Agro-morphological characterization of upland rice accessions

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ABSTRACT: The agro-morphological characterization is fundamental in order to provide information for plant breeding programs. The aim of the present study was to characterize 146 accessions of upland rice (*Oryza sativa* L.), based on qualitative and quantitative agro-morphological descriptors. The experiment was conducted in Recife, state of Pernambuco, Brazil, using a randomized block design with three replicates. Polymorphism was observed among 12 of 14 qualitative characters evaluated, whereas significant differences ($p < 0.05$) were observed for 11 of the 14 analysed quantitative traits. Genetic variance was higher than environmental variance and the average inheritability coefficients were above 80 % for all characters, which ensures the predominance of the genetic components in the differences observed among accessions. On the cluster analysis for qualitative traits the accessions were classified in two groups with a total of 18 duplicates, whereas for the quantitative traits three groups were obtained with few subgroups. The principal component analysis for quantitative traits showed great dispersion of the accessions. The most divergent group of accessions included the genotypes Mitsukasane, Mie, Tomoe mochi, Ooba kirishima and Nourin mochi 6, which showed a higher number of spicklets per plant. There is high variability among the rice accessions from the germplasm collection studied, which presents great importance for breeding programs or for genetic studies on this species.
Keywords: genetic variability, germplasm, ex-situ conservation, pre-breeding

Introduction

Agro-morphological characterization of germplasm accessions is fundamental in order to provide information for plant breeding programs (Lin, 1991). Several researchers reported the use of agro-morphological markers in the characterization and study of rice (*Oryza sativa* L.) germplasm diversity. Li et al. (2000) obtained consistent results analyzing the correlation between genetic and morphological differentiation in 111 accessions of rice from the Japonica and Indica groups. Yawen et al. (2003) studied the genetic diversity on 5285 accessions of indigenous rice in China and found considerable morphological variation among accessions. In India, Patra and Dhua (2003) analyzed the agro-morphological diversity of upland rice and in Vietnam, Fukuoka et al. (2006) assessed the variability in agronomic characters among landraces of aromatic rice populations. Using 42 agro-morphological characters associated with 39 SSR markers, Bajracharya et al. (2006) examined the genetic relationships among 147 high altitude rice landraces from Jumla, Nepal. Seetharam et al. (2009) characterized 30 rice genotypes comprising landraces, pure lines, somaclones, breeding lines and varieties specifically adapted to costal saline environments using SSR markers and morphological characters. Yibo et al. (2010) investigated morphological and genetic diversity in 11 surviving populations of *O. rufipogon* Griff. from Hainan Island, China, and reported a clear morphological differentiation among or within populations.

This type of characterization has also been used on wild species in Brazil. Rosa et al. (2006) characterized eight populations of *O. glumaepatula* Steud. collected in different hydrographic basins and Veasey et al. (2008) analyzed the genetic variability among the four wild rice species occurring in South America, reporting agro-morphological variation for *O. glumaepatula*, followed by *O. latifolia*.

The aim of the present study was to characterize 146 upland rice genotypes using agro-morphological characters and to provide useful information to facilitate the choice of genitors for rice plant breeding programs.

Materials and Methods

One hundred and forty-six accessions of upland rice were assessed in this study (Table 1). Three Brazilian cultivars were used as controls: IAC 202, IAC 47 and Bonança.

The experiment was carried out in Recife, state of Pernambuco in northeast Brazil, (08°01' S; 34°56' W - 10.3 m altitude), from March to July 2007, during the agricultural year in the region. The mean temperature during the experiment was 23.8 °C and the index annual rainfall was 1.193 mm.

Seeds were germinated in polystyrene trays with a substrate composed of *Pinus* husk, vermiculite, fine peat, macro and micro-nutrients. Twenty-eight days after emergence, the most vigorous seedlings of each genotype were transplanted to the field, following the procedure reported by Villela and Furlani Júnior (1996). The statistical experiment design was a randomized block with three replicates. Each plot consisted of a row of six plants spaced 0.15 m apart, with the rows spaced 0.40 m apart.

The accessions were characterizated according to descriptors established by the International Rice Research Institute and the International Board for Plant Genetic Resources (IRRI, 1980). A total of 14 qualitative (Table 2) and 14 quantitative descriptors (Table 3) were used. The qualitative descriptors were: leaf color (LC), leaf pubescence (LP), lodging resistance (LR), internode

Table 1 – List of accessions of upland rice from Japan from the germplasm collection of Universidade Federal Rural de Pernambuco - UFRPE and the Brazilian cultivars (controls) studied.

N°	Acc.	Genotype	N°	Acc.	Genotype	N°	Acc.	Genotype	N°	Acc.	Genotype
1	1	Kunihikari mochi	39	144	Miyamae okute	77	261	Kahei	115	337	(337)
2	2	Senshou	40	153	Col/Fukuti/1965*	78	263	Tamasari 3	116	339	Owari 79
3	3	Fukuton	41	156	Tachiminori	79	264	Miyakonojoo mochi	117	343	Tamasari mochi
4	8	Shin hakaburi	42	159	Minami hata mochi	80	268	Ookuma nishiki	118	352	Rikuu 15
5	12	Senshou ibaragi 1	43	164	No mochi	81	269	Nourin mochi 6	119	355	Col/ Miyazaki/1963*
6	16	Namekata mochi	44	171	Oosumi	82	271	Taishou nishiki	120	357	Rikuu 22
7	23	Sonobe mochi	45	172	Oohataho	83	273	Shina mochi	121	364	Fujimizu bansei
8	25	Seion uruchi	46	173	Nourin 11	84	274	Nagae wase	122	365	Iwate kinsen 1
9	27	Gaisen mochi	47	175	Tomoe mochi	85	276	Arabiya mochi	123	367	Bansei tarou
10	29	Shiro hige	48	177	Nourin 16	86	277	Tozo mochi	124	368	Shiro uzura
11	36	Nakaahara mochi	49	183	Yashino mochi	87	278	Urasar	125	369	(369)
12	38	Nourin mochi*	50	184	Akayakan	88	279	Ootama	126	370	(370)
13	41	Iwata hata mochi	51	186	Kirishima*	89	280	Okabo mochi	127	373	Mogami uruchi 1
14	44	Hassaku mochi	52	189	Okabo	90	284	Furuwase	128	374	Gaisen*
15	45	Mitsukasane	53	191	Col/Fukuti/1965*	91	285	Hirakawa okute	129	378	Okka modoshi
16	48	Mie	54	199	Kahee	92	286	Nourin 7	130	379	Mino senshutsu
17	50	Wase esoshima mochi	55	200	Hitachi nishiki	93	287	Oiran	131	380	Rikutou
18	52	Mizuhoshi	56	202	Ooba kirishima	94	289	Shinhoku daiou mochi	132	382	Kurohige
19	55	Oohata mochi	57	203	Horarin	95	290	Riku araki	133	383	Mogami chikanari 1
20	56	Miyako	58	206	Taishou mochi	96	293	Suzume shirazu	134	384	Kounoso rikutou 2
21	57	Yoridashi	59	214	Kaneko mochi	97	294	Col/Miyazaki/1963*	135	386	Minami hata mochi
22	69	Saitama senshou	60	216	Iwate kurumi wase 1	98	295	Hideshirazu mochi	136	387	Wase shinshuu
23	70	Kirishima*	61	217	Col/Miyazaki/1963*	99	299	(299)	137	389	Igisu mochi
24	74	Aichi rikutou 1	62	218	Toukyo haneko	100	302	Kazusa wase	138	394	Susono mochi
25	78	Yonoyuki mochi	63	219	Gaisen (4x)*	101	304	Shinkuko mochi	139	395	Seta gaisen
26	79	Dango mochi	64	228	Tariu saku mochi	102	308	Hikouki gome	140	397	Korotou mochi
27	80	Sangoku	65	229	Col/Tokushima/1967*	103	310	Senshou*	141	401	Ishiyakushi mochi
28	82	Terenzu	66	230	Miyanishiki	104	312	Col/Ooita/1964	142	402	Shiro hige
29	99	Eika ine	67	235	Hatamurasaki	105	314	Taiwan mochi	143	407	Edogawa
30	127	Hakamuri 20	68	236	Toga	106	315	Urasan	144	408	Gose yonkoku
31	129	Esojima mochi	69	239	Col/Miyazaki/1963*	107	317	Owari mochi	145	410	Shizouka
32	130	Esojima	70	248	Col/Tokushima/1967*	108	320	Nourin mochi 2	146	413	Chousen
33	131	Mino	71	250	Jouon	109	322	Senshou*	147	420	IAC 202**
34	133	Nourin mochi*	72	252	Oota wase	110	325	Gaisen mochi 909	148	421	IAC 47**
35	134	Suzume shirazu	73	253	Ine mochi	111	330	(330)	149	422	Bonança**
36	136	Yamato nishiki	74	256	Shizuoka	112	331	Rikuu			
37	139	Nourin mochi 1	75	257	Hiderishirazu	113	335	Rikuu 23			
38	140	Nourin mochi 17	76	260	Kozo	114	336	Ohata wase			

Acc. – Accessions; *Different accessions with the same name; **Controls.

color (IC), stigma color (SC), presence and distribution of awn per panicle (PDAP), apiculus and/or awn color (AAC), lemma and palea color (LPC), glumella pubescence (GP), panicle type (PT), threshability (Th), seed coat color (SCC), endosperm type (ET), and grain shape (GS). The quantitative descriptors were: flag leaf length (FLL), flag leaf width (FLW), culm length (CL), culm diameter (CD), number of tillers per plant (NTPP), flowering cycle (FC), maturation cycle (MC), number of panicles per plant (NPP), panicle length (PL), number of spikelets per panicle (NSPP), panicle fertility (PF), ratio between length and width of the grain (RGLW), 1000-grain weight (TGW) and plant production (PP).

Table 2 – Qualitative descriptors used to evaluate 146 upland rice accessions from Japan and three Brazilian cultivars (controls).

Descriptors	Observed phenotypic classes	Evaluation phase
Qualitative		
Leaf color (LC)	1 - light green; 2 - green; 3 - dark green; 4 – purple.	Early flowering
Leaf pubescence (LP)	1 - glabrous; 2 - intermediate; 3 - pubescent.	Early flowering
Lodging resistance (LR)	1 - absent; 2 - plants with moderate lodging; 3 - plants strongly lodged.	After maturation
Internode color (IC)	1 - green; 2 - gilded; 3 - purple; 4 - purple stripes.	Grain filling
Stigma color (SC)	1 - white; 2 - light green; 3 - yellow; 4 - purple.	Flowering
Presence/distribution of awn per panicle (PDAP)	1 - absent; 2 - awns on panicle extremity; 3 - awns throughout the panicle.	After grain filling
Apiculus and/or awn color (AAC)	1 - straw color; 2 - gilded; 3 - red; 4 - purple; 5 - brown; 6 - green; 7 - black.	After grain filling
Lemma and palea color (LPC)	1 - straw color; 2 - gilded or with gilded lines; 3 - straw color with brown stains; 4 - brown; 5 - reddish; 6 - straw color with purple lines; 7 - purple; 8 - black; 9 - white.	Maturation
Glumella pubescence (GP)	1 - absent/very weak; 2 - present.	Flowering
Panicle type (PT)	1 - grouped; 2 - intermediate; 3 - open.	Maturation
Threshability (Th)	1 - difficult (less than 25 % of the grains were removed); 2 – intermediate (from 25 % to 50 % of the grains were removed); 3 – easy (more than 50 % of the grains were removed).	After maturation
Seed coat color (SCC)	1 - white; 2 - light brown; 3 - brown; 4 - red; 5 - purple.	After maturation
Endosperm type (ET)	1 - non-glutinous; 2 - intermediate; 3 - glutinous.	After maturation
Grain shape (GS)	1 – round (length/width ratio was less than 1.50); 2 - semi-round (ratio ranged from 1.50 to 2.00); 3 - semi-elongated (ratio from 2.01 to 2.75); 4 – elongated (ratio from 2.76 to 3.50); 5 - very elongated (ratio larger than 3.50).	After maturation

Table 3 – Quantitative descriptors used to evaluate 146 upland rice accessions from Japan and three Brazilian cultivars (controls).

Descriptors	Observed phenotypic classes	Evaluation phase
Quantitative		
Flag leaf length (FLL)	Arithmetic means of the six random samples.	Anthesis
Flag leaf width (FLW)	Arithmetic means of the six random samples.	Anthesis
Culm length (CL)	Arithmetic means of the six random samples.	Grain filling
Culm diameter (CD)	Arithmetic means of the six random samples.	Grain filling
Number of tillers per plant (NTPP)	Arithmetic means of the six samples.	Grain filling
Flowering cycle (FC)	Number of days from plant germination until 50 % of the plants in each plot flowered.	After flowering
Maturation cycle (MC)	Number of days until 50 % of the panicles were mature.	After maturation
Number of panicles per plant (NPP)	Arithmetic means of the six samples.	After maturation
Panicle length (PL)	Arithmetic means of the six random samples.	After maturation
Number of spikelets per panicle (NSPP)	Arithmetic means of the six random samples.	Maturation
Panicle fertility (PF)	Arithmetic means of the six ramdom samples.	After maturation
Ratio between length and width of the grain (RGLW)	Arithmetic means of the six random samples.	After maturation
1000-grain weight (TGW)	Arithmetic means of the six random samples.	After maturation
Production per plant (PP)	Arithmetic means of the six random samples.	After maturation

For the quantitative characters the statistical analyses were performed using the F test and in order to group the accessions, the Scott and Knott (1974) test was used. Statistical significance was set at 5 % ($p < 0.05$) and the GENES software was used for all tests (Cruz, 2006). The software PAST (Hammer et al., 2001) was used for the cluster and principal component analyses. Qualitative and quantitative traits data were analyzed separately.

The qualitative traits were transformed into binary data considering the presence or absence (1/0) of each character state. The Jaccard similarity coefficient was estimated for qualitative traits, while Euclidean distances were obtained for the quantitative traits. UPGMA (Unweighted pair group method with arithmetic mean) was the clustering method used for both qualitative and quantitative data.

Results and Discussion

Polymorphism was found in 12 of the 14 qualitative traits studied; the non-polymorphic traits were the internode color (light green) and panicle type (intermediate). Panicle type (PT) is generally affected by water deficiency before flowering, because this condition changes the angle of the panicle branches and the density of the grains (Bonow et al., 2007). Internode color (IC) often shows variation on color tonality depending on the age of the plants and the soil fertility conditions. Plants usually present a dark green tonality on high soil fertility and a light green one on low soil fertility (Fonseca et al., 2002), which agrees with the soil type used in this study, a franc-clay and low fertility one.

For the traits stigma color (SC) and glumella pubescence (GP), two alternative forms or types were observed. White (65 %) and purple (35 %) genotypes were observed for SC, while presence (76 %) and absence (24 %) of the pubescence were found in GP. Veasey et al. (2008) reported variation within and among populations of *O. glumaepatula* for stigma color, with three populations 100 % white, four populations 100 % purple, and the others with varying degrees for each color, while white was the only color found on the other South American wild rice species (*O. latifolia*, *O. grandiglumis* and *O. alta*).

The characters showing higher variability were leaf pubescence (74 % pubescent, 20 % glabrous and 6 % intermediate), lodging resistance (37.5 % absent, 37.5 % few lodged and 25 % moderate), presence and distribution of awn per panicle (PDAP) (55 % absent, 23 % present only at the end of the panicle and 22 % present on all panicle), threshability (73 % easy threshability, 21 % intermediate and 6 % difficult), endosperm type (31 % glutinous endosperm, 42 % intermediate and 27 % not glutinous), and grain shape (74 % semi-long, 20 % long, 5 % tightly long and 1 % semi-rounded grain shape). The grain shape character also showed the highest variation in studies conducted in Pakistan by Siddiqui et al. (2007). Although this character is mentioned as qualitative, its evaluation is carried out as a quantitative trait, according to the grain dimentions. The major variation observed was probably due to polygene action and the influence of environmental causes. In relation to PDAP, while the awn is present its length should be influenced by the soil fertilization and plant density (Fonseca et al., 2002). Studies carried by Bisne and Sarawgi (2008) to characterize 32 aromatic rice accessions of Badshah Bhog group from IGKV, Raipur, Chhattisgarh germplasm, found the highest variation among accessions for the traits leaf blade colour, lemma and palea colour, apiculus colour, and lemma and palea pubescence.

The cluster analysis for the qualitative traits using the Jaccard similarity coefficient classified the accessions into two groups (Figure 1). However, the scatter graph from agro-morphological qualitative traits obtained by principal components showed that the accessions did not form distinct groups, with a wide dispersion among the accessions (Figure 2). The first and second components represented 21.1 % and 11.5 % of total variation observed among accessions, respectively. A total of 18 duplicates were found in the cluster analysis (Figure 1), including the following accessions: 14-125, 5-8, 44-128, 27-28, 25-83, 133-142, 78-144, 51-109-118-138, 61-91, 33-48, 85-104, 110-111-112, 89-101-132, 65-77-78-87-120-121-140, 143-145, 8-10-39-49, 7-102 and 88-105. None of these duplicates included accessions with the same genotype name. However, Fukuoka et al. (2006), in
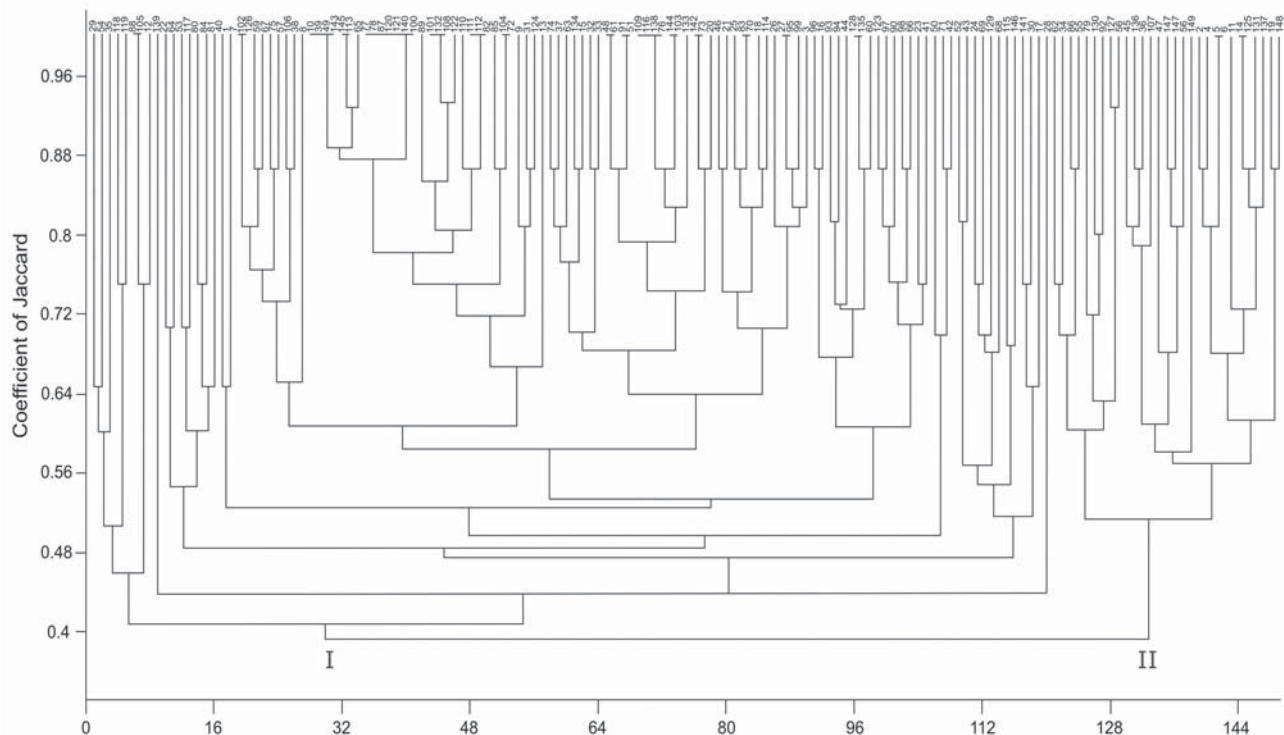

Figure 1 – Dendrogram of similarity patterns by the UPGMA method based on Jaccard similarity coefficient estimated from 14 qualitative agromorphological traits analyzed in 146 accessions of Japanese upland rice and three cultivars (controls) used in the experiment.
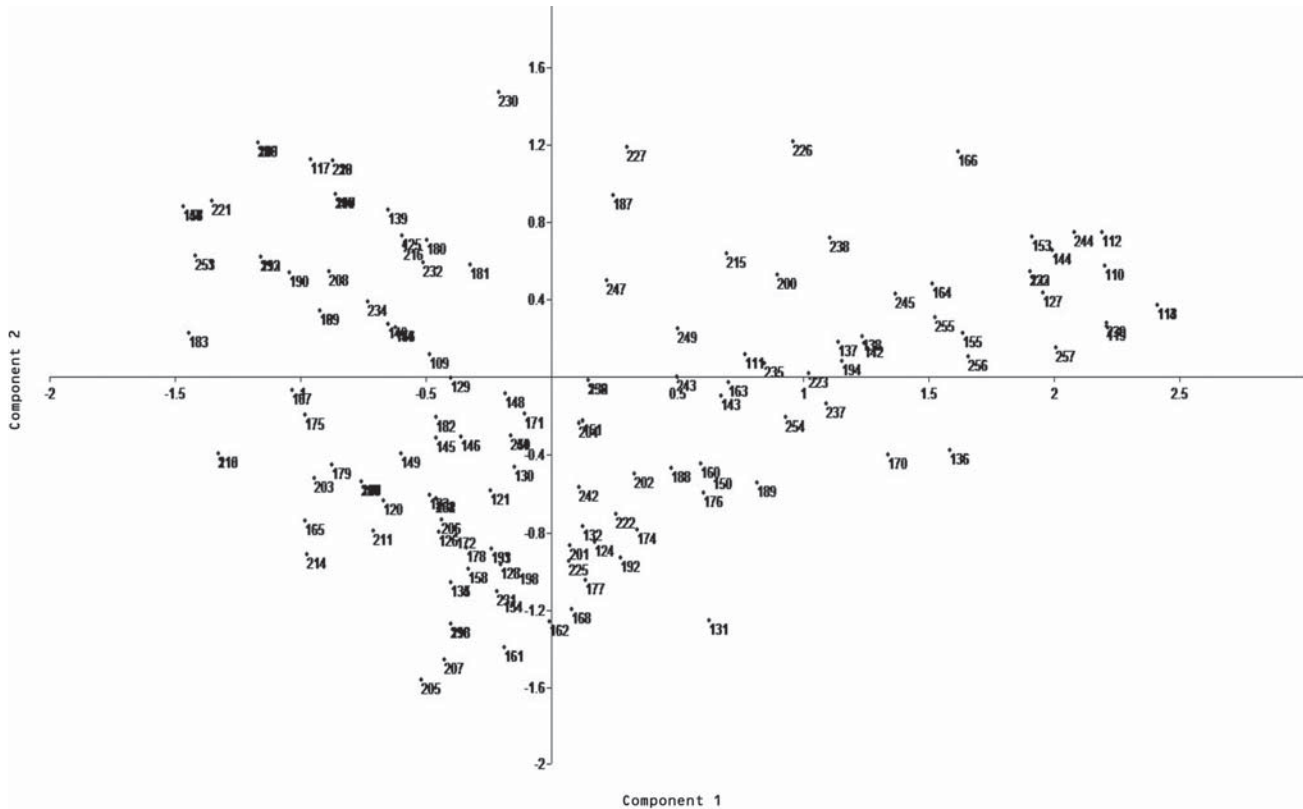
Figure 2 – Scatter graph of 146 accessions of Japanese rice upland germplasm collection of the Universidade Federal Rural de Pernambuco - UFRPE and cultivars (controls) used in the experiment from 14 qualitative agro-morphological traits.

Table 4 – Analysis of variance for 14 quantitative traits[1] for 146 upland rice accessions from Japan and three Brazilian cultivars (controls).

| Sources of variation | DF | Mean squares[3] | | | | | | | | | | | | | |
		FLL	FLW	CL	CD	NTPP	FC	MC	NPP	PL	NSPP	PF	RGLW	TGW	PP
Replications	2	11.93	0.02	297.57	0.01	6.30	13.83	92.24	2.42	0.47	74.68	5.38	0.07	25.13	71.47
Treatments	148	168.92*	0.30^{ns}	598.80*	0.04^{ns}	9.29*	165.81*	11.94*	6.79*	19.88*	5590.06*	279.86*	0.50^{ns}	38.57*	79.38*
CV (%)[2]		6.59	4.11	7.95	3.95	9.99	1.64	1.04	10.45	4.88	10.38	3.62	4.29	5.70	24.23
Average		41.28	1.98	95.68	0.56	6.09	71.72	104.90	6.14	21.93	107.83	84.94	2.63	28.17	15.21

[1]FLL-flag leaf length; FLW-flag leaf width; CL-culm length; CD-culm diameter; NTPP-number of tillers per plant; FC-flowering cycle; MC-maturation cycle; NPP-number of panicles per plant; PL-panicle length; NSPP-number of spikelets per panicle; PF-panicle fertility; RGLW-ratio grain length/width; TGW-1000-grain weight; PP-production per plant; DF – degrees of freedom. [2]CV – coefficient of variation. [3]*Significant at a 0.05 probability level, by F test.; ^{ns}not significant at a 0.05 probability level, by F test.

studies with aromatic rice landraces, concluded that significant variation may be found among genotypes with the same name.

Considering the 14 quantitative traits analyzed in this study, differences among accessions ($p < 0.05$) were found for 11 traits (Table 4). The non-significant traits were flag leaf width, culm diameter and the ratio culm/width of the grain. Veasey et al. (2008) also found significant differences and high variability for 11 populations of *O. glumaepatula*, mainly for the characters number of tillers, plant height at flowering, leaf length and width, culm length, days to heading, panicle number, panicle height, flag leaf length, spikelet length and awn length.

The coefficients of variance (CV%) showed an optimum experiment precision, with values below 11 % for all characters,

except for PPP (CV = 24.2 %). The analysis performed by Patra and Dhua (2003) had CV values below 27.1 % for all agronomic traits evaluated, except for the character number of panicles, directly related to grain production, showing a CV value of 30.7.

Results concerning the estimates of variance components among accessions indicate that the variance observed was due to genetic factors, as the values obtained for the b index (CVg/CVe) were above 1 for all characters (Table 5). When the b index is higher than 1, there are favorable conditions for selecting superior genotypes considering the predominance of genetic factors rather than environmental factors (Vencovsky and Barriga, 1992). The traits number of spikelets per panicle, culm length, panicle fertility, flowering cycle and flag leaf length

showed higher genetic variance values, 1821.59, 180.30, 90.13, 54.81 and 53.85, respectively (Table 5). The estimate of the average inheritability among accessions was high, over 82 % for all quantitative traits. The better prediction of the environmental component of phenotypic variance, helps the more realiable estimation of both broad and narrow sense heritability, and so the better planning program for cross and self pollinated plants improvement (Fahliani et al., 2010).

The Scott and Knott (1974) ($p < 0.05$) analysis allowed the formation of several groups among accessions for all characters (not shown data). The flag leaf length character classified the accessions in eight groups. The group with the highest average showed a variation from 58.2 cm (accession 121) to 64.3 cm (accession 147), while the group with the lowest average varied from 25.9 cm (accession 10) to 30.5 cm (accession 90). Eight groups were obtained for the character flag leaf width, varying from 2.52 cm (accession 6) to 2.7 cm (accession 99) for the group with higher scores and from 1.36 cm (accession 91) to 1.63 cm (accession 137) for the group with lower scores.

The culm length (CL) trait, related to plant height, classified the accessions in five groups. The higher values varied from 131.1 cm (accession 137) to 139.3 cm (accession 125), while the lower values varied from 58.5 cm (accession 127) to 86.8 cm (accession 114). The accessions presenting higher means for CL were 125 (369 – without denomination), 148 (IAC 47), 68 (Toga)

Table 5 – Estimates of the variance components, phenotypic and genetic parameters of 14 quantitative traits for 146 upland rice accessions from Japan and three Brazilian cultivars (controls).

Character[1]	Phenotypic and genetic parameters[2]					
	$\hat{\sigma}_f^2$	$\hat{\sigma}_e^2$	$\hat{\sigma}_g^2$	h_m^2 (%)	CVg	Index b
FLL	56.301	2.47	53.85	95.63	17.78	2.70
FLW	0.10	0.00	0.10	97.79	15.77	3.84
CL	199.60	19.30	180.30	90.33	14.03	1.77
CD	0.01	0.00	0.14	98.87	21.27	5.39
NTPP	3.10	0.12	2.97	96.01	28.31	2.83
FC	55.27	0.46	54.81	99.17	10.32	6.31
MC	3.98	0.39	3.59	90.13	1.81	1.74
NPP	2.26	0.14	2.13	93.94	23.75	2.27
PL	6.63	0.38	6.25	94.25	11.40	2.34
NSPP	1863.35	41.77	1821.59	97.76	39.58	3.81
PF	93.29	3.16	90.13	96.62	11.18	3.09
RLWG	0.17	0.00	0.16	97.45	15.30	3.57
TGW	12.86	0.86	12.00	93.33	12.30	2.16
PP	23.46	4.53	21.94	82.90	30.80	1.27

[1]FLL-flag leaf length; FLW-flag leaf width; CL-culm length; CD-culm diameter; NTPP-number of tillers per plant; FC-flowering cycle; MC-maturation cycle; NPP-number of panicles per plant; PL-panicle length; NSPP-number of spikelets per panicle; PF-panicle fertility; RLWG-ratio grain length/width; TGW-1000-grain weight; PP-production per plant.[2] $\hat{\sigma}_f^2$ = phenotypic variance; $\hat{\sigma}_e^2$ = environmental variance; $\hat{\sigma}_g^2$ = genetic variance; h_m^2 (%) = average heritability coefficient; CVg = coefficient of genetic variance; CVe = coefficient of experimental variation; Index b = CVg/CVe.

and 137 (Igisu mochi), with 139.3 cm, 132.5 cm, 132.2 cm and 131.1 cm, respectively, all considered of an intermediate height. However, 10.7 % of the accessions [25 (Yonoyuki mochi), 35 (Suzume shirazu), 58 (Taishou mochi), 59 (Kaneko mochi), 60 (Iwate kurumi wase 1), 66 (Miyanishiki), 69 (Col/Miyaza-ki/1963), 75 (Hiderishirazu), 90 (Furuwase), 100 (Kazusa wase), 103 (Senshou) and 127 (Mogami uruchi 1)] showed CL means below 80 cm, which is why they were considered semi-dwarf plants. The character culm diameter classified the accessions into 14 groups, which shows the high variability among accessions for this trait. The highest value was presented by accession 117 (Tamasari mochi), with 0.97 cm, followed by accessions 123 (Bansei tarou), 5 (Senshou ibaragi 1), 131 (Rikutou), 42 (Minami hata mochi), 14 (Hassaku mochi), 81 (Nourin mochi 6) and 37 (Nourin mochi 1), all with means above 0.8 cm. The group with the lower values showed a variation from 0.38 cm (accession 79) to 0.42 cm (accession 108).

Ten groups were obtained for the character number of tillers per plant, with accession 10 (Shiro hige) presenting the highest mean, 14.8 cm, followed by accessions 110 (Gaisen mochi 909), 145 (Shizuoka), 59 (Kaneko mochi), 111 (330-without denomination) and 87 (Urasar), with means above 10 tillers per plant. The accessions that had the lowest means for this trait varied from 3.1 (accession 11) to 4.3 (accession 99). As for the number of panicles per plant, eight groups were obtained, with accessions 140 (Korotou mochi), 110 (Gaisen mochi 909), 59 (Kaneko mochi) and 85 (Arabiya mochi) producing the higher number of panicles, around 10 panicles per plant. The lower means, between 3.1 to 4 panicles per plant, were presented by accessions 133 (Mogami chikanari 1), 131 (Rikutou), 95 (Riku araki), 40 (Col/Fukuti/1965), 82 (Taishou nishiki), 5 (Senshou ibaragi 1), 19 (Oohata mochi) and 83 (Shina mochi). Sarhadi et al. (2009), studying native aromatic rice cultivars from north, east and northeast of Afghanistan, and check cultivars from Japan, Thailand and India, found panicle number per plant ranging from 8 ± 1.5 to 13 ± 1.3, and observed that this trait was not correlated with grain number per panicle.

The trait panicle length classified the accessions in seven groups. Accessions 147 (IAC 202), 47 (Tomoe mochi), 137 (Igisu mochi), 36 (Yamato nishiki) and 11 (Nakaahara mochi) presented the higher means, 28.7 cm, 28.2 cm, 27.3 cm, 27.0 cm and 26.8 cm, respectively. Accessions 35 (Suzume shirazu), 48 (Nourin 16) and 100 (Kazusa wase) showed the lower means for this character, 16.5 cm, 16.0 cm and 15.7 cm, respectively.

Plant yield, number of panicles per plant and amount of fertile spicklets are some of the main components of rice production. The trait number of spicklets per plant classified the accessions in ten groups. The accession that showed the highest mean, 302 spicklets, was 81 (Nourin mochi 6), followed by accessions 56 (Ooba kirishima), 147 (IAC 202), 16 (Mie), 47 (Tomoe mochi), 149 (Bonança) and 15 (Mitsukasane), with 267.5, 264.9, 219.2, 218.5, 212.3 and 205.0 spicklets, respectively. The lowest means for this trait showed a variation from 40.4 (accession 58) to 73.9 spicklets (accession 49). Grain number per panicle in Afghan native rice cultivars ranged from 69 to 169 with most Afghan cultivars showing more than 100 grains per panicle (Sarhadi et al., 2009), which is a desirable character for breeding programs. Therefore, the accessions in our study showed much higher values for this trait.

As for the character panicle fertility, the accessions were classified in eight groups: genotypes Col/Miyazaki/1963 (accession 97), Shiro hige (accession 10), Bansei tarou (accession 123), Kahee (accession 54), Nourin mochi (accession 12) and Oosumi (accession 44) showed the higher means, 97 %, 96.6 %, 96.5 %, 96.5 %, 96.2 % and 96.1 %, respectively; all of them resulted in fertility values above 90 %. Six groups were obtained for the trait 1000-grain weight. The higher means varied from 33.7 g (accession 86) to 36.2 g (accession 72), while the lower means varied from 19.5 g (accession 56) to 21.5 g (accession 96). This trait ranged from 20 to 32 g in the Afghan cultivars (Sarhadi et al., 2009).

Finally, character plant production classified the accessions in four groups. The genotypes that presented the higher means for this trait were Oota wase (accession 72), 35.6 g per plant, Bansei tarou (accession 123), 33.8 g per plant, Jouon (accession 71), 31.1 g per plant and Nourin mochi 1 (accession 37), 31.0 g per plant. The group that showed the lower means varied from 4.6 g per plant (accession 35) to 13.0 g per plant (accession 38). These same traits showed variation among 147 rice accessions in studies conducted by Bajracharya et al. (2006). In studies of ecogeografic and genetic diversity based on morphological characters of indigenous rice in China, Yawen et al. (2003) found wide variations for characters related to production, such as length of the panicle (10-36 cm) and grain number per panicle (30-340).

Considering the crop development period, the flowering cycle (FC), which is very important in the definition of the maturation cycle (MC) and was the most efficient trait in discriminating the accessions, varied considerably among accessions. It allowed 17 groups to be formed. Accession 53 (Col/

Fukuti/1965) showed the highest mean, a flowering cycle of 95.3 days, followed by accessions 48 (Nourin 16) and 129 (Okka modoshi), 88.3 and 88 days, respectively. Accessions 136 (Wase shinshuu), 76 (Kozo) and 45 (Oohataho), 55 days, and accession 75 (Hiderishirazu), 54 days, showed flowering cycles shorter than the other accessions. Seven groups were obtained for character MC: the longer cycle was presented by genotype Tamasari mochi (accession 117), an average of 115 days, followed by accessions 81 (Nourin mochi 6), 53 (Col/Fukuti/1965), 48 (Nourin 16) and 55 (Hitachi nishiki), 115, 112.7, 112, 112 and 110.7 days, respectively. The genotypes that presented shorter cycles varied from 100.7 days (accession 62) to 103.3 days (accession 133). Variations in the cycle can occur due to season sowing and weather conditions (Fonseca et al., 2002).

In the cluster analysis for the quantitative traits using the Euclidean distance, three groups were formed (Figure 3). One of the groups (group I) classified the accessions 56, 147 and 81 as more divergent than the others, for presenting higher number of panicles, fertile spikelets and plant production, which are important agronomic characters. The analysis of the descriptors used showed that the number of panicles per plant was the most important character in the group classification. The scatter graph considering the quantitative traits showed that accessions 56 (Ooba kirishima), 81 (Nourin mochi 6) and 147 (IAC 202, control), belonging to the most divergent group in the cluster analysis (group I), were also more divergent for the principal component analysis (PCA), followed by accessions 15 (Mitsukasane), 16 (Mie), 47 (Tomoe mochi) and 149 (Bonança, control) (Figure 4), which belong to a subgroup in group 2 of the cluster analy-
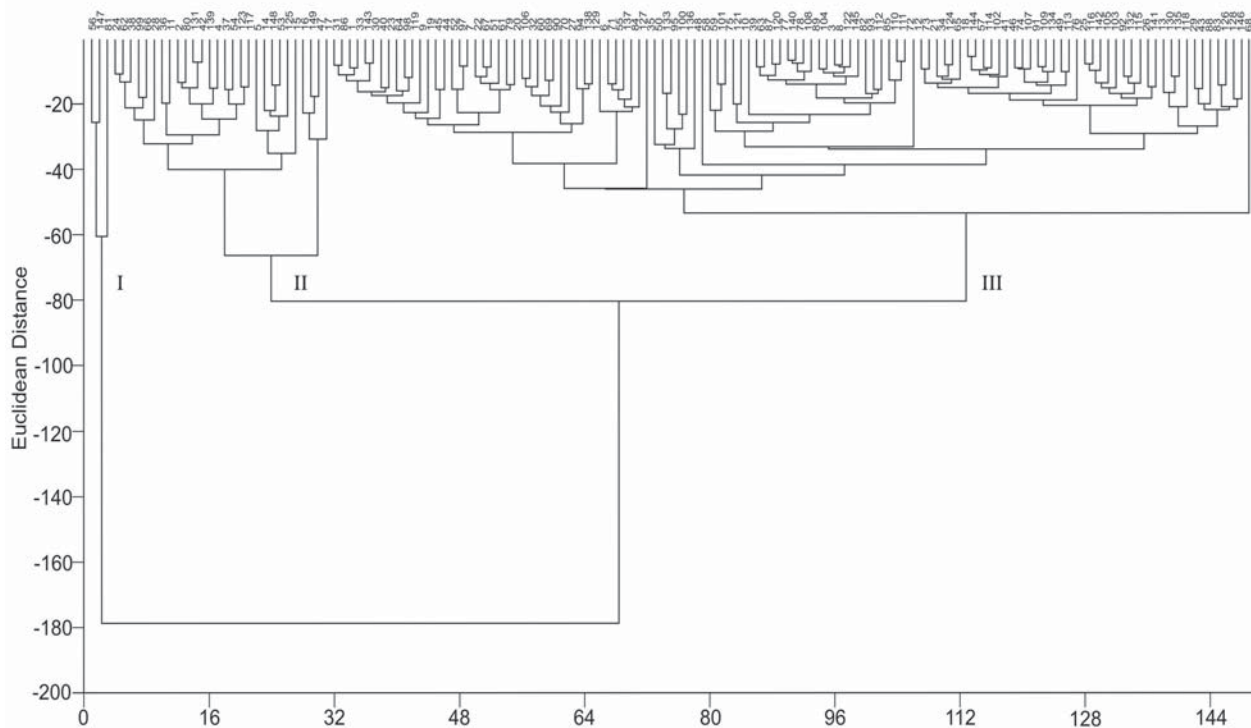

Figure 3 – Dendrogram of similarity patterns by the UPGMA method based on the average Euclidean Distance estimated from 14 quantitative agro-morphological traits analysed in 146 accessions of Japanese rice and and cultivars used in the experiment.
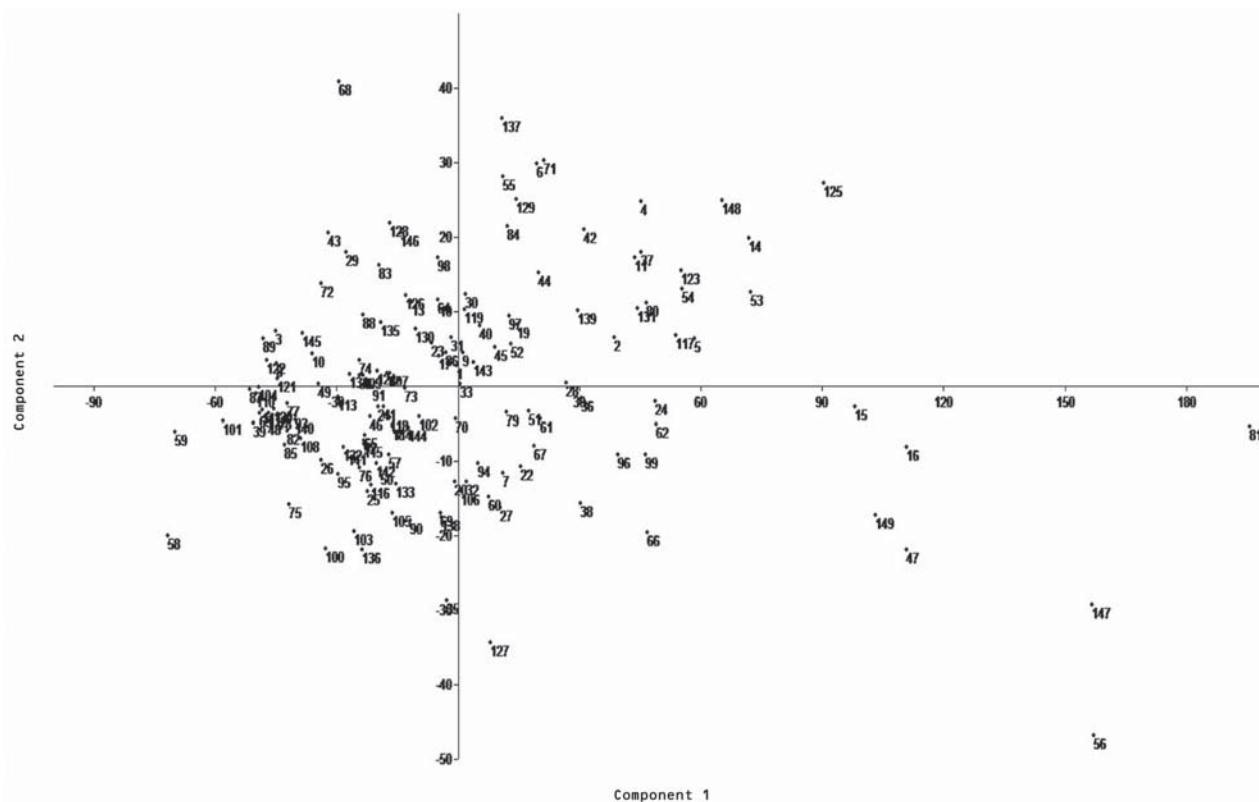
Figure 4 – Scatter graph of 146 accessions of Japanese rice upland germplasm collection of the Universidade Federal Rural de Pernambuco - UFRPE and cultivars (controls) used in the experiment from 14 quantitative agro-morphological traits.

sis. These seven accessions had high number of spicklets per plant, while accessions 47 and 147 showed high panicle lengths; accession 147 showed high flag leaf lengths as well. This last accession is the genotype IAC 202, one of the controls used in this study. The first and second components in the PCA represented 83.1 % and 8.4 % of the total variation among accessions. If the initial components accumulate a relatively high percentage of total variation, generally above 80 %, they satisfactorily explain the variability among individuals (Madia et al., 1979).

No duplicates were identified among the studied accessions for quantitative traits in the cluster analysis (Figure 3), which means there is a high diversity among the accessions for these traits. Cluster analysis based on agro-morphological diversity assessment in rice was also reported in several studies, such as Ghalain (2006), Naik et al. (2006), Hien et al. (2007), Sarawgi and Bhisne (2007), Mathure et al. (2010), Li et al. (2010) and Zhang et al. (2010). Seetharam et al. (2009) characterized 30 rice genotypes comprising landraces, pure lines, somaclones, breeding lines and varieties by SSR markers and morphological characters. At Euclidian distances the genotypes were grouped into five clusters and the PCA components explained 38.4 % of total variation. Therefore, all data presented in this study allowed the identification of cultivars with distinct morphological traits that could be used as potential parents to facilitate high resolution QTL mapping and validate candidate genes responsible for quantitatively agronomic characters (Li et al., 2010).

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