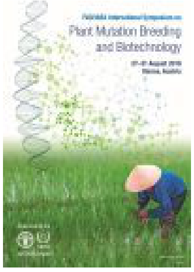

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THE POWER OF NEXT-GENERATION SEQUENCING IN RAPIDLY IDENTIFYING (EPI)GENETIC CAUSAL MUTATIONS

The advent of next-generation sequencing has accelerated forward genetic screens and can simultaneously achieve the typical steps of marker discovery, genetic mapping and identification of causal mutations. Initially applied in model organisms, an increasing number of studies emerge on crops. There is a wide variety of strategies to perform genetic mapping and the choice of an optimal approach depends on many factors, such as the genetic architecture and penetrance of the trait of interest, the applied mutagenesis and mutational load, the recombination frequency of the species, and the available resources. We will illustrate some of these aspects and their influence on the choice of crossing schemes and on the optimal use of next-generation sequencing. Besides genetic causes of agronomically important traits, a recent landmark study revealed that DNA methylation changes are responsible for a yield-reducing somaclonal variant of oil palm. Current research is focusing on a stable maintenance of epigenetic changes, so that they might become interesting targets for breeding. We will introduce a novel tool that enables the reliable and efficient identification of DNA methylation differences in whole populations of plants. Resulting epi-allele groups can serve as a basis for association studies.

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