

Genetic Diversity of Released Rice Varieties Derived From a Global Exchange and Evaluation Network

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The continuous breeding of lines with narrow genetic base may cause rice varieties to be susceptible to abiotic and biotic stresses. Thus, genetically diverse germplasm that are well-adapted to adverse conditions need to be continually used in rice breeding programs. To this end, the International Network for the Genetic Evaluation of Rice (INGER; <http://seeds.irri.org/inger/>) was established in 1975 to facilitate the exchange and evaluation of genetically diverse germplasm from various sources worldwide. To date, more than 25,000 unique breeding lines and genbank accessions have been distributed by INGER to 85 countries. Of these, several hundreds have been directly released as varieties in more than 60 countries and thousands more have been used as breeding materials. Understanding the genetic diversity of these released varieties could yield clues as to the impact of this global exchange and evaluation network on rice varietal improvement worldwide.

Objectives

- To determine the genetic variation of varieties directly released through INGER through agronomorphological characterization and microsatellite marker analysis
- To evaluate the genetic diversity of varieties released within each country

Methodology

- 176 varieties commercially released in 60 countries analyzed together with 15 SNP reference collections (McNally et al., 2009) for genetic diversity. Figure 1 shows the number of varieties released per country.

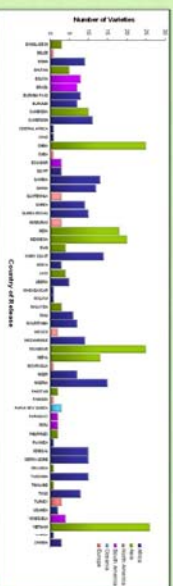


Fig. 1. Distribution of released varieties in 60 countries.

Agromorphological characterization

- 32 morpho-agronomic traits evaluated on the basis of *Bioversity International's Descriptors of Rice (2002)*, *UPVOY guidelines for the Conduct of Tests for Distinctness, Uniformity and Stability for Rice (2004)* and *Standard Evaluation System (1996)*
- Similarity analysis using Gower's coefficients using R version 2.9.2 (Ihaka and Gentleman 2009)

Microsatellite marker analysis

- 50 SSR markers covering the 12 rice chromosomes assayed to determine genetic variation and scores compared with those of 15 SNP reference collections

- Genetic similarity based on Dice coefficient and clustering based on unweighted pair-group method of arithmetical means (UPGMA) performed using NTSYS-pc 2.02e (Rohlf 1997)
- Trends of genetic diversity based on country of release visualized in radial trees and average dissimilarity obtained using DARWIN 5.0.156 (Perrier, X, and J.P. Jacquemoud-Collet 2006)
- STRUCTURE 2.3.1 (Pritchard et al. 2009) used to infer population structure using 10,000 iterations; model allowed admixture and correlated allele frequency

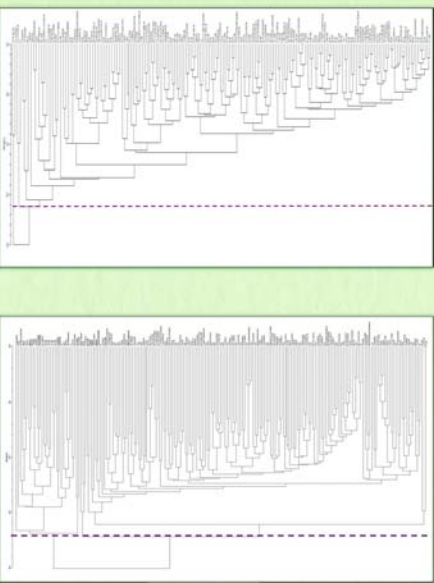


Fig. 2a. Dendrogram of 176 released varieties based on agronomorphological data.

Fig. 2b. Dendrogram of 176 released varieties and 15 SNP reference collections based on marker data.



Fig. 3. Genetic diversity of 176 released varieties of release (DARWIN 5.0)

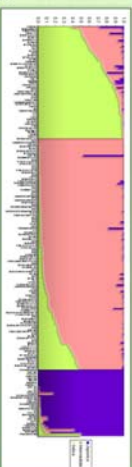


Fig. 4. Population structure of 176 released varieties and 15 SNP reference collections (STRUCTURE 2.3.1 at k=5).
 * Each color represents a country

Results

- No distinct major clusters were observed in the agronomorphological data; at 0.27 dissimilarity, 11 overlapping clusters were detected (Fig. 2a).
- Microsatellite marker analysis detected 380 alleles; at approximately 0.69 dissimilarity, two major clusters separated Japonica and Indica varieties, branching out into four sub-clusters at 0.65 (Fig. 2b); 0.56 average dissimilarity was computed among the 176 released varieties.
- At 5% level of significance, trends of clustering of agronomorphological and microsatellite marker data showed weak correlation (0.2468) based on Cramer's V coefficient and Spearman correlation coefficient (0.1822).
- Each sub group was composed of varieties released in different countries (Fig. 3) and an average dissimilarity of 0.52 was computed within the country of release.
- LnP(D) increased with K from 1 to 10 and the knee was seen at k=3; three sub groups diverged and differentiated the released varieties (Fig. 4).

Conclusions

- Microsatellite marker data better characterized the genetic diversity of released varieties than agronomorphological data did since it defined clusters of different variety groups.
- Based on SSR data, varieties that were released in different countries through INGER are genetically diverse.
- Direct varietal releases within each country have high genetic diversity.

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