

# SNP MARKERS FOR GENETIC STUDIES AND PREDICTION OF MONOGENIC TRAITS IN OIL PALM

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MPOB INFORMATION SERIES • ISSN 1511-7871 • JUNE 2011

MPOB TT No. 482

**M**arker-assisted selection (MAS) is the selection of desirable genotypes in conventional breeding using DNA-based diagnostic tools (Ibitoye and Akin-Idowu, 2010). By applying MAS, palms with the desired genotype can be differentiated early by their DNA, even before the characteristic trait can manifest itself visually. The availability of genetic maps, on which DNA markers such as Simple Sequence Repeats (SSRs) and Single Nucleotide Polymorphisms (SNPs) associated with the genes controlling selected traits of interest (*e.g.* the fruit colour gene and the shell gene) can be located, will facilitate the application of MAS.

Single DNA base differences between homologous DNA fragments are referred to as Single Nucleotide Polymorphisms. SNPs represent the most frequent type of genetic polymorphisms, and provide an important source of molecular markers that are useful in genetic mapping (Angaji, 2009), map-based positional cloning (Angaji, 2009), the detection of marker-trait gene associations through linkage and linkage disequilibrium (LD) mapping (Jehan and Lakhanpaul, 2006), and the assessment of genetic relationships between individuals (Jehan and Lakhanpaul, 2006; Hakim *et al.*, 2010). SNPs are therefore useful for marker assisted selection, positional cloning and gene isolation. SNPs can also help the breeders select for high-yielding varieties with desirable characteristics, including resistance to pests and diseases, and tolerance to environmental stresses.

## OIL PALM SNP MARKERS

Based on the existing sequences generated from the hypomethylated regions of the oil palm genome (Budiman *et al.*, 2005), MPOB has developed oil palm SNP markers, and has selected and extensively tested some of these markers. Our efforts have led to the identification of a subset of 63 SNP markers that can be used

to predict for monogenic traits as well as for general DNA fingerprinting of oil palm. An SNP array comprising a panel of these 63 SNP markers (named VALOPS1) has been developed, and can be made available to interested parties from the oil palm industry to evaluate their planting materials. This SNP array can be used in internal R&D programmes of industry members for either DNA fingerprinting or for the identification of markers linked to specific traits.

Research aimed at identifying and locating SNP genetic markers in oil palm is an on-going effort. The scheme for SNP marker development is illustrated in *Figure 1*. SNP markers linked to the fruit colour and shell genes are included in MPOB's SNP array VALOPS1. These markers being located close to the shell and fruit colour genes cosegregate with these genes and can hence be used to predict for the traits. Preliminary verification of these SNP markers has indicated the potential of using them to predict fruit colour and to differentiate the fruit forms.

## TESTING SNP MARKERS LINKED TO THE FRUIT COLOUR AND SHELL GENE LOCI

The SNP markers in the VALOPS1 array which include SNP markers linked to the fruit colour and shell genes have been tested on a small scale. The linkage of these markers to the *virescens* gene and the shell gene was tested on oil palm from several independent crosses with genetic backgrounds different from that of the mapping population used to generate these markers. The results indicate the ability of several of these markers to differentiate the fruit forms with an accuracy of 85%-90% in several of the populations tested (*Figure 2*). For the fruit colour trait, results indicate that several SNP markers have the ability to predict fruit colour with a certainty of greater than 90% (*Figure 3*). As part of our efforts in validating and improving the utilisation of these SNP markers, we would like to propose a collaborative effort with industry

ISSN 1511-7871



9 771511 787001

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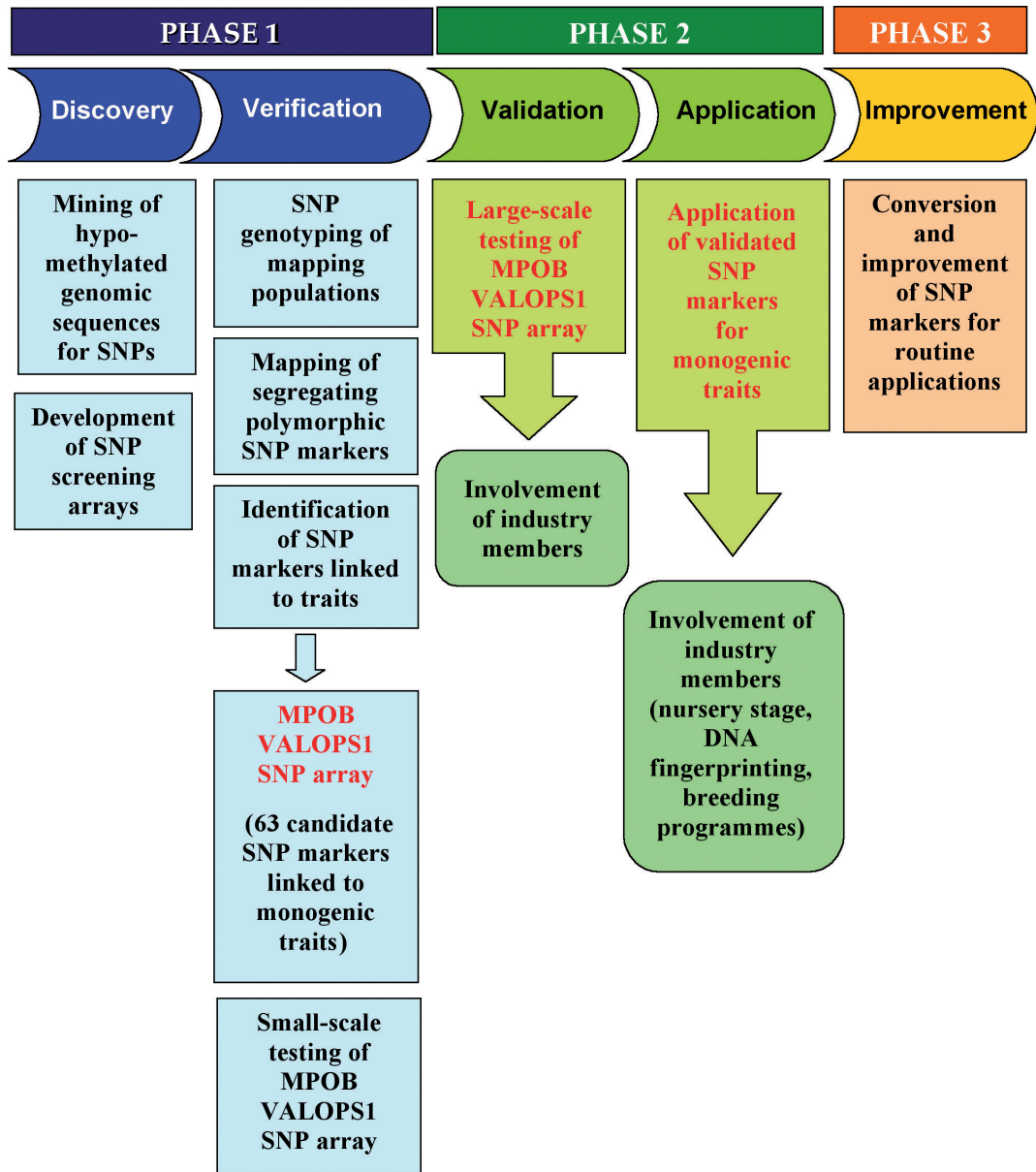


Figure 1. Development scheme for oil palm SNP markers.

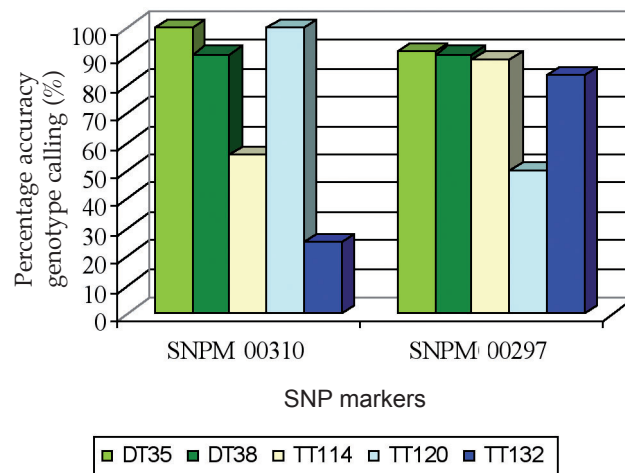


Figure 2. Validation of SNP markers for differentiating oil palm fruit forms on five independent populations (DxT, TxT).

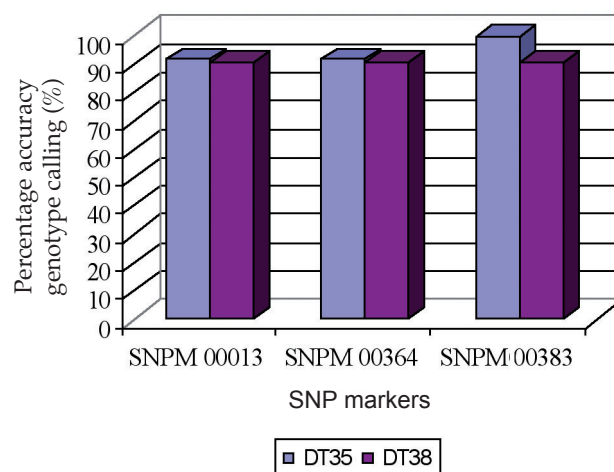


Figure 3. Validation of SNP markers for prediction of fruit skin colour on two independent populations (DxT).

members/ interested parties to test the SNP markers on a much larger scale and over a wider range of samples from different genetic backgrounds. This is to ascertain the suitability of each of these SNP markers towards the samples tested based on their genetic background. It is part of MPOB's efforts to continue to find markers more tightly linked to the monogenic traits.

### BENEFITS

- The SNP markers can be used as a predictive and selection tool in the oil palm nursery.
- The SNP markers allow for the application of marker-assisted selection in conventional oil palm breeding.
- VALOPS1 can be used for general DNA fingerprinting of oil palm.

### PROPOSED COLLABORATION

- To collaborate with industry members/ interested parties in applying MPOB's oil palm SNP array VALOPS1 to evaluate their planting materials.
- To enlist the participation and collaboration of industry members/interested parties in providing materials for genetic studies and testing of the SNP markers for the prediction of oil palm fruit skin colour and/or for differentiating oil palm fruit forms.

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