

# Genetic Structure of *Oryza rufipogon* Griff. In Malaysia

Ngu, M.S.<sup>1</sup>, Wickneswari, R.<sup>1</sup>, Abdullah, M. Z.<sup>2</sup>

<sup>1</sup>School of Environmental and Natural Resources Sciences, Faculty Science and Technology, Universiti Kebangsaan Malaysia, 43650 Bangi, Selangor, Malaysia

<sup>2</sup>Gene Bank, MARDI Seberang Perai, P.O.Box 203, 13200 Kepala Batas, Pulau Pinang, Malaysia

## Introduction

*Oryza rufipogon* Griff. (AA genome, 2n=24) is widely distributed in the tropics and subtropics of monsoon Asia. But in Malaysia, this species can only be found in northern part of peninsular Malaysia (Abdullah et al. 1991). As the progenitor of the Asian cultivated rice (*O. sativa*), *O. rufipogon* has been proven to be a valuable gene pool for rice genetic improvement and thus plays a critical role in rice breeding. Recent field investigations indicated that the current geographic range of *O. rufipogon* in Malaysia was significantly decreased, and the extant populations have been gradually reduced in size because of decades of habitat destruction and degradation from agriculture and urbanization. However, our knowledge of the genetic structure of this agriculturally important species in Malaysia is rather limited. In this study, we used 30 highly polymorphic SSR markers to investigate the genetic diversity and population genetic structure of *O. rufipogon* in Malaysia. This study was carried out using *O. rufipogon* accession IRGC#105491 and 176 individuals of *O. rufipogon* collected from four states, i.e. Penang(Seberang Prai), Kedah, Kelantan and Terengganu.

## Materials and Methods

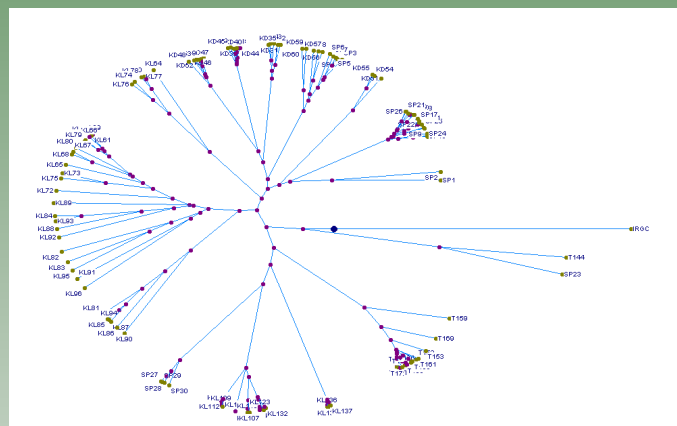
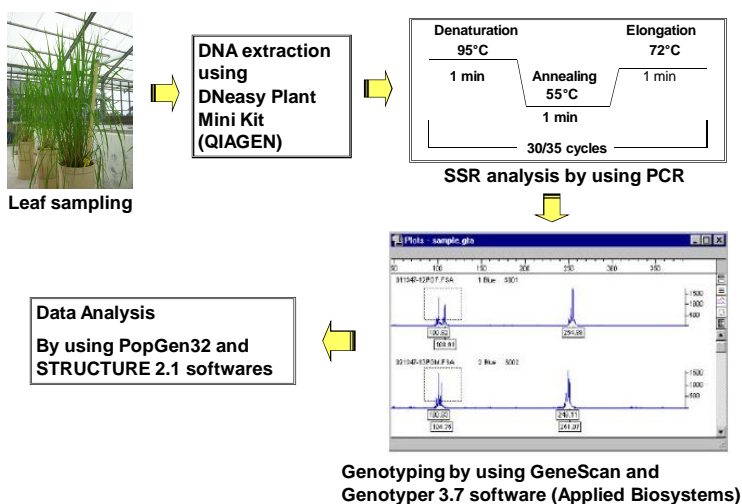


Figure 1 Dendrogram of the 176 individuals of *O. rufipogon* and accession IRGC105491 using UPGMA clustering method based on Nei's (1978) unbiased genetic distance

## Summary

At the species level, 445 alleles ranging from 66bp to 286bp in size were detected. The overall fixation indices for all the polymorphic loci in each population were positive (0.1372). The indirect estimate of multilocus outcrossing rate ( $t_m$ ) at population level of 76% showed that this species is predominantly out-crossing. The genetic differentiation between the four populations was 0.20, indicating that 80 % of the genetic variation was within populations. This moderate genetic differentiation might be due to a combination of factors such as, limited seed dispersal, short viability of pollen and fragmentation of the populations. UPGMA clustering based on Nei's genetic distance and Bayesian clustering analysis using STRUCTURE program grouped the 177 individuals of *O. rufipogon* into 17 clusters with slight differences.

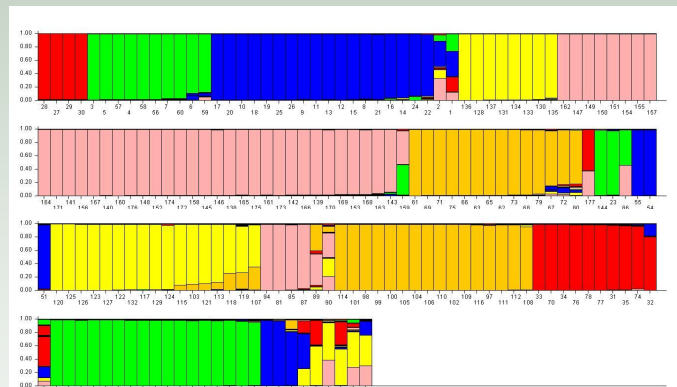


Figure 2 Population genetic structure analysis of 176 individuals of *O. rufipogon* and accession IRGC105491 using STRUCTURE 2.1 software.

## Results

Table 1 Estimates of genetic diversity for 4 populations of *O. rufipogon*

Population	N	Aa	Ae	Mean Heterozygosity	
				Ho	He
Seberang Perai	30	6.63	3.55	0.557	0.697
Kedah	30	7.67	4.78	0.595	0.746
Kelantan	77	11.87	5.50	0.631	0.798
Terengganu	39	4.23	2.10	0.549	0.449
Mean		7.60	3.98	0.583	0.673

## Conclusions

*Oryza rufipogon* refugia populations in Malaysia maintain high genetic diversity within populations despite the continuing habitat destruction. Restricted gene flow and random genetic drift maybe acting together resulting in extensive subdivision of the remnant populations in Malaysia. As one of the most important gene pool for rice breeding, practical conservation actions such as barriers around paddy fields are essential to maintain the genetic integrity of the species and prevent genetic pollution of cultivated rice.

## Acknowledgement

This project is supported by the Ministry of Science, Technology and Environment, Malaysia (IRPA 01-03-03-0001 BTK/ER/01)

## References

1. Abdullah et al. 1991. MARDI report 145.
2. Nei TM. 1978. *Genetics* 89: 583-590.