlation and the stability analyses were based on the main components of the GGE biplot and analyzed using PBSTAT-GE software (**www.pbstat.com**).

3. Results and Discussion

3.1. Agronomic performance of inbred lines

This study evaluated the yield performance and stability of 14 inbred lines from landrace varieties compared to two superior varieties (Inpago 12 and Rindang 2) under different irrigation types in Bengkulu, Indonesia. The combined analysis of variance indicated wide variability in the lines under testing (Table 3), which suggests that the lines interacted differentially regarding yield component performance; therefore, further general adaptability and stability analysis across lines should be followed before their selection for release as new varieties.

Table 3
Mean square of combined analysis of variance across environment of yield component of 14 inbred lines

Source of variance	Df	Panicle length	Number of Productive Tiller per hill	Filled grain per panicle	Unfilled grain per panicle (%)	1000-grain Weight (g)	Grain weight per hill (g)	Yield (tonnes/ha)

Environment (E)	4	38.21**	359.49**	18,356.66**	524.74**	50.88**	9,464.23**	324.66**
Replication/R	5	0.24	2.06	92.26	35.44**	1.30*	21.90	2.04**
Genotype (G)	15	8.92**	49.11**	839.64**	235.55**	12.24**	444.43**	31.46**
GxE	60	2.80**	13.96**	1,156.62**	74.51**	1.88**	372.63**	11.96**
Residuals	75	0.39	1.10	53.53	7.77	0.44	15.27	0.57

*, ** Significant at the 0.05 and 0.01 probability levels, respectively

Yield response is a combination of yield components, namely panicle length, number of productive tillers, number of filled grains, 1000-grain weight, and grain weight per hill (Table 4). The appearance of the agronomic characteristics showed that the panicle length of 24.85–27.04 cm was significantly different from that of Rindang 2. The number of productive tillers ranged from 9.68–15.22, which was significantly different from that of Rindang except for G1(BKL3-RS1-1-253-18), while G7(BKL1-B3-261-3) surpassed Inpago 12 check varieties. The number of filled grains per panicle and percentage of empty grains ranged from 112.99–151.57, and 14.65–25.75, respectively. The 1000-grain weight was quite low, relatively, at 26.45–28.52. In contrast, the weight of filled grains per hill ranged from 22.46 g in G1(BKL3-RS1-1-253-18) to 42.82 g I G11(BKL3-B1-265-7), as shown in Table 4.

Tabel 4

Agronomic performance of genotypes tested in different location yield trials.

Genotype	Panicle length	Number of Productive Tiller per hill	Filled grain per panicle	Unfilled grain per panicle (%)	1000-grain Weight (g)	Grain weight per hill (g)	Grain yield (tonnes/ha)
1	27.04^{a}	9.68^{gh}	120.22^{efg}	25.75^{bc}	27.01^{defg}	22.46^{i}	5.97^{h}
2	25.51^{cde}	10.17^{g}	112.99^{h}	23.46^{cd}	27.22^{cdef}	24.98^{hi}	6.07^{gh}
3	26.36^{b}	10.09^{g}	119.73^{fg}	22.38^{de}	27.86^{b}	28.53^{fg}	6.73^{fg}
4	25.97^{bc}	10.39^{fg}	118.33^{fgh}	19.11^{fg}	26.91^{defg}	31.30^{ef}	7.28^{ef}
5	24.85^{f}	13.59^{d}	129.27^{bc}	15.65^{hi}	27.35^{bcde}	38.69^{bc}	10.31^{b}
6	25.01^{ef}	13.53^{d}	126.87^{bcd}	14.94^{i}	26.45^{g}	37.25^{cd}	9.06^{c}
7	26.00^{bc}	15.63^{a}	129.49^{bc}	17.47^{gh}	26.52^{g}	41.87^{ab}	10.20^{b}
8	25.62^{cd}	13.74^{cd}	121.42^{defg}	22.45^{de}	27.63^{bc}	35.44^{cd}	8.07^{d}
9	26.04^{bc}	15.43^{ab}	123.72^{cdef}	19.81^{fg}	27.50^{bcd}	42.37^{a}	8.76^{c}
10	25.23^{def}	13.78^{cd}	126.41^{bcde}	14.65^{i}	28.52^{a}	41.50^{ab}	10.47^{ab}
11	25.90^{bc}	15.22^{ab}	115.09^{gh}	18.30^{fg}	27.18^{cdef}	42.82^{a}	8.02^{d}
12	25.83^{bc}	11.85^{e}	131.48^{b}	20.43^{ef}	26.58^{g}	34.50^{de}	6.89^{f}
13	25.93^{bc}	13.07^{d}	151.57^{a}	18.63^{fg}	26.69^{fg}	42.27^{a}	11.14^{a}
14	25.87^{bc}	11.14^{ef}	130.34^{b}	23.65^{cd}	27.01^{defg}	35.32^{cd}	7.74^{de}
pago 12	22.71^{g}	14.62^{bc}	120.36^{defg}	27.44^{b}	23.29^{h}	34.69^{de}	7.87^{de}
indang 2	26.32^{b}	9.07^{h}	116.77^{gh}	32.66^{a}	26.87^{efg}	26.25^{gh}	5.13^{i}

LSD 5%	0.55	0.93	6.52	2.48	0.59	3.48	0.67
CV	2.43	8.34	5.87	13.24	2.46	11.16	9.29

Numbers in one column followed by the same letter show no significant difference based on the LSD test at 5%; CV = coefficient of variance

All genotypes tested in Aur Gading had a mean yield of 4.52 tons/ha, while G9(BKL2-B2-263-5) had the highest value of 6.41 tons/ha (Table 5). However, this was the lowest compared to other environments. The irrigation system relies only on rainfall, and farmers usually cultivate this grain once a year. This is encouraging because some of the genotypes tested in this environment were above the average yield of the Rindang 2, the check variety. Therefore, this line can be considered a potential line for cultivation as upland rice or under rainfed systems. It differs from the Sungai Serut and Talang Benih environments supported by a technical irrigation system, with a mean grain yield of 12.65 tons/ha and 9.82 tons/ha. The highest yield grouping comprised G13(BKL4-B1-268-10), G10(BKL2-B3-264-6), G7(BKL1-B3-261-3), and G5(BKL1-B1-259-1), and was found in the Sungai Serut.

Table 5
Means of grain yield (tonnes/ha) in 5 environments of 14 genotypes

Genotype	Grain yield (tonnes/ha)					Mean
	Aur Gading (AG)	Desa Semarang (DS)	Sawah Dendam (SD)	Sungai Serut (SS)	Talang Benih (TB)	
G1	3.18	4.76	4.58	5.57	11.52	5.92
G10	4.97	9.55	11.82	14.85	11.18	10.47
G11	3.85	5.50	6.60	17.37	6.79	8.02
G12	4.15	4.48	4.48	15.96	5.40	6.89
G13	4.57	11.38	12.22	15.24	12.29	11.14
G14	3.85	6.34	6.25	15.73	6.56	7.74
G2	3.28	4.34	4.69	8.84	9.14	6.06
G3	5.21	4.14	4.36	9.01	10.93	6.73
G4	4.39	4.32	5.09	7.51	15.10	7.28
G5	5.19	8.14	10.16	13.11	14.96	10.31
G6	4.93	5.93	7.18	13.52	13.76	9.06
G7	4.37	7.47	10.33	16.31	12.52	10.20
G8	4.55	5.93	7.26	15.21	7.39	8.07
G9	6.41	5.84	7.43	16.84	7.26	8.76
Inpago 12	5.07	7.36	7.82	12.07	7.05	7.87
Rindang 2	4.37	4.30	6.40	5.29	5.29	5.13
Mean	4.52	6.23	7.29	12.65	9.82	8.10
LSD 0.05	1.12	0.80	0.56	0.56	2.49	0.57
CV (%)	14.10	7.33	4.22	2.52	14.48	9.40

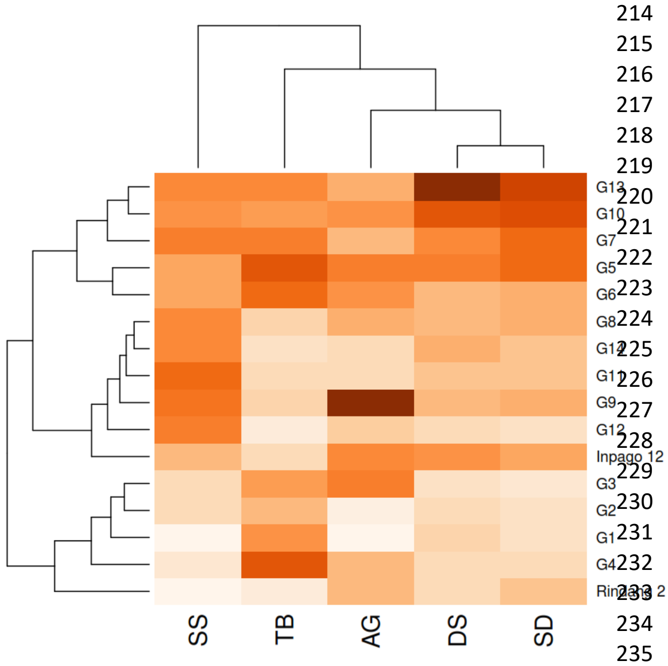

Fig 1. GxE Heat-map genotypes tested at five environments (AG = Aur Gading; DS = Desa Semarang; SD = Sawah Dendam; SS = Sungai Serut; TB = Talang Benih). Data described according to the mean yield of the genotypes in five environments. High values are indicated in brown and low values in white.

Some of the lines had a yield potential of over 5 tons/ha, and some genotypes even exceeded the check varieties, namely Inpago 12 and Rindang 2. Furthermore, G10(BKL2-B3-264-6), G13(BKL4-B1-268-10), G5(BKL1-B1-259-1), and G7(BKL1-B3-261-3) had a potential yield of more than 10 tons/ha, thereby exceeding the check varieties of 7 tons/ha and 5 tons/ha, as shown in Table 5. These lines have agronomic characteristics of new varieties, namely the number of productive tillers > 13, the number of filled grains > 126 grains / panicle, and the percentage of empty grains < 19% per panicle according to SES IRRI (2013) (Table 4).

The GxE heat-map described according to the mean yield of the genotypes in five environments is shown high values in brown and low values in white (Fig 1). The highest-yielding group was comprised of genotype G13(BKL4-B1-268-10), G10(BKL2-B3-264-6), G7(BKL1-B3-261-3), and G5(BKL1-B1-259-1), with the highest yields being found in Sungai Serut. Furthermore, the moderate-yield group contained G8(BKL2-B1-262-4), G14(BKL4-B3-270-12), G11(BKL3-B1-265-7), G9(BKL2-B2-263-5), G12(BKL3-B3-267-9), and Inpago 12 in Sungai Serut (SS). Meanwhile, the low-yield group comprised G3(BKL4-RS1-2-257-22), G2(BKL4-RS1-1-256-21), G1(BKL3-RS1-1-253-18), and G4(BKL4-RS1-3-258-23) in Talang Benih (TB). The highest grain yield of 12.65 tons/ha was discovered in Sungai Serut, followed by 9.82 tons/ha, 7.23 tons/ha, 6.23 tons/ha, and 4.52 tons/ha in TB, Sawah Dendam, Desa Semarang, and Aur Gading, respectively, as shown in Table 5.

3.2. Parametric Stability Analysis

The parametric stability analysis showed that G10(BKL2-B3-264-6), G13(BKL4-B1-268-10), G5(BKL1-B1-259-1), G7(BKL1-B3-261-3), and Inpago 12 had variance coefficient (CVi) values of 34.61%, 35.49%, 37.68%, and 32.64% and environmental variance ($S_i^{(2)}$) values of 3.13, 5.48, 4.51, 1.74, respectively, as shown in Table 6. These genotypes are stable because the two values are relatively close to 0. Based on the variance coefficient and environmental variance values, they are classified as genotypes with static stability (Becker and Leon, 1988). Genotypes G10(BKL2-B3-264-6), G13(BKL4-B1-268-10), G5(BKL1-B1-259-1), and G7(BKL1-B3-261-3) had b_i values of 1.02, 1.05, 1.06, and 1.42, and grain productivity of 10.47, 11.14, 10.31, 10.2 tons/ha over the total mean, respectively, as shown in Table 4. According to Finlay and Wilkinson (1963), a genotype with a regression coefficient (b_i) of 1 and a mean yield greater than the total mean is regarded as stable, with high adaptability to all environments.

Table 6
Parametric stability analysis: coefficient of variability, environmental variability, regression coefficient and regression deviation, and stability in 14 genotypes, and 2 checks in 5 environments

Genotype	Y_i (tonHa^{-1})	CV_i	bi	P_b$_i$	S^2d_i	P_s^{2}d$_i$	W_i^2	D_i	StabVar (σ^2)
G1	5.97	53.89	0.51**	0.006	9.96***	0.000	40.34	8.45	22.2
G10	10.47	34.61	1.02 ns	0.899	3.11***	0.000	10.19	7.12	4.97
G11	8.02	66.73	1.51**	0.004	7.19***	0.000	32.86	7.94	17.93
G12	6.89	73.88	1.35*	0.044	9.50***	0.000	34.41	8.36	18.81
G13	11.14	35.49	1.06 ns	0.744	5.46***	0.000	17.36	7.6	9.06
G14	7.74	59.36	1.28 ns	0.106	5.65***	0.000	21.04	7.64	11.17
G2	6.07	44.88	0.79 ns	0.231	1.11***	0.004	5.93	6.69	2.53
G3	6.73	45.48	0.73 ns	0.125	4.94***	0.000	18.57	7.5	9.76
G4	7.28	62.65	0.79 ns	0.230	18.97***	0.000	59.53	9.92	33.16
G5	10.31	37.68	1.06 ns	0.707	4.50***	0.000	14.53	7.41	7.45
G6	9.06	46.92	1.24 ns	0.161	2.90***	0.000	11.95	7.08	5.97
G7	10.2	45	1.42*	0.017	0.48 ns	0.053	9.48	6.55	4.56
G8	8.06	51.51	1.20 ns	0.258	3.37***	0.000	12.52	7.18	6.3
G9	8.76	52.13	1.21 ns	0.227	7.70***	0.000	25.74	8.03	13.86
Inpago 12	7.87	32.64	0.71 ns	0.094	1.74***	0.000	9.56	6.83	4.61
Rindang 2	5.13	16.7	0.11***	0.000	0.54*	0.040	34.93	6.56	19.11

Y: overall mean of yield. LSD 0.05: 0.17; CVi: coefficient of variability (Francis and Kannenberg); b: coefficient of regression to index the environment (Finlay and Wilkinson; Eberhart and Russel). Stable (a=0.05): 0.9 - 1.1 P_bi : P-value for b with null hypothesis b=1; s^2d: deviation of regression (Eberhart and Russel); P_s^2di: P-value for s^2d with null hypothesis s=0; W_i^2 : Wricke ecovalence; Di: Hanson's parameter stability; StabVar : Shukla *stability variance* (σ^2)

Wricke (1962) developed the ecovalence method (W_i^2), which measures the contribution of each genotype to the total square of the genotype × environment interactions. A genotype is considered stable assuming it has a low ecovalence value. The analysis showed that the stable genotypes were G10(BKL2-B3-264-6), G2(BKL4-RS1-1-256-21), G7(BKL1-B3-261-3), and Inpago 12, with low ecovalence values of 10.19, 5.93, 9.48, and 9.56, respectively (Table 6).

The stability evaluation method applied by Hanson (1970) was used to investigate the total genotype in a few environments concerning D_i parameters. Stable genotypes such as G2(BKL4-RS1-1-256-21), G7(BKL1-B3-261-3), Inpago 12, and Rindang 2 had low D_i values of 6.69, 6.65, 6.83, and 6.56, respectively (Table 6).

The stability parameter designed by Shukla (1972) is based on the concept that genotypes with the smallest StabVar (σ2) are the most stable. G10(BKL2-B3-264-6) (4.97), G2(BKL4-RS1-1-256-21) (2.53), G7(BKL1-B3-261-3) (4.56), and Inpago 12 (4.61) (Table 4) were the most stable lines, while G4(BKL4-RS1-3-258-23) and G1(BKL3-RS1-1-253-18) were the most unstable. The results obtained using both methods (CVi and σ2) showed that G10(BKL2-B3-264-6) and G7(BKL1-B3-261-3) were the most stable lines.

3.3. Nonparametric stability analysis

The nonparametric stability method is based on the ratio of the genotype rank to each environment. A genotype is stable assuming it ranks the same in several environments (Kang, 1988; Nassar and Huehn, 1987; Fox et al., 1990; Huehn, 1990). The Kang yield and stability index (YS_i) combined the genotype yield and Shukla stability variance into one statistical test. Kang and Pham (1991) stated that rank-sum is another nonparametric stability statistic regarded as yield, and Shukla (1972) stability variance was used as the selection criteria. This analysis realized a score of 1 for yield and stability, thereby permitting the identification of stable genotypes. Furthermore, the genotypes with the maximum and minimum yields were both assigned to rank 1. Ranks based on yield and stability variance were attached to each genotype. The genotype with the minimum rank-sum was the most desirable one. Moreover, when a genotype has a YS_i > mean, then YSinya is selected. The genotypes with (+), namely G10(BKL2-B3-264-6), G13(BKL4-B1-268-10), G5(BKL1-B1-259-1), G6(BKL1-B2-260-2), G7(BKL1-B3-261-3), G8(BKL2-B1-262-4), and G9(BKL2-B2-263-5), were selected based on YS_i, as shown in Table 7.

The two stability methods designed by Nassar and Huehn (1987) are S1 and S2. Moreover, both methods are based on the ranking of the genotypes in the number of environments. Genotypes with slight changes in rank are more stable (Becker and Leon, 1988). The variance of S1 and S2 (Zi (1) as well as Zi (2)) is smaller than the value of Table Z (Tables Chi-sq Zi (1), Zi (2)), which implies that the genotype is stable. The sums of Zi (1) = 16.63 and Zi (2) = 8.73 are smaller than the Chi-sq Sum Zi (1) table. However, when Zi (2) = 26.29, it indicates that the stability ratings of the tested genotypes were insignificantly different. Fox et al. (1990) suggested a nonparametric superiority measure for general adaptability using graded ranks from cultivars. The ranking was carried out at each location. In addition, the number of sites where the genotypes occurred in the upper, middle, and lower third of the rankings is calculated. Those that occur mostly in the upper third are considered widely adapted cultivars. Based on Fox et al. (1990), those discovered in the top three ranked environments tested were identified as properly adapted genotypes. Following this method, G5(BKL1-B1-259-1), G10(BKL2-B3-264-6), G13(BKL4-B1-268-10), G7(BKL1-B3-261-3), and G9(BKL2-B2-263-5) were properly adapted to these environments, unlike the others, as shown in Table 7. Genotypes with small NPi (1), NPi (2), NPi (3), and NPi (4) values are considered to be more stable. Based on these values, G2(BKL4-RS1-1-256-21), G5(BKL1-B1-259-1), G11(BKL3-B1-265-7), G8(BKL2-B1-262-4), and Inpago 12 were more stable than the others, as shown in Table 7.

Table 7

The result of the analysis non-parametric stability

Genotype	YSi	Si(1)	Zi(1)	Si(2)	Zi(2)	Si(3)	Si(6)	TOP	NPi(1)	NPi(2)	NPi(3)	NPi(4)
G1	-9	6.20	0.35	27.80	0.37	5.15	1.21	0	3.40	0.26	0.39	0.51
G10	10 +	6.20	0.35	24.70	0.10	6.42	2.33	2	3.60	0.72	0.93	1.29
G11	0	5.40	0.00	25.70	0.17	10.52	1.83	1	2.80	0.28	0.49	0.59
G12	-6	7.90	2.95	41.25	3.43	7.00	1.31	0	5.10	0.43	0.50	0.68
G13	11 +	7.40	1.92	35.30	1.69	8.00	3.00	2	4.40	0.88	1.33	1.85
G14	-2	4.80	0.12	15.00	0.34	7.40	1.80	0	3.00	0.27	0.35	0.48
G2	-8	3.60	1.29	8.50	1.39	1.63	0.59	0	2.20	0.17	0.20	0.28
G3	-7	6.80	0.97	31.30	0.87	13.04	2.15	1	4.20	0.35	0.46	0.63
G4	-4	6.80	0.97	35.30	1.69	11.80	2.00	1	4.00	0.33	0.53	0.68
G5	9 +	4.60	0.22	13.30	0.54	9.36	2.55	3	2.80	0.93	0.74	1.05
G6	6 +	6.40	0.52	26.00	0.19	3.21	1.27	1	3.80	0.54	0.69	0.97
G7	8 +	5.80	0.10	22.50	0.01	8.20	2.29	2	3.60	0.90	0.87	1.18
G8	1 +	2.80	2.78	5.00	2.27	0.75	0.50	0	1.60	0.20	0.25	0.35
G9	5 +	7.20	1.57	34.80	1.58	12.90	2.97	2	4.70	0.78	0.91	1.24
Inpago 12	-1	4.80	0.12	14.50	0.39	7.73	2.22	0	2.80	0.56	0.46	0.65
Rindang 2	-10	7.20	1.57	36.70	2.05	2.67	0.96	0	4.40	0.29	0.40	0.53

YS: Kang's yield and stability index; '+': selected genotypes having YSi> mean of 8.10; Si(1), Si(2), Si(3), Si(6): Nassar and Huehn's nonparametric stability parameters; SumZi(1) : 16.63; SumZi(2) : 17.61; Chi-sqtabelZi(1), Zi(2): 8.73; Chi-sqtabelSumZi(1), SumZi(2): 26.29; TOP: Fox's TOP - Number of sites at which the genotype occurred in the top third of the ranks; NPi(1), NPi(2), NPi(3), NPi(4): Thennarasu's nonparametric stability parameters

Table 8

Spearman correlation between stability parameters

	Yi	CVi	bi	s2di	Wi2	Di	StabVar	YSi	Si(1)	Si(2)	Si(3)	Si(6)	TOP	NPi(1)	NPi(2)	NPi(3)
Yi																
CVi	0.25															
bi	0.59*	0.24														
s2di	0.14	0.76**	0.01													
Wi2	0.46	0.54*	0.40	0.76**												
Di	0.14	0.76**	0.01	1.00**	0.76**											
StabVar	0.46	0.54*	0.40	0.76**	1.00**	0.76**										
YSi	1.00**	0.25	0.59*	0.14	0.46	0.14	0.46									
Si(1)	0.10	0.11	0.19	0.38	0.57*	0.38	0.57*	0.10								
Si(2)	0.24	0.20	0.30	0.44	0.70**	0.44	0.70**	0.24	0.97**							
Si(3)	-0.22	0.20	0.01	0.42	0.25	0.42	0.25	-0.22	0.29	0.28						
Si(6)	-0.68**	-0.27	-0.36	0.12	-0.13	0.12	-0.13	-0.68**	0.27	0.15	0.73**					
TOP	0.78**	0.22	0.46	0.00	0.19	0.00	0.19	0.78**	-0.15	-0.06	-0.59*	-0.82**				
NPi(1)	0.08	0.09	0.15	0.33	0.51*	0.33	0.51*	0.08	0.98**	0.93**	0.32	0.30	-0.20			
NPi(2)	-0.72**	-0.40	-0.27	-0.15	-0.25	-0.15	-0.25	-0.72**	0.30	0.16	0.50*	0.86**	-0.81**	0.36		
NPi(3)	-0.76**	-0.19	-0.36	0.09	-0.06	0.09	-0.06	-0.76**	0.48	0.36	0.50*	0.84**	-0.88**	0.50	0.88**	
NPi(4)	-0.75**	-0.26	-0.36	0.03	-0.13	0.03	-0.13	-0.75**	0.48	0.35	0.46	0.84**	-0.83**	0.51*	0.92**	0.99**

**, **:significant at 0.05 and 0.01*

Parametric and nonparametric methods have their advantages and disadvantages; each method describes a particular way of looking at the GE interaction phenomenon. Each of these approaches complements the other for interpreting GE interactions, so it was finally determined that a clear picture of the interaction as a genotype was differentially sensitive to the environment (Dehghani et al., 2016). Correlation analysis is beneficial for breeders in interpreting the results of both methods.

3.4. Correlation of the relationship between stability parameters

The regression coefficient b_i was correlated with Y_i (0.59), and all stability parameters were tested. YS_i was negatively correlated with Si (6) (−0.68), NPi (2) (−0.72), NPi (3) (−0.76), and NPi (4) (−0.75). There was a strong and positive correlation (r = 1.00) between the mean yield (Y_i) and YS_i, S^2_{di}, and D_i, as well as W21 and Stabvar, while TOP had a positive correlation of 0.78 (Table 8).

The Spearman correlation analysis of the stability parameters indicated that Y_i, YS_i, TOP, and b_i had a positive correlation, as shown in Table 8. This is consistent with studies carried out by Becker and Leon (1988) and Mut et al. (2010), which found a correlation between Y_i and the TOP stability parameter. Selection to improve yield is expected to change grain yield stability by increasing the TOP parameter (Abdipour et al., 2017; Goksoy et al., 2019). It was directed toward the development of site-specific genotypes by optimizing environmental conditions. Genotypes tend to produce poor yields when planted in a less optimal environment and will produce high yields when planted in an optimal environment. The regression coefficient b_i was correlated with Y_i and all the tested stability parameters. YS_i was negatively correlated with $S_i^{(6)}$, NPi (2), NPi (3), and NPi (4). Similarly, there was a strong and positive correlation (r = 1.00) between the mean results and YS_i, S^2_{di}, and D_i, as well as W21 and Stabvar. Furthermore, TOP had a positive correlation of 0.78, indicating a stability parameter suitable for identifying high-yield genotypes (Mut et al., 2010; Abdipour et al., 2017).

The principal component analysis correlating the genotype with the yield and stability parameters is shown in Fig 2. Genotypes that are close to the stability parameter are considered “stable” or “good.” The results of the biplot analysis showed that G13(BKL4-B1-268-10), G10(BKL2-B3-264-6), G5(BKL1-B1-259-1), G7(BKL1-B3-261-3), and G9(BKL2-B2-263-5) had the highest stable yields based on the TOP stability parameters and were strongly correlated with YS_i and b_i (Fig 2, Table 8). This makes sense because TOP is calculated based on the number of locations where the genotypes had the highest yield rank.

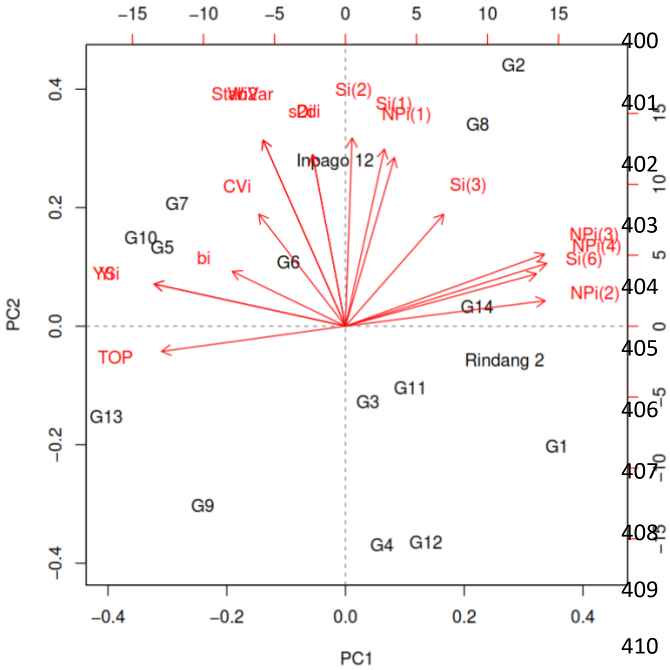

Fig 2. Mapping of stability parameters of 14 genotype base on PCA biplot

3.5. GGE biplot analysis

Biplot analysis was used to interpret the AMMI model, as indicated by AMMI1 and AMMI2. The AMMI1 biplot is a plot of the main effect (yield) and the score for the first principal component (PC1). In contrast, the AMMI2 biplot is a plot of the first (PC1) and the second (PC2) principal component scores. The results of the AMMI variance analysis showed that the interaction with the main component 1 (PC1) was significant at a probability level of less than 1% (Table 9). The effective breakdown of the genotype × environment interaction into four main components showed three essential components. The contribution of diversity explaining the indicators used to observe the relationship between genotypes and environment trials was 100%. However, by conducting biplot analysis, which reduced all the indicators into two-side dimensions, the information that could be explained was about 88%. Two principal components (PC1 and PC2) were used to construct the GGE-biplot graph, explaining 53% and 35.1% (Fig 3, 4, and 5), It meant that biplot analysis has already represented enough information on the relationship among those two indicators.

Table 9

Analysis of variance of AMMI model

Source of variance	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Environment (E)	4	1296.28	324.07	158.27	0.00
Replication/E	5	10.24	2.05	3.53	0.01
Genotype (G)	15	454.38	30.29	2.53**	0.01

GxE	60	717.73	11.96	20.61**	0.00
PC1	18	497.07	27.62	47.58**	0.00
PC2	16	117.91	7.37	12.70**	0.00
PC3	14	93.29	6.66	11.48**	0.00
PC4	12	10.17	0.85	1.46*	0.16
Residuals	73	42.37	0.58		

*, ** Significant at the 0.05 and 0.01 probability levels, respectively

GGE biplot graphs are better than the AMMI in the mega-environmental analysis for evaluating genotypes. The GGE biplot is more descriptive on G + GE and comprises the productive part of the biplot properties. GGE biplots have been used to analyze mega-environments (Kebede and Getahun, 2017; Zulqarnain et al., 2017), for genotype evaluation (Islam et al.) and evaluation of environmental trials (Tekdal and Kendal) and to analyze heterotic patterns (Kannababu et al., 2017), and their applications are becoming popular in quantitative analysis and plant breeding. The polygon visualization in the GGE biplot is practical and elegant. This method divides the environment into several groups and predicts the ideal genotype (Yan and Kang, 2003).

The analysis of discriminativeness and the representativeness of the environments produced genotype rankings relatively close to the mean. In Desa Semarang and Sawah Dendam, G13(BKL4-B1-268-10) had the highest yield, followed by G10(BKL2-B3-264-6), G5(BKL1-B1-259-1), G7(BKL1-B3-261-3), and G6(BKL1-B2-260-2), as shown in Fig 3.

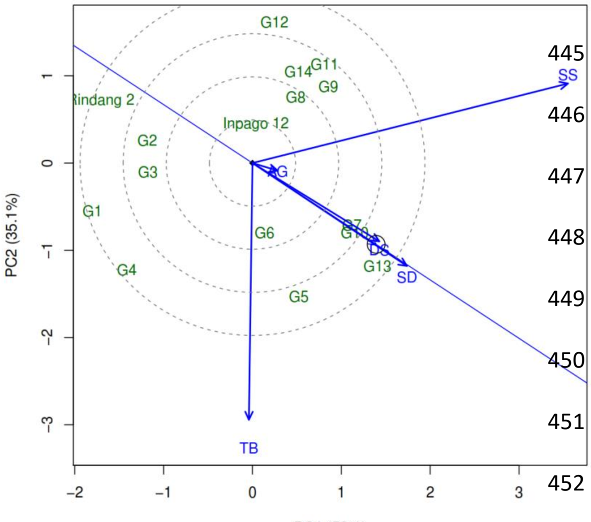

Fig 3. Biplot showing the discriminating ability and the representativeness of environments from 14 genotypes and five environment trials

These results were consistent when analyzed based on the highest mean grain yield ratings tested in the five environments (Fig 4). The genotype determined using the biplot in respect to the most extended vector was combined with G × E = 0 and represented by dots and arrows. It was a stable and high-yield genotype. Fortunately, G13(BKL4-B1-268-10), G10(BKL2-B3-264-6), and G7(BKL1-B3-261-3) were ideally stable because their projections in AEA were close to zero. However, those close to the ideal genotype were G5(BKL1-B1-259-1) and G6(BKL1-B2-260-2). The deficient yield genotypes were Rindang 2, G1(BKL3-RS1-1-253-18), G2(BKL4-RS1-1-256-21), G3(BKL4-RS1-2-257-22), and G12(BKL3-B3-267-9), because it was located far from the ideal ones.

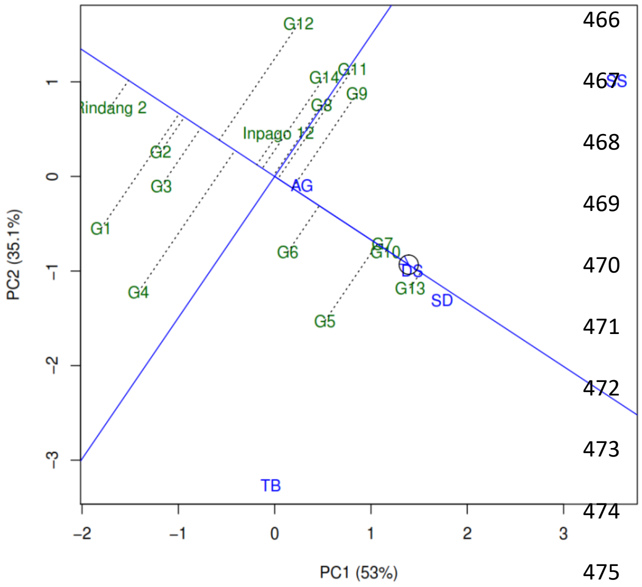

Fig 4. Mean versus stability biplot for grain yield showing the stability and performance of each genotype

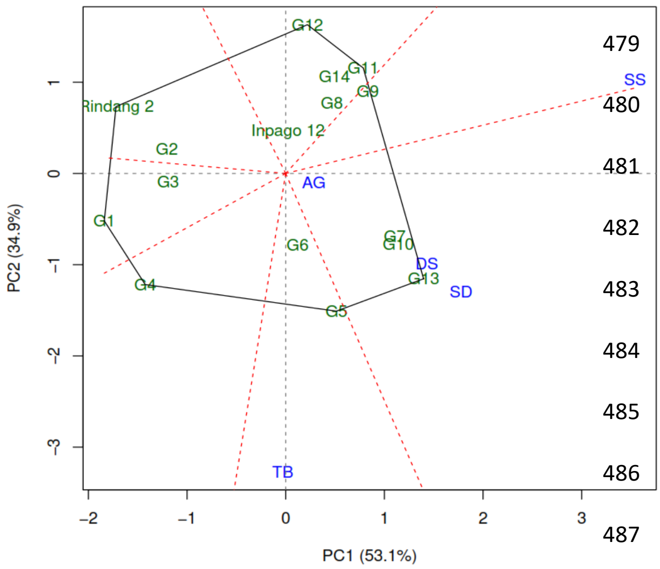

Fig 5. GGE biplot with mega-environment sectors: which won where biplot for grain yield showing identification of winning genotypes and their related mega-environments

The polygon is drawn from the position of the point farthest to the axis (0, 0), which then forms an angle. Therefore, all genotypes are present in the polygon. Subsequently, a perpendicular line is drawn from the axis (0, 0) to each side of the polygon, dividing the location into sectors, with each having a different genotype angle. Apparently, in each sector, the genotype suited at the top of the polygon was identified as the best in all the locations (Yan and Kang, 2003). Seven genotypes were located at the top of the polygon: G5(BKL1-B1-259-1), G13(BKL4-B1-268-10), G11(BKL3-B1-265-7), G12(BKL3-B3-267-9), Rindang 2, G1(BKL3-RS1-1-253-18), and G4(BKL4-RS1-3-258-23) (Fig 5). The genotypes were spread across seven sectors, but only two provided a suitable environment for the genotypes to be tested. The first sector, which comprises G7(BKL1-B3-261-3), G10(BKL2-B3-264-6), and G13(BKL4-B1-268-10), is appropriately adapted to the Sungai Serut, Aur Gading, Semarang Village, and Sawah Dendam environments. The second sector included G6(BKL1-B2-260-2) and G5(BKL1-B1-259-1), which were precisely adapted to the environment in TB.

Stability analysis using several methods can help breeders make decisions quickly and comprehensively to obtain stable superior genotypes. It can be done by comparing the results of the statistical relationship between them (Shukla et al., 2015; Goksoy et al., 2019). We compared the results of several methods to determine the yield stability of the lines (Table 10).

Table 10

A summary of the stability analysis using a parametric, nonparametric, and GGE biplot to determine the yield stability of the inbred lines

Methods	Parameters	Stability	Stability Lines
Parametric stability			
Regression	bi	b=1	**G10**, **G13, G5, G7**
	bi and S2di	b=1; S2di=0	**G10, G5, G6, G7**, G8
Variace	Wi2	Low	**G10**, G2, **G7**, Inpago 12
	σ2	Low	G10, G2, **G7**, Inpago 12
	Di	Low	G2, **G7**, Inpago 12, Rindang 2
	CVi	Low	**G10, G13, G5, G7**, Inpago 12
Nonparametric stability			
	Ysi	YSi> mean	**G10, G13, G5, G6**, **G7**, G8, G9
	Si(3), Si(6)	Zi< Chi-sq-table	all genotipe
	Si(1), Si(2)	Zi< Chi-sq-table	all genotipe
	NPi(1), NPi(2), NPi(3), NPi(4)	Low	G2, **G5**, G8, G11, Inpago 12
	TOP	The top third of the ranks	**G13, G10, G5, G7**, G9
GGE biplot			
	discrimitiveness vs. representativeness		**G13, G10, G5, G7, G6**
	mean vs. stability		**G13, G10, G5, G7, G6**
	which−won−where		**G13, G10, G5, G7, G6**

Bold letters indicated the stable genotype frequency of each parameter

Based on parametric stability analysis as well as the results of nonparametric analysis, the genotypes that had high frequency were G10 (BKL2-B3-264-6), G7 (BKL1-B3-261-3), G13 (BKL4-B1-268-10), and G5 (BKL1-B1-259-1); meanwhile, the biplot GGE analysis showed that there was an additional stable genotype, G6(BKL1-B2-260-2) (Table 10). Overall, the results of this study indicated that there were four consistently stable lines based on parametric and nonparametric stability analyses: G10(BKL2-B3-264-6), G7(BKL1-B3-261-3), G13(BKL4-B1-268-10), and G5(BKL1-B1-259-1). The GGE approach methods showed consistent stability, with lines G13(BKL4-B1-268-10), G10(BKL2-B3-264-6), G5(BKL1-B1-259-1), G7(BKL1-B3-261-3), and G6(BKL1-B2-260-2) showing high-yield potential, wide adaptation, and stability, and these should be tested more widely as candidates for new varieties.

4. Conclusion

Landrace varieties are a source of germplasm that can be developed into new superior varieties that are resistant to biotic or abiotic stress through plant breeding programs. Multilocation trials are essential in plant breeding as well as in other studies carried out in the field of agronomy. A combination of agronomy and plant breeding is needed to improve plant characteristics and stability tests before releasing new varieties. A single stability analysis method may not be sufficiently representative to determine the stability performance of genotypes across environments. In this study, we evaluated 14 inbred lines in five environmental trials. Stability analysis uses a parametric approach, nonparametric approach, and GGE biplot. This study indicated that there were four consistently stable lines based on parametric and nonparametric stability analyses: G10(BKL2-B3-264-6), G7(BKL1-B3-261-3), G13(BKL4-B1-268-10), and G5(BKL1-B1-259-1). The GGE approach methods showed consistent stability, and lines G13(BKL4-B1-268-10), G10(BKL2-B3-264-6), G5(BKL1-B1-259-1), G7(BKL1-B3-261-3), and G6(BKL1-B2-260-2) showed high-yield potential, wide adaptation, and stability, and it is recommended to be tested more widely at least 3-6 replications must be carried out for each trial in order to obtain a representative as a candidate for new varieties. Genotypes G7(BKL1-B3-261-3), G10(BKL2-B3-264-6), and G13(BKL4-B1-268-10) were more adapted to the Sungai Serut, Aur Gading, Semarang Village, and Sawah Dendam environments, while G6(BKL1-B2-260-2), and G5(BKL1-B1-259-1) were properly adapted to the environment in Talang Benih. Furthermore, this study is expected to be able to solve the problem of providing superior varieties originating from breeding programs through the developing of landraces varieties for high yield, wide adaptation, stability, and resistance to biotic and abiotic stress.

Comment [R2]: Rivised comment 2; we hav revised and added sentences in the conclusio as highly recommended in the widely trials.

Declaration of Competing Interest

All authors declare that they have no conflict of interest

Acknowledgments

The authors would like to thank the Directorate of Research and Community Service, Ministry of Education and Culture Republic of Indonesia, which supported this research through multi-year nationally competitive research (2018-2020) (Project no.052/SP2H/LT/DRPM/2018). Special thanks to Rosi Anandya, Aji Satrio, and Ahmad Zubaedi for their assistance in field experiments. We are grateful to the Head of Research and Community Board, Dean of the Agricultural Faculty, and Head of the Department of Crop Production at the University of Bengkulu to facilitate this research.

CRediT authorship contribution statement

Reny Herawati: Suggested the main idea of research, experimental design, data analysis, writing the original draf and editing paper. Angelita Puji Lestari, Nurmegawati: investigation and supervising the research work in the the field, reviewing and editing of the paper. Dwi Wahyuni Ganefianti: data interpretation, reviewing, and editing of draft paper. Atra Romeida: project administration, reviewing and editing of the paper.

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Dear Editor Annals of Agricultural Sciences,

Thank you for your e-mail dated December 1, 2021, informing us of the editorial decision on our manuscript “Comparative Study on the Stability and Adaptability of Different Models to Develop a High-Yield Inbred Line from Landrace Rice Varieties”, AOAS-D-21-00348R2”.

We would like to express our appreciation to the editor for the time and effort that had been spent in processing our paper. We confirm that the paper has been appropriately revised in accordance with your comment, and the revised manuscript has been uploaded to the Editorial Manager.

Once again, sincere thanks for the time and effort in further processing our revised manuscript.

Sincerely,
Reny Herawati et al

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Dear Dr Herawati,

Your submission entitled "Comparative Study on the Stability and Adaptability of Different Models to Develop a High-Yield Inbred Line from Landrace Rice Varieties" has been received by Annals of Agricultural Sciences.

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Dear Editor in Chief
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Thank you for your e-mail dated December 3, 2021, informing us of the editorial decision on our manuscript “Comparative Study on the Stability and Adaptability of Different Models to Develop a High-Yield Inbred Line from Landrace Rice Varieties”, AOAS-D-21-00348R2”.

We would like to inform you that we have edited the revision and we confirm that the paper has been appropriately revised in accordance with your comment and the comments made by the reviewer. The revised manuscript has been uploaded to the Editorial Manager.

Once again, sincere thanks for the time and effort in further processing our revised manuscript.

Sincerely,
Reny Herawati et al

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Round 3:

Response to Reviewer 2/editor (Comments)

Editor

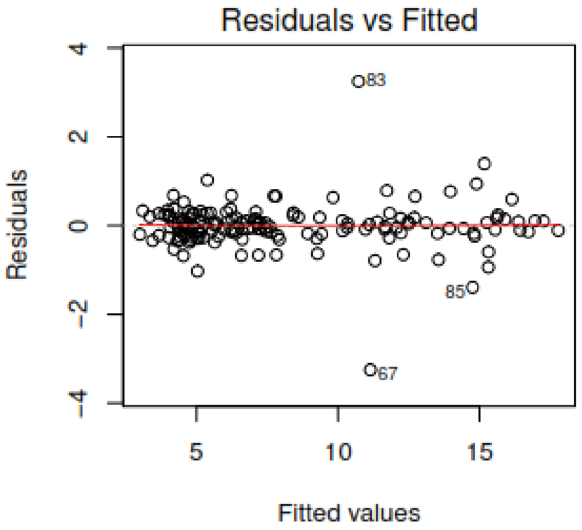
Is the experiment carried out with two replicates only?
How did you perform the statistical analysis with 2 replicates only?

First, add the comments of the reviewer and your responses to them since he isn't evaluate them yet.
Second, the confidence in the results and conclusion is very important. How is the specialist in statistics recommend to design a field experiment based on 2 replicates only. For sure, it will affect the experimental error, SE, SD and the p value which is sensitive to sample size. the minimum replicates for experiment is 3 or 4. This type of weakness must be resolve or provide an evidence from well documented source for trusted statisticians go with your opinion.

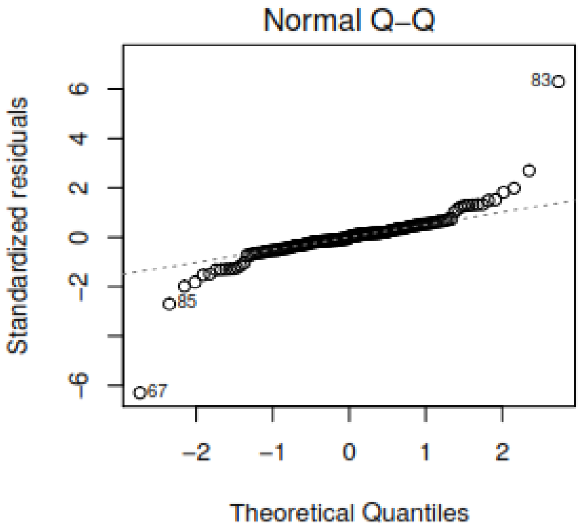
Replies to Reviewer/editor:

Comment: First of all, we deeply appreciate your helpful comments, As the reviewer pointed out, this study carried out with two replicates consisted of 14 lines and two check varieties grown in five locations. This is commonly applied by breeders if the number of seeds is limited. Previous study of GxE interaction analysis and AMMI models were performed using two replicate (Francis and Kannenberg, 1978; Alwala et al., 2010; Tekdal and Kendal., 2018; Li et al., 2018; Singh et al., 2019). Meanwhile, Zobel et al. (1988) state that most trials had four replicates, but some only two or three can be executed for the yield trial; which of 980 possible plots, 912 were actually harvested. We used a plot measuring 5 m x 5 m with a population of 625 per plot, quite representative for the sample size.
Multilocation trials are experiments that carried out in several different locations, but using the same design and treatment. Overall, the total variance of responses divided into three sources of variance, namely: main effect of genotype, main effect of location/enviroment, and the effect of interaction between genotype and location.To perform a multilocation analysis, several assumptions must be met. As for the assumptions that must be met to perform analysis of variance is as following (Steel and Torrie, 1980):
1. The experimental residuals are normally distributed: the homogeneity of the residual variance can be formally tested using the test Barlett.
2. The experimental residuals are independent: the randomness of the experimental residue can be plotted between the estimated value of the experimental residue with the estimated response value (Mattjik and Sumertajaya, 2013). The residual are mutually independent if the plot made does not form a certain pattern or clear model. The formal method used for testing independent residuals is the runs test.
3. The experimental residuals have a large variance homogeneous: tests for normal distributed residuals are used, namely the Kolmogorov-Smirnov test. The residuals are normally distributed if the value is p-value $\geq \alpha$

The results of the analysis using PBSTAT-GE software showed that the assumption of the data has met the normality and homogeneity of the residuals. Figure 1 shows the distribution of residues forming a relatively linear pattern of dots and not indicates a deviation normality. Residual homogeneity is visible in Figure 2 which shows the distribution of residue is around line 0 and does not form a certain pattern. It means that our data has met the eligible assumptions for F-test and so on. Furthermore, We recommended for a wider trial with a national scope, at least 3-6 replicates should be carried out for each experiment in order to obtain representative as a candidate for a new variety.



Figur 1



Figur 2

As the reviewer suggested, we have revised and added sentences in the **Results and Discussion sections** highlighted with red color, on page 6, lines 190-198. We do not display the results of the analysis of data assumptions because there are too many pictures that have been presented which focus more on the object of research. As the reviewer's suggestion, we recommended for a wider trial with a national scope, at least 3-6 replicates should be carried out for each experiment on the **Conclusion** sections highlighted with red color. Those was stated on page 19, lines 573-575.

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Reny Herawati <reny.herawati@unib.ac.id>

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Title: Comparative Study on the Stability and Adaptability of Different Models to Develop a High-Yield Inbred Line from Landrace Rice Varieties
Annals of Agricultural Sciences

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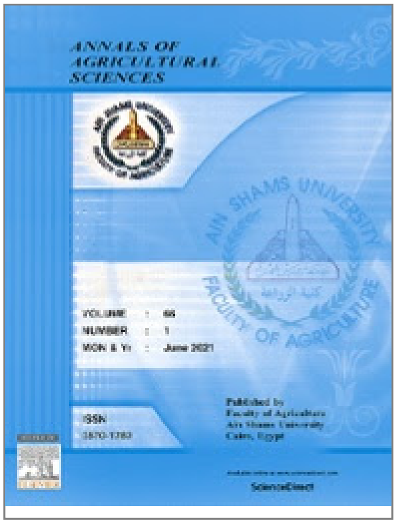

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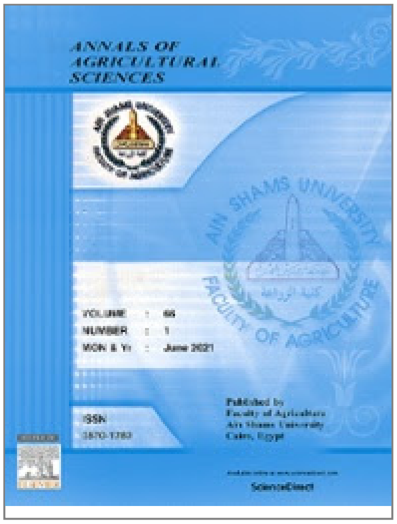

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