RESEARCH ARTICLE

GENETIC ANALYSIS AND QTL MAPPING OF AGRO-MORPHOLOGICAL TRAITS IN LOWLAND RICE (*ORYZA SATIVA* L.) UNDER DROUGHT CONDITIONS

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A R T I C L E I N F O	A B S T R A C T
	The present study was undertaken to evaluate lowland rice genetic variability associated with agro-morphological traits under drought condition. A set of 250 recombinant inbred lines (RILs) from the cross between rice parental cultivarIR64 (sensitive to drought) and ITA112 (tolerant to drought) were used. The experiment was performed at Banfora in Burkina Faso using randomized complete block design with 2 replications. High genetic variability was observed for all studied traits. Moderate to high heritability in broad sense were observed for almost studied traits. Grain yield recorded positive correlation with all traits except day to 80% maturity and number of tillers. Using inclusive composite interval mapping software (ICIM), a total of 7 QTLs were identified for this study distributed on 5 chromosomes (2; 3; 4; 5; 6) and associated with day to 50% heading (QTL$_{50DH}$), day to 80%maturity (QTL$_{80DM}$), Biomass (QTL$_{Biom}$), flag leaf width (QTL$_{FLW}$), plant height (QTL$_{PH}$), panicle length (QTL$_{PL}$) and percentage of fertile spikelet (QTL$_{PFS}$). The percentage of phenotypic variance (PVE) explained by QTLs ranged from 5.45 to 14.58%. QTL$_{50DH}$, QTL$_{80DM}$ and QTL$_{Biom}$ were overlapped in same region on chromosome 3, which was in accordance with correlation results among the traits.

INTRODUCTION

Among cereals, rice (*Oryza sativa* L.) is one of the most important food crops in the world. It is member of genus *Oryza* and family Poaceae. In addition to cultivated species that are *Oryza sativa* (2n= 24 AA), grown worldwide and *Oryza glaberrima* (2n=24 AA) grown in Africa (Sajid *et al.*, 2015). Unlike other cereals, rice is cultivated across a much wider range of ecosystems, including irrigated, rainfed upland, rainfed lowland, flooded, and deepwater ecosystems across tropical and temperate climate conditions (Dixit *et al.*, 2014). It Rice is the principal food for the two-thirds of world population. It represent an important place in human nutrition, providing 20% of the calories and 15% of proteins consumed by world's population (Sajid *et al.*, 2015).

Rice is grown in 117 countries across all habitable continents. According to FAOSTAT (2014), rice production covered a total area of about 163 mha with a global production of about 740 mt and an average yield of about 4,539 kg / ha. The Asian continent ranks first with over 90.1% of world production, followed by America, Africa, Europe and Oceania. China is the leading in production with 206.5 million tons followed by India (157.2 million tons), Indonesia (70.8 million tons), Bangladesh (52.2 million tons) and Viet Nam with 44.9 million tons (FAOSTAT, 2014). It is a staple food for millions of people in Africa. It is grown and consumed in more than 40 countries among the continent. More than 20 million farmers in Africa are engaged on rice production and about 100 million people are dependent on it directly for their livelihood (Nwanze *et al.*, 2006). In sub Saharan Africa, rice yield has increased from 2.2 t/ha in 2000 to 2.7 t/ha in 2013 (Yao *et al.*, 2016). This yield is low compared with the average yield reported in Asia (4.6 t ha–1), South America (5.2 t ha–1) and North America (8.6 t ha–1) in 2013.

Several factors including insect, diseases, abiotic stress have contributed to low productivity in Africa. Among the major constraints, abiotic factors particularly drought constitutes a serious obstacle for rice production. Drought is the major abiotic stresses affecting plant growth and reducing crop productivity. Crop yield losses due to drought were estimated at 70% (Lang *et al.,* 2013). Thus, where rice is grown, drought is one of the main factors that cause important reduction in yield.

In order to reduce the loss of rice yield caused by drought, new drought tolerant rice varieties are required. Hence, improved tolerance to drought is a goal in rice improvement programs. Drought tolerance is mostly conditioned by many of components responses which interact. Moreover, drought tolerance is a complex trait controlled by minor and major genes and is dependent on the environment; it is one of the most difficult traits to study (Sabouri *et al.*, 2013). Therefore, selection based on the phenotype only, would be difficult for such traits (Dashti *et al.*, 2007). The advent of molecular markers has revolutionized genetic analysis of complex traits. Thus, molecular markers have been widely used to identify quantitative traits loci (QTLs) for complex traits, particularly those that are polygenic in nature such as drought.

The identification of genes or QTLs is one of the prerequisites for rice improvement for drought tolerance using marker

assisted selection (MAS). Recent studies have identified QTLs for various agro-morphological traits under drought condition in rice using for almost studies SSR markers (Sabouri *et al.*, 2013; Lang *et al.*, 2013; Sajid *et al.*, 2015; Ye *et al.*, 2015). Thus using single nucleotide polymorphism (SNP) markers that are more polymorphic than SSR marker can gives more in formatives. According to Rafalski *et al.*, (2002) single nucleotide polymorphism (SNP) markers constitutes a powerful tool for genetic applications due to low assay costs, high genomic abundance, co-dominant inheritance, potential for high throughput analysis and relatively low genotyping error rates. The objectives of the present study were (i) to evaluate genetic variability of rice agro-morphological traits under drought condition and analyse the relationships between these traits, (ii) to identify QTLs associated with agro-morphological traits under drought condition in bi-parental rice population genotyped with SNPs markers using Kompetitive Allele Specific PCR (KASP) genotyping system.

MATERIALS AND METHODS

Plant materials and experimental design

A population of 250 RILs was developed at Africa Rice center research station (6º25.415N and 2º19.684E; altitude: 21 m) located at Cotonou in Benin Republic through single seed descent from a cross between the two *Indica* parental lines IR64 and ITA112. IR64 is considered as a high yielding cultivar; however it is susceptible to drought in contrast to ITA112 witch is highly tolerant to drought. RILs and their two parents were evaluated in field under drought condition in 2014 from February to July (dry season). The experiment was performed in Banfora site (N: 10°63067 W: 004°77846) located in West of Burkina Faso using randomized complete block design with 2 treatments and 2 replications. The distance between rows and plants was 20 cm. Each line was grown in 3 rows with 15 plants per row. Experiment were managed following high input system with 300 kg of fertilizers (NPK + urea) and optimum weed and pest management. Two weeks cycling drought treatment was imposed from 45 days after sowing (around tillering stage) by withholding irrigation at the paddy field.

Trait measurements

The RILs population was assessed for 12 agro-morphological traits including number of tillers (NT), day to 50% heading (50DH, days after sowing), day to 80% physiological maturity (80DM, days after sowing), plant height (PH, cm), flag leaf length (FLL, cm), flag leaf width (FLW, cm), panicle length (PL, cm), percentage of fertile spikelet (PFS), number of panicle per m^2 (NP/m^2), biomass (Biom), 1000-grain weight (1000GW) and yield (kg/ha) under drought condition.

Genotyping

Young fresh leaves (2-3 week old) of each RILs and parental plants were sampled for DNA isolation. The genomic DNA was extracted using cetyltrimethylammoniumbromide (CTAB) method (Saghai-Maroof *et al.* 1994). Quality and quantity of DNA was checked by running aliquots of DNA samples on a 1% agarose gel. DNA was then normalized and shipped to the LGC Genomics genotyping laboratory in UK (http://www.lgcgenomics.com) as described in the user's manual. A total of 369 SNPs markers distributed throughout the rice genome were used for this study. Markers were initially screened on the two parents to identify the polymorphic markers. The segregating markers (250) were then used for genotyping in whole RILs population using Kompetitive Allele Specific PCR genotyping system (KASP) assay at LGC Genomics genotyping laboratory in UK.

Statistical analysis

Phenotyping analysis

The data recorded on 12 agro-morphological traits from the RILs studies, were subjected to statistical analysis. Analysis of variance (ANOVA) was performed to access the genotype effect and their interaction using the general linear model (GLM) implemented in Genstat 13th edition software (Payne *et al.*, 2011). In order to assess and quantify the genetic variability among the RILs for the characters under study the variance components and values of heritability were estimated for each trait. The frequency distributions of all the traits were performed to test the skewness of the traits towards the parents. Correlation analysis was performed using the same software to determine relationship between the characters under drought condition.

QTL analysis

Inclusive Composite Interval Mapping (ICIM) was used to detect QTL-marker for the agro-morphological traits under drought condition using QTL IciMapping software (Meng *et al.*, 2015). The LOD value of 2.5 was selected as the minimum to declare the presence of a QTL in a given genomic region. In addition, additive effects of the detected QTLs and the percentage of phenotypic variance (PVE) explained by each QTL were also estimated.

RESULTS

Phenotyping of mapping population

The mapping population, have been phenotyped extensively for 12 agro-morphological traits. Frequency distribution of RILs and their parents for all the characters studied showed normal distribution pattern (Figure 1). For each of these traits the two parents present significative differences except for flag leaf width. Some RILs showed lower values than their parents for any studied characters, whereas some others showed higher values than the parents, suggesting the involvement of multiple genes with quantitative inheritance for these agro-morphological traits under drought condition.

Analysis of variance of these phenotyping data revealed significant differences between RILs for all characters except flag leaf length, number of panicles and 1000 grains weight (Table 1). The genetic parameters estimated revealed low (<10%) to high (>20%) values of phenotypic (PCV) and genotypic coefficient of variation (GCV); however PCV was always higher than GCV for all the characters studies. The broad-sense heritability (H²b.s) estimate varied from 1.61% to 83.08%, respectively for flag leaf length (FLL) and yield. Almost the characters studies had moderate (comprising from 30 to 60%) to high heritability (>60%) except the number of tillers (NT), number of panicle (NP), flag leaf length (FLL), flag leaf width (FLW) and 1000 grains weight (1000GW). This result indicates that these characters could be easily improved through conventional selection.
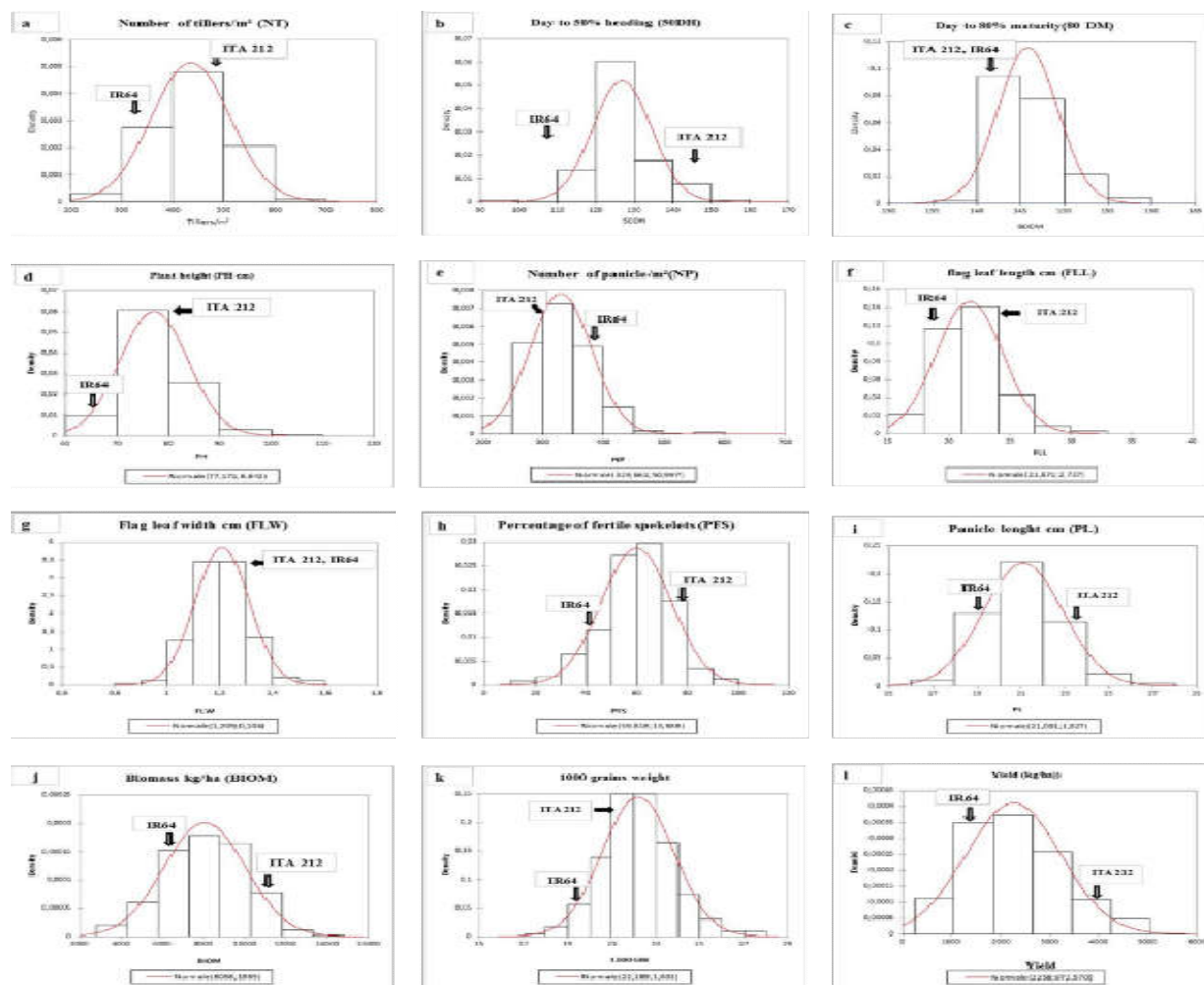
Figure 1 Frequency distribution for 12 agro-morphological in rice under drought of IR64 x ITA212 RILs populations. (a) number of tillers per m2, (b) : day to 50% heading, (c): day to 80% maturity, (d): plant height, (e): number of panicle, (f): flag leaf length, (g): flag leaf width, (h): percentage of fertile spikelet, (i): panicle length, (j): biomass, (k): 1000 grains weight, (k): yield.

Tableau 1 Mean of parents and RILs and estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and broad sense heritability (H^2b.s) for 12 agronomical traits under drought

Traits	MEANS				f proba	GCV	PCV	H^2b.s
	ITA212	IR64	Range	RILs				
NT	321.14	441.41	130 - 775	435.6 ± 8.60	*	7.91	17.02	21.57
50DH	142.24	121.41	64 - 158	126.7 ± 0.59	***	4.75	5.95	63.83
80DM	152.9	145.51	138 - 163	145.7 ± 0.24	***	1.93	2.33	68.4
PH (cm)	79.25	67.22	53.4 -106.6	77.33 ± 0.50	***	6.71	8.39	63.97
NP	332.4	391.73	140 - 625	329.1 ± 6.02	ns	4.83	14.77	10.71
FLL (cm)	22.22	18.07	11 - 39	21.7 ± 0.34	ns	1.54	12.13	1.61
FLW (cm)	1.17	1.16	0.7 - 1.9	1.21 ± 0.02	*	2.97	8.34	12.71
PSF	35.81	63.93	13.43 - 95	60.39 ± 1.44	***	12.01	22.01	29.75
PL (cm)	22.89	18.69	14 - 29	21.11 ± 0.19	***	4.83	8.44	32.8
Biom (g)	10887.5	7150	2450 - 13950	8050 ± 124.55	***	21.59	24.6	77.01
1000GW (g)	22.28	20.8	11.25 - 31.28	22.21 ± 0.18	ns	2.2	6.76	10.62
Yield (kg/ha)	3804.53	1052.32	187.7 - 5125	2258 ± 50.11	***	37.54	41.19	83.08

NT: number of tillers, **50DH:** day to 50% heading, **80DM:** day to 80% physiological maturity, **PH**: plant height, **FLL:** flag leaf length, **FLW**: flag leaf width, **PL:** panicle length, **PFS:** percentage of fertile spikelet, **NP:** number of panicle per m^2, **Biom**: biomass, **1000GW:** 1000-grain weight,

Relationship between agro-morphological traits under drought condition in rice

Knowledge about correlation degree between the characters is a key factor in plant breeding. Hence, the correlation analysis is necessary to determine the direction of selection. The correlation coefficients among the agro-morphological traits under drought condition in this study were given in Table 2. Significant and positive correlations were observed between biomass under stress and 1000 grains weight (0.1876), day to 50% heading (0.2577), day to 80% maturity (0.2258), flag

leaf length (0.1604), flag leaf width (0.2549), number of tillers (0.1584), number of panicles (0.2225), plant height (0.4217), panicle length (0.287) and yield (0.3965). Day to 80% maturity showed also positive and high significant correlation with day to 50% heading (0.7532), biomass (0.2258) and panicle length (0.2664), whereas it showed negative correlation with number of panicles (-0.0722), number of tillers (-0.0356), percentage of fertile spikelet (-0.4784), 1000 grains weight (-0.4041) and yield (-0.0275). Similar, significant and positive correlation were obtained

between yield per hectare and 1000 grains weight (0.3502), biomass (0.3965), flag leaf width (0.1356), percentage of fertile spikelet (0.254), plant height (0.4375) and panicle length (0.2566) under drought condition. Among these characters, plant height gives the highest correlation coefficient value with yield following by biomass and 1000 grains weight under drought. In addition, panicle length showed positive correlation with all the characters studies except number of panicle, number of tillers and percentage of fertile spikelet.

except the percentage of fertile spikelet. Overlapping of QTLs for different traits was identified in this study. For example, QTLs for day to 50% heading (QTL_{50DH}), day to 80% maturity (QTL_{80DM}) and biomass (QTL_{Biom}) under drought stress were mapped to id3000946 - id3001701 region on chromosome 3. Positive values (>0) of additive effects were obtained with the QTLs related to day to 50% heading, day to 80% maturity, flag leaf width, panicle length and biomass. Therefore, the favorable alleles for these QTLs came from the resistant parent ITA212.

Table 2 Correlation coefficients among agronomic traits of rice recombinant inbred lines under drought conditions

Traits	1000GW	50DH	80DM	Biom	FLL	FLW	NP	NT	PFS	PH	PL
1000GW	-										
50DH	-0.29**	-									
80DM	-0.40**	0.75**	-								
Biom	0.18**	0.2-**	0.22**	-							
FLL	0.16*	0.139ns	0.09ns	0.16*	-						
FLW	0.005ns	0.03ns	0.04ns	0.25**	0.24**	-					
NP	0.06ns	-0.05ns	-0.07ns	0.22**	-0.04ns	-0.004ns	-				
NT	0.21**	0.03ns	-0.03ns	0.15*	0.035ns	0.043ns	0.14*	-			
PFS	0.52**	-0.35**	-0.47ns	0.002ns	-0.01ns	-0.025ns	-0.03ns	0.19**	-		
PH	0.38**	0.17**	0.12ns	0.42**	0.41**	0.13*	-0.07ns	0.08ns	0.14*	-	
PL	0.14*	0.22**	0.26**	0.28**	0.39**	0.24**	-0.13*	-0.04ns	-0.05ns	0.52**	-
yield	0.35**	0.03ns	-0.02ns	0.39**	0.12ns	0.13*	0.03ns	-0.004ns	0.25**	0.43**	0.25**

NT: number of tillers, **50DH:** day to 50% heading, **80DM:** day to 80% physiological maturity, **PH:** plant height, **FLL:** flag leaf length, **FLW:** flag leaf width, **PL:** panicle length, **PFS:** percentage of fertile spikelet, **NP:** number of panicle per m², **Biom**: biomass, **1000GW:** 1000-grain weight, *: significant at 0.05 probability level, **: Significant at 0.01 probability level; **ns**: no significant.

Identification of QTL for agro-morphological traits under drought condition

Firstly a total of 369 SNPs markers were used to screen the two parental genotypes IR64 and ITA212. Among the screened 369 SNPs markers, 253 (68.56%) markers showed polymorphism between IR64 and ITA212. These polymorphic markers were used for genotyping the 230 RILs.

Phenotypic data obtained for all agro-morphological traits studied were analyzed together with genotyping data for all mapped using QTL IciMapping software. The results from Inclusive Composite Interval Mapping (ICIM) showed seven QTLs for seven various agro-morphological traits under drought stress in this study (Table 3, Figures 2 and 3). The seven QTLs identified in the RILs population were distributed on five chromosomes (Table 3). Thus, QTLs for day to 50% heading (50DH), day to 80%maturity (80DM), Biomass (Biom) are located in chromosome 3 and QTLs for fag leaf width (FLW), plant height (PH), panicle length (PL) and percentage of fertile spikelet (PFS) are respectively located in chromosomes 2; 4; 5 and 6.

However, some negative values of additive effects were obtained with the QTLs for plant height (-4.92) and percentage of fertile spikelet (-3.76) indicating that the favorable alleles were contributed by the susceptible parent IR64.

DISCUSSION

Phenotypic variation

The present study was undertaken to discover QTLs and marker-trait association from the mapping population derived from the cross between drought resistant (ITA212) and susceptible (IR64) parents followed by screening with SNPs markers and subsequently, identify the potential QTLs and markers linked to agro-morphological traits under drought condition. The mapping population consisting of 230 RILs exhibited significant variation for all traits studied except flag leaf length, number of panicles and 1000 grains weight.

Table 3 QTLs detected for agro-morphological traits under drought stress in IR64 × ITA212 recombinant inbred lines using Inclusive Composite Interval Mapping (ICIM)

Traits	QTLs	Chr	Position	Interval Markers Left - right	LOD	PVE (%)	Additive effect	Parent donor of drought resistance QTL
50DH	QTL_{50DH}	3	13	id3000946 - id3001701	4.3	8.71	2.36	ITA212
80DM	QTL_{80DM}	3	10	id3000946 - id3001701	3.51	7.11	1.03	ITA212
PH	QTL_{PH}	4	1	id4000734 - K_id4001733	2.7	14.58	-4.92	IR64
FLW	QTL_{FLW}	2	95	id2009666 - id2009758	3.31	6.42	0.02	ITA212
PFS	QTL_{PFS}	6	6	id6000402 - K_id6000911	2.69	5.45	-3.76	IR64
PL	QTL_{PL}	5	88	K_id5007714 - id5009481	2.94	6.03	0.45	ITA212
Biom	QTL_{Biom}	3	10	id3000946 - id3001701	3.91	8.07	712.50	ITA212

50DH: day to 50% heading, **80DM:** day to 80% physiological maturity, **PH:** plant height, **FLW:** flag leaf width, **PL:** panicle length, **PFS:** percentage of fertile spikelet, **Biom**: biomass

The LOD value and the phenotypic variance explained (PVE) were respectively ranging from 2.69 for QTL_{PFS} to 4.3 for QTL_{50DH} and from 5.45% for QTL_{PFS} to 14.58% for QTL_{PH} (Figure 2). The PVE was less than 10% for all traits studied

This result indicates huge genetic variability existing among the genotypes. So, the parents used for crossing were genetically different.
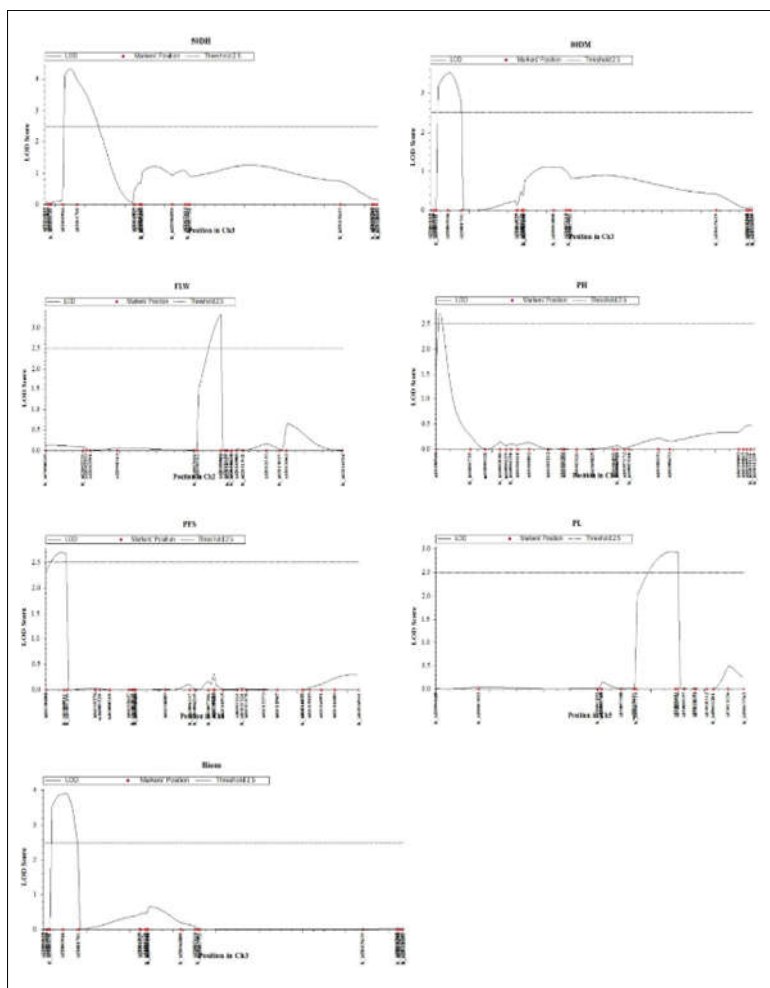
Figure 2 QTLs detected for rice agro-morphological traits under drought condition

50DH: day to 50% heading,
80DM: day to 80% maturity,
PH: plant height,
FLW: flag leaf width,
PL: panicle length,
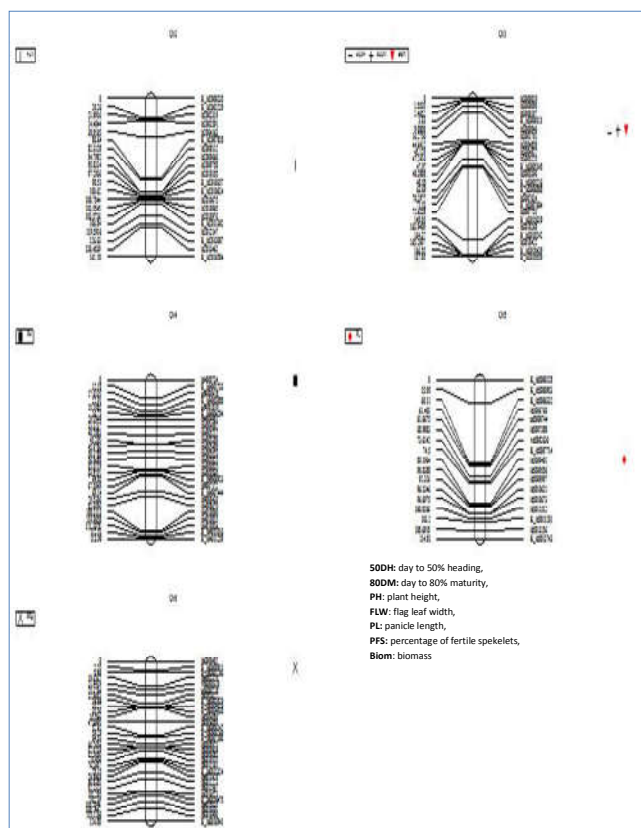**PFS:** percentage of fertile spekelets,
Biom: biomass

Figure 3 Mapping of QTLs day to 50% heading, day to 80% physiological maturity, plant height, flag leaf width, panicle length, percentage of fertile spikelet and biomass under drought condition.

Similar variation and transgressive segregation for various morphological and production traits under drought condition have been reported earlier in several rice lines by Gomez *et al.*, (2006), Amiri Fahliani *et al.*, (2011) and Ahmad *et al.*, (2015). Estimation of genetic variability revealed a magnitude of variation from low too high for PCV and GCV for the traits studied. Also, PCV values were higher than GCV values for all the characters, indicating that the expression of these characters was influenced by environment. Similar results were reported by Lafitte *et al.*, (2004), Gomez *et al.*, (2010) and Sabouri *et al.*, (2013) in rice agronomical traits under drought. The minimum difference between GCV and PCV values were estimated for all the characters except number of panicles (NP), flag leaf length (FLL), flag leaf width (FLW) and percentage of spikelet fertile (PSF) under drought condition indicated minimum environmental influence. Manikya and Reddy (2011); Singh Alok *et al.*, (2015) and Anis *et al.*, (2016) also reported that the PCV was higher than GCV indicating the influence of environment on the characters and also reported the reduction in genetic variance under severe stress condition. High GCV and PCV coupled with high heritability were observed for the characters biomass (Biom) and yield. This indicates the lesser influence of environment in expression of these characters and prevalence of additive gene action in their inheritance. Thus, these characters could be easily improvement through conventional methods under drought conditions. The characters day to 50% heading (50DH), day to 80% maturity (80DM) and plant height (PH) had high heritability with low PCV and GCV, indicating that the characters were governed by both non-additive gene actions. These results are accordance with those of Sadimantara *et al.*, (2014), Sedeek and El-Wahsh (2015); Singh Alok *et al.*, (2015) and Anis *et al.*, (2016).

Correlation analysis

Correlation analysis of characters can be used as tool for indirect selection. In this study, day to 80% maturity showed significant and positive correlation with day to 50% heading and biomass. Also, the character yield showed significant and positive correlation with 1000 grains weight, biomass, flag leaf width, percentage of fertile spikelet, plant height and panicle length under drought condition, indicating that simultaneous selection for these characters would result in improvement of yield. Similar finding are already notified in previous studies (Gomez *et al.*, 2010; Ahmad *et al.*, 2015). Plant height showed a negative correlation with the character number of panicles under drought. Thus, lower plant height results to higher panicle number. This result is in accordance to those of Spielmeyer *et al.*, (2002) and Ahmad *et al.*, (2015). In addition plant height, biomass and 1000 grains weight gives the highest correlation coefficient value with yield under drought. This finding indicated that these characters will be considered in simultaneous selection on enhancing the yield under drought for next population. Similar findings also observed in the study made by Dashti *et al.*, (2007) and Gomez *et al.*, (2010).

QTLs linked to agro-morphological traits under drought

The DNA of the two parents (IR64 and ITA212) was surveyed and 253 (68.56%) of the 369 SNPs primers generated informative polymorphism between the parents. Despite a relatively low number of SNPs markers used in this cross, the parents exhibited high level of polymorphism as both are indica ecotypes. High level of polymorphism had already been reported between the parents by previous studies (Sabouri *et al.*, 2013 and Ye *el al.*, 2015). In contrast, a low level polymorphism was reported between the parents in the intra-sub-specific and even in inter-sub-specific crosses of rice (Price and Tomos 1997; Ali *et al.*, 2000 and Gomez *et al.*, 2010). This low polymorphism between parents can be attributed to its origin. Varshney *et al.* (2007) suggested also that the low level of polymorphism can attributed to the marker techniques used.

In this study, the 253 SNPs DNA markers were performed to search potential QTL regions. Using ICIM method, a total of seven QTLs were located that associated with day to 50% heading (50DH), day to 80% maturity (80DM), Biomass (Biom), fag leaf width (FLW), plant height (PH), panicle length (PL) and percentage of fertile spikelet (PFS) under drought condition. The map position and characteristics of QTLs associated with the seven traits under drought condition are presented in Figures 3. The QTL associated to 50DH (chromosome 3 near id3000946 - id3001701) was already mapped to a similar region in previous studies (Lafitte *et al.*, 2004; Gomez *et al.*, 2006). In addition QTLs associated to PL and PSF located in chromosome 5 and 6 were also mapped near the same region by several studies (Kamoshita *et al.*, 2008; Sabouri *et al.*, 2013; Ye *et al.*, 2015). Overlapping of QTLs for different traits was observed in this study. Some QTLs identified for some traits in drought condition were co-localized. Thus, QTLs associated with 50DH, 80DM and Biom under drought stress were mapped to id3000946 - id3001701 region on chromosome 3. These findings were supported by the correlation analysis among traits. Similar collocation of QTLs associated to agronomical traits under drought were reported in the same region early in rice by Gomez *et al.*, (2010) and Lang *et al.*, (2013). Whether this region might contain one or more key genes for drought resistance ability in this mapping population needs to be further tested. Others QTLs associated with PH (chromosome 4) and FLW (chromosome 2) mapped here were also located early in previous studies (Nguyen *et al.*, 2013; Dixit *et al.*, 2014).

The QTLs identified various agronomical traits under drought stress in this study, which individually explained 5.45 to 14.58% of the phenotypic variation (PVE). The low and high (PVE) were obtained respectively with QTLS associated to PSF and PH. According to Collard *et al.* (2005), QTL accounting for more than 10% of phenotypic variation (PVE) are major QTL. Based on this delineation, PVE values were high for QTL associated to PH. There for, this QTL is could be considered as QTL major. Several researchers used this approach to establish marker phenotype association where the phenotypes possessed continuous distribution. These results are in accordance with those of Nguyen *et al.*, (2013). Based on the values of additive effect recorded by QTLs identified, both parents contain favorable QTLs affecting this trait, suggesting the likelihood of recovering transgressive segregants. Majority of favorable alleles of QTLs associated with PH and PSF were contributed by the susceptible parent (IR64). Similar results were early reported by Bernier *et al.* (2007); Kumar *et al.* (2007) and Dixit *et al.* (2014).

CONCLUSION

The lowland rice RILsused in this study showed significant variation in agro-morphological traits under drought condition. Seven QTLs linked to various agro-morphological under drought stress in field condition were identified. Colocation of QTLs associated with day to 50 heading, day to 80% maturity and biomass traits was observed in these rice RILs. In conclusion, the present study has identified QTLs linked to drought tolerance traits in locally adapted *indica* ecotypes and may be useful for improved breeding programs using marker assisted selection (MAS) for drought tolerance in rice.

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