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Development of Core Collection with Heuristic Method in Rice (*Oryza sativa* L.)

Hun-Ki Chung, Kyu-Won Kim, Jong-Wook Chung, Jung-Hee Lee, Jung-Ro Lee, Kyung-Ho Ma, Jae-Woong Yu, Anupam Dixit, Eun-Gi Cho, Yong-Jin Park*

National Institute of Agricultural Biotechnology, Rural Development Administration, Suwon-441-707, Republic of South Korea

Objectives

In order to obtain the core set with high genetic diversity and minimum redundancy, we developed another approach known as A* algorithm, a kind of admissible heuristic (hereafter called advanced M strategy). Core sets with heuristic method were evaluated and were shown maximum genetic diversity with minimum accessions.

Materials and Methods

1. Plant materials: Rice (*Oryza sativa* L.)
2. Methods: Genotyping with SSR markers, Cluster analysis, Development of Heuristic methods, Evaluation of core sets, Shannon-Weaver Diversity Index (SDI)

Results and Discussion

Modified admissible heuristic method using A* algorithm was developed to obtain the core set with high diversity and minimum redundancy among accession. Program module was constructed at the web-based execution on NIAB web services. 10,368 characterized accessions among passport data in Genebank at RDA were analyzed. Core set developed by advanced M strategy were consisted of 168 accessions and represented a full retention of the entire collection and enhancement 22% of genetic diversity, which reduced the entire accessions about 98.78%. As evaluation of percentage of the character difference, there was not significantly difference in means, variances, range, and coefficient variance between the core collection and the entire collection. But as even distribution of characters, there was difference in means and variances between core collection and the entire collection. The further adaptation of genotype data, core set of 91 accessions were constructed with genotype data of SSR marker among 872 accessions. To evaluation of diversity, Shannon-Weaver Diversity Index (SDI) between core set and entire collection were analyzed. Overall SDI value of core set and the entire collection is 17.87, 14.06, respectively. And core set has evenly allelic distribution. This results suggested that advanced M strategy of designing admissible heuristic method might be efficient way to retain the genetic diversity and reducing the redundancy of the entire collection.

Table . Shannon and Weaver Diversity Index (SDI) results among passport data.

	World collection		Heuristic strategy	
	No. of samples	SDI	No. of samples (%)	SDI
<i>Variety types</i>				
<i>Indica</i>	5,749	46.39	194 (3.37)	54.52
<i>Japonica</i>	3,937	42.90	161 (4.09)	53.31
<i>Javanica</i>	497	43.61	109 (21.93)	47.73
<i>Hybrid</i>	90	44.77	61 (67.78)	48.23
<i>Tongli</i>	21	37.13	20 (95.24)	37.31
<i>Eco-strains</i>				
<i>Landrace</i>	1,016	43.97	118 (11.61)	49.96
<i>Breeding Variety</i>	268	38.35	90 (33.58)	41.02
<i>Breeding Lines</i>	1,046	36.62	122 (11.66)	42.90

Table . Comparison among core collections by different sampling strategies with 11 quantitative traits in Rice

Core collections	MD%	VD%	CR%	VR%
<i>P strategy</i>	0.24	-0.46	59.29	99.30
<i>R strategy</i>	-0.23	-1.76	59.29	98.47
<i>Heuristic</i>	0.12	2.95	100.00	102.83

Table . Shannon and Weaver Diversity Index (SDI) results among SSR marker.

	RM21	RM48	RM206	RM214	RM247	RM249	Total
M strategy	2.21	3.32	3.56	3.25	2.74	2.80	17.87
Entire	1.68	2.52	3.04	2.64	1.97	2.21	14.06
Ratio	1.32	1.32	1.17	1.22	1.39	1.27	

* Corresponding author: Yong-Jin Park, TEL: 031-299-1821; E-mail: yjpark@rda.go.kr