

Full Length Research Paper

Genetic diversity of salt tolerance rice landraces in Vietnam

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Accepted 7 May, 2009

A collection of 200 salt tolerance rice landraces was assessed for genetic diversity using quantitative agro-morphological characters. ANOVA showed highly significant differences (LSD 0.01) among the traits assessed such as grain length, grain width, number of unfilled grains, 1000-grain weight, leaf length and leaf width except panicles per plant and yield. Correlation coefficients showed that all the traits were highly correlated with each other except yield.. The diversity indices (H') for quantitative descriptors were high ranging from 0.68 to 0.95. Overall the mean diversity index for all traits was 0.88). Cluster analysis generated by UPGMA grouped the 200 rice landraces into six clusters with similarity coefficient of 20.61. The six clusters were distinct in terms of culm length, number of filled grains, panicle length, panicles per plant, grain length, grain width, yield and biomass.

Key words: Rice, genetic, landraces, diversities.

INTRODUCTION

Traditional varieties, some times called landraces or local or farmer varieties form the foundation on which to build better crop plants. Landraces are generally considered to be a rich source of genetic variation. Furthermore, local varieties provide farmers with alternatives in areas where modern crop varieties are not well adapted and contribute to diversity at the field level. However, for rice the number of traditional varieties being planted has reduced, with a few productive and relatively uniform high-yielding varieties dominating the rice landscape (Tran, 2000). Traditional rice varieties though had been documented to have contributed to the origin of 1,709 modern rice varieties in Asia; it can be traced to 11,592 traditional varieties. The pedigrees of IRRI breeding lines and varieties until 1994 can be traced to hundreds of traditional varieties most from Asian countries (Tran, 2000). Genetic diversity is the basic foundation for a species survival. According to Brown et al. (1989), the processes of recombination and gene mutation guarantee continuous inputs for new variants, environmental adaptation and random drift genetic diversity in time and space. Shape the distri-

bution of the easiest and most common tool for gauging genetic diversity is measuring morphological or phenotypic trait differences (Jarvis et al., 2000). Available evidence indicates that farmers use certain phenotypic features of plants for selection and identification (Jarvis et al., 2000). Hence morphological traits are linked to genetic diversity. Therefore giving names to these varieties indicates that farmers have some understanding about the crop genetic diversity in their fields (Jarvis et al., 2000).

Many authorities asserts that characterization and evaluation of diversity among traditional varieties will provide plant breeders information necessary in the identification of initial materials for hybridization to produce varieties with improved productivity and quality (Buu et al., 2002). Therefore the objectives of this study were to: 1. Assess genetic diversity of the traditional rice varieties in the genebank of Cuu Long Rice Research Institute, Vietnam 2. Ascertain the correlation among the rice characters for use in rice improvement.

MATERIALS AND METHODS

Plant materials

A total of 200 accessions of traditional rice varieties obtained from Cuu Long Rice Research Institute genebank, Vietnam was used for

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the study, The detailed passport information of these accessions is provided by Lang et al. 2007.

Agro-morphology- based diversity analysis

The 200 traditional rice varieties were planted in the field at the Cuu Long Rice Research Institute (CLRRI), Vietnam during the 2006/2007 wet season. Seeds were sown in raised seedbeds and 18 - 21 day old seedlings were transplanted at one seedling per hill at a spacing of 15 x 20 cm. The standard cultural management practices for rice were followed (Bui, 1986; Buu et al., 1999).

Data collection

Data were collected for quantitative traits following the Descriptors for Rice *Oryza sativa* L. (IBPGR-IRRI Advisory Committee, 1980). The following is the list of morphological and agronomic traits and the number of samples that were measured to assess diversity and relationships of the different rice accessions (Table 1).

1. Panicle length (cm) at maturity measured from the base to the tip of the panicle from 10 randomly selected primary panicles per accession per replication.
2. Number of panicles per plant from 10 randomly selected primary panicles per accession per replication.
3. 1000 g weight at 14% MC from 5 randomly selected primary panicles per accession per replication.
4. Culm length (cm) measured from the ground level to the base of the panicle (from 10 randomly selected primary panicles per accession per replication).
5. Days to maturity- when 80% of the grains are fully ripened on a per replication (Bui, 1986).
6. Number of filled grains)- per panicle from 5 randomly selected primary panicles per accession per replication.
7. Number of unfilled grains per panicle from 5 randomly selected primary panicles per accession per replication.
8. Yield-obtained from the harvested plants in each replication. Harvested grains were threshed, cleaned, dried, and weighed for each accession per replication. Moisture content (MC) per plot was determined immediately after weighing using a moisture meter.

Yield = wt. of harvest (g)/ no. of hills harvest x no. of possible hills x MF

Where; $MF = \frac{100 - MC}{86}$ of the harvest grains

9. Biomass-weight of 10 plants harvested from each accession per replication. Harvested plants were dried before weighing.

$$10.) \text{HarvestIndex} = \frac{\text{EconomicYield}}{\text{BiologicalYield}} \times 100$$

Where; Economic Yield is the total weight of grain harvest from 10 plants per accession per replication and Biological Yield is the total grain weight and biomass from 10 plants per accession per replication.

RRL: Rate root length. The root will measure at 30 days stress NaCl (EC = 12 DS/m)

Data analysis

Analysis of variance: The agro-morphological data collected were

analyzed by analysis of variance to verify the genetic variations among the traits measured. Non significant traits based on the F-test, were not considered for further analyses.

Shannon-weaver diversity index: Diversity indices for the various traits were computed using the following formula (Shannon and Weaver, 1949):

Where; n is the number of phenotypic classes for a character and p_i is the portion of the total number of entries belonging to the i class. The standardised Shannon -Weaver diversity index ranging from 0 to 1 was obtained by dividing H' by the \log_2 of the total number of phenotypic classes. H' for each of the morpho-agronomic descriptors of each variety was computed using MS Excel. Mean phenotypic diversity index was computed for the pooled diversity estimates per descriptor.

Correlation analysis: Correlation coefficients (r) among agro-morphological traits were calculated by using SAS program.

Distance matrix: Distance matrix was calculated by means of Euclidean Distance Coefficient (Sneath and Sokal, 1973):

Where; $E_{ij} = 0$ to ∞ , the larger the value, the more distant the degree of relationship
 X_i and X_j are the standardized values for the i th and j th characters in k th varieties.

Cluster analysis: Cluster analysis for agro-morphology-based genetic distance matrix was generated using UPGMA clustering method of the NTSYS program. The results of the UPGMA were used to draw the dendrogram of the 90 traditional varieties.

Principal component analysis: Principal component analysis was done using NTSYS and SAS programs.

RESULTS AND DISCUSSION

Diversity analysis using agro-morphological characters

The Table 2 showed that highly significant differences among the various traits in the 90 traditional varieties were obtained for grain length, grain width, number of unfilled grains, 1000-grain weight, leaf length and leaf width. Differences were not significant for panicles per plant.

Analysis of variance

The mean, range (maximum and minimum), standard deviation, coefficient of variation (CV), mean standard error, and F value of the quantitative traits assessed is presented in Table 2. The results showed that most of the quantitative traits were highly variable. For instance, the early and late maturity dates were 135 and 153 days, respectively. In general maximum values obtained for yield and number of filled grain was 145.6 g \approx 3.44 tons/ha and 303 g for the variety Nep lemand Thang coi, respectively. Highly significant differences (LSD 0.01) were also observed for number of unfilled grains, 1000 g weight leaf length and leaf width. In contrast, no significant differences were observed for panicles per plant.

Frequency distribution of the varieties with respect to

Table 1. Passport information of the 200 traditional varieties used in the study (Lang et al 2007).

No	Accession	Name of variety	Passport information
1	1	Chiu Han	Kiengiang, Vietnam, 104°40'- 105°32'40 longitude and 9°23'50" – 10°32'30" latitude
2	2	HTA 88086	Wetland rice, Thailand, 15 00 N, 100 00 E
3	3	HTA 88086	Wetland rice, Thailand, 15 00 N, 100 00 E
4	4	Lua Huong	Lua nuoc troi, Longan, Vietnam, 105°30' 30"-106°47' 02" longitude and 10°23'40"-11°02' 00" latitude, alluvial soil
5	5	Lua Huong	Lua nuoc troi, Longan, Vietnam, 105°30' 30"-106°47' 02" longitude and 10°23'40"-11°02' 00" latitude, alluvial soil
6	6	Ca Hom	Deep water rice, Songhau, Western Vietnam, 106° 48'32" east longitude and 10°35'19" north latitude
7	7	Trung Dung	Songhau, Western Vietnam, 106° 48' E longitude and 10° 20' north latitude
8	8	Trung Dung	Songhau, Western Vietnam, 106° 48' E longitude and 10° 20' N latitude
9	9	Lua Ba Trang	Mekong Delta, Southeast Vietnam, 106°48'32" E longitude and 10° 35'19" N latitude
10	375	Mua So 43	Cambodia, 102nd -108th eastern longitude and 10th -15 th parallels of northern latitude
11	11	HTA 88085	Wetland rice, Thailand, 15 00 N, 100 00 E
12	12	Mot Bui Co Don	Camau peninsula, Vietnam, 104°80 – 105°5 longitude and 8°30 – 9°10 latitude, saline soil
13	13	Mot Bui Co Don	Camau peninsula, Vietnam, 104080 - 10505 longitude and 8030 - 9010 latitude, saline soil
14	15	HTA8037	Wetland rice, Thailand, 15 00 N, 100 00 E
15	16	Co To	Upland rice, Angiang, Vietnam, 105°35 longitude and 10°57 north latitude
16	17	Nang Sao Do Mien Nam	Camau Peninsula, Vietnam, 104080 - 10505 longitude and 8030 - 9010 latitude, saline soil
17	18	HTA 88060	Wetland rice, Thailand, 15 00 N, 100 00 E
18	19	Ao Gia Te	Kien giang, Vietnam , 104040'- 105032'40" longitude, 9023'50- 10032'30", alkaline alluvial soil
19	20	HTA 88085	Wetland rice, Thailand, 15 00 N, 100 00 E
20	21	Bong Cu Tim	Southeast Vietnam, 105048'43" - 106022'48" longitude and 10057'08"-11046'36' latitude , alluvial soil
21	22	Co Na	Lua nuoc troi, Longan, Vietnam, 105030' 30"-106047' 02" longitude and 10023'40"-11002' 00' latitude , alluvial soil
22	23	Co Na	Lua nuoc troi, Longan, Vietnam, 105030' 30"-106047' 02" longitude and 10023'40"-11002' 00" latitude, alluvial soil
23	26	Ro Dinh Vo Den	Taynguyen, Vietnam
24	27	HTA 88080	Wetland rice, Thailand, 15 00 N, 100 00 E
25	29	Nang Sen Ran	Songhau, Western Vietnam, 106 0 48'32" east longitude and 10 0 35'19" north latitude
26	31	HTAFR 88085-14	Wetland rice, Thailand, 15 00 N, 100 00 E
27	32	HTA 88085	Wetland rice, Thailand, 15 00 N, 100 00 E
28	33	HTA 85035	Wetland rice, Thailand 100 00 longitude and 1500 latitude

Table 1. contd.

29	34	HTA 85035	Wetland rice, Thailand, 15 00 N, 100 00 E
30	36	Nep Mua	Mekong Delta Vietnam, 106 0 48'32" east longitude and 10 0 35'19" north latitude
31	37	HTA 88086	Wetland rice, Thailand, 15 00 N, 100 00 E
32	38	Nanh Chon	Vungtau, Vietnam, 107'05" east longitude, 10'50" north latitude
33	39	Nanh Chon	Vungtau, Vietnam, 107'05" east longitude, 10'50" north latitude
34	40	HTAFR 81031	Wetland rice, Thailand, 15 00 N, 100 00 E
35	41	HTAFR 81031	Wetland rice, Thailand, 15 00 N, 100 00 E
36	42	Goi 2	Lua nuoc troi, Longan, Vietnam, 105030' 30"-106047' 02" longitude and 10023'40"-11002' 00" latitude, alluvial soil
37	43	Lua F5	Baria, Southeast Vietnam, 107'05" east longitude, 10'50" north latitude
38	45	Lua F5	Baria, Southeast Vietnam, 107'05" east longitude, 10'50" north latitude
39	52	Chet Xanh	Wetland rice, Tu giac Longxuyen, Vietnam, 105°35 longitude and 10°57 north latitude
40	58	Nho Thom	Lua nuoc troi, Tiengiang, Vietnam, 106 0 48'32" east longitude and 10 0 35'19" north latitude
41	59	Nho Thom	Deep water rice, Songhau, Western Vietnam, 106 0 48' east longitude and 10 0 20' north latitude
42	60	KT	Deep water rice, Songhau, Western Vietnam, 106 0 48'32" east longitude and 10 0 35'19" north latitude
43	61	HTA 88086	Wetland rice, Thailand, 15 00 N, 100 00 E
44	376	Mua so 43	Cambodia, 102 nd -108 th eastern longitude and 10 th -15 th parallels of northern latitude
45	65	Mi Ban To Bo	Kiengiang, Vietnam, 104040'- 105032'40"longitude and 9023'50- 10032'30" latitude, alkaline alluvial soil
46	66	Mi Ban To Bo	Kiengiang, Vietnam, 104040'- 105032'40" longitude, 9023'50- 10032'30" latitude
47	67	Nang Thom Hat Lua	Lua nuoc troi, Longan, Vietnam, 105030' 30"-106047' 02" longitude and 10023'40"-11002' 00" latitude , alluvial soil
48	68	Do Lun	Plain of Reeds, Vietnam, 105030' 30"-106047' 02" longitude and 10023'40"-11002' 00" latitude, alluvial soil
49	69	Mong Chim	Lua nuoc troi, Kiengiang, Vietnam, 104040'- 105032'40 longitude and 9023'50" – 10032'30" latitude
50	70	Nang Phet Don	Tiengiang, Vietnam, 106 0 48'32" east longitude and 10 0 35'19" north latitude
51	378	Thang Coi	Camau Peninsula, Vietnam, 104080 – 10505 longitude and 8030 – 9010 latitude, saline soil
52	379	Mua so53	Cambodia, 102 nd -108 th eastern longitude and 10 th -15 th parallels of northern latitude.
53	263	Tien Nu	Tayninh, Vietnam, 105048'43" – 106022'48" longitude and 10057'08"-11046'36" latitude, alluvial soil
54	264	Tien Nu	Tayninh, Vietnam, 105048'43" – 106022'48" longitude and 10057'08"-11046'36" latitude, alluvial soil
55	265	Tien Nu	Tayninh, Vietnam, 105048'43" – 106022'48" longitude and 10057'08"-11046'36" latitude, alluvial soil
56	266	Nang Ut Som	Deep water rice, Songhau, Western Vietnam, 106 0 48'32" east longitude and 10 0 35'19" north latitude
57	267	Bong Sen	Deep water rice, Songhau, Western Vietnam, 106 0 48' east longitude and 10 0 20' north latitude

Table 1. contd.

58	268	Cao Don	Western Vietnam, 105048'43" - 106022'48" longitude and 10057'08"-11046'36" latitude, alluvial soil
59	269	Nep Lem	Plain of reeds, Vietnam, 105030' 30"-106047' 02" longitude and 10023'40"-11002' 00" latitude, alluvial soil
60	270	Ba Reo	Southeast Vietnam, 105048'43" - 106022'48" longitude and 10057'08"-11046'36" latitude, alluvial soil
61	271	Lua Thuoc Co	Longan, Vietnam, 105030' 30"-106047' 02" longitude and 10023'40"-11002' 00" latitude
62	296	Mua So 68	Longan, Vietnam, 105030' 30" longitude and 10023'40" latitude
63	299	Trang Cut	Deep water rice, Songhau, Western Vietnam, 106 0 48'32" east longitude and 10 0 35'19" north latitude
64	300	Trang Cut	Deep water rice, Songhau, Western Vietnam, 10 0 20' north latitude and 106 0 48' east longitude
65	303	Trang Tep	Camau peninsula, Vietnam, 104080 - 10505 longitude and 8030 - 9010 latitude, saline soil
66	304	Mua So 19	Cambodia, 102nd -108th eastern longitude and 10th -15 th parallels of northern latitude
67	305	Mua So 19	Cambodia, 102nd -108th eastern longitude and 10th -15 th parallels of northern latitude
68	306	Trang Quang	Cambodia, 102nd -108th eastern longitude and 10th -15 th parallels of northern latitude
69	307	Mua So 58	Cambodia, 102nd -108th eastern longitude and 10th -15 th parallels of northern latitude
70	308	LPT 123	Wetland rice, Thailand, 15 00 N, 100 00 E
71	309	Gian Cao 69B	Southeast Vietnam, 105048'43" - 106022'48" longitude and 10057'08"-11046'36" latitude, alluvial soil
72	310	Gian Cao 69B	Southeast Vietnam, 105048'43" - 106022'48" longitude and 10057'08"-11046'36" latitude, alluvial soil
73	311	Lua Mem	Southeast Vietnam, 105048'43" - 106022'48" longitude and 10057'08"-11046'36" latitude, alluvial soil
74	312	Lua Mem	Songhau, Western Vietnam, , 106 0 48'32" longitude and 10 0 35'19" latitude
75	313	Nang Cua	Songhau, Western Vietnam, 106 0 48' east longitude and 10 0 20' north latitude
76	314	Troi Cho	Songhau, Western Vietnam, 106 0 48' east longitude and 10 0 20' north latitude
77	315	Canh Nong Lun	Southeast Vietnam, 105048'43" - 106022'48" longitude and 10057'08"-11046'36" latitude, alluvial soil
78	316	Mong Chim Lun	Kiengiang, Vietnam, 104040' - 105032'40 longitude and 9023'50" - 10032'30" latitude, Acid sulfate soil
79	317	Mua So 69	Cambodia, 102nd -108th eastern longitude and 10th -15 th parallels of northern latitude
80	318	Ba Bui	Camau peninsula, Vietnam, 104080 - 10505 East longitude and 8030 - 9010 North latitude, saline soil
81	374	Bang Rut	Southeast Vietnam, 105048'43" - 106022'48" longitude and 10057'08"-11046'36" latitude, alluvial soil
82	362	Mua So 44	Cambodia, 102nd -108th eastern longitude and 10th -15 th parallels of northern latitude
83	363	Tau Vang	Deep water rice, Songhau, Western Vietnam, 10 0 20' north latitude and 106 0 48' east longitude

Table 1. contd.

84	365	Tau Vang	Angiang, Vietnam, 10°57 north latitude and 105°35 longitude
85	366	Tau Vang	Wetland rice, Tu giac Longxuyen, Vietnam, 105°35 longitude and 10°57 north latitude
86	368	Nang Tay Dum	Wetland rice, Tu giac Longxuyen, Vietnam, 105°35 longitude and 10°57 north latitude
87	369	Nang Tay Dum	Lua noi, Tugiach Longxuyen, Vietnam. 105°35 longitude, 10°57 north latitude
88	405	Song Doi	Wetland rice, Songhau, Western, Vietnam, 106 0 48'32" east longitude, 10 0 35'19" north latitude
89	372	Rong Xanh	Camau peninsula, Vietnam, 104080 - 10505 longitude 8030 - 9010 altitude, saline soil
90	373	Rong Xanh	Plain of Reeds, Vietnam, 105030' 30"-106047' 02" longitude and 10023'40"-11002' 00" latitude, alluvial soil
91	374	Bang Rut	Southeast Vietnam, 105048'43" - 106022'48"longitude and 10057'08"-11046'36" latitude, alluvial soil
92	375	Mua so 43	Mekong, 102nd -108th eastern longitude and 10th -15th parallels of northern latitude
93	376	Mua so 43	Mekong, 102nd -108th eastern longitude and 10th -15th parallels of northern latitude
94	378	Thang coi	Camau Peninsula, Vietnam, 104080 - 10505 longitude and 8030 - 9010 latitude, saline soil
95	379	Mua so 53	Mekong
96	380	Mbakit	Kien giang
97	381	Mbakit	Kien giang
98	382	Lua Ba Trang	Mekong Delta, Southeast Vietnam, 106 0 48'32" east longitude and 10 0 35'19" north latitude
99	384	Nang tay	Mekong
100	387	Nang thuoc	Mekong
101	388	Nang thuoc	Mekong
102	389	Nang thuoc	Mekong
103	390	Nahng nah	Mekong
104	391	Nahng nah	Mekong
105	392	Nahng nah	Mekong
106	393	Nahng nah	Mekong
107	394	Nahng nah	Mekong
108	395	Nong nghiep	Mekong
109	396	Bang minh coc	Mekong
110	397	Bang minh coc	Mekong
111	400	Bang tay me	Mekong
112	401	Nen con sam	Mekong
113	402	Trang lon	Mekong
114	404	Thang con	Mekong
115	405	Song doi	Wetland rice, Songhau, Western, Vietnam, 106 0 48'32" east longitude, 10 0 35'19" north latitude
116	408	Mua so 42	Mekong
117	409	Mua so 45	Mekong
118	433	LPT 123	Mekong
119	434	Nang Chi	Mekong
120	435	Do sao	Mekong
121	436	Trang lun	Mekong
122	437	Ba Thiet Xanh	Mekong
123	438	Do sao muon	Mekong

Table 1. contd.

124	439	Mua so 5	Mekong
125	440	Thom Mx	Mekong
126	442	Nha Trang	Mekong
127	443	Trang ong 7	Mekong
128	444	Mua so 23	Mekong
129	445	Khong ten	Mekong
130	446	Trang phuoc 2	Mekong
131	447	Cong Ca	Mekong
132	448	Mua so 47	Mekong
133	449	SG Giai Phong	Mekong
134	450	Tieu Nhum	Mekong
135	451	Nang loan	Mekong
136	452	Nep ao gia	Mekong
137	476	Tau binh rau	Mekong
138	477	Nho do	Mekong
139	478	Trang hoa binh	Mekong
140	481	Gie noi 1035	Mekong
141	493	Nang Tay	An Giang
142	494	Mua so 5	Mekong
143	1331	Hai sung	Mekong
144	1332	Nep chuot che	Kien Giang
145	1333	Nep chuot che	Kien Giang
146	1334	Nep chuot che	Kien Giang
147	1348	Mashuri	An Giang
148	1349	Tep trang	Mekong
149	1350	Nep nhung	Mekong
150	1351	Trang lun	Mekong
151	1352	Kien Giang lon	Kien Giang
152	1353	Bong dinh	Mekong
153	1356	Rong xanh	Camau peninsula, Vietnam, 104080 - 10505 longitude 8030 - 9010 altitude, saline soil
154	1357	Lua soi vang	Mekong
155	1359	Chiem do	Mekong
156	1364	Hue ky Bd	Mekong
157	1365	Nang soi	Mekong
158	1376	Lua noi	Mekong
159	1377	K297	Mekong
160	1390	Truong hung	Mekong
161	1391	Den vo do ruot	Mekong
162	1392	Cach met	Mekong
163	1396	Nep mo	Mekong
164	1397	Nang co	Mekong
165	1398	Barvul runtai	Mekong
166	1399	PCR93206	Mekong
167	1400	Than nong mua	Mekong
168	1437	Lua Do	Mekong
169	1438	Ca Dung Go Cong	Mekong
170	1439	Ca Dung Go Cong	Mekong
171	1440	Mui Ruoc	Mekong
172	1441	Nep Tha	Mekong
173	1442	Ca Dung Do	Mekong
174	1443	Ca Dung Do	Mekong

Table 1. contd.

175	1465	Nep Tau Huong	Mekong
176	1467	Bang Rut	Southeast Vietnam, 105048'43" - 106022'48" longitude and 10057'08"-11046'36" latitude, alluvial soil
177	1468	Ta Lay	Mekong
178	1469	Nang Thom Ben Luc	Long An
179	1470	Nang Thom Ben Luc	Long An
180	1471	Rohyd Wrar6	Mekong
181	1484	K302	Mekong
182	1488	Nang So Lon LA	Long An
183	1489	Nang Thom Can Duoc	Long An
184	1490	Tai Nguyen Can Duoc	Long An
185	1491	Nang Quoc	Mekong
186	1492	Chum Ruot Xanh	Mekong
187	1493	Lua Nen	Mekong
188	1494	Mong Chim Do	Mekong
189	1495	Nang Triet	Mekong
190	1496	Nang Thom Can Duoc	Long An
191	1497	K229	Mekong
192	1498	Mot Bui Lun	Mekong
193	1499	Nang Le	Mekong
194	1500	Ca Tha Tia	Mekong
195	1501	Nang Phet Don	Tiengiang, Vietnam, 106 0 48'32" east longitude and 10 0 35'19" north latitude
196	1503	Nang Thom Ben Luc	Long AN
197	1505	Nha Trang	Mekong
198	1506	Lua Cai Lay	Mekong
199	1507	Nep Lem	Plain of reeds, Vietnam, 105030' 30"-106047' 02" longitude and 10023'40"-11002' 00" latitude, alluvial soil
200	1509	Ca Dung Ket	Mekong

Quantitative traits data collected included

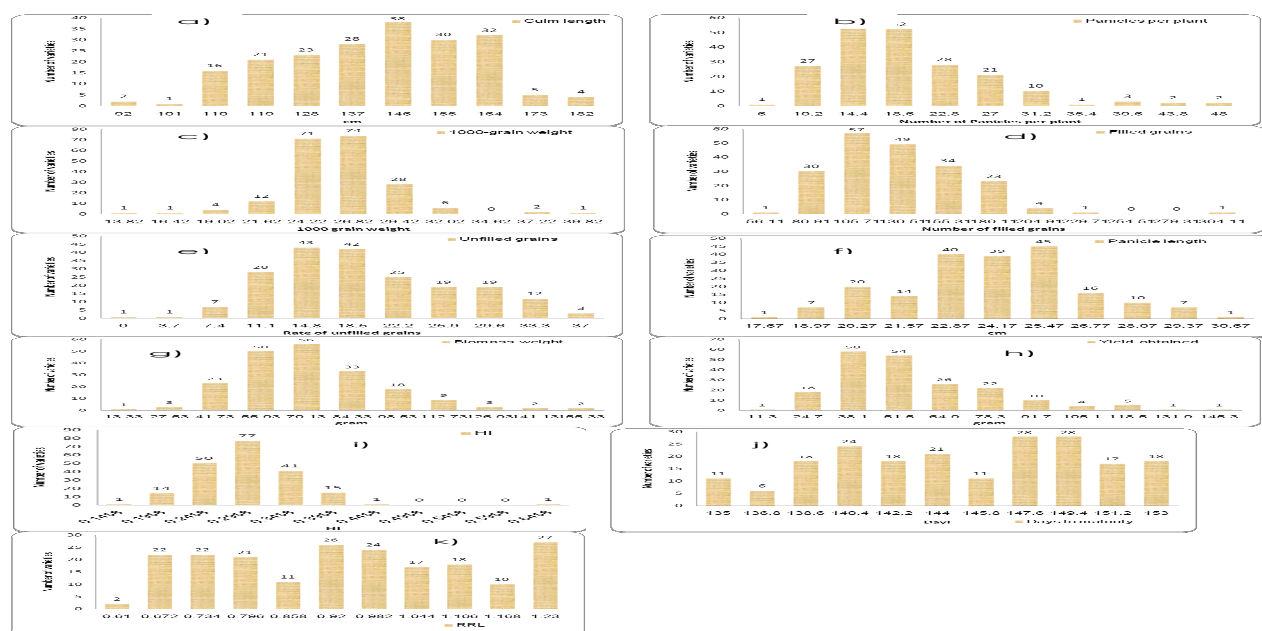
maturity, culm length, panicles per plant, number of filled grains, number of unfilled grains, 1000-g weight, yield, biomass, RRL and harvest index showed the diversity of traditional varieties Figure 1. These quantitative characters were found to be significant at 1% and all measurements were not too far from normal distribution. Distribution of varieties for the number of filled grains was slightly skewed to the right with only a few varieties near the maximum value (Figure 1a). For traits like number of unfilled grains, leaf length, yield and panicles per plant, unimodal distributions were observed with most varieties skewed to the left of the curve. Such distribution is favorable particularly with respect to number of unfilled grains because lower number of unfilled grains would mean higher yield. This is an important objective for most plant breeders in improving present day varieties. It was and still being considered as one of the major breeding objectives in developing rice varieties. (No evidence elsewhere to support the discussions presented) Grain width, biomass and harvest index showed normal distribution. With

regards to maturity, almost half of the varieties investigated exhibited long maturity duration.

Analysis of variance (ANOVA) showed high variability among the varieties in terms of number of unfilled grains, yield, number of filled grains, and biomass (Table 2 -15). For 1000 g weight, only six varieties had weight less than 20 g (Figure 1g,) (No the axes do not corresponds that is, vertical is number of varieties but horizontal is RRL! Therefore need to revisit this). Since the trait is one of the most important components of yield, the materials can be important source for development of varieties with higher grain weight. This study also found out that most of the varieties are tall. Only 40 varieties had heights less than 120 cm (Figure 1a). Nowadays, reduced culm length is most preferred in modern varieties (Khush, 1997). The semi-dwarf stature contributed most to production of grains during the green revolution due to associated improvements in harvest index and reduced lodging under heavy dosage of fertilizer (Hargrove et al., 1980). Regarding maturity, most varieties matured after 138 days

Table 2. Mean and range of different quantitative traits assessed among 200 traditional rice varieties, Vietnam, 2006/07.

Characters/Traits	N	Mean	Std dev	Sum	Min	Max	Cv%	Mean Std. error	F. value	PR > F
Culm-length	270	146.11	15.87	39451	105	180	6.861	14.79258	1.34	0.1366
Filled Grain	270	123.63	38.19	33380	47.67	255.7	22.74	36.06945	2.01	0.0044
Panicle Length	270	23.821	2.932	6432	15.75	31.13	7.726	2.821036	2.4	0.0004
Panicles/ Plant	270	14.785	6.687	3992	6	39	37.68	6.693207	1.35	0.1289
Grain Length	270	9.3307	0.799	2519	7.557	10.92	2.066	0.798559	20.54	<.0001
Grain Width	270	2.8766	0.256	776.67	2.15	3.53	2.368	0.256588	12.68	<.0001
Unfilled Grain	270	88.207	57.9	23816	10	333	51.91	55.77563	2.68	<.0001
1000-grain weight	270	24.661	3.371	6659	17.69	40.24	5.672	3.380738	21.24	<.0001
Maturity	270	146.59	6.276	39579	135	153	0	5.881775	Infity	<.0001
Leaf length	270	35.111	8.404	9480	19	63	16.02	8.424106	2.7	<.0001
Leaf width	270	1.2089	0.247	326.4	0.6	2	12.3	0.216889	3.08	<.0001
Yield	270	103.82	45.17	28030	21.23	283.6	37.69	45.29111	1.08	0.3701
Biomass	270	61.678	25.6	16653	10	150	33.27	28.086	2.64	<0.0001
Harvest index	270	0.627	0.040	56.44	0.48	0.82	0.001	0.004	3.02	0.0110

**Figure 1.** Frequency distribution of the varieties with respect to maturity, culm length, panicles per plant, leaf length, leaf width, grain length, grain width, number of filled grains, number of unfilled grains, 1000-g weight, yield, biomass and harvest index showed the diversity of traditional varieties.

Therefore, the challenge still exists for breeders to develop varieties with shorter duration without sacrificing yield.

In general, morphological characterization showed that most traditional varieties had have difference traits. The variation in agro-morphological characters discussed above can be explained by the genetic variation among the varieties examined. This variability can be utilized as raw materials for plant breeders to improve rice for better plant type, better grain quality and higher photosynthetic

efficiency.

Correlation among agro-morphological traits

Correlation coefficients among the traits measured are shown in Table 16. Number of panicles per plant was highly correlated with yield ($r = 0.797$) and biomass ($r = 0.718$) indicating that varieties with more panicles also have higher yields. Significant correlations were also

Table 3. ANOVA for culm length among 200 traditional varieties.

Source	DF	Sum of squares	Mean square	F value	PR > F
Model	201	49853.19	547.8	5.45	<.0001
Error	178	17889.10	100.5		
Total	269	67742.30			

Table 4. ANOVA for number of filled grains of 200 traditional varieties.

Source	DF	Sum of squares	Mean square	F value	PR > F
Model	201	251715.11	2766.100	3.50	<.0001
Error	178	140684.22	790.3608		
Total	269	392399.40			

Table 5. ANOVA for number of unfilled grains of 200 traditional varieties.

Source	DF	Sum of squares	Mean square	F value	PR > F
Model	201	528645.14	5809.28	2.77	<.0001
Error	178	373215.23	2096.71		
Total	269	901860.38			

Table 6. ANOVA for panicle length among 200 traditional varieties.

Source	DF	Sum of squares	Mean square	F value	PR > F
Model	201	1710.023	18.79	5.5	<.0001
Error	178	602.899	3.38		
Total	269	2312.92			

Table 7. ANOVA for number of panicles per plant among 200 traditional varieties.

Source	DF	Sum of squares	Mean square	F value	PR > F
Model	201	6503.23	71.46	2.30	<.0001
Error	178	5524.30	31.03		
Total	269	1207.54			

Table 8. ANOVA for grain length among 200 traditional varieties.

Source	DF	Sum of squares	Mean square	F value	PR > F
Model	201	165.27	1.81	48.85	<.0001
Error	178	6.617	0.03		
Total	269	171.89			

Table 9. ANOVA for grain width among 200 traditional varieties.

Source	DF	Sum of squares	Mean square	F value	PR > F
Model	201	16.85	0.185	39.91	<.0001
Error	178	0.826	0.004		
Total	269	17.68			

Table 10. ANOVA for 1000 grain weight of 200 traditional varieties.

Source	DF	Sum of squares	Mean square	F value	PR > F
Model	201	2709.1	29.77	15.21	<.0001
Error	178	348.32	1.95		
Total	269	3057.43			

Table 11. ANOVA for maturity of 200 traditional varieties.

Source	DF	Sum of squares	Mean square	F value	PR > F
Model	201	10595.3	116.4	Infity	<.0001
Error	178	0.00000	0.0000		
Total	269	10595.3			

Table 12. ANOVA for leaf length of 200 traditional varieties.

Source	DF	Sum of squares	Mean square	F value	PR > F
Model	201	13365.53	146.8	4.64	<.0001
Error	178	5633.13	31.64		
Total	269	18998.6			

Table 13. ANOVA for leaf width of 200 traditional varieties.

Source	DF	Sum of squares	Mean square	F value	PR > F
Model	201	12.50	0.137	6.22	<.0001
Error	178	3.933	0.022		
Total	269	16.43			

Table 14. ANOVA for yield of 200 traditional varieties.

Source	DF	Sum of squares	Mean square	F value	PR > F
Model	201	276184.2	3034.9	1.98	<.0001
Error	178	272577	1531.3		
Total	269	548761.2			

Table 15. ANOVA for biomass of 200 traditional varieties.

Source	DF	Sum of squares	Mean square	F value	PR > F
Model	201	101346.36	1113.69	2.64	<.0001
Error	178	74954.6	421.09		
Total	269	176300.96			

found between culm length and number of filled grains ($r = 0.602$), panicle length ($r = 0.596$). This association can be explained by the principle of morphogenic compatibility in rice plant architecture. Other traits that were strongly correlated with culm length and panicle length, number of unfilled grains, 1000-g weight, yield and biomass. Ma-

turity was found to be poorly correlated with other agromorphological traits. It exhibited negative correlation with ten other traits and only slightly correlated with biomass ($r = -0.026$), panicles per plant ($r = -0.072$) and yield ($r = -0.044$). In the analysis of quantitative traits, the range of the coefficients of variability was high. It varied from the

Table 16. Correlation coefficients among 11 agro-morphological traits of 200 traditional rice varieties, Vietnam, 2006/07.

	Culm length	Panicles per plant	1000 g weight	Filled grains	Unfilled grains	Panicle length	Biomass-weight	Yield obtained	HI	Days to maturity	RRL
Culm length	1.000	-0.283	0.003	0.602**	0.108	0.596**	0.163	0.087	0.055	0.114	-0.130
Panicles per plant	-0.283	1.000	0.048	-0.113	-0.013	-0.108	0.718**	0.797**	0.345*	-0.072	0.098
1000-grain weight	0.003	0.048	1.000	-0.360	0.078	0.004	0.007	0.070	0.152	-0.141	-0.008
Filled grains	0.602**	-0.113	-0.360	1.000	-0.182	0.518**	0.226	0.394	0.365	0.147	0.007
Unfilled grains	0.108	-0.013	0.078	-0.182	1.000	0.082	-0.026	-0.100	-0.139	-0.056	-0.059
Panicle length	0.596**	-0.108	0.004	0.518**	0.082	1.000	0.169	0.220	0.246	0.131	-0.093
Biomass-weight	0.163	0.718**	0.007	0.226	-0.026	0.169	1.000	0.793**	0.016	-0.026	-0.009
Yield-obtained	0.087	0.797**	0.070	0.394*	-0.100	0.220	0.793**	1.000	0.556**	-0.044	0.106
HI	0.055	0.345	0.152	0.365*	-0.139	0.246	0.016	0.556	1.000	-0.030	0.119
Days to maturity	0.114	-0.072	-0.141	0.147	-0.056	0.131	-0.026	-0.044	-0.030	1.000	-0.048
RRL	-0.130	0.098	-0.008	0.007	-0.059	-0.093	-0.009	0.106	0.119	-0.048	1.000

Indicate the level of significance by *

* P=0.05 and **P=0.01

HI: Harvest index; RRL: relation root length (EC = 12 DS/m)

many traits such as unfilling, color, shape. This shows that the seed length less variation compared to another characters, second some traits are also have lowest values indicated that it less variation with the environment. The variation in grain characters such as size, shape and color are useful in distinguishing the different landraces or traditional varieties. These traits can be considered as the most stable characters as exemplified by their coefficients of variability. The highest values is unfilling grain (34%) indicated that this character more effected by the environment and cultural management practices of the farmer. The means of measurements of quantitative traits were higher. The variation in grain characters such as (yield for salt tolerance and some line susceptible with salt stress) are useful in distinguishing the different landraces or traditional varieties.

Shannon-Weaver Diversity Indices among 200 Traditional rice Varieties

Table 17 presents the Shannon-Weaver diversity indices (H') of the 11 quantitative agro-morphological traits. The H' ranged from 0.68 - 0.95 with a mean of 0.88. The highest and lowest diversity index of 0.94 and 0.68 was observed for grain width and 1000 grain weight, respectively. However, no significant differences was observed among culm length ($H' = 0.92$), filled grains ($H' = 0.92$), panicles/plant etc. Overall, the 200 traditional varieties held in the Cuu Long genebank exhibited high diversity in the agro-morphological characters assessed. This therefore means that the collections can be available resource for developing rice varieties for Mekong Delta. In addition, this information will also be useful for germplasm managers in

planning for future germplasm acquisitions (Again evidences from related/other studies are needed to support the assertion).

Cluster analysis among traditional varieties

The 200 traditional rice varieties were classified based on agro-morphological markers using UPGMA and SAHN clustering methods (Figure 2). At similarity coefficient of 20.61 (abstract is talking of 20.61) please harmonise this, the dendrogram generated three clusters: I, II, III and many subcluster. Characters that were distinct in the formation of the 6 clusters included origin of the varieties and 11 agro-morphological characters (especially culm length, filled grains and RRL). The clusters are as follows: Cluster I consisted of one traditional variety, namely 378-Thangcoi. Cluster II included 9 traditional varie-

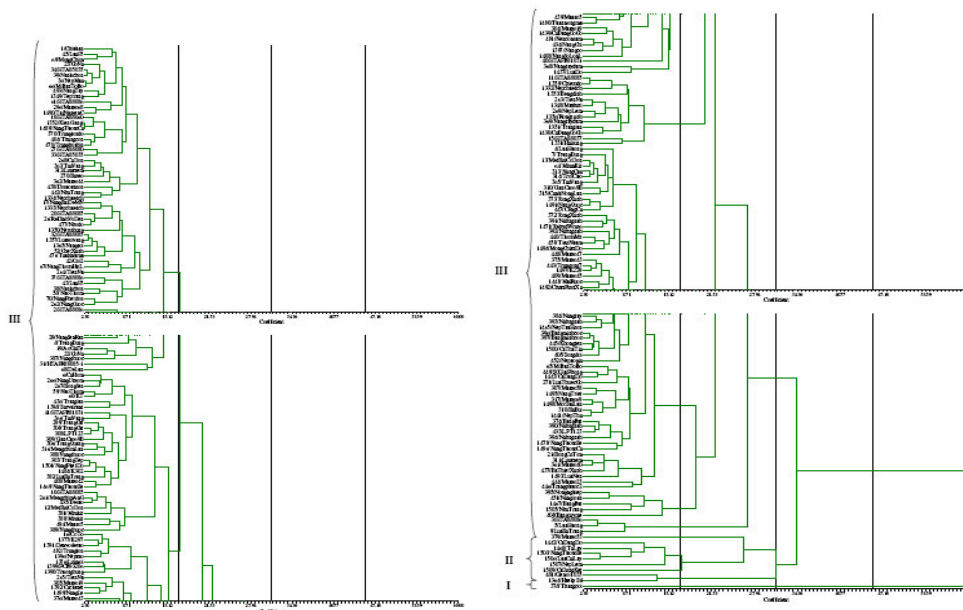


Figure 2. Dendrogram of 200 traditional rice varieties based on Euclidean distance coefficients estimated from the 11 agro-morphological traits.

Table 17. Shannon-Weaver diversity indices for quantitative traits of the 200 traditional rice varieties, Vietnam, 2006/07.

Traits	H'
Culm-length	0.92
Filled Grain	0.92
Panicle Length	0.90
Panicles/ Plant	0.92
Grain Length	0.88
Grain Width	0.95
Unfilled Grain	0.85
1000-grain weight	0.68
Maturity	0.82
Leaf length	0.85
Leaf width	0.91
Yield	0.94
Biomass	0.85

ties. Cluster III includes most traditional varieties. The varieties in this cluster were collections from different places: Southeast Vietnam (seven varieties), Songhau, Western Vietnam and (An Giang) (four varieties each), Camau Peninsula Vietnam (three varieties) and Kien-giang, Plain of Reeds, Longan, Longxuyen of Vietnam and Mekong river (one variety each). These show that although these varieties came from different places, they are grouped together because of close similarities in terms of quantitative traits. They may also have descended from related parents (Harlan, 1965).

The multivariate analysis showed significant differences among the 200 traditional rice varieties. The growing environment of the region likely influenced the structure and level of morphological variation among the rice landraces. Analyses of variation in quantitative traits among the accessions were important in discriminating these rice landraces. Although they were collected from different areas, they were grouped together suggesting that they may have probably originated from the same population. As man moved to different places, they bring and maintain genotypes where continuous selection adapted these genotypes to their places, hence changing genetic constitution of the original variety (Harlan, 1965).

Conclusions

Knowledge of the traits and information on the genetic variation and relationships in germplasm is crucial in determining the value of the collection for utilization and in deciding conservation strategies. Agro-morphological characters have provided valuable information about ge-

netic diversity of rice collection in CLRR. Quantitative agro-morphological characters of 200 accessions were analyzed using hierarchical clustering, correlation coefficient, principal component analysis and analysis of variance. Diversity of the collection was analyzed using Shannon-Weaver diversity index. Although, this study has shown significant differences in agro-morphological traits of the traditional rice varieties. There is need for further study to confirm these findings. Additionally, extensive molecular marker analysis using more primers may

need to be considered for relevant application and efficient attainment of breeding objectives in rice improvement. Continue analysis to study correlation among the characters and to relate results between morphological characters and molecular markers is recommended.

ACKNOWLEDGEMENTS

We would like to express our gratitude to CP7 program for the support and help to carry out this work. We are also grateful to IRRI, Travinh, Bac Lieu province and CLRRRI for the support rendered.

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