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Technologies for Genetic Analysis Based on Genomic Information

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Introduction

For the past decade, plant scientists have aspired to breed by design. However, with the fast development of genomics-based genotyping tools and the availability of hundreds of functional genes/alleles connected to significant characteristics, it may finally be feasible to transform this lasting aspiration into a realistic reality. Rice has a relatively simple genome in comparison to other crops, and its genome makeup and genetic behaviour have been thoroughly studied. Recently, rice has been chosen as a model crop for breeding by design. The main aspect of breeding by design is to integrate functional genes/alleles in an optimal genetic background, which necessitates high throughput genotyping tools to test for predicted genotypes. With a considerable quantity of genome resequencing data and high-throughput genotyping methods accessible, a variety of genomics-based genotyping systems have been created. These systems are commonly employed in genetic mapping, target trait integration via marker-assisted backcrossing, pyramiding, recurrent selection, and genomic selection.

Description

We describe and discuss recent interesting developments in rice genomics-based genotyping technologies and their implications in molecular breeding. Variations in all key trait-related genes However, due to a lack of genomic knowledge and high throughput genotyping technologies, this approach was rarely used in empirical breeding. Since the rice genome was sequenced, substantial advances in functional genomics of rice have provided breeders with several tools and resources to undertake breeding by design. The rapid accumulation of rice genome resequencing data not only aided in the discovery of functional Quantitative Trait Loci or genes, but also offered various polymorphic genome sequences for molecular marker creation. Simultaneously, a number of molecular marker test systems with varying throughputs have recently been created [1].

All of these accomplishments have therefore transformed the notion of "design" into a real breeding activity. By design, this paper focuses on the recent development of genomics-based genotyping technologies and their applications in rice molecular breeding. Molecular markers are frequently utilised in genetic research and the production of novel varieties. To suit the needs of genetic research or breeding programmes in rice, many genotyping methods have been developed. Restriction Simple Sequence Polymorphism and Fragment Length Polymorphism Repeats are the first and second generation markers' representatives. They were crucial in the creation of rice genetic maps and the identification of trait-related locus genes. Breeders continue to utilise SSR markers to help them genotype screen for specific characteristics. This analysis will concentrate on the most recent advancements in high throughput genotyping systems, notably DNA array platforms and nextgeneration sequencing technology [2].

Recently, a variety of array-based genotyping technologies have been developed, and some of the representatives, such as Restriction Site-Associated DNA Single Feature Polymorphism and Single Nucleotide Polymorphism, have been thoroughly tested. RAD markers use short DNA tags as probes to discover genetic variations associated to specific restriction sites throughout the genome. RAD markers have been utilised successfully in genotyping both individuals and segregating bulks. SFP markers detect polymorphic signals caused by differential hybridization of distinct alleles to DNA probes arranged on a microchip. Affymetrix microarrays with 25 nucleotide probes have been demonstrated to be effective and easy for identifying a high number of SFPs in rice [3].

SNPs are the most prevalent DNA markers that are uniformly dispersed across the whole genome. SNP markers may target almost any gene or site. A SNP array with a high density may test a large number of SNP markers in a high throughput way. In the last decade, SNP array-based genotyping platforms have emerged as one of the most popular solutions for gene QTL mapping and marker-assisted crop breeding. Furthermore, with the increasing accumulation of rice genome resequencing data, SNP-based markers will continue to be employed more broadly than any other form of marker. Although SNPs may be discovered using PCR or Sanger sequencing, array-based detection approaches are preferable since they can meet a variety of genotyping criteria [4].

SNPs may now be identified at a range of throughputs, depending on the aims. Several firms have created SNP assay systems, including Illumina's SNP chip platforms, Affymetrix's SNP array platform, GenomeLab's SNPstream genotyping system, and the TaqMan OpenArray genotyping system. Because Illumina and Affymetrix SNP arrays are more extensively utilised in the rice community, they will be explored in greater depth here. The combination of Veracode and GoldenGate technology on Illumina's BeadXpress Reader can genotype 48-SNP, 96-SNP, 192-SNP, or 384-SNP persample. SNPs and their surrounding sequences are utilised to create locus-specific and allele-specific primers for the GoldenGate test. This technology, which can test hundreds of individual samples in a short amount of time, is both dependable and reasonably priced. Several 384-SNP assays using this platform have recently been developed and utilised for both variation evaluation and genetic diversity analysis in rice. Because of its high-throughput sample processing capabilities, this low-density SNP array device is suitable for genotyping of early generation breeding materials.

The identification of appropriate parental lines is an important phase in all breeding projects. Breeders seek to choose varieties with comparable genetic backgrounds for particular trait development so that homozygous progenies can be created in early generations. Breeders, on the other hand, prefer to employ varieties with significantly diverse genetic backgrounds to generate a novel variety with numerous new features, so that progenies have a greater chance of integrating various allelic variants. Breeders can quickly discover the genetic backdrop to their expectations using genomics-based genotyping tools. Furthermore, high density genetic markers may be employed to predict combinability in rice to achieve higher hybrid vigour [5].

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Conclusion

Breeding by design is an excellent method for creating novel varieties, but its full potential is now unrealized due to our inadequate understanding of the molecular and biochemical networks that drive trait development and the effects of gene-environment interactions. We know practically all of the rice gene structures now that the whole genome sequence has been annotated, but the mechanisms of action for the majority of them remain unknown. We know very little about gene interactions and how they influence trait development. Despite the fact that a considerable number of accessions have been re-sequenced, the rich allelic variants found in rice germplasm need to be investigated further. Aside from the necessity for high throughput genotyping technologies, breeders also want precise phenotyping tools, as well as the ability to detect environmental effects on offspring.

Conflict of Interest

None.

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