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'Sharei' Weedy Collection, Found in Ganghwa Island, Maintains a Unique Population Structure

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강화도 수집 '샤레'벼 집단의 유전특성

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ABSTRACT: A total of 29 simple sequence repeat (SSR) markers were used to analyze the genetic diversity and population structure of Korea weedy rice (*Oryza sativa* L.). A total of 243 alleles were detected with an average of 8.4 per locus among 114 rice accessions. Major allele frequency (M_{AF}) ranged from 0.22 to 0.98 and the average is 0.52. The averages of gene diversity and polymorphic information content (PIC) values were 0.61 and 0.57, with a range from 0.04 (SSS) to 0.87 (RM241) and from 0.04 (SSS) to 0.86 (RM241), respectively. In cluster analysis, 90.4% of accessions (shared > 70% membership with one of five clusters) were classified as members of each cluster, whereas 9.6% accessions showed evidence of mixed population ancestry. The Korea weedy rice, 'Sharei rice' collected from isolated island, 'Ganghwa' appears to be a very primitive rice cultivar for being separately grouped from *indica* and *japonica*. It might have changed its genetic background along with adaptation to such an isolated region. This result showed that the collected weedy rice accessions have valuable sources of gene diversity for future rice improvement breeding programs.

***Key words*:** Weedy rice, Genetic diversity, Population structure, SSR

Weedy rice, also known as red rice, is a species of rice (*Oryza sativa* L.). Populations of weedy rice are found in many rice-producing areas. Weedy rice can be distinguished from the cultivated rice, mainly due to longer primary dormancy, longer culm, pubescent leaves, more tillers, easy seed shattering, red pigmentation of pericarp, seed coat, or both and photoblastism (Suh *et al*., 1992; Chung and Paek, 2003). It was generally considered that weedy rice is a natural hybrid of cultivated rice and wild rice. Long-term sympatric distribution has led to similarities between weedy and cultivated rice through natural hybridization and introgression (Cao *et al*., 2006). Weedy rice has become important resources for breeding and for studying the domestication process of rice (Suh *et al*., 1997; Bres-Patry *et al*., 2001). It possesses useful genes conferring tolerance to various abiotic and biotic stresses (Suh *et al*., 1992; Suh *et al*., 1999). Some red rice strains are disease-resistant (Cho *et al*., 1996). Korean weedy rice strains are also thought to possess tolerance to a wide range of adverse conditions, since they successfully acclimate and adapt to diverse growing environments.

Many of genetic resources have been recently collected and characterized (Cho *et al*., 2010; Chung and Park, 2010; Gao *et al*., 2010). Weedy rice strains (*O. sativa* L., locally called 'Aengmi' and 'Sharei') have been collected from farmers' elds in Korea and their regional distribution and genetics have been studied (Heu, 1988; Suh *et al*., 1992;

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Chung and Park, 2010). There are two strains locally known as 'Red rice' and 'Sharei rice' in an isolated island, in Korea. 'Sharei rice' occurs mainly in Ganghwa Island, and is thus geographically isolated from other weedy sub-populations (Chung and Park, 2010). 'Sharei rice' has almost all the characteristics of 'Red rice', except for the unique shattering pattern, i.e. each grain of a spikelet within the same panicle has a different ripening time and individually shatters upon ripening (Lee *et al*., 2003). In addition, 'Sharei rice' accessions have a shorter culm length than 'Red rice' and landraces (Lee *et al*., 2003). These differences in quantitative traits imply the existent of genetic diversity in rice which might be of future usefulness. Detail analysis of diversity and population structure of that weedy rice is of paramount important.

Several studies have indicated that weedy rice strains appear to be dierentiated into *indica* and *japonica* types (Glaszmann, 1987; Cho *et al*., 1995; Suh *et al*., 1997; Gealy *et al*., 2002). However, Vaughan *et al.* (2001) reported that several samples of weedy biotypes collected in the United States belong not only to the *indica* and *japonica ssp*., but also to the wild rice species *O. rupogon* attribution and *O. nivara* attribution. Therefore, Yu *et al*. (2005) pointed out that different rice-growing locations often show different patterns of genetic diversity, depending on the specic combination of germplasm from which weedy rice emerges.

Plant breeders used traditional morphology and biochemical characteristics to evaluate the genetic diversity, but the use of this evaluation method is restricted especially for a population which has similar genetic characteristics and closely related species. Qualitative traits especially for ones which change along with environmental impact, assessment of genetic diversity is limited (Chen and Nelson, 2004). Such evaluation using morphological characters has the discrimination potential but DNA markers do not undergo like this influences (Bernet *et al*., 2003). Moreover, genetic markers are abundance in genome and revealed a high level of polymorphism which is an advantage in distinguishing between closely related individual (Campos *et al*., 2005).

Simple sequence repeats (SSRs) also known as microsatellites consist of tandem repeat of short nucleotide motif with the length between one to six nucleotides (Bull *et al*., 1999). They are abundant and distributed in nuclear, mitochondrial and chloroplast genome (Barkley *et al*., 2009). SSRs have high level of variation which was believed due to DNA slippage during replication, unequal-crossing over and genetic recombination (Park *et al*., 2009). Moreover, SSRs presented a higher level of polymorphism and a greater information content than AFLPs and RAPDs (Belaj *et al*., 2003). Due to their advantages such as they are co-dominant, multiallelic and mendelian inherited, semi-automated with the use of fluorescence-labeled primer and have high reproducibility and reliability, the usage of SSRs in various studies had increased (Brondani *et al*., 1998; Ji *et al*., 1998; Garris *et al*., 2005; Jatoi *et al*., 2006).

The purposes of this study are to assess the level of genetic diversity and fine population structure of Korean weedy rice and to explore its relatedness to improved variety, landraces and introduced species using SSR markers.

MATERIALS AND METHODS

1. Plant materials

A total of 114 rice (*O. sativa* L.) accessions including 109 from Korea (including 89 Ganghwa Island weedy rice('Sharei rice'), 10 improved variety, and 10 landraces) and 5 from Philippines (introduced species), were used in this study. Accession codes, IT numbers and origin are given in Table 1. All these accessions were obtained from the National Agrobiodiversity Center of Rural Development Administration (RDA), Republic of Korea (http://genebank.rda.go.kr).DNA extraction and SSR assay

DNA was extracted from freeze-dried leaves of 15-day-old seedlings of each accession using a DNA extraction kit (Qiagen). The relative purity and concentration of extracted DNA was then checked using NanoDrop ND-1000 (NanoDrop Technologies Inc., Wilmington, DE, USA). The final DNA concentration was adjusted to 20ng/iL.

Markers were chosen according to their location on the rice genetic map and their suitability for high-throughput genotyping. 29 SSR markers distributed on the 12 chromosomes were employed to analyze population structure (Table 2). All SSR marker information is available in GRAMENE (http://www.gramene.org/). Two different marker types were used for SSR assays. A three-primer system (Schuelke, 2000) was used that includes a universal M13 oligonucleotide (TGTAAAACGACGGCCAGT) labeled with one of the fluorescent dyes 6-FAM, NED, or HEX, which allows PCR products to be triplexed during electrophoresis. A special forward primer composed of the concatenation of the M13 oligonucleotide and the specific forward primer was used with the normal reverse primer for SSR PCR amplification.

PCR amplification was performed in a total volume of 20 μL containing 20 ng genomic DNA, 2 μM of the specific primer, 4 μM M13 universal primer, 6 μM normal reverse primer, 1x PCR buffer, 0.2 mM dNTP, and 0.5 U Taq polymerase. Conditions of the PCR amplification were as follows: 94°C (3 min); 30 cycles at 94°C (30 s), the appropriate annealing temperature (45 s), and 72°C (45 s); followed by 20 cycles at 94°C (30 s), 53°C (45 s), 72°C (45 s); and a final extension at 72°C for 20 min. The PCR products of three microsatellites were mixed together in a ratio of FAM:

Table 1. Passport data and Inferred Populations of 114 rice accessions used in this study.

NO.	Code	IT NO.	Variety	Origin	5 Population
1	1-WD	213559	WD-3-1-B	Korea	Admixture
2	2-WD	213560	WD-7-1-B	Korea	4
3	3-WD	213561	WD-8-1-B	Korea	5
4	4-WD	213563	WD-10-1-B	Korea	5
5	5-WD	213564	WD-11-1-B	Korea	4
6	6-WD	213565	WD-13-1-B	Korea	5
7	7-WD	213568	WD-18-1-B	Korea	Admixture
8	8-WD	213569	WD-20-1-B	Korea	5
9	9-WD	213570	WD-21-1-B	Korea	5
10	10-WD	213571	WD-24-1-B	Korea	3
11	11-WD	213572	WD-25-1-B	Korea	3
12	12-WD	213573	WD-26-1-B	Korea	3
13	13-WD	213574	WD-28-1-B	Korea	5
14	14-WD	213576	WD-31-1-B	Korea	4
15	15-WD	213577	WD-35-1-B	Korea	5
16	16-WD	213578	WD-36-1-B	Korea	5
17	17-WD	213579	WD-37-1-B	Korea	3
18	18-WD	213580	WD-38-1-B	Korea	5
19	19-WD	213582	WD-41-1-B	Korea	Admixture
20	20-WD	213583	WD-43-1-B	Korea	5
21	21-WD	213584	WD-44-1-B	Korea	5
22	22-WD	213585	WD-45-1-B	Korea	5
23	23-WD	213586	WD-46-1-B	Korea	5
24	24-WD	213587	WD-49-1-B	Korea	5
25	25-WD	213590	WD-52-1-B	Korea	Admixture
26	26-WD	213592	WD-57-1-B	Korea	5
27	27-WD	213594	WD-61-1-B	Korea	5
28	28-WD	213595	WD-63-1-B	Korea	5
29	29-WD	213596	WD-64-1-B	Korea	5
30	30-WD	213597	WD-65-1-B	Korea	Admixture
31	31-WD	213598	WD-66-1-B	Korea	Admixture
32	32-WD	213599	WD-67-1-B	Korea	5
33	33-WD	213600	WD-68-1-B	Korea	4
34	34-WD	213601	WD-69-1-B	Korea	5
35	35-WD	213602	WD-70-1-B	Korea	5
36	36-WD	213603	WD-71-1-B	Korea	5
37	37-WD	213604	WD-72-1-B	Korea	5

Table 1. Continued-1

NO.	Code	IT NO.	Variety	Origin	5 Population
38	38-WD	213605	WD-73-1-B	Korea	4
39	39-WD	213606	WD-74-1-B	Korea	4
40	40-WD	213607	WD-75-1-B	Korea	5
41	41-WD	213608	WD-76-1-B	Korea	5
42	42-WD	213609	WD-77-1-B	Korea	5
43	43-WD	213610	WD-78-1-B	Korea	5
44	44-WD	213611	WD-80-1-B	Korea	5
45	45-WD	213612	WD-81-1-B	Korea	5
46	46-WD	213614	WD-91-1-B	Korea	5
47	47-WD	213616	WD-97-1-B	Korea	Admixture
48	48-WD	213617	WD-98-1-B	Korea	4
49	49-WD	213619	WD-100-1-B	Korea	2
50	50-WD	213620	WD-101-1-B	Korea	2
51	51-WD	213621	WD-102-1-B	Korea	4
52	52-WD	213623	WD-104-1-B	Korea	2
53	53-WD	213624	WD-107-1-B	Korea	4
54	54-WD	213625	WD-109-1-B	Korea	4
55	55-WD	213626	WD-110-1-B	Korea	2
56	56-WD	213627	WD-111-1-B	Korea	2
57	57-WD	213628	WD-112-1-B	Korea	2
58	58-WD	213629	WD-113-1-B	Korea	2
59	59-WD	213630	WD-118-1-B	Korea	2
60	60-WD	213631	WD-119-1-B	Korea	2
61	61-WD	213633	WD-123-1-B	Korea	2
62	62-WD	213634	WD-124-1-B	Korea	2
63	63-WD	213635	WD-125-1-B	Korea	2
64	64-WD	213636	WD-126-1-B	Korea	2
65	65-WD	213637	WD-127-1-B	Korea	Admixture
66	66-WD	213638	WD-128-1-B	Korea	2
67	67-WD	213639	WD-129-1-B	Korea	2
68	68-WD	213640	WD-130-1-B	Korea	2
69	69-WD	213641	WD-131-1-B	Korea	2
70	70-WD	213642	WD-132-1-B	Korea	3
71	71-WD	213643	WD-134-1-B	Korea	2
72	72-WD	213644	WD-135-1-B	Korea	3
73	73-WD	213645	WD-137-1-B	Korea	4
74	74-WD	213646	WD-140-1-B	Korea	3

Table 1. Continued-2

NO.	Code	IT NO.	Variety	Origin	5 Population
75	75-WD	213647	WD-142-1-B	Korea	3
76	76-WD	213648	WD-143-1-B	Korea	3
77	77-WD	213649	WD-146-1-B	Korea	3
78	78-WD	213650	WD-147-1-B	Korea	3
79	79-WD	213651	WD-159-1-B	Korea	3
80	80-WD	213653	WD-168-1-B	Korea	3
81	81-WD	213655	WD-175-1-B	Korea	3
82	82-WD	213658	WD-180-1-B	Korea	3
83	83-WD	213659	WD-185-1-B	Korea	3
84	84-WD	213660	WD-192-1-B	Korea	admixture
85	85-WD	213661	WD-194-1-B	Korea	3
86	86-WD	213666	WD-202-1-B	Korea	admixture
87	87-WD	213667	WD-203-1-B	Korea	admixture
88	88-WD	213668	WD-204-1-B	Korea	2
89	89-WD	213669	WD-205-1-B	Korea	2
90	90-IR	1883	IR24	Philippines	1
91	91-IR	1894	IR29	Philippines	1
92	92-IR	1898	IR30	Philippines	1
93	93-IR	1902	IR34	Philippines	1
94	94-IR	1907	IR38	Philippines	1
95	95-BL	6197	Milyang21	Korea	1
96	96-BL	6202	Milyang23	Korea	1
97	97-BL	7084	Sinpung	Korea	4
98	98-BL	7085	Jaegeon	Korea	4
99	99-BL	7098	Jinheung	Korea	4
100	100-BL	191781	Ilpumbyeo	Korea	4
101	101-BL	191816	Sangjubyeo	Korea	4
102	102-BL	191828	Juanbyeo	Korea	4
103	103-BL	191829	Hwaseonchalbyeo	Korea	4
104	104-BL	191849	Hwajungbyeo	Korea	4
105	105-LL	5660	Nokdudo	Korea	4
106	106-LL	8289	Jaeraedo	Korea	4
107	107-LL	5679	Dadajo	Korea	4
108	108-LL	8382	Jeonggeumjo	Korea	4
109	109-LL	5044	Guwangdo	Korea	4
110	110-LL	10275	Neulbyeo	Korea	4
111	111-LL	10631	Jjokjebichal	Korea	4
112	112-LL	10727	Heukpi	Korea	4

Table 1. Continued-3

NO.	Code	IT NO.	Variety	Origin	5 Population
113	113-LL	6556	Sando	Korea	4
114	114-LL	10721	Hwaseongbatchal	Korea	4

IT NO: introduction number of National Agrodiversity Center of RDA (Rural Development Administration) in Republic of Korea.

Table 2. Total number of alleles and genetic diversity index for 29 simple sequence repeat (SSR) loci in the 114 accessions.

Marker	Map Position	Size Range	N_A[a]	rare alleles[b]	M_{AF}[c]	GD[d]	PIC[e]
RM21	11	131-165	10	7	0.33	0.76	0.73
RM44	8	99-157	11	5	0.36	0.79	0.77
RM48	2	125-233	17	12	0.32	0.83	0.81
RM206	11	125-233	24	20	0.39	0.81	0.79
RM214	7	111-155	13	7	0.32	0.83	0.81
RM228	10	103-151	8	5	0.41	0.68	0.63
RM231	3	168-192	6	3	0.70	0.47	0.43
RM232	3	135-169	13	9	0.37	0.79	0.76
RM235	12	93-127	8	4	0.57	0.62	0.59
RM241	4	100-140	15	9	0.22	0.87	0.86
RM246	1	90-114	9	4	0.37	0.74	0.71
RM247	12	131-165	12	9	0.65	0.56	0.54
RM249	5	119-153	13	9	0.35	0.79	0.76
RM253	6	126-144	8	4	0.30	0.76	0.71
RM257	9	144-170	13	7	0.27	0.84	0.82
SBE	2	204-218	3	1	0.90	0.19	0.18
SSS	6	197-215	3	2	0.98	0.04	0.04
WxOligo	6	118-218	5	3	0.63	0.52	0.46
RM310	8	150-204	11	7	0.36	0.76	0.72
RM3322	5	120-136	5	2	0.76	0.40	0.38
RM3718	7	154-162	3	0	0.52	0.55	0.46
RM3857	2	116-158	8	2	0.32	0.80	0.77
RM6144	10	135-141	2	0	0.69	0.43	0.34
RM6165	2	170-194	3	1	0.91	0.17	0.16
RM6629	4	59-83	4	1	0.64	0.50	0.42
RM12676	2	252-256	2	0	0.56	0.49	0.37
RM16427	4	271-289	4	1	0.65	0.51	0.44
RM19159	5	167-191	6	3	0.52	0.64	0.58
RM23455	8	308-314	4	2	0.71	0.45	0.40
Total			243	139			
Mean			8.4		0.52	0.61	0.57

[a] Number of alleles, [b] Number of alleles that <5 allele frequency, [c]Major allele frequency, [d] Gene diversity, [e] Polymorphic information content.

HEX:NED = 1:3:4, which was varied depending on the amplification intensity for individual markers as determined with the ABI PRISM 3100 Genetic Analyzer (Applied Biosystems, Foster City, CA, USA). PCR products labeled with HEX and NED were added in higher amounts, and those labeled with FAM were added in lower amounts because of the different signal intensities of these fluorescent dyes. The mixed PCR product of 1.5 μL was combined with 9.2 μL Hi-Di formamide and 0.3 μL of an internal size standard, Genescan-500 ROX. The samples were denatured at 94°C for 3 min and analyzed in an ABI PRISM 3100 Genetic Analyzer (Applied Biosystems). Molecular weights, in base pairs, of the microsatellite products were estimated with Genescan software ver.3.7 (Applied Biosystems) by the local Southern method. The individual fragments were assigned as alleles of the appropriate microsatellite loci with Genotyper software ver.3.7 (Applied Biosystems).

2. Data analysis

Basic statistics were calculated using the genetic analysis package PowerMarker V 3.23 (Liu and Muse, 2005) for diversity measurements at each microsatellite locus, including the total number of alleles (N_A), allele frequency, major allele frequency (M_{AF}), gene diversity (GD), and polymorphism information content (PIC). Genetic distances between each pair of accessions were measured by calculating the shared allele frequencies using PowerMarker V3.23.

Population structure was determined and identification of admixed individuals performed using the model-based software program, Structure 2.2 (Pritchard *et al*., 2000; Falush *et al*., 2003). In this model, a number of populations (K) are assumed to be present, each of which is characterized by a set of allele frequencies at each locus. Individuals in the sample are assigned to populations (clusters), or jointly to more populations if their genotypes indicate that they are admixed. All loci are assumed to be independent, and each K population is assumed to follow Hardy-Weinberg equilibrium. Posterior probabilities were estimated using a Markov Chain Monte Carlo (MCMC) method. The MCMC chains were run for 100,000 burn-in period lengths, followed by 200,000 iterations using a model allowing for admixture and correlated allele frequencies. At least three runs of Structure were performed by setting K from 2 to 10, and an average likelihood value, L (K), across all runs was calculated for each K. The model choice criterion to detect the most probable value of K was Δ K, which is an ad hoc quantity related to the second order change of the log probability of data with respect to the number of clusters inferred by Structure (Evanno *et al*., 2005). An individual was assigned to a group more than 70% of its genome fraction value derived from that group.

RESULTS

1. SSR polymorphism

The SSR polymorphism was measured in terms of the numbers of alleles, gene diversity, and PIC using PowerMarker 3.23 software (Liu and Muse, 2005). The 29 SSR markers revealed 243 alleles across the 114 rice accessions, with an average of 8.4 alleles per locus (Table 2). The allele size ranged from 59 to 314 bp. The allelic richness per locus varied widely among the markers, ranging from 2 (RM6144 and RM12676) to 24 (RM206) alleles. The result showed that rare alleles (frequency < 0.05) comprised 57.2% of all alleles, whereas intermediate (frequency 0.05–0.50) and abundant alleles (frequency > 0.50) comprised 37.0% and 5.8% of all detected alleles, respectively. This result indicated that most alleles concentrated at a low frequency among the rice accessions studied (Fig. 1, Table 2). The gene diversity and PIC values ranged from 0.04 (SSS) to 0.87 (RM241) and from 0.04 (SSS) to 0.86 (RM241), with an average of 0.61 and 0.57, respectively. The major alleles frequency per locus varied from 0.22 (RM241) to 0.98 (SSS) with the average of 0.52, (Table 2).

2. Genetic diversity

The genetic distance-based analysis was performed by calculating the shared allele frequencies among the 114 accessions, and an unrooted phylogram (Fig 2) was computed using PowerMarker 3.23 and Mega 4 software (Tamura *et al*., 2007). The colours were used to stained according to the result of model-based cluster analysis. In the phylogram, all rice accessions clustered into five main groups (POP 1, 2, 3, 4, and 5), with the exception of 11 accessions (admixture). POP1 comprised 7 accessions

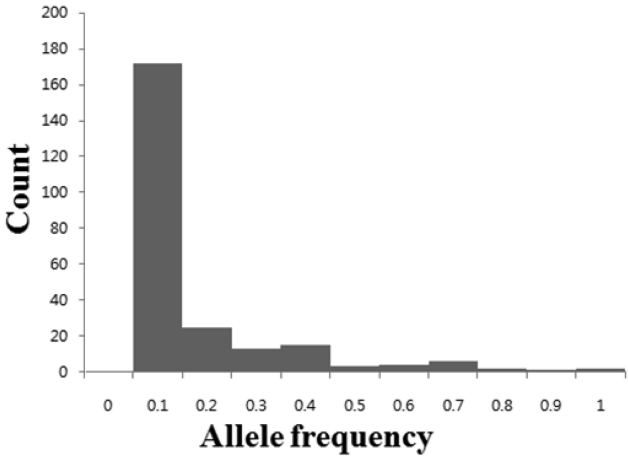

Fig. 1. Histogram of allele frequencies for all 243 alleles in the 114 rice accessions.

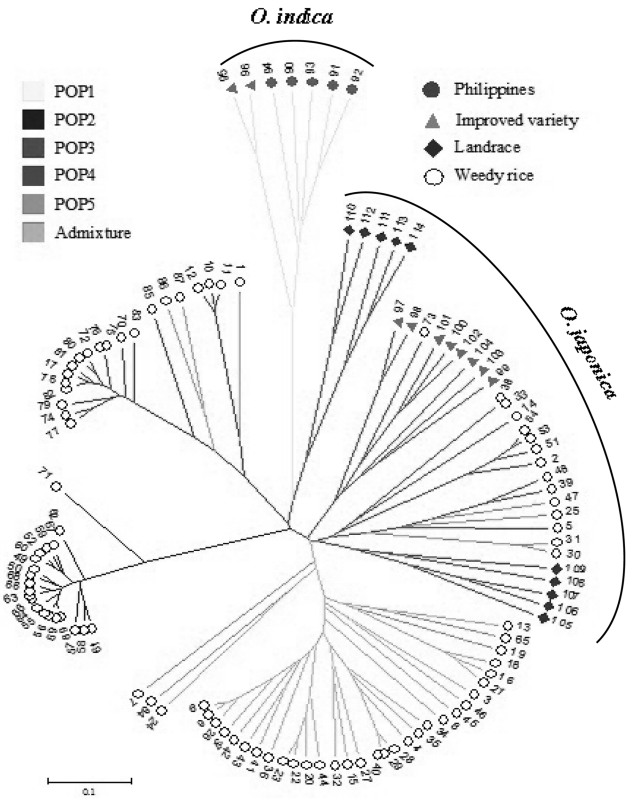

Fig. 2. UPGMA dendrogram based on a genetic distance matrix among 114 rice accessions from Korea and Philippines. The colors of the branches correspond to those of the model-based populations (POP1-POP5, Admixture).

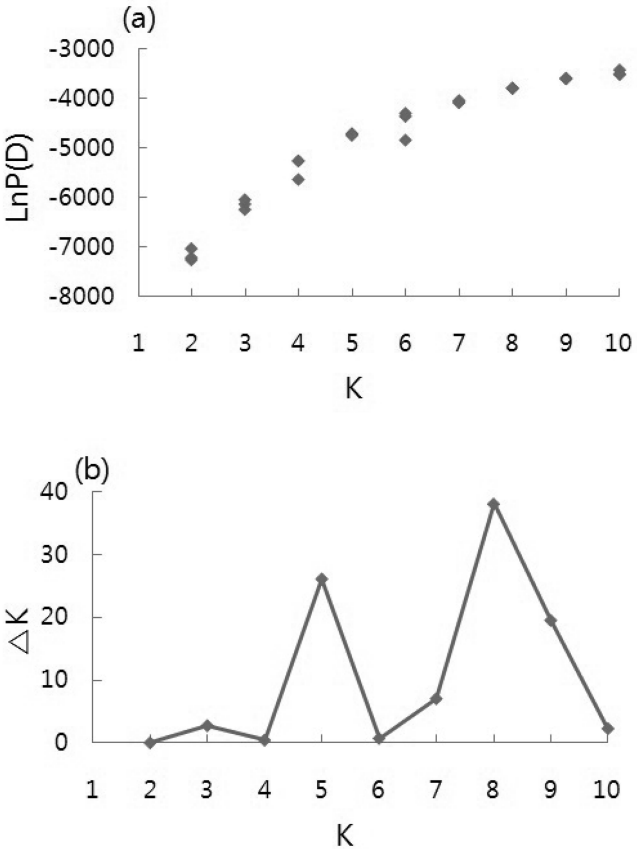

Fig. 3. (a) The Bayesian log probability data [LnP (D)] by increasing K. (b) Magnitude of Δ K as a function of K (Evanno *et al*. 2005) .

(including 5 Introduced species from Philippines and 2 Improved variety), POP2 comprised 20 accessions of 'Sharei rice', POP3 comprised 17 accessions 'Sharei rice', POP4 comprised 29 accessions (including 11 accessions of 'Sharei rice', 8 improved variety and 10 landraces) and POP5 comprised 30 accessions of 'Sharei rice', respectively.

3. Population structure analysis

The model-based clustering method was performed using all 114 accessions and 29 SSR markers. However, inference of the exact value of K (gene pool) was not straightforward because the estimated log–likelihood values appeared to be an increasing function of K for all examined values of K. Therefore, it may not be possible to find the true value of K (Fig. 3a). Thus, another ad hoc quantity (Δ K) was used (Evanno *et al*., 2005) to overcome the difficulty of interpreting the real K value. The relatively high value of Δ K for 114 accessions were for K = 5 and K= 8 (Fig. 3b). However, the highest number of accessions assigned to one specific cluster with a probability higher than 90% was obtained with k = 5, while with K = 8 this percentage dropped to

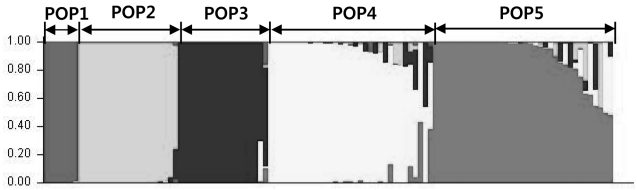

Fig. 4. Model-based membership of 114 rice accessions (*O.sativa*) using STRUCTURE. Colors represent model-based populations for 5 inferred clusters.

84.2% of the total number of accessions, thus indicating the presence of complex relationships among accessions. At K = 5, all 114 accessions were divided into 5 clusters (Fig. 4). Analysis of these data identified the major substructure groups when the number of clusters was set at 5 with the relatively high value of Δ K and high probability of accessions assigned to one specific cluster (Maccaferri *et al*., 2005). The relatively small value of the alpha parameter (α = 0.0319) indicated that most accessions originated from one primary ancestor, with a few admixed individuals (Ostrowski *et al*., 2006).

Of the 114 rice accessions, 103 (90.4%) shared > 70% membership with one of five clusters and were classified as members of that cluster, whereas 11 accessions (9.6%) were categorized as admixture forms with varying levels of membership shared among the five clusters (Table 1).

DISCUSSION

The study of genetic diversity and population structure of Korea rice using 29 SSR (microsatellite) markers depicted high divergence among 114 rice accessions. Cui *et al.* (2010) presented that the number of alleles detected and gene diversity was strongly correlated with the number of accessions used. However, it might be influenced by the different accessions used in each study (Zhao *et al*., 2009).

The model-based structure analysis used here revealed the presence of five populations among the selected core set. Similar pattern of grouping of accessions was found when the two results developed by different clustering methods (genetic distance matrix and model based membership) were compared (Figs. 3, 4). The distribution of the 114 accessions that shared at least 70% ancestry with one of the five inferred groups is summarized in Table 1 and Fig. 2. Clear cut was found between introduced accessions from Philippines (*indica*) and Korean weedy accessions (*japonica*). Two out of 10 improved accessions were closely related to *indica* and the others were related to *japonica*. It was astonishing that most of weedy accessions 'Sharei rice' collected from Ganghwa Island were separately grouped from both *indica* and *japonica* rice. 'Sharei rice' remains distinct from other weedy rice with it prominent characters of unique shattering pattern (Lee *et al*., 2003) and shorter culm lengths (87-111 cm) (Chung and Park, 2010). Our finding aligned with the result for 152 weedy rice accessions previously analyzed with isozyme and RAPD markers (Suh *et al*., 1997). Although Korea is not included in the list of origin of rice, it can't be argued that it has long history of rice cultivation. 'Sharei rice' appears to be a very primitive rice cultivar for it was separately grouped in our analysis. It might have changed its genetic background along with adaptation to such an isolated region. The origin of weedy rice has been suggested to involve the three routes; (i) from wild colonizing plants through selection towards adaptation to continuous disturbance, along with domestication, (ii) from hybrids between wild and cultivated races and (iii) from abandoned domestic varieties through selection towards a less intimate association with humans (Babker, 1974; de Wet and Harlan, 1975; Oka, 1988).

In addition to the groups indentified by this analysis, 9.6 % of accessions showed evidence of mixed population ancestry. The mixture is likely the result of breeding and domestication history, which have had large effects on the diversity structure. The independent population histories of the groups have shaped gene pools (Garris *et al*., 2005).
Human-mediated gene flow may play an important role within a population due to breeding in rice for its self fertilization nature (Zhao *et al*., 2009). In other words, in self-pollinated species, one would predict a greater partitioning of diversity among rather than within populations in the absence of human-mediated gene flow between populations by breeding (Liu *et al*., 2003).

Assessment of genetic diversity is an essential component in germplasm characterization and conservation. Therefore, several researches; Lu *et al.* (2009) on American rice, Cheng *et al.* (2009) on Africa, Asia, Europe and South America rice, Chung and Park (2010) on Korean weedy rice and Cui *et al*. (2010) on South Asia rice, have carried out. Zhu *et al*. (2004) pointed out that high selection pressure for good grain quality and repeated use of the same parental origin with proven yielding ability in the breeding program, result in significant genetic erosion of the local rice gene pool and cause a narrow genetic base for rice cultivars. In the context of breeding for the development of improved varieties, a wide genetic diversity will be of great important. The results derived from analyses of genetic diversity could be used for designing effective breeding programs to broaden the genetic base of commercially grown varieties. Here we reported the diverse arrays of Korean weedy and landrace rice using SSR markers. The result will support the required information for breeding programs and crop improvement practices of rice.

적 요

본 연구는 강화도에서 수집한 샤레벼 자원의 유전적 다양성 수준과 집단의 특성을 구명하기 위해 몇몇 Indica(5점), Japonica(8점) 및 통일형(2점) 품종과 재래종(10점) 및 강화도 수집 샤레벼 89점을 포함한 총 114개 벼 자원에 대하여 유전적 다양성과 집단의 구조 분석을 수행하였으며, 이를 통하여 향후 육종을 위한 소재로 활용할 수 있는 기초 정보를 제공하고자 본 실험을 수행하였다.

1. 114점의 벼 자원에 대하여 29개 SSR 마커에 의해 얻어진 allele는 총 243개이고, 마커당 평균 allele 수는 8.4개를 보였다. 유전적 다양성을 나타내는 genetic diversity와 PIC 값의 범위는 각각 0.04~0.87, 0.04~0.86 이였으며, 평균은 각각 0.61, 0.57로 관찰되었다.

2. 유전적 거리와 STURUCTURE를 이용하여 집단의 구조를 분석한 결과 70% 확률로 5개의 subpopulation으로 나눌 수 있었으며, 9.6%는 유전적으로 혼입된 형태를 나타냈다.

3. 강화도에서 수집된 샤레벼 89점 중 11개 자원은 japonica형의 국내육성품종 (8점) 및 재래벼(10점)와 POP4에 속했고, 11개 자원

은 혼입된 형태이며, 67개 자원은 POP2(20점), POP3(17점), POP5(30점)에 포함되었다.

강화 수집 샤레벼는 차후 국내 벼 품종의 유전적 다양성을 확대하고, 육종 소재로 활용할 수 있는 중요한 재료가 될 것이다.

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