

6. Morphological and SSR characterization of four strains of Dandong weedy rice (*Oryza sativa* L.)

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To characterize four new strains of weedy rice (*Oryza sativa* L.) found in farmers' fields in Dandong (40°07'N, 124°23'E), Liaoning Province, China. The weedy rice (WL, WS, BL and BS), 3 standard indica testers (Nanjing11, Nantehao and IR36), 3 standard japonica testers (Qiuguang, Zaoshajing and Balilla), one American red rice (Accession number: 15936 in the germplasm bank at China National Rice Research Institute) and 2 strains of Dongxiang wild rice (DY1 and DY2) were grown for phenotyping and genotyping with a set of 19 SSR markers capable of distinguishing between indica and japonica rice (Fan et al., 2000).

Six phenotypic traits including glume hair, phenol reaction, length of the first to second rachis internode, glume color at heading, leaf hair and grain length/width ratio were recorded (Table 1). The score of each trait was added up, 0-8 scores are typical indica, 9-13 scores are indica, 14-17 scores are japonica, and 18-24 are typical japonica (Cheng, 1993).

Results indicated that weedy rice strain WL (straw hull with long awn) belonged to typical japonica type with a total score of 18, strains WS (straw hull with short awn), BL (black hull with long awn) and BS (black hull with short awn) all were japonica with total scores of 14, 15 and 17 respectively.

For genotyping, a total of 86 alleles were examined (4.53 alleles/locus with a range from 2 to 7.5 alleles/locus). Five alleles were weedy rice specific at loci RM217, RM228, RM247, RM248 and RM250. 8 out of 19 SSR markers (42.1%) showed polymorphisms among the weedy rice. four markers (RM18, RM25, RM202 and RM250) showed differences between WS and the other strains of weedy rice. Three markers (RM20, RM228 and RM247) showed polymorphisms between WL and the other weedy strains. SSR pattern was highly similar between BL and BS except a single locus at RM259. Cluster analysis showed that the weedy rice, wild rice and japonica testers were grouped together in one group. The red rice and indica testers were clustered into another group. The japonica group was divided into two sub-clusters at 0.80 similarity level, one sub-cluster consisted of all strains of weedy rice and the other consisted of two Dongxiang wild rice. The genetic similarity coefficient was 0.82 between weedy rice and the japonica testers, and was 0.73 between Dongxiang wild rice and weedy rice, indicating that weedy rice was more closely related to japonica rice than wild rice. The result supported that weedy rice belonged to japonica rice similar to cultivars (Fig. 1).

Table 1 Morphological performance of the weedy rice and indica/japonica testers

Line	Glume hair	Phenol reaction	Internode length (cm)	Glume color	Leaf hair	Length/width ratio	Score	Type
IR36	0	0	0	0	1	3	4	Typical Indica
Nanjing11	0	1	0	0	3	4	8	Typical Indica
Nantehao	0	1	0	1	3	4	9	Indica
Balilla	4	4	4	2	3	4	21	Typical japonica
Zaoshajing	0	3	4	2	4	4	17	Japonica
Qiuguang	4	4	3	2	4	4	21	Typical japonica
WS	0	0	4	2	4	4	14	Japonica
WL	0	4	4	2	4	4	18	Typical japonica
BS	0	2	4	3	4	4	17	Japonica
BL	0	1	3	3	4	4	15	Japonica

Analysis of indica and japonica differentiation of the weedy rice showed that indica, japonica, weedy rice and wild rice were distinguishable at axial direction (Fig. 2). The red rice was distributed with the indica testers, showing differentiation towards indica and cultivated rice. The weedy rice were distributed with the japonica testers showing differentiation towards japonica and cultivated rice. No difference was observed between BS and BL using 19 SSR markers, they appeared in a single spot in the chart. The two

strains of Dongxiang wild rice collected from two natural populations showed a differentiation tendency towards japonica, this result was consistent with the research based on isozyme, RAPD and rDNA (Wang et al., 1994).

In summary, we concluded that the Dandong weedy rice belong to japonica rice similar to cultivar and possibly originated from ancient cultivars or introgression of modern varieties.

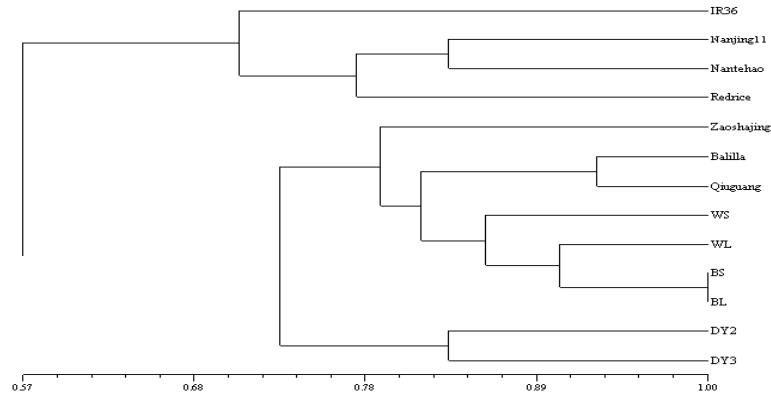


Fig. 1 Cluster analysis of the weedy rice. DY1, Dondxiang wild rice 1; DY2, Dongxiang wild rice 2.

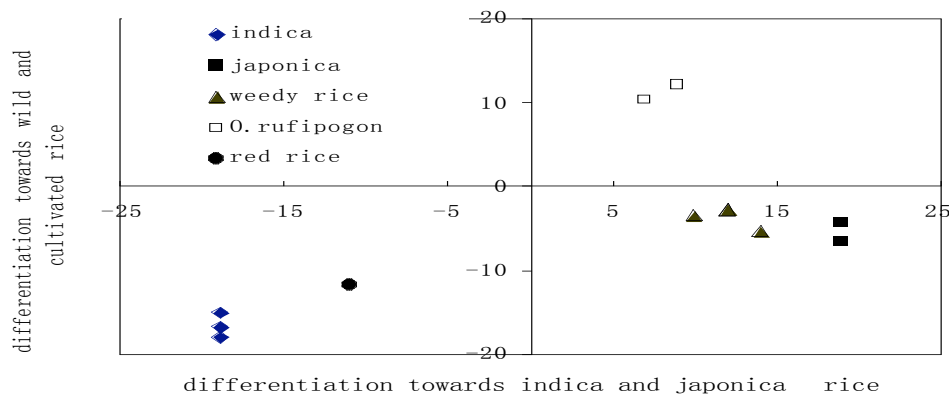


Fig 2. Genetic and evolutionary relationship of Dandong weedy rice

References

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