



ASSESSING THE EARLY-SEASON VIGOR OF A DIVERSE RICE POPULATION BY USING MORPHOPHYSIOLOGICAL TRAITS

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SUMMARY

Early-season vigor is an important morphological determinant of a crop's growth rate and duration. It results from metric parameters, such as light interception and dry matter production, loss, and partitioning. Formulating screening tools to assess early-season vigor by using root and shoot characteristics will be useful for identifying genotypes with superior performance during the juvenile growth stages. A 2-year study was conducted by using a sunlit pot culture set-up to assess genetic variation among 100 rice genotypes for shoot and root traits and several physiological parameters at the seedling growth stage (25–30 days after sowing). Given the absence of a significant year or experimental period × genotype interaction for the traits measured, the 2-year data were combined for each genotype. Individual (IVRI) and cumulative response indexes (CVRI) were estimated for each trait for all genotypes. Genotypes were classified into different categories by using CVRI values and standard errors. The majority of the genotypes exhibited low vigor (43%), followed by genotypes with moderate (33%) and very low (16%) vigor. However, five and three genotypes showed high- and very-high vigor, respectively. The CVRI values varied from a low value of 21.36 for RU1404196 to 36.17 for N-22, the most vigorous genotype. The high-vigor genotypes can be valuable genetic resources for developing new varieties with high early-season vigor as well as for physiological studies on canopy development for optimum light interception and weed competitiveness. The information and

methods generated by this study can also be useful in identifying promising rice lines with potentially high vigor in rice breeding programs.

Keywords: Rice (*Oryza sativa* L.), early-season vigor, morphophysiological traits, classification, principal component analysis

Key findings: High vigor during early-season is essential for rapid canopy development and water- and nutrient-acquiring root system development. Genotypic differences for early-season vigor were observed among new and untested rice lines. These differences will help rice breeders develop new rice cultivars.

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INTRODUCTION

Rice (*Oryza sativa* L.), first grown in Southeast Asia 10,000 years ago, is cultivated in over 100 countries globally and serves as the staple food for one half of the global population (Fageria, 2007). In 33 developing nations where rice is consumed as the primary staple food, rice provides 27% of dietary energy needs, 20% of nutritional protein needs, and 3% of dietary fiber (Kennedy *et al.*, 2002). Rice, therefore, is under enormous pressure in terms of keeping its productivity in pace with population growth and dietary demands. In Asia, for example, the demand for rice is predicted to increase by 69% over the next 30 years due to population growth (Hossain, 1997). Although the United States accounts for less than 2% of global rice production, it is a major rice exporter and accounts for 12%–14% of the annual global rice exports (Childs and Livezey, 2006).

In recent years, the yields of improved inbred rice varieties grown under favorable conditions, such as those found in the US, have plateaued and even declined in some countries

due to various challenges related to biotic and abiotic stresses (Redoña, 2004). Rice productivity, which is already facing resource limitations in terms of land and water availability, is under enormous pressure to keep pace with a continuously increasing population. Technological advances in rice production systems must be made to meet future rice demands. One approach to minimize the gap between rice production and future demand is to develop varieties with a broad range of adaptations to diverse growing conditions. For example, breeding programs may select varieties adapted to dry, direct seeding, or aerobic cultivation to combat water scarcity (Cabangon *et al.*, 2002).

Another example is selecting for more extended, more expansive root systems that will increase water and nutrient uptake. This approach requires multidisciplinary collaboration among breeders, physiologists, and other plant scientists to select genotypes adapted to variable environmental conditions (Dingkuhn *et al.*, 2015). However, research on rice root growth is limited because plant

systems below ground are generally arduous to study, and strong interactions with unmeasured variables can complicate results.

Mississippi is one of the five rice-producing states in the US mid-South, where producers typically plant from March to April primarily through drill-seeding. According to studies conducted from 2007–2014, the optimal time to plant rice in Mississippi to avoid yield reduction is between the 20th of March and the 13th of April (Golden *et al.*, 2014). A major yield-limiting factor in the US mid-South is erratic rainfall and high temperatures during the summer season. Walker (2013) showed that rice planted earlier within this window typically produces higher, more stable yields than later-planted crops. Therefore, the selection of rice genotypes that are well suited for early planting may help producers optimize their growing conditions throughout the growth of their crop plants.

Early-season growth is a critical phase for rice that influences canopy development, tillering, and, ultimately, the overall crop stand. Early-season vigor is a crucial trait that allows the plant to rapidly access resources, conferring the capability to compete with weeds and pests (Namuco *et al.*, 2009). It is a complex trait that is manifested by the capacity of seedlings to accumulate leaf area and shoot biomass rapidly. It is a summation of a genotype's capability to germinate uniformly, synchronize emergence, and proliferate in growth (Chen *et al.*, 2015). Vigor, a complex trait, can be simplified for genetic improvement by dissecting it further into component traits of less genetic complexity, such as leaf area, leaf size, tiller number, leaf expansion rate, and leaf appearance (Rebetzke

et al., 2007; Maydup *et al.*, 2012). Improving early-season vigor is considered as the most relevant and useful strategy for mitigating poor and uneven crop stand establishment, thus combating one significant constraint in direct-seeded rice systems (Okami *et al.*, 2015; Kumar *et al.*, 2009; Singh *et al.*, 2017a; Singh *et al.*, 2017b, Lone *et al.*, 2019).

Measuring and identifying important traits to screen and classify rice genotypes for early-season vigor is valuable for selecting new varieties and developing genotypes that are better suited for the US mid-South production system. In recent years, the development of technologies, such as optical scanners and analytical software, has aided the development of studies on early vigor. For example, the WinRHIZO ocular scanner (Regent Instruments Inc., Canada) is a precise, rapid, and simple instrument that is used to analyze the root characteristics of cereals (Wijewardana *et al.*, 2015; Singh *et al.*, 2017b; Singh *et al.*, 2018). Genotypes were categorized into various stress-tolerant groups on the basis of single and cumulative value indexes (Singh *et al.*, 2017b). Others have used principal component analysis (PCA) to rank genotypes into various groupings (Asif *et al.*, 2010). The application of these techniques in screening root parameters in diverse rice germplasm pools can help identify new donors and genotypes with early-season vigor, which is essential for crop stand establishment in the U.S. mid-South rice production system. The objectives of this study were (1) to evaluate the root and shoot morphology and growth of rice genotypes of temperate origin during the seedling growth stage; (2) to develop a method to assess early-

season vigor variability; and (3) to characterize rice genotypes on the basis of vigor response indexes.

MATERIALS AND METHODS

Seed materials and facility

In this study, 100 genotypes from the Mississippi State University (MSU) rice breeding program in Stoneville, Mississippi, were utilized. MSU's breeding program uses this germplasm to develop new varieties adapted to the US mid-South. Approximately 95% of these genotypes are tropical *japonica* varieties, the predominant subspecies grown in the US mid-South, whereas 5% are *indica* varieties, the rice subspecies commonly grown in Asia. Approximately 70% of the genotypes were breeding lines under development, and 30% were commercially released varieties. Of the released varieties, 25 have been released for commercial use in the US mid-South.

The experiments were conducted at the Environmental Plant Physiology Laboratory at MSU's Rodney Foil Plant Science Research Facility located near Starkville, Mississippi, during the 2015 and 2016 growing seasons. In 2015, the experiment was conducted from June to July over 30 days. In 2016, the investigation was conducted from August to September, again for 30 days. The environmental conditions for these two experiments are shown in Table 1. In both studies, rice plants were sown in 6 L polyvinylchloride pots that were 15.2 cm in diameter and 30.5 cm in height and filled with a custom soil mixture of three parts

sand to one part topsoil and 500 g of gravel at the bottom of each pot. The rooting medium was classified as sandy loam (87% sand, 2% clay, and 11% silt). The bottom of each pot was sealed with a plastic cap, and a hole 0.5 cm in diameter was drilled at the bottom for drainage. Initially, eight seeds were sown at a depth of 3 cm in each pot. After emergence, the plants were gradually thinned to a single plant in each pot. In both experiments, the pots were organized by using a randomized complete block design in three rows (replication) with 100 pots per row. Rice genotypes were assigned randomly to each of the 100 pots. Plants were exposed to natural sunlight and irrigated three times per day (0800, 1300, and 1700 h) via an automated and computer-controlled drip system with full-strength Hoagland's nutrient solution (Hewitt, 1952) designed for optimum plant growth. Plant growth and development, as well as root and shoot morphological features, were assessed 30 days after sowing (DAS).

Parameter measurements

Shoot growth and development traits

The following morphological characteristics were measured: leaf number (LN), plant height (PH), the total number of tillers (TN), and dry biomass (leaves, stems, roots, and total dry weights, g plant⁻¹). Biomass was oven-dried at 75 °C for 72 h before being weighed. Shoot weight was calculated by summing the leaf and stem weight for each genotype. The root/shoot ratio was calculated by dividing root weight (RW) by the sum of leaf weight and stem weight for each genotype. The

Table 1. Environmental details, including solar radiation, average relative humidity, and mean temperature, during the experimental period for each year.

Environmental condition	Experiment 1			Experiment 2		
	Mean	Max	Min	Mean	Max	Min
Temperature (°C)	27.27 ± 0.4	31.6	22.1	28.5 ± 0.2	31	26.3
Relative humidity (%)	76.1 ± 1.2	88.5	67.0	75.9 ± 1.5	90	54.6
Solar radiation (MJ m ⁻² day ⁻¹)	23.62 ± 0.8	29.0	12.6	21.3 ± 0.7	26.7	13.4

leaf area (LA) was determined by using a leaf area meter (Li-3100 leaf area meter, Li-COR Inc., Lincoln, NE).

Root morphology, architecture, and root parameters

At 30 DAS, plant growth was terminated by separating plant shoots from the roots at the soil surface level. All soil media were washed from the roots, which were subsequently placed between moist paper towels until further analysis. WinRHIZO Pro optical scanner (Version 2009, Regent Instruments, Inc.), adjusted to acquire root images at 800 × 800 dpi resolution, was utilized to analyze the roots. The WinRHIZO Pro software was used to analyze nine root parameters, including root surface area (RSA), average root diameter (RAD), cumulative root length (RL), root volume (RV), number of forks (RNF), number of tips (RNT), and number of crossings (RNC). The longest root length (LRL) was measured with a ruler, and root number (RN) was counted manually. After scanning, the roots were placed in paper bags and dried at 75 °C for 3 days before determining the dry weight.

Vigor indexes utilized

For each experiment, the individual vigor index (I) for each parameter was calculated by dividing the value of each genotype (V_i) by the maximum

value (V_x) among the genotypes for the given parameter (Eq. 1).

$$I = V_i/V_x. \quad [\text{Eq. 1}]$$

Then, the values of the cumulative vigor response index (CVRI) were estimated as the sum of all individual indexes for all parameters for each genotype (Eq. 2).

$$\begin{aligned} \text{CVRI (1)} = & (PH_i/PH_x) + (TN_i/TN_x) + \\ & (LN_i/LN_x) + (LA_i/LA_x) + (LW_i/LW_x) + \\ & (SW_i/SW_x) + (RW_i/RW_x) + \\ & (SHW_i/SHW_x) + (RS_i/RS_x) + (TW_i/TW_x) \\ & + (RL_i/RL_x) + (RSA_i/RSA_x) + (AD_i/AD_x) \\ & + (RV_i/RV_x) + (T_i/T_x) + (LRL_i/LRL_x) + \\ & (RN_i/RN_x) + (SPAD_i/SPAD_x) + \\ & (Fv/Fm_i/Fv/Fm_x). \end{aligned} \quad [\text{Eq. 2}]$$

The total vigor response index (TVRI) was determined as the sum of all CVRIs from each experiment (Eq. 3).

$$\text{CVRI (1)} + \text{CVRI (2)} = \text{TVRI}. \quad [\text{Eq. 3}]$$

Finally, the total vigor response indexes and standard deviations (SD) were used to classify genotypes into very low-to-low, moderate, high, and very high vigor at early-season growth and developmental stages.

Data analysis

Analysis of variance for root and shoot traits was performed by using the Proc

GLM procedure in SAS 9.4 (SAS Institute, 2011). Genotype was considered as a fixed effect, whereas replication within the experiment was considered as a random effect. The separation of means was performed by using the least significant difference (LSD) test at $P = 0.05$. The standard error of each mean was calculated by using SigmaPlot version 13 (Systat Software Inc., San Jose, CA). The correlation and regression coefficients for shoot and root parameters among rice genotypes were obtained by using the Pearson correlation (PROC CORR) and (PROC REG) procedures in SAS. Principal component analysis (PCA) was performed on the correlation matrix of 100 genotypes and 19 response variables comprising PH, TN, LN, LA, LW, SW, RW, SHW, RS, TW, RL, RSA, AD, RV, T, LRL, RN, SPAD, and Fv/Fm by using the PRINCOMP procedure of SAS (SAS Institute, 2011). The results were abridged in biplots by using SigmaPlot version 13 (Systat Software Inc., San Jose, CA).

RESULTS AND DISCUSSION

Morphophysiological traits

Through the joint analysis of variance for the two studies, significant variability among the genotypes for all morphophysiological parameters measured, except for the leaf number of the main stem (LN) and quantum efficiency of fluorescence (Fv/Fm), was observed (Table 2). Selection for superior genotypes based on growth and yield at a single location or trial in a year may not be advantageous (Shrestha *et al.*, 2012; Annicchiarico, 1994). However, given that 90% of the genotype \times year interaction of

traits was not significant (Table 2), the 2-year data for each genotype were combined. The evaluation of genotypes for the stability of performance under varying environmental conditions, including seasonal experiments, is an essential part of any breeding program. Moreover, genetic variation is a crucial factor that enhances the plant's survival within its cultivated environment (Tariku *et al.*, 2013; Diwan, 2006).

Growth parameters

A crucial component for accelerating the expansion of newly developed crop genotypes, including rice, is the rapid and precise phenotypic assessment of genotypes under different environmental conditions, including planting them year after year. Despite technological innovations that describe genomes cheaply and rapidly, the ability to quickly and accurately measure plant performance remains a limiting factor in plant breeding and genetics.

Traits, such as seedling or plant height and dry weight, have been identified as useful indicators of seedling and early vigor (Regan *et al.*, 1992). A significant variation ($P < 0.001$) among genotypes in plant height, with a low of 15.3 cm (RU1404157 and RU1404196) to a high of 22 cm (CL Jazzman and RU1401102) and an average of 18.8 cm (Table 3), was identified. In rice, early vigor is mainly attributed to high leaf area index (LAI) during the vegetative stage (Okami *et al.*, 2011). A 126% change was recorded among genotypes between high 3.3 (CL 152) and low 2.6 (RU1404196) leaf number with an average of 230.5 cm². The rate of early leaf area development

Table 2. Analysis of variance across 100 rice genotypes and 2-year treatments and their interactions (genotypes by year) with rice morphophysiological parameters measured 30 days after planting: PH, TN, LN, LA, LW, SW, SHW, RS, TW, RL, RSA, AD, RV, T, LRL, RN, SPAD, and Fv/Fm.

S.O.V	PH	TN	LN	LA	LW	SW	RW	SHW	RS	TW	RL	RSA	AD	RV	T	LRL	RN	SPAD	Fv/Fm
Geno- types	***	***	N.S	***	***	**	***	***	**	**	**	***	***	***	***	*	**	**	N.S
Year 1	**	***	*	***	**	**	**	***	**	***	**	***	**	**	N.S	**	**	**	N.S
Year 2	**	**	N.S	***	**	*	**	**	N.S	***	*	**	*	**	*	***	*	*	*
Years	N.S	N.S	N.S	N.S	*	N.S	**	N.S	*	N.S	*								
G x Y	N.S	N.S	N.S	N.S	N.S	N.S	**	N.S	*	N.S									

† *, **, and *** represent significant differences at the 0.05, 0.01, and 0.001 *P* level, respectively.

†† NS represents non-significant differences at the 0.05 *P* level.

Table 3. Means of PH, TN, LN, LA, LW, SW, RW, SHW, RS, and TW of 100 rice genotypes.

No.	Genotype name	Measured growth parameters									
		PH	TN	LN	LA	LW	SW	RW	SHW	RS	TW
1	14CLPYT033	16.1	9	2.8	196.5	1.5	1.9	0.7	3.4	0.2	3.8
2	14CLPYT108	17.2	9.3	2.8	221.2	1.5	1.5	0.7	2.9	0.3	3.2
3	14CVPYT094	16.5	8.7	2.8	264.8	1.8	1.8	0.8	3.6	0.2	4
4	14CVPYT144	19.7	9.3	2.9	196.7	1.8	1.9	0.7	3.7	0.2	4
5	COLORADO	17.3	10	2.9	215.2	1.7	1.9	0.6	3.5	0.2	3.8
6	Bowman	16.3	8	2.9	210.4	1.4	1.3	0.7	2.7	0.3	3.2
7	CAFFEY	19.4	9.7	2.9	238.1	2	2	0.7	4	0.2	4.3
8	CHENIERE	17.6	9.5	3	174.4	1.4	1.6	0.7	3	0.2	3.4
9	CL Jazzman	22	8.5	3	211.4	1.4	2.2	0.7	3.6	0.2	4
10	CL111	21.2	9	3	261.5	1.9	1.9	0.8	3.8	0.2	4.1
11	CL142-AR	20.9	8.3	3	174.5	1.4	1.5	0.7	2.9	0.2	3.3
12	CL151	19.5	10.7	3	233.1	1.7	1.9	0.6	3.6	0.2	3.9
13	CL152	19.4	10.3	3.3	248.2	1.8	1.9	0.7	3.7	0.2	4.1
14	CL163	16.3	7.7	3	204.9	1.2	1.4	0.7	2.6	0.3	2.9
15	CL172	19.4	10	3.2	240.4	1.7	1.9	0.7	3.6	0.2	4
16	CL271	20.4	8.5	3	305	2.1	2.2	0.8	4.3	0.2	4.8
17	Cocodrie	20.3	8.5	2.9	287.6	1.7	1.9	0.7	3.5	0.2	3.8
18	NIPONBARE	15.8	7.8	2.6	219.6	1.5	1.2	0.7	2.7	0.3	3
19	ANTONIO	18.9	8.8	3.1	266.8	1.6	1.9	0.7	3.4	0.2	3.8
20	El Paso 144	16.2	11.5	3	341	2	2	1	4.1	0.3	4.5
21	GSOR100390	20.7	10.3	3	251.4	2.2	2.4	0.8	4.6	0.2	5
22	GSOR100417	20.4	10	2.8	263.4	1.7	1.7	0.5	3.4	0.2	3.8
23	GSOR101758	15.3	11.3	2.7	268.5	1.4	1.3	0.7	2.7	0.3	3
24	RU1104122	18.6	7.3	2.7	188.2	1.4	1.4	0.7	2.8	0.3	3.2

Table 3 (cont'd).

No.	Genotype name	Measured growth parameters									
		PH	TN	LN	LA	LW	SW	RW	SHW	RS	TW
25	CLJZMN	21.2	8.7	3	240.8	1.7	1.7	0.7	3.4	0.2	3.8
26	INIA Tacuari	17.4	5.7	3	123.6	1.2	1.1	0.7	2.3	0.3	2.6
27	IRGA409	20.9	12.7	3.1	354.8	1.9	2.2	0.7	4.1	0.2	4.5
28	JES	17.9	12.7	3	360.6	1.8	1.8	0.7	3.6	0.2	4
29	JUPITER	16.4	8.2	3	225.1	1.8	1.8	0.8	3.6	0.2	4
30	LA 2008	20.4	9.3	2.9	186.9	1.6	1.6	0.7	3.2	0.2	3.5
31	LA 2134	21.3	10.3	2.8	238.8	1.5	1.6	0.6	3.1	0.2	3.5
32	LAKAST	17.8	7.8	3	203.6	1.4	1.5	0.9	2.9	0.3	3.3
33	MERMENTAU	19	8.2	2.9	195.5	1.5	1.7	0.8	3.1	0.3	3.5
34	Presidio	18.3	7.7	3.1	211.9	1.4	1.3	0.7	2.7	0.3	2.9
35	Rex	17.2	9.8	2.9	318.4	2	2.3	0.9	4.3	0.2	4.8
36	RoyJ	18.6	8.3	2.9	231.8	1.6	1.7	0.6	3.3	0.2	3.6
37	RU0603075	18.5	17.3	3	490.5	2.4	2.4	0.9	4.8	0.2	5.3
38	RU1201024	18.9	7.7	3	227.9	1.7	1.6	0.8	3.2	0.2	3.6
39	RU1201047	20.2	8	2.8	189.1	1.5	1.7	0.8	3.2	0.2	3.5
40	RU1201136	17.3	7.3	3.1	208.6	1.4	2.3	0.6	3.7	0.2	4
41	RU1204156	17.4	9.3	2.9	237.1	1.5	1.9	0.7	3.3	0.2	3.6
42	RU1204197	19.5	9.2	2.9	220.4	1.6	1.9	0.8	3.5	0.2	3.9
43	RU1301084	17.9	7.5	3.1	215.5	1.6	2	0.8	3.7	0.2	4.2
44	RU1301093	18.8	7.2	3	208.8	1.5	1.6	0.7	3.1	0.3	3.5
45	RU1301102	18.2	9.7	2.9	179.6	1.4	1.8	0.7	3.2	0.2	3.6
46	RU1302192	20.4	10	2.6	262.3	1.8	1.9	0.8	3.7	0.2	4.1
47	RU1303138	16.3	15	2.7	497.8	2.4	2.2	1	4.6	0.2	5.2
48	RU1303181	19.3	8.2	3	210.7	1.5	1.6	0.6	3.1	0.2	3.4
49	RU1304114	17.9	9.8	2.8	262.6	1.7	1.6	0.7	3.3	0.2	3.6
50	RU1304122	19.4	8.3	3.2	218.2	1.7	1.7	0.6	3.4	0.2	3.7
51	RU1304154	19.9	8.3	3	262.3	1.7	1.7	0.8	3.4	0.3	3.8
52	RU1304156	21.9	8	2.9	217.4	1.7	1.7	0.7	3.4	0.2	3.8
53	RU1305001	20.6	8.8	2.7	247.8	1.8	1.7	0.8	3.5	0.2	4
54	RU1401067	19.3	7	3.2	212	1.4	1.8	0.6	3.1	0.2	3.4
55	RU1401070	18.1	6.8	3.1	196.2	1.3	1.5	0.6	2.8	0.2	3.1
56	RU1401090	19.2	8.3	3	156.1	1.4	1.6	0.6	2.9	0.2	3.3
57	RU1401099	18.4	8.8	2.9	226.1	1.7	1.9	0.8	3.6	0.2	4
58	RU1401102	22	8.7	3	230.5	1.6	2.1	0.7	3.7	0.2	4
59	RU1401145	19.1	8.2	2.9	144.6	1.2	1.5	0.8	2.7	0.3	3.1
60	RU1401161	18.9	7.8	3.2	216.1	1.6	1.6	0.6	3.2	0.2	3.5
61	RU1401164	20.8	10.8	3	238.3	1.7	2	0.6	3.7	0.2	4.1
62	RU1402005	19.3	9.8	3	241.2	1.8	1.8	0.7	3.6	0.2	4
63	RU1402031	19.6	10.7	2.9	228.3	1.7	1.9	0.7	3.6	0.2	4
64	RU1402065	19.1	10.3	2.8	194.9	1.7	2	0.6	3.7	0.2	4.1
65	RU1402115	19.6	10.2	2.9	262.7	1.9	1.9	0.6	3.7	0.2	4.2
66	RU1402131	21.3	10.2	2.8	306	2.1	2.1	0.7	4.3	0.2	4.7
67	RU1402134	20.9	10	2.9	294.2	1.8	1.8	0.6	3.6	0.2	4
68	RU1402149	19.3	8	2.9	192.8	1.4	1.8	0.5	3.2	0.2	3.4
69	RU1402174	17.3	9	2.9	167.2	1.4	1.5	0.6	2.9	0.2	3.1
70	RU1402189	20.4	7.7	3.1	197.4	1.4	1.8	0.7	3.2	0.2	3.5

Table 3 (cont'd).

No.	Genotype name	Measured growth parameters									
		PH	TN	LN	LA	LW	SW	RW	SHW	RS	TW
71	RU1402195	20.6	10.3	2.7	281.9	1.8	1.6	0.6	3.4	0.2	3.7
72	RU1403107	17.7	6.7	3	181.4	1.4	1.6	0.6	3	0.2	3.3
73	RU1403126	17.8	9	3	211	1.6	1.8	0.6	3.4	0.2	3.8
74	RU1404122	16.4	9	2.7	168.2	1.2	1.4	0.8	2.5	0.3	2.9
75	RU1404154	20.6	7.7	2.8	235.3	1.7	1.6	0.7	3.3	0.2	3.7
76	RU1404156	18.1	7.8	3	199.7	1.4	1.5	0.7	2.9	0.2	3.2
77	RU1404157	15.3	7.8	2.6	149.3	1	1.1	0.6	2.1	0.3	2.3
78	RU1404191	19.2	9.2	2.9	273.3	1.9	1.6	0.6	3.5	0.2	3.9
79	RU1404193	21.4	7.7	3	196.3	1.5	1.4	0.6	2.9	0.2	3.2
80	RU1404194	17.2	6.8	2.9	162.3	1.2	1.3	0.7	2.4	0.4	2.7
81	RU1404196	15.3	8	2.6	106.6	0.9	1.4	0.5	2.3	0.3	2.5
82	RU1404198	17.8	8.5	2.8	202.7	1.8	1.7	0.8	3.4	0.3	3.9
83	RU1504083	18.1	7.5	2.8	221.6	1.4	1.8	0.8	3.2	0.3	3.6
84	RU1504100	18.9	8	3.1	236.7	1.6	1.7	0.7	3.3	0.2	3.7
85	RU1504114	19.9	7.7	2.9	215.6	1.5	1.5	0.7	2.9	0.4	3.3
86	RU1504122	18.9	9.5	3	241.4	1.7	2	0.7	3.7	0.2	4.1
87	RU1504154	19.8	8.3	3.1	191	1.4	1.7	0.8	3.1	0.3	3.6
88	RU1504156	17.8	7.8	2.8	171.1	1.3	1.5	0.6	2.8	0.3	3.1
89	RU1504157	20.1	10	2.9	234	1.8	2	0.7	3.8	0.2	4.1
90	RU1504186	18.9	8.5	2.9	215	1.4	1.7	0.6	3.1	0.2	3.4
91	RU1504191	19.1	9.5	3.1	218.2	1.6	1.6	0.6	3.2	0.2	3.6
92	RU1504193	20.1	7.8	3	194.6	1.4	1.6	0.7	3	0.2	3.4
93	RU1504194	18.8	7.2	2.7	151.4	1.3	1.6	0.5	2.8	0.2	3.1
94	RU1504196	19.9	8.7	3	269.2	1.8	1.6	0.7	3.3	0.2	3.7
95	RU1504197	15.6	9.2	2.9	209.5	1.4	1.4	0.7	2.8	0.3	3.2
96	RU1504198	18.2	8	3	190.8	1.4	1.4	0.6	2.8	0.2	3.1
97	Sabine	17.4	9	2.8	166.4	1.3	1.7	0.7	3	0.3	3.4
98	Taggart	18.6	7.3	2.9	183.2	1.5	1.8	0.7	3.3	0.2	3.7
99	Thad	17.7	7.8	2.9	201	1.5	1.7	0.7	3.2	0.2	3.6
100	N-22	19.4	14.5	2.7	539.1	3.1	2.6	1.2	5.7	0.2	6.5
	Mean	18.8	9	2.9	230.5	1.6	1.7	0.7	3.3	0.2	3.7

(early vegetative vigor) is a determinant of the resource colonization and yield competitiveness of the rice seedling (Zhao *et al.*, 2006), as well as yield potential (Dingkuhn *et al.*, 1999); in these experiments, genotype N-22 had the highest LA.

The lowest PH, LN, LA, LW, and RW were recorded for RU140196. These results might account for the least vigor shown by this genotype among the 100 genotypes. Lines RU1404157 and Tacuari from INIA had

the lowest TN, SW, and SHW values among genotypes, also reducing vigor. On the other hand, N-22 showed the highest LA, LW, SW, RW, SHW, and TW among genotypes, placing it in the high-vigor index category (Tables 2.3 and 2.6). A total of 76% of the genotypes were below the grand average for RW (0.7 g) and RS (0.2), whereas 45% of genotypes exceeded the general average for SHW (3.3 g) and TW (3.7 g). Fukai and Cooper (1995) stated that seedling vigor is the plant's capability to emerge

rapidly from soil or water and establish itself before its competitors (Bastiaans *et al.*, 2011). Several parameters that are closely associated with seedling vigor are considered relevant in determining crop vigor. Rapid emergence is a crucial trait for successful crop establishment (Namuco *et al.*, 2009).

Genetic variation among genotypes can be used as a screening tool during rice growth stages for vigor-related traits, including plant height, tiller number, canopy ground cover, and early crop biomass production, in seedlings (Netnet 2012; Caton *et al.*, 2003; Zhao *et al.*, 2006). In a screening study by Cairns *et al.* (2009), early vigor indicators were measured, including shoot length, shoot biomass, leaf area, and the number of roots; root biomass; partitioning coefficients; and growth rates. Phenotypic correlation among related traits can be combined and used to define early vigor. In agreement with the study of Saito *et al.* (2010), this study showed that genotypes with high or above-average values for morphological or growth parameters can be identified as vigorous cultivars. This result provided clues for the selection of varieties that will display the best survival and competitiveness (Table 3).

Root parameters

The optimal establishment of root system architecture by currently cultivated rice genotypes increases the chances of improving their adaptation to different abiotic stresses and, subsequently, performance. The mean values of each root parameter of the 100 rice genotypes are shown in Table 4. Significant variation in root length among the tested genotypes was

observed, ranging from 4276.6 cm (RU1303138) to 8445.7 cm (RU1303138), with an average of 6011.3 cm (Table 4). As for growth parameters, genotypes RU1404194 and GSOR101758 had the lowest average for over half (62%) of the root growth and development parameters for RL, RSA, RV, LRL, and RN, making them the least vigorous among the 100 genotypes (Tables 4 and 6). However, genotypes N-22 and RU0603075 had the highest averages for 62% of the root growth and development parameters, including RSA, AD, RV, and T, making them among the most vigorous (Tables 4 and 6). Approximately 198% and 199% reductions in variability among genotypes in the root number of tips and root numbers compared to other traits, respectively, were observed, as well as the presence of the strong positive correlation between them (Tables 4 and 5). Half (52%) of the genotypes exceeded the overall average for RL, T, and RN, whereas 62% of the genotypes were above the overall average for RSA, RV, and LRL (Table 4).

The early emergence of a vigorous crop stand enables better root anchorage. It improves nutrient absorptive capacity (Farooq *et al.*, 2011), and root hairs protect the water status of young root tissue (Tanaka *et al.*, 2014). Multiple studies have identified links between root traits and crop productivity (Kell, 2011), and other studies used root length as a representative indicator for seedling vigor (Redoña and Mackill, 1996). Deep roots enable the plant to access water that is stored in the deep layers of the soil substratum (Wasson *et al.*, 2012). Haling *et al.* (2013) confirmed that root tips with large diameters exhibit improved root

Table 4. Means of RL, RSA, AD, RV, T, LRL, RN, SPAD, and Fv/Fm of 100 rice genotypes.

No.	Genotype name	Root parameters					Physiological parameters			
		RL	RSA	AD	RV	T	LRL	RN	SPAD	Fv/Fm
1	14CLPYT033	6011.4	753.4	0.4	8.3	31196.8	35.3	60.7	38	0.7
2	14CLPYT108	4897.3	683.2	0.5	7.6	32785.8	36.7	53.2	39.7	0.7
3	14CVPYT094	6591.4	925.7	0.5	10.5	38511.5	41.7	53.5	39.9	0.6
4	14CVPYT144	6412.8	881.6	0.4	9.8	38085.7	39.7	54	39.7	0.7
5	COLORADO	6672.3	813.1	0.4	9.2	37827.7	37.2	70.8	40.1	0.7
6	Bowman	6453.6	836.1	0.4	8.8	31820.2	41.2	50	41.8	0.7
7	CAFFEY	6713.7	994	0.5	11.9	34366.3	43.8	60	40.4	0.8
8	CHENIERE	5624	780.4	0.4	8.8	34283.8	42.5	53.7	36.8	0.8
9	CL Jazzman	5778.7	817	0.5	9.4	32443.3	40.2	59.8	40.8	0.7
10	CL111	6233.9	870.3	0.4	10	33523.5	42.7	57.5	39.5	0.7
11	CL142-AR	6190.9	823.6	0.4	8.9	37716.7	45.2	47.8	41.4	0.7
12	CL151	6093.2	784.3	0.4	8.2	40199.2	41.2	51.2	35.6	0.7
13	CL152	7148.8	949.6	0.4	10.1	39925.3	40.3	61.8	35.9	0.6
14	CL163	5469.2	605	0.4	6.4	33674.2	40.2	45.3	40.3	0.7
15	CL172	5884.7	872.5	0.5	10.4	30607.5	40.3	59.5	39.4	0.7
16	CL271	6812.7	993.2	0.5	11.9	33986.2	40.8	54.3	40.4	0.7
17	Cocodrie	6031.3	800.4	0.4	8.6	31780.3	38.5	52.7	41.3	0.6
18	NIPONBARE	6713.1	799.8	0.4	7.7	40761.2	38.5	69	37.2	0.7
19	ANTONIO	5697.3	773.1	0.4	8.6	32523.2	37.3	54.7	38.7	0.7
20	El Paso 144	7385.9	861.3	0.4	9.1	38545.7	41.8	69.8	37	0.7
21	GSOR100390	7663.6	1073.6	0.5	12.2	35136.5	42.2	63.7	38	0.7
22	GSOR100417	5584.2	854.1	0.5	10.6	27563.3	35	55	38.8	0.7
23	GSOR101758	4276.6	631.9	0.5	7.7	27493.5	33.8	53.7	37.4	0.8
24	RU1104122	5162.7	707.3	0.4	7.9	25522.2	38.8	49.3	39.3	0.8
25	CLJZMN	5920.4	842.9	0.5	9.7	35934.5	42	63	37.5	0.6
26	INIA Tacuari	5871.1	579.5	0.4	5.5	32523.7	38.2	48.2	39.9	0.8
27	IRGA409	6901.5	1094	0.5	14.2	35070.8	46.7	69.3	42.4	0.7
28	JES	7022.1	1018.3	0.5	12.1	43166.8	41.5	76	39.6	0.7
29	JUPITER	6233.3	889.4	0.5	10.1	31380	41.8	60.2	42.1	0.7
30	LA 2008	5355.4	699.2	0.5	8.4	30146.3	39.8	44	41.4	0.6
31	LA 2134	6238.7	807	0.4	8.5	43324.7	39.3	58.2	38.3	0.7
32	LAKAST	5675.9	807.8	0.5	9.3	29882.2	43	53.2	41.8	0.5
33	MERMENTAU	5759.3	806.1	0.4	9.1	34764	38.3	62.3	36.6	0.6
34	Presidio	5312.5	573	0.4	5.5	36649	39.5	49.5	37.1	0.8
35	Rex	6956	1042.6	0.5	12.9	37401.2	40.5	69.8	41.3	0.9
36	RoyJ	7124.6	817.7	0.4	8.6	35772	42.8	55.7	40.6	0.7
37	RU0603075	7419.8	1293.2	0.6	18.7	48164	42.3	69.5	38.7	0.6
38	RU1201024	5725.1	844.1	0.5	9.9	27257.3	40.3	58	43.2	0.7
39	RU1201047	5920.1	792.1	0.4	8.5	30102.7	44.2	45.2	39.7	0.7
40	RU1201136	6017.2	796.9	0.4	8.6	27555.8	41.8	53.5	40.3	0.7
41	RU1204156	5508.2	710.7	0.4	7.5	36427.3	37.2	55.2	34.9	0.7
42	RU1204197	6659.7	853.7	0.4	9	36835.8	40.5	59.7	39.1	0.7
43	RU1301084	5954.1	743.7	0.4	8.4	27439.5	41	59.8	43	0.7
44	RU1301093	5568.6	753.6	0.4	8.4	30143	39	54.5	44.3	0.7
45	RU1301102	7035.9	952.5	0.4	10.4	37464.8	42	65.5	40.1	0.7

Table 4 (cont'd).

No.	Genotype name	Root parameters						Physiological parameters		
		RL	RSA	AD	RV	T	LRL	RN	SPAD	Fv/Fm
46	RU1302192	5806.2	923.9	0.5	11.9	26201.3	42.3	66.8	41.9	0.7
47	RU1303138	8445.7	1352.8	0.5	18	47124.5	43.8	80.2	44.5	0.7
48	RU1303181	5390	714.4	0.4	7.6	31882	43	48.8	40.8	0.6
49	RU1304114	6135.3	803.7	0.4	8.5	34293	37	59.7	38.4	0.7
50	RU1304122	6195.4	846.7	0.4	9.5	33487.5	37.7	57	39.8	0.9
51	RU1304154	5716.6	807.3	0.4	9.3	33689.8	38.2	58	38	0.8
52	RU1304156	6247.2	767.8	0.4	8.1	35902.8	40	52.2	41	0.8
53	RU1305001	7420.7	1059.5	0.5	12.2	36285.8	41.7	56.2	42	0.7
54	RU1401067	5132.9	715.1	0.5	8.3	27180	37.7	52.5	41.7	0.7
55	RU1401070	5446.1	725.9	0.4	7.8	27939.8	42.7	46.8	42.9	0.8
56	RU1401090	5426.2	744.1	0.4	8.2	30864.7	43.3	53	39.1	0.8
57	RU1401099	6610.8	917.2	0.5	10.3	36093.7	40.5	51.2	41.1	0.7
58	RU1401102	5730.7	803.8	0.5	9	28930.7	40	60.2	39.4	0.6
59	RU1401145	4824.9	645.7	0.4	7.6	24317.8	37	52.5	42.7	0.7
60	RU1401161	5863.4	767.6	0.4	8.1	33153.7	43	52.2	37.5	0.8
61	RU1401164	6377	939.2	0.5	11.5	33867.5	41.8	60.7	40.1	0.8
62	RU1402005	6005.6	781.6	0.4	8.3	35149.2	42.3	55.5	41.5	0.6
63	RU1402031	6640.8	917.9	0.4	10.2	36466.8	42.7	55.2	40	0.7
64	RU1402065	6073.6	902.9	0.5	10.8	35501.5	43.2	64.5	40.9	0.7
65	RU1402115	6987.5	975.7	0.5	11.3	42342.7	40.2	69.3	40.3	0.7
66	RU1402131	6930.3	1009.4	0.5	11.8	32744.7	43.2	68.5	39.7	0.7
67	RU1402134	6551.4	893.9	0.4	9.8	35335.8	38.7	68.2	38.2	0.7
68	RU1402149	6175.9	742.8	0.4	7.2	34012	39.3	48.8	39.6	0.7
69	RU1402174	4612.6	619.9	0.4	6.8	26159.3	41.3	57.5	37	0.9
70	RU1402189	5700.9	751.4	0.4	8	32759.8	43	51.7	39.4	0.7
71	RU1402195	5019.7	711.7	0.4	8.1	27102.8	38.8	59.3	40.7	0.7
72	RU1403107	6668	776.9	0.4	8.1	39361.3	38.2	54	39.2	0.6
73	RU1403126	5686.8	823.4	0.5	9.8	34991.3	43.5	48	40.4	0.7
74	RU1404122	4655.2	639.6	0.4	7.1	27679	38.8	44.8	43.5	0.7
75	RU1404154	5731.9	722.9	0.4	7.5	28985.2	39.3	46.5	39.2	0.7
76	RU1404156	5615.1	742.7	0.4	7.9	29668	39.2	58.5	38.6	0.7
77	RU1404157	4534.1	595.4	0.4	6.3	33050.8	38.8	46	35.4	0.6
78	RU1404191	6009.1	840	0.5	9.5	36309.2	39.3	54.8	42.2	0.7
79	RU1404193	5754.7	756.7	0.4	8	37619.5	39.3	53.7	40	0.7
80	RU1404194	5503.8	598.9	0.4	5.6	31776.3	41.5	45	36.5	0.6
81	RU1404196	4436.2	523.7	0.4	5	32676.5	36	40.8	35.7	0.7
82	RU1404198	5652.3	661.4	0.4	6.6	30430.3	41.3	61.2	38	0.8
83	RU1504083	5974.6	748	0.4	7.5	31388	40.7	44.8	39.1	0.7
84	RU1504100	5895.1	839.8	0.4	9.7	33118	41.3	57.5	42.1	0.5
85	RU1504114	5075.8	704.1	0.4	7.9	28998.2	39.7	50	39	0.7
86	RU1504122	6066.6	794.9	0.4	8.5	37411	38.3	58.3	40.1	0.6
87	RU1504154	6305	817.3	0.4	8.7	36307	39.8	57.2	39.7	0.7
88	RU1504156	4903.2	630.5	0.4	6.7	32340.5	37.5	56.2	40.2	0.8
89	RU1504157	6120.5	885.4	0.5	10.3	30177.3	41.5	57.5	38.5	0.6
90	RU1504186	5725.6	719.7	0.4	7.3	30346.3	41.3	56.7	40.7	0.7
91	RU1504191	5746.8	811.5	0.5	9.2	30356.7	40	50.2	40.3	0.8
92	RU1504193	5592.2	740.5	0.4	8.1	29395.8	41.3	51.5	40.2	0.7

Table 4 (cont'd).

No.	Genotype name	Root parameters						Physiological parameters		
		RL	RSA	AD	RV	T	LRL	RN	SPAD	Fv/Fm
93	RU1504194	5113.2	636.9	0.4	6.4	31182.5	39.3	55.3	40.7	0.8
94	RU1504196	6245.6	866.6	0.4	9.6	31805.8	39.7	57.8	41.4	0.8
95	RU1504197	5289.8	711.1	0.4	7.7	26089.2	44	47.8	43	0.6
96	RU1504198	5297.3	743.1	0.4	8.4	28851.8	42.5	44.2	42	0.6
97	Sabine	6188.5	775.4	0.4	7.9	35137.3	39.8	57.5	42.4	0.7
98	Taggart	6027.4	797.7	0.4	8.5	35199.5	41.7	58.5	42	0.7
99	Thad	6156.5	840.9	0.4	9.2	31051.5	39	56.7	41.6	0.7
100	N-22	8010.4	1444.8	0.6	21.3	45658.8	42.8	81.5	40	0.6
	Mean	6011.3	816.3	0.4	9.2	33538.4	40.4	56.5	39.9	0.7

penetration to the soil. Root growth and development parameters, such as RL, RV, RSA, and root thickness, determine root hydraulic conductance, which can potentially increase water uptake by rice under water-limited conditions (Henry *et al.*, 2012; Singh *et al.*, 2017b). In this study, rice genotypes with higher values for RL, RV, RSA, and RD might be desirable and show increased potential productivity under water-limited growth conditions.

Genetic diversity is essential to improve the desirable traits of new cultivars. The rice gene pool is genetically highly diverse, as reflected by the number of landraces existing today (Sujay, 2007). The differences in root growth (RSA and RL) among rice cultivars may be due to the genetic differences in their root hydraulic conductivity (Henry *et al.*, 2012). Similar to the present study, studies by Jaleel *et al.* (2009) and Lone *et al.* (2019) identified variability in root growth and proliferation among rice lines in the seedling stage. The genotypic variation shown by root length and some identified root traits in this study suggested that these traits can be selected for in any prebreeding program and

supplemented by relevant marker-aided selection and direct phenotypic screening (Reynolds *et al.*, 2012).

Physiological parameters

Identifying the relationships between growth performance and seedling physiological parameters can permit the early selection of genotypes. Rice genotypes have yet to be classified on the basis of genotypic differences for physiological traits. The SPAD index value indicates the relative greenness of leaves and is a measure of chlorophyll content. The SPAD index value ranged from 34.9 (RU1204156) and to 44.5 (RU1404194) with an average of 39.9 (Table 4). A significant difference ($P < 0.05$) in the SPAD index value was observed between genotype \times year interaction; this indicates that genotypes differed in chlorophyll concentration in response to different seasons and that this difference was heritable (Table 2). In this study, 80% of rice genotypes exceeded the general average (0.7) in fluorescence (Fv/Fm), with minimum and maximum fluorescence observed in LAKAST (0.5) and RU1304122 (0.9), respectively.

Table 5. Estimates of simple correlations among the parameters of the 100 rice genotypes.

	TN	LN	LA	LW	SW	RW	SHW	RS	TW	RL	RSA	AD	RV	T	LRL	RN	SPAD	Fv/ Fm
Plant height (PH)	0.01 n.s	0.17 ***	0.13 *	0.25 ***	0.23 ***	0.07 n.s	0.17 ***	0.19 ***	0.15 **	0.19 ***	0.24 ***	0.13 *	0.18 **	0.05 n.s	0.18 **	0.07 n.s	-0.02 n.s	-0.10 n.s
Tiller number (TN)		0.23 ***	0.64 ***	0.59 ***	0.4737	0.29 ***	0.58 ***	0.52 ***	0.56 ***	0.32 ***	0.53 ***	0.36 ***	0.61 ***	0.27 ***	0.14 *	0.48 ***	-0.2 ***	-0.41 ***
Leaf number of main stem (LN)			0.04 n.s	0.02 n.s	0.02 n.s	0.01 n.s	0.01 n.s	0.01 n.s	0.01 n.s	0.03 n.s	0.02 n.s	0.08 n.s	0.01 n.s	0.01 n.s	0.10 n.s	0.01 n.s	-0.01 n.s	-0.01 n.s
Leaf area (LA)				0.80 ***	0.56 ***	0.43 ***	0.54 ***	0.57 ***	0.49 ***	0.41 ***	0.67 ***	0.49 ***	0.73 ***	0.24 ***	0.24 ***	0.52 ***	0.13 ***	-0.31 ***
Leaf dry weight (LW)					0.65 ***	0.48 ***	0.71 ***	0.69 ***	0.65 ***	0.54 ***	0.77 ***	0.50 ***	0.79 ***	0.30 ***	0.31 ***	0.59 ***	0.11 ***	-0.39 ***
Stem dry weight (SW)						0.37 ***	0.64 ***	0.62 ***	0.59 ***	0.47 ***	0.64 ***	0.39 ***	0.64 ***	0.25 ***	0.26 ***	0.54 ***	-0.12 ***	0.39 ***
Root dry weight (RW)							0.47 ***	0.24 ***	0.43 ***	0.32 ***	0.48 ***	0.30 ***	0.52 ***	0.14 ***	0.15 ***	0.36 ***	-0.03 ***	-0.05 n.s
Shoot dry weight (SHW)								0.75 ***	0.98 ***	0.52 ***	0.65 ***	0.37 ***	0.65 ***	0.35 ***	0.23 ***	0.56 ***	-0.09 n.s	-0.45 ***
Root shoot ratio (RS)									0.68 ***	0.47 ***	0.66 ***	0.45 ***	0.70 ***	0.31 ***	0.26 ***	0.50 ***	-0.06 n.s	-0.41 ***
Total dry weight (TW)										0.48 ***	0.59 ***	0.32 ***	0.59 ***	0.33 ***	0.21 ***	0.53 ***	0.07 ***	0.42* **
Root length (RL)											0.78 ***	0.04 n.s	0.54 ***	0.71 ***	0.28 ***	0.45 ***	-0.08 n.s	-0.26 ***
Root surface area (RSA)												0.46 ***	0.92 ***	0.48 ***	0.39 ***	0.62 ***	0.02 n.s	0.38 ***
Average root diameter (AD)													0.69 ***	0.16 **	0.25 ***	0.39 ***	-0.13 *	-0.22 ***
Root volume (RV)														0.27 ***	0.38 ***	0.63 ***	-0.09 n.s	-0.38 ***
Tip number (T)															0.09 n.s	0.27 ***	-0.06 n.s	-0.23 ***
Longest root length (LRL)																0.15 **	-0.13 *	-0.07 n.s
Root number (RN)																	0.09 n.s	-0.61 n.s
Chlorophyll content (SPAD)																		0.27 ***

† *, **, and *** represent significant differences at the 0.05, 0.01, and 0.001 P level, respectively.

†† n.s represents nonsignificant differences at the 0.05 P level.

Simple correlation matrix

When the genetic correlation is strong between two traits, the selection of one character causes a response in the other automatically (Falconer, 1964), potentially aiding the plant breeder in crop improvement. Table 5 shows the estimated simple correlation matrix among the parameters measured in the 100 rice genotypes. Significant correlations were observed among the root and growth parameters, except for LN. The relationship between shoot dry weight and total dry weight showed the highest positive considerable association (98%) among all shoot, root, and physiological parameters, followed by the relationship between root surface area and root volume (92%). The lowest negative correlation was observed between root-shoot ratio and fluorescence (Fv/Fm) at 45%. The results of this study were consistent with those of previous reports on rice (Farooq *et al.*, 2009). The differences observed for aboveground parts (LN, LA, and TN), chlorophyll content (SPAD value), and root growth (RN, RL, and RSA) might have contributed to the observed cultivar differences similar to those observed in previous studies (Jaleel *et al.*, 2009; Farooq *et al.*, 2011).

Categorization of rice genotypes

CVRI and PCA

Rice genotype classification is a complex process. Morphological, ecological, and population characteristics have been used to classify wild and cultivated rice (Counts and Lee, 1987; Pang *et al.*, 1995). Different qualitative and quantitative aspects have also been

utilized (Fatokun *et al.*, 1986). Rice diversity panels created on the basis of genetic makeup, geographic origin, the ecosystem of adaptation, and the genetic levels of improvement can be used to identify naturally occurring trait combinations (Jahn *et al.*, 2011). Understanding physiological changes to improve photosynthetic efficiency in rice is one of the key components in current physiological research (Reynolds *et al.*, 2012).

In this study, the CVRI values for year₁ and year₂ for each rice genotype or cultivar were derived by summing individual vigor response indexes for all root and shoot parameters of the 100 evaluated rice genotypes (Table 6). The CVRI-based technique was used to identify genotypes that were very low, low, moderate, high, and very high in terms of their vigor response index.

The 100 rice genotypes were classified into five groups on the basis of the CVRI and standard error of the mean (Table 5). Sixteen genotypes were classified as having very low vigor response; 43 were classified as having low vigor; 33 as having moderate vigor; and 5 (JUPITER, 28.77; RU1402131, 29.07; El Paso 144, 29.39; JES, 29.69; and IRGA409, 30.71) as highly vigorous. However, only 3 genotypes (RU0603075, 33.94; RU1303138, 34.08; and N-22, 36.17) were classified as very highly vigorous. N-22 also displayed a high level of consistency in terms of vigor traits during the two experimental years (Table 6). Rice genotypes with moderate, high, and very high vigor responses are genotypes with good productivity potential. The high correlation coefficient (r^2) observed between the CVRI of the 100 rice genotypes and experimental year₁ or

Table 6. Classification of 100 rice genotypes based on combined response indexes for morphophysiological traits during the seedling growth stage, 30 days after planting.

Very low 21.36–23.75	Low 23.75–26.13	Moderate 26.13–28.51	High 28.52–30.90	Very high 30.91–33.28
RU1404196 (1.36)	RU1401070 (23.78)	RU1304156 (26.19)	JUPITER (28.77)	RU0603075 (33.94)
RU1404157 (21.59)	RU1404156 (24.21)	LA 2134 (26.20)	RU1402131 (29.07)	RU1303138 (34.08)
INIA Tacuari (22.91)	RU1504114 (24.24)	RU1504154 (26.20)	El Paso 144 (29.39)	N-22 (36.17)
RU1404122 (23.03)	RU1303181 (24.29)	RU1304154 (26.23)	JES (29.69)	
RU1504156 (23.03)	RU1401090 (24.38)	RU1404191 (26.25)	IRGA409 (30.71)	
RU1504194 (23.06)	RU1404193 (24.51)	RU1402005 (26.28)		
RU1104122 (23.13)	RU1504186 (24.57)	RU1504186 (26.35)		
CL163 (23.24)	RU1402149 (24.57)	CLJZMN (26.38)		
GSOR101758 (23.25)	RU1401067 (24.58)	RU1504196 (26.50)		
RU1401145 (23.41)	RU1504193 (24.62)	RU1504157 (26.65)		
RU1404194 (23.43)	Bowman (24.68)	14CVPYT144 (26.67)		
RU1504198 (23.44)	LA 2008 (24.70)	RU1504122 (26.80)		
RU1402174 (23.50)	RU1301093 (24.71)	CL172 (26.85)		
14CLPYT108 (23.65)	RU1404154 (24.75)	RU1402065 (27.04)		
Presidio (23.65)	RU1402195 (24.81)	14CVPYT094 (27.09)		
RU1504197 (23.72)	RU1504083 (24.81)	RU1204197 (27.11)		
	14CLPYT033 (24.86)	RU1401099 (27.16)		
	RU1204156 (24.86)	COLORADO (27.22)		
	RU1201047 (24.90)	RU1302192 (27.31)		
	Thad (25.09)	Rex (27.32)		
	RU1402189 (25.10)	RU1402134 (27.36)		
	ANTONIO (25.12)	RU1401164 (27.41)		
	NIPONBARE (25.12)	RU1402031 (27.59)		
	LAKAST (25.13)	RU1304122 (27.79)		
	GSOR100417 (25.17)	RU1301102 (27.80)		
	CHENIERE (25.18)	CL271 (27.82)		
	RU1403107 (25.19)	CL111 (27.85)		
	RU1201136 (25.20)	CL152 (27.87)		
	Taggart (25.25)	RoyJ (27.88)		
	RU1401161 (25.27)	GSOR100390 (27.90)		
	Sabine (25.31)	RU1305001 (28.16)		
	MERMENTAU (25.35)	RU1402115 (28.25)		
	RU1504100 (25.43)	CAFFEY (28.38)		
	RU1403126 (25.49)			
	RU1404198 (25.53)			
	Cocodrie (25.57)			
	CL142-AR (25.61)			
	RU1504191 (25.69)			
	RU1201024 (25.79)			
	CL151 (25.79)			
	RU1304114 (25.86)			
	RU1401102 (25.87)			
	RU1301084 (25.95)			

year₂ ($r^2 = 0.77$, $P = 0.0001$ and $r^2 = 0.76$, $P = 0.0001$, respectively), indicated that the response of genotypes to all parameters was almost the same for year₁ and year₂ (Figure 1).

The correlation coefficient between CVRI and either shoot or root vigor indexes ($r^2 = 0.92$, $P = 0.0001$) ($r^2 = 0.93$, $P = 0.0001$, respectively) were high and similar (Figure 2). This similarity suggested that either root or shoot parameters might be sufficient for evaluating early vigor, and selection based on either index may be sufficient for classification; however, shoot traits are easier to measure than root traits. Linear regression showed no significant relationship between the physiological traits and the combined vigor response index, suggesting that morphological parameters are major contributors to genotypic variability compared with the two physiological parameters observed in this study.

Rice genotypes with strong early vigor are useful for crop establishment in direct-seeded systems, especially in upland growing environments (Namuco *et al.*, 2009). The strength of relationships between growth performance and physiological parameters was analyzed by using correlations in multivariate analysis, including PCA. This approach has been used as a data density technique for preserving total variance and minimizing mean square estimated errors (Ingebritsen and Lyon, 1985). In this study, PCA was performed to recognize the principal components of shoot, root, and physiological parameters that best described the vigor response of the 100 genotypes and to identify low-, intermediate-, and high-stability rice genotypes. The intermediate- and high-stability lines

were then selected because our goal was to categorize the genotypes in accordance with their vigor response and their consistency or stability.

More than 70.1% of the total variation among genotypes was explained by the first three PCs (Figures 3 and 4). The first principal component (PC1) versus the second (PC2) could be interpreted in lieu of positive values for LN, SPAD, and Fv/Fm and RS to a lesser extent. In other words, the eigenvectors of PC1 had high positive values for LW, LN, LA, RV, RN, TW, and SHW and, to a lesser degree, RS, LN, Fv/Fm, and SPAD (Figure 4). Therefore, genotypes N-22, RU1303138, RU0603075, IRGA409, JES, and REX were considered as having high vigor stability because of their relatively high scores for PC1 and PC2. By contrast, RU1404196, RU1404157, RU1404193, GSOR101758, and NIPONBARE could be classified as having low stability because they have relatively small values for RS, LN, Fv/Fm, and SPAD. Even though both the methods used the same data and slightly different ways of computation, the vigor response index was much simpler and could be used as a valid screening method for identifying genotypic variations and assigning relative scores.

As a result, the biplot of PC1 vs. PC2 grouped the rice genotypes RU1401070, RU1402149, and RU1104122, which had been classified as moderately stable or intermediate varieties, into the "intermediate" sector of the graph. The CVRI analysis (Figure 2) identified Fv/Fm and SPAD as unuseful parameters for the vigor response index to classify rice genotypes. The PC1, PC2, and PC3 scores collectively contributed to the rice genotype separation for vigor

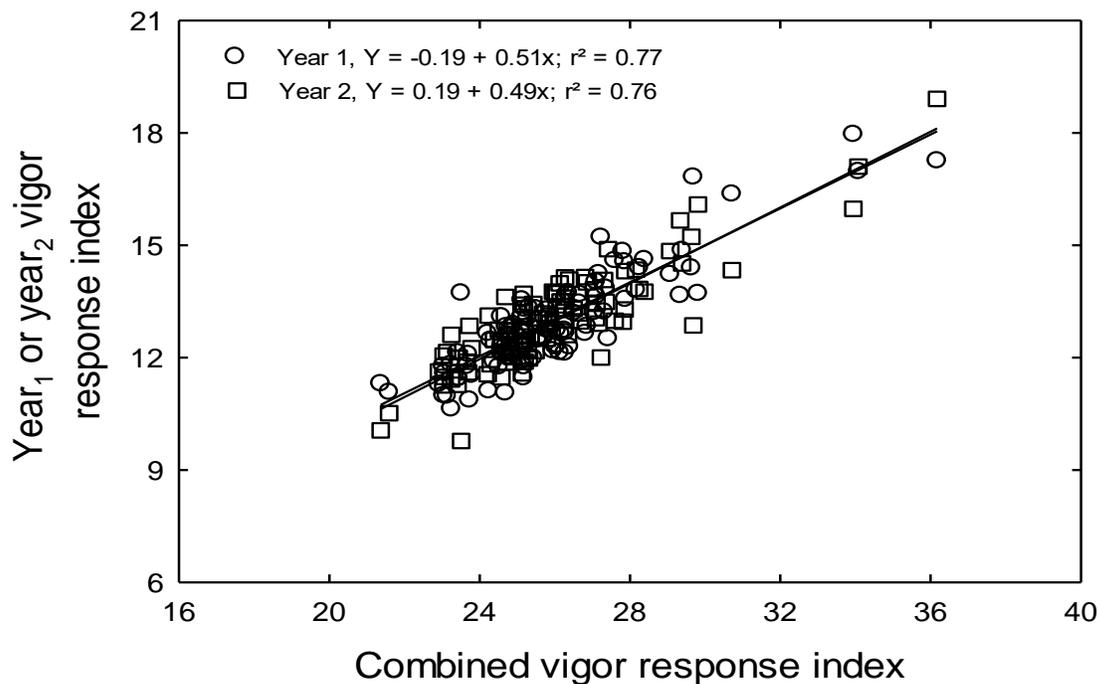


Figure 1. Relationship between the combined vigor response indexes and year 1 or year 2 vigor response indexes of 100 rice genotypes.

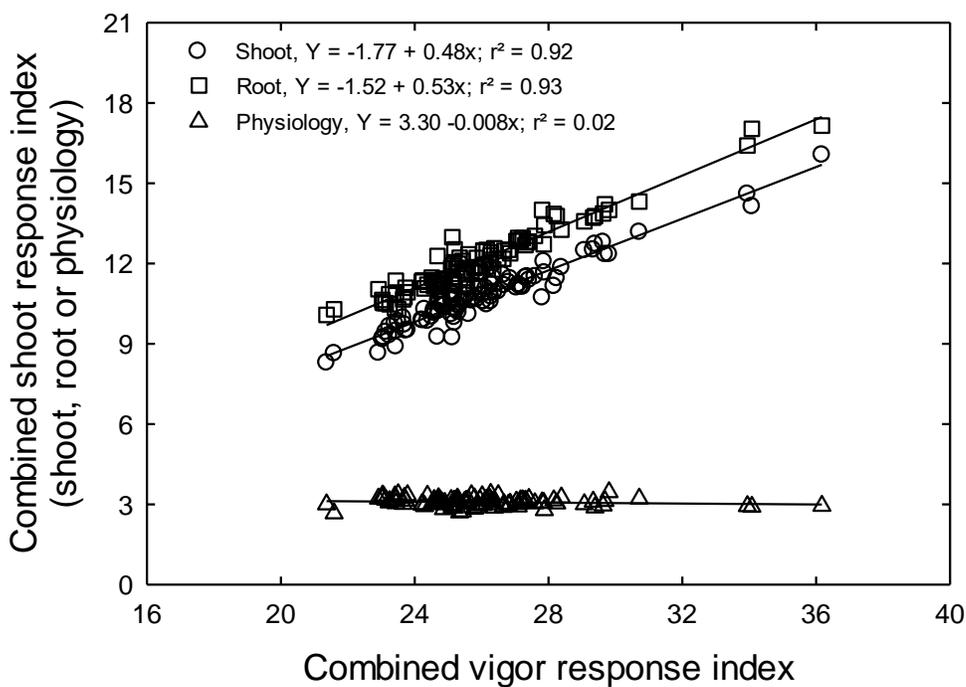


Figure 2. Relationship between the combined vigor response indexes and shoot, root, or physiological combined vigor response indexes of 100 rice genotypes.

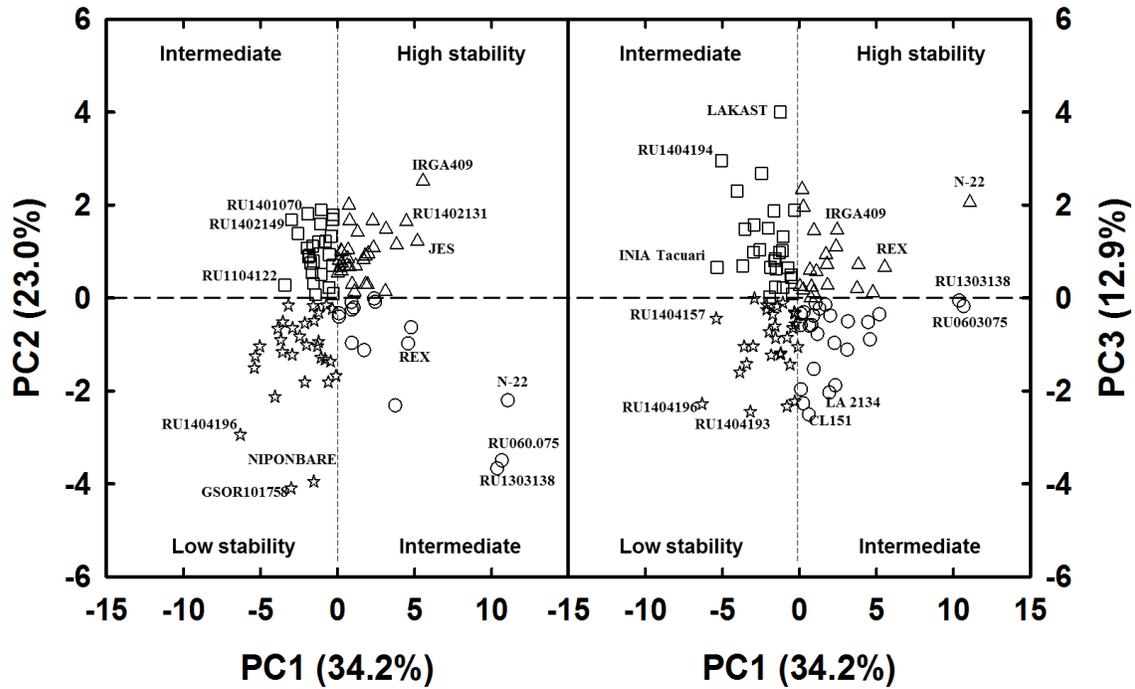


Figure 3. PCA biplot for the first two principal components (PC) scores, PC1 vs. PC 2 and PC 1 vs. PC 3, related to the classification of 100 rice genotypes for early-season vigor response indexes and rice genotypes.

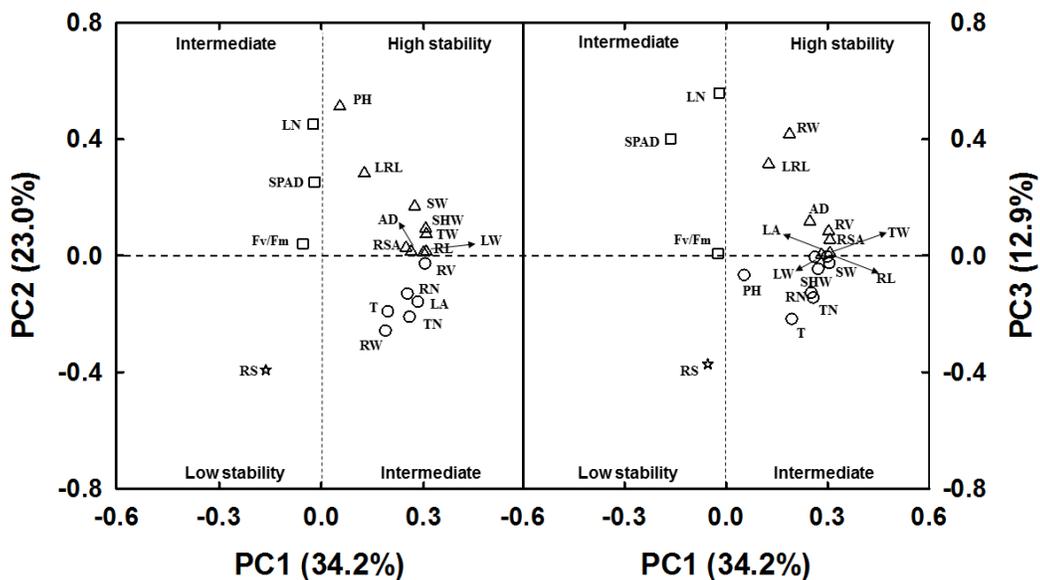


Figure 4. PCA biplot for the first PC scores, PC1 vs. PC 2 and PC 1 vs. PC 3, related to the classification of 100 rice genotypes for early-season vigor response indexes based on traits.

response stability. PCA was utilized to group the genotypes into the low- and high-stability groups. TW, RL, LW, TN, RN, RSA, RN, and SHW were shown to be the parameters that best described rice genotype stability. The evaluation of genotypes for the stability of performance under varying environmental conditions is an essential part of any breeding program (Tariku *et al.*, 2013). Therefore, this experiment can be repeated under various environmental conditions for high-quality genotype selection.

CONCLUSIONS

Significant genotypic variability was observed for the morphophysiological traits related to early-season vigor. The limited physiological parameters, such as chlorophyll content based on SPAD and fluorescence (Fv/Fm), measured in this study, were not significantly different among genotypes. They may not be useful as screening tools for the early-season vigor of rice. The CVRI derived from the root, shoot, and physiological parameters, however, showed not only variability among rice genotypes but also a significant positive correlation with shoot and root parameters. This result indicated that shoot and root morphological traits are essential for identifying variability and classifying rice genotypes into various vigor groups. However, it is based on the limited number of physiological traits observed in this study during the early stages. Therefore, caution is needed for a broader statement. Moreover, by using PCA, total plant weight, root length, leaf weight, total tiller numbers, root volume, root surface

area, root number, and shoot weight were identified as the best parameters for defining the vigor response stability of rice genotypes. The PCA and CVRI methods used in this study collectively identified low, moderate, and highly stable rice genotypes. Based on these screening methods, the rice genotypes N-22, REX, IRGA 409, RU1303138, and RU0603075, were identified as having stably high vigor and may be useful as genetic donors for early-season vigor to improve this critical economic trait in new rice cultivars.

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