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# RICE SCREENING WITH HYDROPONIC DEEP-FLOW TECHNIQUE UNDER SALINITY STRESS

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## SUMMARY

Salinity is one of the main abiotic stresses affecting rice crops. It considerably affects the growth and yield traits of rice, especially rice planted in coastal areas. The development of rice genotypes adapted to salinity requires effective screening and intensive selection. Selection in the seedling stage is ineffective because it cannot predict and quantify the productivity of a genotype under stressed conditions. Therefore, selection in the generative phase by considering yield traits is important. The main aim of this study was to determine selection in the generative phase and environment under a hydroponic culture with a deep flow technique (DFT). The study was laid out in with a randomized complete block design comprising two factors (cultivars and NaCl concentrations) with three replications in a greenhouse from April 2020 to June 2020 at the Department of Agronomy, Faculty of Agriculture, Hasanuddin University, Indonesia. Five rice cultivars, i.e., 'Inpari-34 Salin Agritan', 'Ciherang', 'IR-29', 'Inpari-29', and 'Jeliteng', were tested at three NaCl levels, i.e., 0, 60, and 120 mM. Data analysis was carried out on genetic and multivariate factors. On the basis of results, the 60 mM level of NaCl was recommended for the screening and selection of salinity-tolerant genotypes. The agronomic characters that could also be used as selection criteria were productive tillers and rice yield per plant. Therefore, the hydroponic DFT is suggested and recommended to be the best method for the controlled screening of salinity in the generative phase of rice crops.

**Keywords:** Hydroponic deep flow technique, genotype salinity screening, environment, genotype by environment interaction, productive tillers, grain yield, *Oryza sativa* L.

**Key findings:** Results revealed that a deep-flow hydroponic system has the potential to be used for the screening and selection of tolerant rice genotypes under salinity stress. This study also recommended using the traits of productive tillers and grain yield as selection criteria with a critical level of 60 mM NaCl for screening rice genotypes under hydroponic DFT.

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## INTRODUCTION

In most Asian countries, rice is grown as an important staple food crop and also exported to support the economy. However, rice yield has several constraints, with abiotic stresses, such as salinity, being the major ones. For a country like Indonesia wherein coastal areas are enormous, salinity has become a considerable obstacle in the expansion of rice areas to enhance yield.

Salinity affects various aspects of plant growth and physiology at different stages. At the early stage, it causes the inhibition of water absorption; rice plants, therefore, experience drought, which results in the closure of the stomata with reduced plant growth (Yamamoto *et al.,* 2011; Negrao *et al.,* 2016). The build-up of ions under persistent and prolonged saline conditions causes leaf poisoning and later causes leaf death (Munns and Tester, 2008). Rachman *et al.* (2007) reported that in Indonesia, the saline area is approximately 440 300 ha and is divided into medium saline (304 000 ha) and ultimate saline (140 300 ha) areas. Rad *et al.* (2012) also reported that elevating salinity to 6 dS/m can reduce rice productivity by 50%. Therefore, the assembly of salinity-tolerant rice cultivars is an effective and efficient solution to increase yield.

The management of salinity tolerant rice cultivars is largely dependent on three factors, i.e., the screening method, selection environment, and selection traits (Anshori *et al.,* 2018). In general, the screening approach is closely related to the critical phase of the plant. Several past findings have revealed that the germination phase (Mokhtar *et al.,* 2015; Diaguna *et al.,* 2017), seedling phase (Zeng *et al*., 2001; Ali *et al.,* 2014; Anshori *et al.,* 2021), and generative phase (Moradi and Ismail, 2007) are the critical phases of rice plants under salinity. Screening in the early seedling phase in static hydroponic culture is frequently used to measure the tolerance level of a rice genotype (Ali *et al.,* 2014). This method is considered to be time-efficient, and stress levels can be well controlled in this approach. However, this screening method has several weaknesses, one of which is that the stress imposed precludes the plants from reaching the generative phase. Ismail *et al.* (2013), Kranto *et al.* (2016), and Sen *et al.* (2017) stated screening in the vegetative phase has a relatively low correlation with that in the generative phase. Additionally, the use of static hydroponic has a weakness wherein the low solubility of oxygen in nutrient solutions affects plant growth (Ginting, 2008; Pudjiwati and Asmina, 2019). Therefore, controlled genotype screening for salinity stress in the generative phase is an area for further development.

Several studies on rice screening for salinity in the generative phase have been conducted. However, in some of the studies, soil media (Moradi and Ismail 2007; Safitri *et al.,* 2016; Anshori *et al.,* 2018) and inert material, i.e., sand, gravel (Egdane *et al.,* 2003), were used for growing and screening of the rice genotypes. The difference in growing media is considered cannot effectively the growing environment of genotypes. Given that different media have different effects with different levels of salinity and nutrients, the environmental interaction might be highly complex (Kranto *et al.,* 2016).

The use of a dynamic hydroponic system, such as the deep flow technique (DFT), could be highly effective and is an alternative to screening rice for salinity in the generative phase. This hydroponic system enables nutrient circulation by flooding roots with nutrient solutions. The circulation system increases the amount of dissolved oxygen in the nutrient solution, hence optimizing water absorption and plant growth (Yoshida *et al.*, 1997; Bonachela *et al.,* 2010; Ningrum *et al.,* 2014). This method is expected to increase the objectivity and balance of screening rice for tolerance to salinity stress. However, this technique requires a critical environment and specific selection criteria to achieve tangible results. Consequently, the main aim of this study was to evaluate the application of hydroponic DFT and to determine the environment and character selection suitable for the screening of rice genotypes under salinity.

## MATERIALS AND METHODS

This study, which focused on rice screening under salinity, was conducted in the greenhouse from April 2020 to June 2020 at the Department of Agronomy, Faculty of Agriculture, Hasanuddin University, Indonesia. The generative phase was carried out on nutrient culture in accordance with Egdane *et al.* (2003). The research material comprised five rice cultivars ('Inpari-34 Salin Agritan', 'Ciherang', 'IR-29', 'Inpari-29', and 'Jeliteng'), planting media, water, AB mix, and NaCl. Several other tools, such as a seed tub, a pH meter, and an EC meter, were also required to run the hydroponic DFT.

The experiment was laid out in a randomized complete block design with three salinity stress levels, i.e., 0, 60, and 120 mM NaCl, and three replications. Each unit of the hydroponic DFT culture represented one stressed environment, and each cultivar was replicated three times. Therefore, 45 experimental units were established, and each unit consisted of three rice seeds.

The seedlings were allowed to grow for 15 days before their transplantation into nutrient culture media. The hydroponic DFT installation was constructed on polymerizing vinyl chloride pipes. Each pipe had planting holes of 5 cm in diameter with a 20 cm space between two holes. The pipes were flooded with nutrient solutions. The seedlings were planted inside a net pot container that was set in the pipe holes in a certain way to ensure that the roots were in contact with the nutrient culture solution. The nutrient culture solution was AB mix with a concentration of 5 mL per liter of water. The volume of the nutrient solution was 120 L per nutrient bath. Salinity stress was induced 65 days after transplanting. Salinity treatments were applied gradually to avoid osmotic shock; in the first stage of NaCl administration, 50% of the treatment concentration was applied. After 3 days, the treatment concentration was increased to 60 and 120 mM NaCl. The application of 1 N NaOH or HCl was performed every 2 days to maintain the pH of the solution within the range of 5.5 to 6.5.

### Data recorded

The data on the following variables were recorded: plant height, number of leaves, number of tillers, number of productive tillers, flowering time, chlorophyll a and b, total chlorophyll, fresh shoot weight, dry shoot weight, fresh root weight, dry root weight, panicle length, flag leaf length, percentage of filled grains, percentage of empty seeds, 100-grain weight, and grain yield per clump.

### Data analysis

Analysis of variance for all the variables was performed in accordance with Steel *et al*. (1997). The parametric characters of cultivars that have a significant interaction with salinity levels were converted into stress tolerance index (STI) characters as an index of tolerance to salinity stress (Anshori *et al.,* 2019). The index formula of Fernandez (1992) was followed:

$$\text{Stress tolerance index (STI)} = \frac{Yp \times Ys}{\bar{Y}p^2}$$

where

Yp = Yield of each cultivar under normal conditions

Ys = Yield of each cultivar under salinity stress

$\bar{Y}p$ = average yield of all the cultivars under normal condition

All the STI traits were further analyzed via correlation analysis. Characters showing correlations with yield were subjected to path, factor, and clustergram analyses. Factor analysis was performed with Minitab 17 software, and RStudio software was used for clustergram analysis.

## RESULTS AND DISCUSSION

The analysis of variance related to growth and yield characters is shown in Table 1. The results indicated that all characters were significantly affected by genotypic diversity. Salinity stress levels also affected almost all the traits, except for height, number of leaves, and flowering time. Meanwhile, the interaction effect between genotype and salinity stress also showed significant effects for almost all the traits, except for the number of leaves and tillers, chlorophyll A and B, and total chlorophyll. Nonetheless, plant height and flowering time were the only two traits that had real significance due to cultivar diversity. However, these traits were not significantly affected by the environment.

Analysis of variance is an indicator in assessing the effectiveness of different factors, including crop plant behavior, to different abiotic stresses. Stress assessments can be made on the basis of three different sources, i.e., genotypes, environments, and their interaction (Anshori *et al.,* 2019, 2021; Farid *et al.,* 2020, 2021). The genotype effect is initially assessed to determine the effectiveness of selection. This was also supported by Syukur *et al.* (2015), who stated that population diversity is the main key in genotype selection. The findings of the present study indicated that genotype diversity had a significant effect on all characters. Therefore, the assessment of the adaptability between genotypes and the screening method was effective. The significant environmental influence on a character indicates that the selection environment is effective in seeing the response of a population to a character (Safitri *et al.,* 2016; Anshori *et al.,* 2021). However, it cannot explain the nature of the tolerance of the genotypes for these characters. Therefore, the assessment based on the effect of interaction becomes the initial basis for assessing the potential of a character to become a selection criterion (Al-Naggar *et al.,* 2015; Akbar *et al.,* 2019; Anshori *et al.,* 2019). Cultivar interaction showed differences in the responses of tolerant and sensitive genotypes to different environmental stresses (Kan *et al.,* 2010; Akçura and Çeri, 2011; Al-Naggar *et al.,* 2015; Safitri *et al.,* 2016; Sitaresmi *et al.,* 2016). The present results further demonstrated that plant height, number of productive tillers, flowering time, fresh shoot weight, dry shoot weight, fresh root weight, dry root weight, panicle length, flag leaf length, percentage of filled grain, percentage of empty grain, 100-grain weight, and grain yield per clump were potential characters for use as selection criteria in hydroponic culture salinity screening in the generative phase. However, the selection criteria must be determined in consideration of the concept of STI.

The STI formation for various traits with significant interaction is shown in Table 2. The formation consists of two types: STI-1 for the salinity stress of 60 mM NaCl and STI-2 for the salinity stress of 120 mM NaCl. In general, STI is one of the tolerance indexes that is commonly used to measure the tolerance level of a genotype under a stressed environment. The STI is dynamic given that it considers the average of all genotypes when measuring the potential tolerance traits of a genotype (Hosseini *et al.,* 2012; Anshori *et al.,* 2019). The use of this tolerance index has been proven by several workers, namely, Anshori *et al.* (2018), who reported on rice plants under salinity stress; Farid and Ridwan (2018), who studied the tolerance of rice plants to drought stress; Anwar *et al.* (2020), who investigated the response of wheat plants to drought stress; and Kumar *et al.*

**Table 1.** Mean squares and repeatability of rice traits under normal and saline environments.

| Charac-ters | Cultivars | Stress | Var : Str | Errors | CV | Vg | Vp | Repeatability |
|---|---|---|---|---|---|---|---|---|
| PH | 5899.721** | 133.414 ns | 103.264* | 40.778 | 7.51 | 20.83 | 61.61 | 33.81 |
| NL | 8.028** | 2.485 ns | 1.876 ns | 0.921 | 13.46 tr | 0.32 | 1.24 | 25.69 |
| NT | 0.715** | 0.912** | 0.219 ns | 0.136 | 12.29 tr | 0.03 | 0.16 | 16.9 |
| NPT | 0.861** | 11.213** | 0.36* | 0.12 | 17.27 tr | 0.08 | 0.2 | 40 |
| FD | 1755.925** | 505.768 ns | 855.735** | 199.736 | 17.84 | 218.67 | 418.4 | 52.26 |
| Chl A | 29.941* | 85.34** | 12.136 ns | 9.487 | 24.19 tr | 0.88 | 10.37 | 8.51 |
| Chl B | 604.257** | 1670.684** | 94.053 ns | 147.247 | 15.53 | −17.73 | 129.52 | −13.69 |
| Chl Tot | 30.385* | 75.99** | 9.057 ns | 8.691 | 18.92 tr | 0.12 | 8.81 | 1.38 |
| SFW | 566.488** | 2871.853** | 175.875** | 14.105 | 12.61 | 53.92 | 68.03 | 79.27 |
| SDW | 55.234** | 134.855** | 15.062** | 2.925 | 15.91 | 4.05 | 6.97 | 58.04 |
| RFW | 40.102** | 146.327** | 24.247** | 3.792 | 14.26 | 6.82 | 10.61 | 64.26 |
| RDW | 1.171** | 0.921* | 0.967** | 0.2 | 19.14 | 0.26 | 0.46 | 56.11 |
| PL | 87.852** | 504.215** | 21.044** | 7.255 | 15.29 | 4.6 | 11.85 | 38.78 |
| FLL | 261.91** | 423.795** | 108.449** | 27.236 | 19.75 | 27.07 | 54.31 | 49.85 |
| PNFG | 0.085** | 2.246** | 0.025** | 0.001 | 10.11 | 0.01 | 0.01 | 88.89 |
| PNUG | 0.12** | 1.02** | 0.112** | 0.022 | 22.71 tr | 0.03 | 0.05 | 57.69 |
| W100 | 0.437** | 1.411** | 0.34** | 0.048 | 14.54 | 0.1 | 0.15 | 66.97 |
| GY | 0.2205** | 23.16** | 0.091* | 0.03 | 15.1 tr | 0.02 | 0.05 | 40.4 |

Notes: tr: the result of transformation √x, ns: not significant, **: significant effect on 1% level, *: significant effect on 5 % level, CV: Coefficient of variance, PH: plant height, NL: number of leaves, NT: number of tillers, NPT: number of productive tiller, FD: flowering days, Chl A: Chlorophyll A, Chl B: Chlorophyll B, Chl Tot: Total Chlorophyll, SFW: fresh shoot weight, SDW: dry shoot weight, RFW: fresh root weight, RDW: dry root weight, PL: panicle length, FLL: flag leaf length, PNFG: percentage number of filled grains, PNUG: percentage number of unfilled grains, W100: Weight of 100 grains, GY: Grain yield.

**Table 2.** STI of selected characters for salinity stress.

| G | E | PH | NPT | FD | SFW | SDW | RFW | RDW | PL | FLL | PNFG | PNUG | W100 | GY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| V1 | STI1 | 1.070 | 0.557 | 1.113 | 0.990 | 1.061 | 1.044 | 1.184 | 0.864 | 0.987 | 0.532 | 4.006 | 0.832 | 0.192 |
| V2 | STI1 | 0.950 | 0.807 | 0.933 | 1.345 | 1.090 | 1.168 | 1.078 | 0.834 | 0.783 | 0.286 | 4.638 | 0.825 | 0.160 |
| V3 | STI1 | 1.024 | 0.526 | 0.899 | 0.277 | 0.590 | 0.682 | 0.812 | 0.671 | 0.966 | 0.148 | 5.387 | 0.896 | 0.044 |
| V4 | STI1 | 1.446 | 0.313 | 1.041 | 0.647 | 0.472 | 0.620 | 0.677 | 1.149 | 1.374 | 0.075 | 5.866 | 0.952 | 0.034 |
| V5 | STI1 | 0.803 | 0.797 | 1.070 | 0.785 | 0.977 | 1.060 | 1.197 | 0.713 | 0.795 | 0.160 | 7.591 | 0.864 | 0.064 |
| V1 | STI2 | 1.165 | 0.344 | 1.121 | 0.537 | 1.177 | 1.090 | 1.291 | 0.626 | 0.738 | 0.447 | 4.567 | 0.748 | 0.016 |
| V2 | STI2 | 0.856 | 0.276 | 1.056 | 0.374 | 0.400 | 0.421 | 0.540 | 0.583 | 0.575 | 0.187 | 5.167 | 0.769 | 0.004 |
| V3 | STI2 | 0.951 | 0.000 | 0.000 | 0.137 | 0.334 | 0.488 | 0.614 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| V4 | STI2 | 1.210 | 0.073 | 1.085 | 0.219 | 0.275 | 0.373 | 0.592 | 0.663 | 1.312 | 0.158 | 5.451 | 0.954 | 0.002 |
| V5 | STI2 | 0.783 | 0.260 | 1.099 | 0.454 | 0.701 | 0.760 | 0.969 | 0.600 | 0.750 | 0.156 | 7.610 | 0.754 | 0.006 |

Notes: G:genotype, E:environment, PH: plant height, NPT: number of the productive tillers, FD: flowering days, SFW: fresh shoot weight, SDW: dry shoot weight, RFW: fresh root weight, RDW: dry root weight, PL: panicle length, FLL: flag leaf length, PNFG: percentage number of filled grains, PNUG: percentage number of unfilled grains, W100: Weight of 100 grains, GY: Grain yield, V1: "Inpari-34 Salin Agritan', V2: 'Ciherang', V3: 'IR-29', V4: 'Inpari-29', V5: 'Jeliteng', STI1: STI 60 mM NaCl, STI2: STI 120 mM NaCl.

**Table 3.** Pearson correlation for selected characters under salinity stress.

| Traits | PH | NPT | FD | SFW | SDW | RFW | RDW | PL | FLL | PNFG | PNUG | W100 | YH |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PH | 1.00 | | | | | | | | | | | | |
| NPT | −0.19 tn | 1.00 | | | | | | | | | | | |
| FD | 0.13 tn | 0.38* | 1.00 | | | | | | | | | | |
| SFW | −0.04 tn | 0.73** | 0.36 tn | 1.00 | | | | | | | | | |
| SDW | −0.12 tn | 0.63** | 0.36* | 0.76** | 1.00 | | | | | | | | |
| RFW | −0.15 tn | 0.66** | 0.30 tn | 0.81** | 0.96** | 1.00 | | | | | | | |
| RDW | −0.17 tn | 0.52** | 0.32 tn | 0.63** | 0.91** | 0.90** | 1.00 | | | | | | |
| PL | 0.43* | 0.48** | 0.75** | 0.54** | 0.26 tn | 0.29 tn | 0.18 tn | 1.00 | | | | | |
| FLL | 0.52** | 0.14* | 0.68** | 0.16 tn | −0.06 tn | −0.03 tn | −0.03 tn | 0.82** | 1.00 | | | | |
| PNFG | 0.08 tn | 0.38* | 0.50** | 0.49** | 0.67** | 0.59** | 0.54** | 0.33 tn | 0.16 tn | 1.00 | | | |
| PNUG | −0.07 tn | 0.36* | 0.79** | 0.18 tn | 0.15 tn | 0.13 tn | 0.19 tn | 0.58** | 0.56** | 0.00 tn | 1.00 | | |
| W100 | 0.23 tn | 0.38* | 0.90** | 0.33 tn | 0.20 tn | 0.18 tn | 0.17 tn | 0.81** | 0.84** | 0.29 tn | 0.77** | 1.00 | |
| GY | 0.00 tn | 0.70** | 0.20 tn | 0.74** | 0.52** | 0.57** | 0.37** | 0.45* | 0.17 tn | 0.62** | −0.08 tn | 0.18 tn | 1.00 |

Notes: PH: plant height, NPT: number of productive tiller, FD: flowering days, SFW: fresh shoot weight, SDW: dry shoot weight, RFW: fresh root weight, RDW: dry root weight, PL: panicle length, FLL: flag leaf length, PNFG: percentage number of filled grains, PNUG: percentage number of unfilled grains, W100: Weight of 100 grains, GY: Grain yield.

**Table 4.** Path analysis for rice yield per plant based on the traits with the highest correlation with STI and yield.

| Traits | NPT | SFW | SDW | RFW | RDW | PL | PNFG | Res |
|---|---|---|---|---|---|---|---|---|
| NPT | 0.43* | 0.41 | −0.63 | 0.44 | −0.11 | −0.08 | 0.24 | 0.42 |
| SFW | 0.31 | 0.57** | −0.76 | 0.54 | −0.14 | −0.09 | 0.31 | 0.42 |
| SDW | 0.27 | 0.43 | −1.00 | 0.64 | −0.19 | −0.04 | 0.42 | 0.42 |
| RFW | 0.28 | 0.46 | −0.96 | 0.66** | −0.19 | −0.05 | 0.37 | 0.42 |
| FDW | 0.23 | 0.36 | −0.91 | 0.60 | −0.21 | −0.03 | 0.34 | 0.42 |
| PL | 0.21 | 0.31 | −0.26 | 0.19 | −0.04 | −0.16 | 0.20 | 0.42 |
| PNFG | 0.16 | 0.28 | −0.67 | 0.39 | −0.11 | −0.05 | 0.63** | 0.42 |

Notes: numbers in bold indicate a direct effect, cross-print R2: 0.58, Res: Residual, NPT: number of productive tiller, SFW: fresh shoot weight, SDW: dry shoot weight, RFW: fresh root weight, RDW: dry root weight, PL: panicle length, PNFG: percentage number of filled grains.

(2015) and Fadhli *et al.* (2020), who explored the response of maize crops to drought stress. Based on these past findings, the overall characteristics of the STI were applicable as the basis for further analysis in this study.

Correlation analysis can be used to identify the best character. In this study, the analysis focused on productivity as the main character (Table 3). The results showed that productive tillers, fresh shoot weight, dry shoot weight, fresh root weight, dry root weight, panicle length, and the percentage of filled grains had a significant correlation with productivity. Similar results were also reported in the past by Fiyaz *et al.* (2011), Gopikannan and Ganesh (2013), Krishnamurthy *et al.* (2013), and Ghosh *et al.* (2016). The present results could become a basis for further in-depth analysis and were in line with the findings of Anshori *et al.* (2019), Fadhli *et al.* (2020), and Farid *et al.* (2020, 2021). Path analysis is suggested as possible in-depth analysis.

Path analysis showed that fresh root weight (0.66), percentage of filled grains (0.63), fresh shoot weight (0.57), and productive tillers (0.43) were the characters with a high direct effect on productivity (Table 4). In general, path analysis is a development of multiple regression analysis and correlation that aims to separate the direct and indirect effects of a character on the main character (Mattjik and Sumertajaya, 2011). In path analysis, the value of the direct influence is often used as a consideration in determining the character of selection (Anshori *et al.,* 2018; Kose *et al.,* 2018; Anshori *et al.,* 2019; Akbar *et al.,* 2019; Anshori *et al.,* 2021). Direct influence is the weight of the variability of a character in influencing the diversity of the main character (Singh and Chaudhary 2007; Manjunatha *et al.,* 2017). Therefore, path analysis can help determine the best secondary character affecting the main character. On the basis of present findings, the traits fresh root weight, percentage of filled grains, fresh shoot weight, and productive tillers can be recommended in screening for salinity tolerance through hydroponic DFT. However, the present results need to be further supported by other multivariate analyses. Kose *et al*. (2018), Farid *et al.* (2020), and Anshori *et al.* (2021) stated that the use of multiple multivariate analyses could increase the precision of the assessment of selection, especially in multiple environmental trials. Other possible multivariate analyses are cluster heat map analysis and factor analysis.

The heat map cluster analysis showed two dendrograms, namely, character grouping (vertical) and genotype grouping (horizontal) (Figure 1). The vertical and horizontal groupings had two major groups. On the basis of STI characterization, the grain yield grouped together with the percentage of filled grains, whereas other group consisted of the number of productive tillers, fresh shoot weight, and fresh root weight. Meanwhile, in genotype grouping, the first group consisted of rice genotypes, i.e., 'Ciherang' ST1, 'Inpari-34 Salin Agritan' STI1, and 'Jeliteng' STI1, whereas the second group consisted of the genotypes 'Inpari-34 Salin Agritan' STI2, 'IR-29' STI1, 'Inpari-29' STI 1, 'Jeliteng' STI2, 'Ciherang' STI2, and 'IR-29' STI2.

Heat map cluster analysis can visualize the kinship pattern of complex variables and is very simple (Guduru *et al.,* 2018; Anshori *et al.,* 2020). The present findings showed that the heat map pattern of each character revealed a regular gradation pattern. This pattern is an indication that these characters were potential selection characters. Similar findings were also reported by Anshori *et al.* (2020) and Virga *et al.* (2020), who concluded that a regular gradation pattern is one of the characteristics of the selection criteria for stress. Genotype grouping indicated that STI-1 (60 mM NaCl) was a potential selection environment in hydroponic DFT screening for salinity stress. In addition, on the basis of this grouping, the cultivars 'Ciherang',

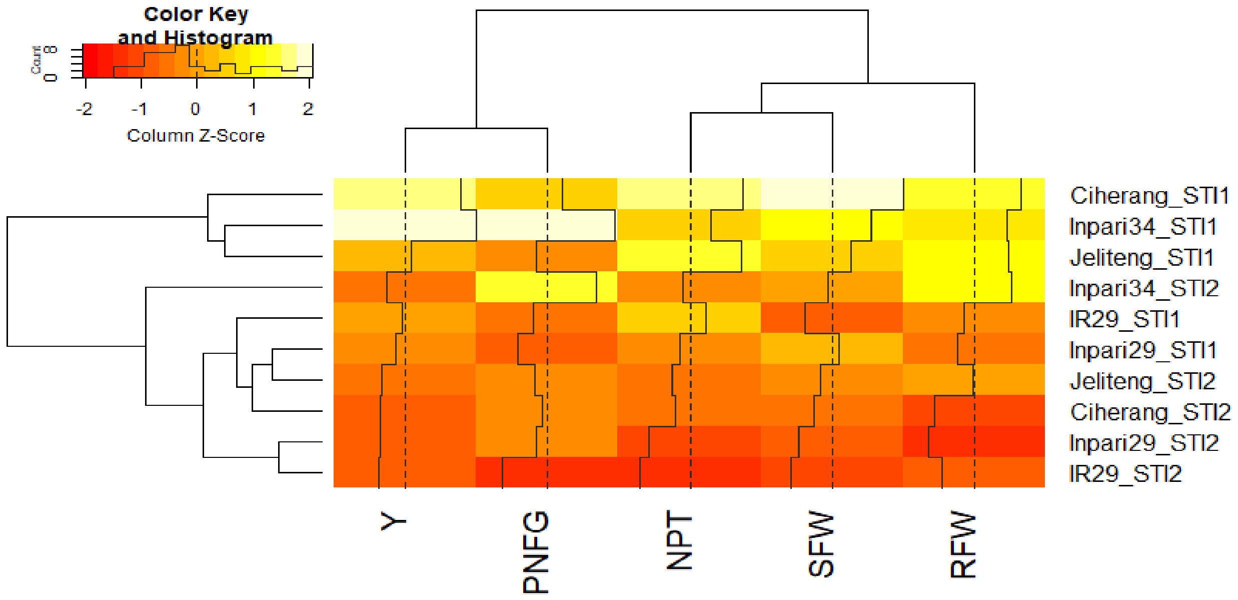

**Figure 1.** Heatmap cluster analysis of the STI of five cultivars based on five selection characters. Y: grain yield, PFG: percentage of filled grains, NPT: number of productive tillers, SFW: shoot fresh weight, RFW: root fresh weight.

**Table 5**. Factor analysis of the characters with the best direct influence on yield.

| Variables | Factor-1 | Factor-2 | Factor-3 | Communality |
|---|---|---|---|---|
| NPT | 0.631 | 0.004 | −0.384 | 0.877 |
| SFW | 0.101 | 0.448 | −0.181 | 0.882 |
| RFW | −0.503 | 0.944 | −0.014 | 0.967 |
| PNFG | −0.271 | −0.128 | 1.000 | 0.974 |
| GY | 0.76 | −0.606 | 0.274 | 0.944 |
| Variance | 1.773 | 1.6132 | 1.2584 | 4.6445 |
| % Var | 0.355 | 0.323 | 0.252 | 0.929 |

Notes: NPT: number of the productive tillers, SFW: fresh shoot weight, RFW: fresh root weight, PNFG: percentage number of filled grains, GY: grain yield.

'Jeliteng', and 'Inpari-34 Salin Agritan' were considered as salt-tolerant genotypes. The grouping of cultivar 'Inpari-34 Salin Agritan' into the tolerant group was also reported by Sembiring *et al.* (2019). By contrast, the rice cultivars 'Inpari-29' and 'IR-29' were classified as the most sensitive genotypes to salinity through hydroponic DFT screening. Cultivar 'IR-29' was also placed in the category of most sensitive rice cultivars by Bhowmik *et al.* (2007), Safitri *et al.* (2016), Chhavi *et al.* (2018), and Anshori *et al.* (2020). This result indicated that screening with the hydroponic DFT could differentiate between the tolerance potential of tolerant and sensitive cultivars. Based on these findings, hydroponic DFT with 60 mM NaCl was found to be most effective in rice screening for salinity stress tolerance.

Factor analysis revealed that the number of productive tillers and productivity were the first factors that determined the diversity of tolerance between rice cultivars under different environmental conditions with loading factor values of 0.631 and 0.76, respectively (Table 5). The second factor was based on the traits fresh shoot weight and fresh root weight, which had loading factor values of 0.448 and 0.944, respectively. Meanwhile, the third factor was the percentage of filled grains with a loading factor value of 1.

Factor analysis is a common multivariate analysis for identifying relationships among random variables internally (Mattjik and Sumertajaya, 2011; Farid *et al.,* 2020). Although this analysis has the same properties as principal component analysis, it serves to reduce small internal variability or covariance. Conversely, large internal covariance in a dimension is increased by the rotation function (Acquaah, 2007; Dormann *et al.,* 2013; Rocha *et al.,* 2018). Therefore, this concept can be feasibly used to assess the capability of potential secondary characters that have covariance relationships. Meanwhile, given that the determination of the main character in factor analysis is based on a factor score above 0.32 (Yong and Pearce, 2013), not all characters were selected to determine the variance in the total diversity of the initial data. Based on the set intersection in the correlation, path, heat map clusters, and factor analyses, the trait productive tillers could be used as a secondary character in supporting potential productivity under salinity stress through hydroponic DFT.

Hasanuzzaman *et al*. (2009), Safitri *et al.* (2016), and Anshori *et al.* (2019) also reported productive tillers as the best secondary character in screening for salinity stress. Generally, productive tillers are an early indicator in supporting rice productivity. Ghosh *et al.* (2016) reported that in the reproductive phase, salinity stress affects the character of yield components, including panicle formation, seed filling, and spikelet sterility, resulting in reduced yield per plant. Stress at the beginning of the flowering phase results in the abnormal formation of rice inflorescence. Therefore, some of the tillers are unable to develop further and to produce panicles. The determination level of tolerance in hydroponic rice begins with panicle formation. The present study showed that the concept of genotype screening for tolerance through hydroponic DFT also follows the same pattern in saline soils and direct processing in the field (Anshori *et al.,* 2019) or artificially (Safitri *et al.,* 2016). In addition, the number of productive tillers was also considered to be a relatively early and quickly observed character with high heritability. Acquaah (2007) stated that the best secondary character or selection criteria is determined by the ease of its observation, high heritability value, and correlation with the main character. Therefore, productive tillers were recommended as a selection criterion in screening rice genotypes under salinity stress through hydroponic DFT.

## CONCLUSIONS

The 60 mM concentration of NaCl and productive tillers were the best environment and selection character for salinity screening in hydroponic DFT. On the basis of salinity screening in the generative phase through hydroponic DFT, the rice cultivars 'Ciherang', 'Inpari-34 Salin Agritan', and 'Jeliteng' were grouped into the tolerant category. On the basis of the results, hydroponic DFT was identified and recommended as the best screening method for salinity in the generative phase of rice crops.

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