ORGANIZATION OF THE PHENOTYPIC AND GENETIC INFORMATION OF RICE BREEDING GERMPLASM IN SRI LANKA USING PEDIMAP TO FACILITATE THE DECISION-MAKING PROCESS IN VARIETAL IMPROVEMENT

P.G.R.G. Rathnayake (S/14/029) Supervisors: **Prof. S.D.S.S. Sooriyapathirana, Dr. U.A.K.S. Udawela,** Rice Research and Development Institute, Bathalagoda.

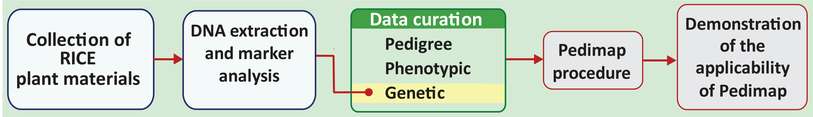
ABSTRACT

Pedimap - a pedigree visualization tool, can be applied to the decisioning of rice breeding programs in Sri Lanka. We organized all the available phenotypic, genetic, and pedigree information using Pedimap to facilitate the breeding decision-making process more simple and efficient. The parentage selection, identifying marker alleles for molecular breeding, and tracing founders of genetic effects can be swiftly conducted using Pedimap.

INTRODUCTION

The decision-making process in a breeding program is crucial for success in rice varietal improvement. The selection of suitable varieties/ genotypes as parents and the determination of the selection methods are the two most critical aspects in breeding, which are entirely performed based on the available information on phenotypes, genotypes, and pedigree (Ragot *et al.,* 2018). However, these data are not properly organized for decision-making for rice breeding in Sri Lanka. A pedigree visualization tool: Pedimap can be used to record and utilize breeding history along with phenotypic and genetic information and illustrate the crosses through pedigrees (Voorips *et al.,* 2012). Therefore, in the present study, we report an attempt to organize the information of the released varieties and the parental genotypes of RRDI breeding programs as a Pedimap database, which is a valuable step to take accurate breeding decisions and speed up the process of releasing novel varieties.

MATERIALS AND METHODS



	A	B	C	D	E	F	G	H	I	J	K
1											
2	POPULATION	=	Sri_Lanka_Rice_Germplasm								
3	UNKNOWN	=	-								
4	NULLHOMOZ	=	$								
5	CONFIRMEDNULL	=	$$								
6	PLOIDY	=	2								
7	NALLELES	=	6								
8											
9	PEDIGREE										
10	NAME	PARENT1	PARENT2	Yield	Maturity	Leaf_color	BPH	GM	BL	BLB	PDT
11	Bg94_1	-	-	4.1	105	Green	S	S	MR	MS	High
12	At354	Bg94_1	Pokkali	6.5	95	Green	MR/MS	MR/MS	MC	S	Sensitive
13											
14											
15	LINKAGEGROUP 12										
16	MAP										
17	RM101	48.2									
18	RM277	62									
19											
20	LOCUS	RM101									
21	ALLELENAMES	110	115	120	125						
22	FOUNDERALLELES	110	110	110	110	115	120				
23											
24	IBDPOSITIONS	48.2	62								
25											
26	ALLELES	RM101									
27	Bg941	140	0	140	0						
28	Pokkali	160	0	180	0						

Figure 1 The input data file structure of the Pedimap database; The input file was created as an MS Excel worksheet, contains four main sections. A: Header, B: Pedigree, C: Marker data and IBD probabilities. The header and pedigree section is compulsory for the program. The final file must be saved as a tab-delimited text (.txt).

RESULTS AND DISCUSSION

• DNA marker analysis - Newly generated data

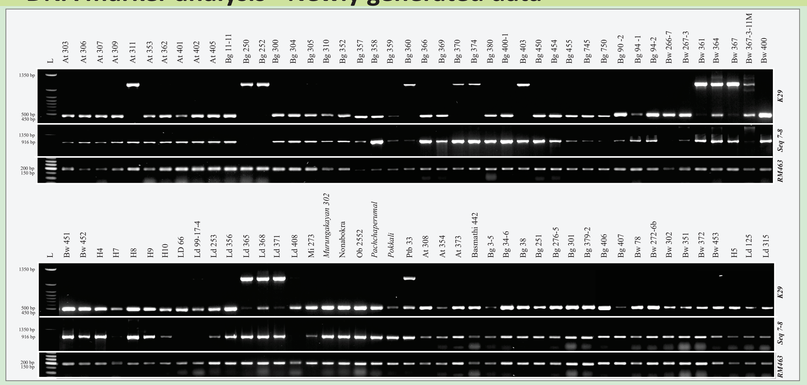


Figure 2 The polymorphism of three co-dominant DNA markers; *K29*, *Seq 7-8*, and *RM463*. Only *K29* and *Seq7-8* showed significant band polymorphism in the 2% agarose gel electrophoresis. However, *RM463* shows a monomorphic band pattern for all 90 rice varieties.

• Applicability of Pedimap for decisioning rice breeding

Example 1: Selecting parents for higher yield (≥ 3.5 mt/ha), Brown plant hopper (BPH) tolerance, short duration (≤125 days), and white pericarp with diverse grain shapes.

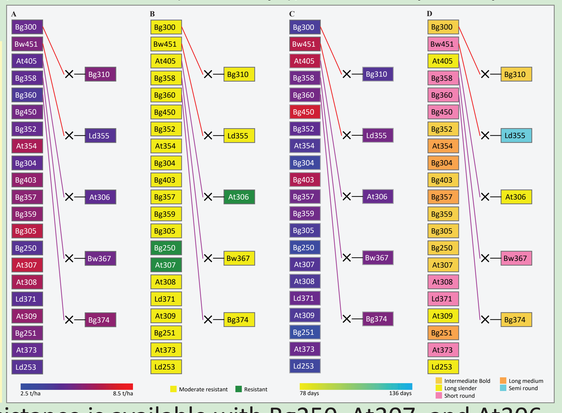


Figure 3 The pedigree visualization for Example 1 A: Yield; B: BPH resistance; C: Maturity period; D: Grain shape. According to the thresholds, a subpopulation of 26 cultivars was identified. The variation of the traits is given according to the color shading, which enables the breeder to select the required parents easily.

The complete BPH resistance is available with Bg250, At307, and At306, while At307 is also recorded for higher yield.

Example 2: Selecting parents for phosphorus deficiency tolerance (PDT), higher yield (≥5.0 mt/ha), short duration (90-105 days), resistance to both BPH and blast, and high/intermediate-high amylose content.

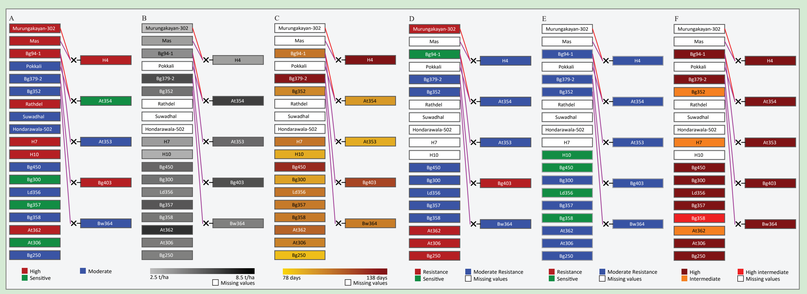


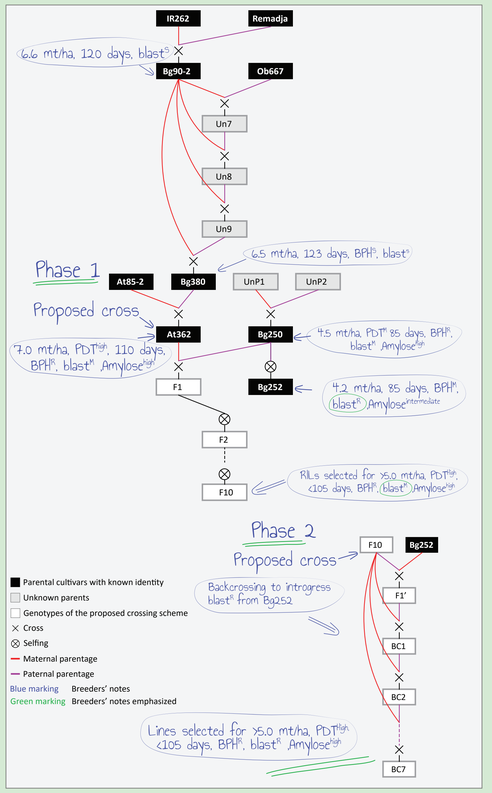
Figure 4 The pedigree visualization for Example 2. A: PDT; B: Yield; C: Maturity period; D: BPH resistance E: BLAST resistance; F: Amylose content.

Among the 24 cultivars with PDT ranks, At362 shows resistance to PD, and BPH, moderate resistance to blast, high yield, average maturity period, and intermediate-high amylose content. Similarly, Bg250 contains alleles for BPH resistance along with moderate yield, shortest maturity period, and high amylose content.

Figure 5 The pedigree visualization for planning a crossing scheme to produce high PDT and complete blast resistance rice variety.

Phase 1: Initial crossing of At362 and Bg250 and pedigree selection to obtain RILs with ≥5.0 mt/ha of mean yield, ≤105 days of the maturity period, resistant to BPH, moderately resistant to blast and high level of amylose content.

Phase 2: Backcrossing with Bg252 as the donor parent to introgress the blast resistance. With the advent of DNA markers and sequencing technologies, the marker alleles, the IBD probabilities, and SNPs data also can be displayed in simple understandable illustrations for breeders using Pedimap. The straightforward accessibility, direct data interpretation with customized views of Pedimap allows visualization and identification of suitable rice cultivars for decision-making with less effort and complete accuracy.



CONCLUSIONS

The pedigree visualization with variations of phenotypic and molecular data using Pedimap is a user-friendly tool to plan rice breeding programs with higher accuracy and resource optimization. The present study explains the applicability of Pedimap as a decision-making tool to streamline the rice breeding programs in Sri Lanka by having precisely characterized breeding germplasm for phenotypic and molecular data.

REFERENCES

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- Voorrips, R.E., Bink, M.C. and Van de Weg, W.E. (2012) Pedimap: software for the visualization of genetic and phenotypic data in pedigrees. Journal of Heredity, 103: 903-907.

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