



Genome-wide polymorphisms between the parents of an elite hybrid rice and the development of a novel set of PCR-based InDel markers

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ABSTRACT. Genome-wide re-sequencing of the Zhenshan 97 (ZS97) and Milyang 46 (MY46) parents of an elite three-line hybrid rice developed in China resulted in the generation of 9.91 G bases of data with an effective sequencing depth of 11.66x and 11.51x, respectively. Detection of genome-wide DNA polymorphisms, single nucleotide polymorphisms (SNPs), short insertions/deletions (InDels; 1-5 bp), and structural variations (SVs), which is an invaluable variation resource for genetic research and molecular marker-assisted breeding, was conducted by comparing whole-genome re-sequencing data. A total of 364,488 SNPs, 61,181 InDels and 6298 SVs were detected in ZS97 and 364,179 SNPs, 61,984 InDels and 6408 SVs were detected in MY46 compared to the 9311 reference sequence. Synteny analysis of the variation revealed a total of 77,013 identical and 181,737 different SNPs and 15,021 identical and 1205 different InDels between ZS97 and MY46, respectively. A total of

180 InDels 3-8 bp in length between ZS97 and MY46 were selected for experimental validation; 160 polymerase chain reaction products were efficiently separated on 6% non-denaturing polyacrylamide gels. Identification of genome-wide variation among the parents of the elite hybrid as well as the set of 160 polymerase chain reaction-based InDel markers will facilitate future genetic studies and the molecular breeding of hybrid rice.

Key words: Breeding; Hybrid rice; InDels; Polymorphisms; Single nucleotide polymorphisms