

Head rice yield in response to water deficit during reproductive stage and aerobic conditions

O. Myint¹, J. H. Mitchell¹, P. J. Snell² and S. Fukai¹

¹ The University of Queensland, School of Agriculture and Food Sciences, Brisbane 4072, Qld, Australia, ohnmar.myint@uq.net.au

² Yanco Agricultural Institute, NSW Department of Primary Industries, Yanco, NSW, 2703, Australia

Abstract

Head rice yield (HRY) is an important criterion to determine milling quality of rice. Traditionally rice is grown under flooded condition however with water scarcity aerobic production has been considered a water saving option. The impacts of an aerobic system or one, which suffers mild water deficit at reproductive stage on HRY has not been determined. A series of experiments were sown across two years to investigate the stability and G×E interaction on HRY of 20 diverse rice genotypes grown under well-watered aerobic conditions (WW) as well as various water deficit (WD). Genotype and G×E were highly significant in all environments. Based on HRY, cluster analysis grouped environments into EG1: poor (48.9%), EG2: favourable (64.3%) and EG3: average (57.6%). Of 6 genotype groups, medium maturity genotypes groups: GG3 and GG5 including Lemont, Jefferson, Amaroo, Sherpa and Calrose had good adaptability under WD at grain filling as well as flowering time. IR 64 (GG1) had poor adaptability across environments and is considered as a susceptible genotype. Genotypes with low amylose achieved high HRY under aerobic condition where there is no water shortage but no relationship with grain yield in any environmental group. The stable and consistent genotypes with high HRY under aerobic and WD conditions will be beneficial for farmers and rice industry in Australia and still needs improving.

Key words: Genotype, favourable environment, flooded, aerobic, water deficit, G×E

Introduction

Rice (*Oryza sativa* L.) consumes about 80% of the total irrigated fresh water resources in Asia and accounts for the highest amount of water use compared to other crops (Bouman et al., 2005). Australian rice farmers in the temperate region of the Riverina, NSW are able to produce among the highest yielding crops in the world (~10.2 t/ha) under permanent water and achieve high water productivity (~1.25 t/ML). However, the Riverina region has been severely affected by water limitations in catchment areas since 2002-03. Limited water availability is a major constraint for cultivation of rice in the traditional permanent water system. As a response option to a looming water-scarcity, a new way of growing rice has been developed and is called the aerobic rice system, which consists of dry-seeded rice cultivation under non-puddled, well-watered but unsaturated and well-drained soils.

The grain yield reduction ranged from 20% to 70% when WD occurred from flowering stage to grain filling stage due to limited current photosynthesis rate (Zhang et al., 2014). WD during reproductive phase and grain filling period affected on rice grain quality especially HRY, grain weight, grain length and width, grain size, amylose and protein content (Bleoussi et al., 2016, Haider, 2015). HRY represents the three-fourths or more of original length of the kernel and less than that is regarded as a broken rice. High HRY is considered a milling quality trait as an economic value in rice industry. Numerous research has been conducted on the effect of WD on GY, but few have included the impact of WD on rice grain quality. Furthermore, there is limited knowledge on genetic variation of head rice yield under WD in aerobic condition. In this paper, we studied the genetic variation of HRY and GY and relationships among quality traits and HRY in 20 contrasting genotypes under well-watered aerobic and several WD conditions.

Methods

Eight experiments evaluating 20 genotypes were conducted over the summer (October-May) in two years (2016-17, 2017-18) under aerobic (well-watered, freely drained soil with no standing water) and WD conditions at Gatton Research Station (27°54'S, 152°34'E, 89 m), The University of Queensland. In 2016-17, three experiments (well-watered throughout (72mm/week), WD imposed for 9day or 16day with two sowing times in a split plot design were conducted in a rainout shelter facility as six environments. Twenty diverse genotypes were allocated as a main plot, while two planting dates were used as a sub-plot. The timing of the WD coincided with the early grain-filling period (Sowing 1) or flowering stage (Sowing 2) of 10 of the 20 genotypes and the rest were at early reproductive stage. Thus, six environments were generated (well-watered Sowing 1 and 2 (17WWS1, 17WWS2), short term (9day; 17WDS1, 17WDS2) and long duration (16day; 17WDS1-L, 17WDS2-L) water deficit. The second sowing was affected by weeds, which caused reduction in plant population. Each experimental unit was assigned in 1.08 m² plot size with 10 cm (between plants) and 15 cm (between rows) by hand in dry direct seeding with a depth of 3-4 cm. In 2017-18, two environments, well-watered (72mm/week) and intermittent water deficit (48mm/week) throughout crop life-cycle were conducted in randomized complete block design with 3 replications. Dry direct seeding at 3 cm depth was achieved with Jang manual planter at a rate of 8 gm⁻¹ in 4m² plot size. Both pre- and post-emergent herbicides

were applied. There was some post-emergence herbicide damage but the plants appeared to have recovered after 15day. Basal fertiliser (Nitrophoska) was applied at the rate of 600 kg ha^{-1} with Urea at the rate 80kg ha^{-1} applied at 30 and 60day after sowing in both years. All grain quality analysis were done at Wet-chemistry Lab, Yanco Agriculture Institute following the protocol of The Department of Primary Industries, NSW.

Statistical analysis

A multiplicative mixed linear model was implemented in AsReml-R (V4.3,VSN international) in the R environments (V4.5.2; R Core Team, <https://www.R-project.org/>) for the analysis. Genotype was treated as a random effect, and residuals were fitted to each 'experiment' separately. An unstructured variance-covariance matrix was used to model genetic effects within experiments as the assumption of equal genetic variance between pairs of experiments was not met. The best spatial model was fitted within each experiments as per Gilmour (1997), where block was treated as a fixed effect, for grain yield of all experiments and quality traits of 18WW, 18WD, 17WWS1, 17WWS2 and 17WDS1. For quality traits of 17WDS1L and 17WDS2L, as a result of limited grain availability, a composite strategy akin to that of Smith et al. (2011) was used. Generalised heritability was estimated from the variance parameter from a single-experiment model, while genetic correlations between traits within experiments were estimated from separate bivariate models. Genotypes and environments were subjected to hierarchical clustering to enable identification of groups of genotypes and environments with similar performance for HRY across experiments. One environment (17WDS2L) did not converge in the analysis process due to high missing values and consequently only 7 environments were considered for quality traits. The squared Euclidean distance was utilised as the proximity measure and incremental sum of squares as the grouping strategy (Ward, 1963) on BLUPs standardised to have zero mean and unit variance within environment vectors.

Results and Discussion

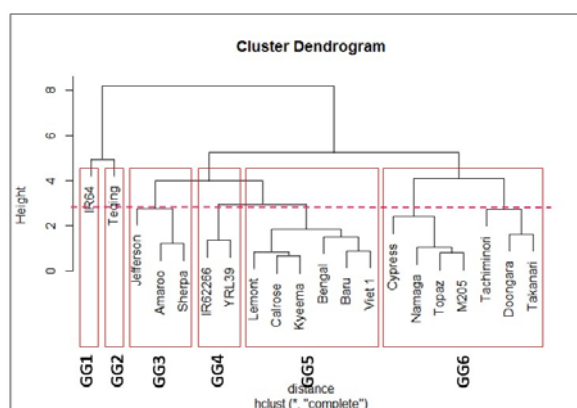
The cluster analysis was truncated at the 3 group levels for environments (EG) and 6 group levels for genotypes (GG) and this retained 62.5 % of the GEI variation for HRY. EG1, was composed of only 1 experiment, namely the first sowing (~grain filling stage) of 9 day short term WD (17WDS1), with a mean HRY of 48.9% was considered a poor environment (Table 1). EG2 comprised of 4 experiments; the two well-watered conditions in 2017 (17WWS1, 17WWS2), and both the well-watered and intermittent water deficit 2018 experiments (18WW and 18WD), with the mean HRY of 64.3% and generally regarded as favourable environment. EG3 consisted of short-term (16-day) WD at grain-filling period (17WDS1L) and (9-day) water deficit at flowering (17WDS2) with HRY of 57.6% and designated as an average environment.

GG1 (IR 64) and GG2 (Teqing) behaved quite differently from others with the lowest HRY across environments. GG5 (Lemont, Calrose, Kyeema, Bengal, Baru and Viet 1) was consistently good in HRY in all EGs with the lowest broken rice. GG3 and GG6 behaved more or less similarly. GG3 consisted of Jefferson, Amaroo, Sherpa; and achieved the highest HRY in EG3 with the lowest amount of broken rice while lower HRY in EG1 and EG3. GG4 (IR62266, YRL39) and GG6 (Cypress, Namaga, Topaz, M205, Tachiminori, Doongara and Takanari) were relatively high HRY and low broken rice (Figure 1(a)). Under favourable environment, GG3 and GG5 were considered as stable genotypes because of their consistent in high HRY in both years. GG4 had reasonably good HRY and moderate stability across all favourable environment. GG2 showed lower HRY under favourable environment but the highest HRY under water deficit (poor and average) environments with the low DoM and bran fraction. Thus, the high interaction effect of genotype by environment was due to GG2. GG3, GG4, GG5 and GG6 obtained higher HRY under favourable environment than others. Based on HRY, GG2 and GG4 were less affected by WD due to late maturing genotypes in EG1 and EG3. The genotypes from GG3 and GG5 were relatively tolerant to WD during grain filling and flowering period (EG1 and EG3). Genotypes from GG1 and GG6 were much more sensitive to WD in both EG1 and EG3 than others (Figure 1(b), Table 1). GG1 and GG3 had higher DoM ($\geq 14\%$) than others. GG3 and GG4 had slightly higher in whiteness than other GGs. Amylose content was lower under EG1 than EG2 and EG3 while higher in protein content. Protein content under EG3 had higher than EG2. The highest amylose and protein content existed in GG1 and GG2 while the least in GG5. Whiteness of GG3 and GG4 ($>71\%$) was slightly higher than GG2 and GG5 (Table 1).

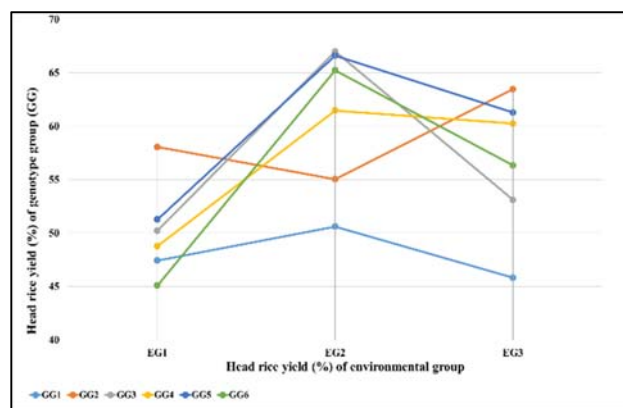
Table 1. The mean grain yield (GY), head rice yield (HRY), broken rice (BR), bran (%), degree of milling (DoM)%, whiteness%, amylose (%), and protein (%) of three genotype groups (GG1,GG2,GG3) in three environment groups

Environment	Poor	Favorable	Average	Mean	Poor	Favorable	Average	Mean
	EG1	EG2	EG3		EG1	EG2	EG3	
HRY (%)					Whiteness(%)			
GG1	47.4	50.6	45.8	48.8	67.7	73.4	66.8	70.7

GG2	58.1	55.0	63.5	57.9	67.3	73.8	67.5	71.0
GG3	50.2	67.0	53.1	60.6	74.0	71.3	71.5	71.7
GG4	48.8	61.5	60.2	59.3	71.3	73.3	70.5	72.2
GG5	51.3	66.6	61.3	62.9	71.8	71.5	69.5	71.0
GG6	45.1	65.2	56.3	59.8	71.0	71.2	68.8	70.5
Mean	48.9	64.3	57.6	60.2	71.4	71.8	69.4	71.0
Broken (%)					AC (%)			
GG1	16.9	18.5	16.2	17.6	19.1	23.5	21.7	22.4
GG2	15.5	16.8	11.3	15.1	26.0	25.5	26.8	25.9
GG3	11.1	5.4	13.9	8.7	18.6	19.2	19.6	19.2
GG4	17.3	8.2	9.8	9.9	15.8	19.3	18.3	18.5
GG5	15.4	5.9	10.4	8.6	17.7	18.4	18.8	18.4
GG6	19.1	6.9	11.4	9.9	18.2	19.3	19.4	19.1
Mean	16.3	7.6	11.6	10.0	18.3	19.5	19.6	19.4
Bran (%)					PC (%)			
GG1	16.4	11.3	10.8	11.9	12.0	9.5	11.0	10.3
GG2	10.2	9.9	7.1	9.1	11.2	8.7	10.5	9.6
GG3	15.6	9.5	11.4	10.9	10.1	8.8	9.5	9.2
GG4	13.8	10.9	8.7	10.7	10.2	8.5	9.5	9.0
GG5	13.8	9.4	9.7	10.1	9.9	8.5	9.4	9.0
GG6	15.2	9.6	10.1	10.5	10.7	9.1	10.1	9.6
Mean	14.5	9.7	9.9	10.5	10.4	8.8	9.8	9.3
DoM (%)					GY (t/ha)			
GG1	20.5	14.1	15.5	15.4	2.2	7.7	1.7	5.2
GG2	12.3	12.2	10.7	11.8	3.3	12.0	2.3	8.0
GG3	19.8	11.6	16.8	14.2	5.2	8.4	3.3	6.5
GG4	16.7	13.5	12.5	13.7	2.4	8.4	1.9	5.7
GG5	16.9	11.4	14.4	13.1	3.5	8.3	2.1	5.8
GG6	19.1	11.7	14.9	13.7	3.8	8.5	2.7	6.2
Mean	18.0	11.9	14.6	13.6	3.7	8.5	2.5	6.1



(a)



(b)

Figure 1. (a) Dendrogram truncated at the Six group level, for hierarchical clustering of the 20 rice genotypes, based on the matrix of standardized (HRY) head rice yield best linear unbiased predictors (BLUPs) tested in the 7 environments (b) Head rice yield (%) of genotype groups response to three different environments

Grain Yield (tha^{-1})

The highest mean GY was observed in EG2 ($8.5\ tha^{-1}$) followed by EG1 ($3.7\ tha^{-1}$), the short term 9-day WD at grain-filling, while the lowest was achieved in EG3 ($2.5\ tha^{-1}$) under 16 day long term WD at grain-filling

and 9 day WD at flowering . Average across EGs, GG1 had the lowest GY while GG2 achieved the highest. GG3 and GG6 had relatively similar GY in average but slightly higher in all EGs than others. These two GGs were stable and high GY in all EGs. The average GY of GG4 and GG5 were almost the same across environment. GG4 was similar GY to GG5 in EG2 and EG3 but lower than in EG1. Interestingly, Genotype groups responded differently to diverse environments. GG2 produced the highest GY (12 tha⁻¹) in EG2 (best HRY environment), but lower GY in EG1 (3.3 tha⁻¹) and EG3 (2.3 tha⁻¹). In contrast, GG3 achieved the highest in EG1 (5.2 tha⁻¹), EG3 (3.3 tha⁻¹) and relatively high in EG2 (8.4 tha⁻¹) (Table 1).

Table 2. Correlation value of head rice yield (HRY) % with its milling quality traits and grain yield for 3 different environment groups: EG1 (poor), EG2 (favourable) and EG3 (Average): **: significant at p=0.01, *: significant at p=0.05, ns: non-significant

Traits	EG1	EG2	EG3
	Poor	Favourable	Average
	HRY	HRY	HRY
Broken rice	-0.58**	-0.96**	-0.85**
Bran	-0.64**	-0.50*	-0.56**
Degree of milling	-0.66**	-0.55*	-0.49*
Whiteness	-0.02	-0.42	0.09
Amylose	0.29	-0.54*	-0.15
Protein	-0.20	-0.26	-0.37
Grain yield	-0.06	-0.07	-0.12

Association of HRY with other quality traits and GY

Associations between HRY and other quality traits and grain yield were analysed within environment groups, EGs (Table 2). HRY was negatively associated with broken rice ($r \geq -0.58^{**}$ to -0.96^{**}), with bran fraction ($r \geq -0.50$ to -0.64^{**}) in all EGs. HRY was significantly correlated with DoM and EG1 had higher DoM ($r \geq -0.66^{**}$) than EG2 ($r \geq -0.55^{*}$) and EG3 ($r \geq -0.5^{*}$). HRY had a negative association with amylose content ($r = -0.54^{*}$) only in EG2. HRY was not associated with GY and protein content in any EG (Table 2).

Conclusion

In this study, HRY and GY were decreased under water deficit environment (EG1 and EG3). GG1 showed a lower mean HRY as well as lower stability because of its poor adaptability in both water deficit and favourable environments. In contrast, GG5 showed a high stability because of their consistent high HRY across environments even though they were not very high yielding. GG2 resulted in high G×E interactions with no stable genotypes identified across different environments. In this study, genotypes from GG3 and GG5 with high HRY across environments were coincided with water deficit at flowering and grain filling period. GG3 and GG5 were good adaptability and stable HRY across environments. GG3 was considered as a stable genotype group in GY. DoM of genotypes was higher in water deficit environment than favorable environment leading to lower HRY, which was associated to higher broken rice and bran percentage supported by findings of Fofana (2010) and Bleoussi (2016). Genotypes with low amylose content achieved high HRY under aerobic well water condition, EG2.

Reference

- BLEOUSSI ET AL. 2016. Effect Of Different Soil Moisture Levels At Reproductive Stage On Rice Grain Quality. *Journal of Agricultural Science and Food Technology* 2, 55-63.
- BOUMAN, B. A. M., PENG, S., CASTAÑEDA, A. R. & VISPERAS, R. M. 2005. Yield and water use of irrigated tropical aerobic rice systems. *Agricultural Water Management*, 74, 87-105.
- GILMOUR, A. R., CULLIS, B. R. & VERBYLA, A. P. 1997. Accounting for natural and extraneous variation in the analysis of field experiments. *Journal of Agricultural, Biological & Environmental Statistics*, 2, 269-293.
- HAIDER, Z., ETAL., 2015. Impact of Drought Stress on Some Grain Quality Traits in Rice (*Oryza sativa*). *Agricultural Research*, 4, 132-138.
- SMITH, A. B., THOMPSON, R., BUTLER, D. G. & CULLIS, B. R. 2011. The design and analysis of variety trials using mixtures of composite and individual plot samples. *Journal of the Royal Statistical Society Series C-Applied Statistics*, 60, 437-455.
- WARD, J. H. 1963. Hierarchical Grouping to Optimize an Objective Function. *Journal of the American Statistical Association*, 58, 236-244.
- ZHANG, B., LI, W., CHANG, X., LI, R. & JING, R. 2014. Effects of favorable alleles for water-soluble carbohydrates at grain filling on grain weight under drought and heat stresses in wheat. *PLoS One*, 9, e102917.