Abstract
SNPs Linked to Key Traits in Hybrids between African and Asian Rice †

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Association analysis was performed to determine trait-associated variants (TAVs) influencing three quantitative agronomic traits, heading date (Hd), tiller number at maturity (T) and 1000-grain weight (TGW) in a population developed by crossbreeding between WAB56-104 (O. sativa) and CG14 (O. glaberrima). DNA derived from progenies with extreme phenotypes (high and low-value) for each trait was bulked, sequenced and then mapped against the reference genome of O. sativa cv Nipponbare for two types of analysis, general association analysis and candidate genes analysis. In the general association analysis, a total of 5152 non-synonymous SNPs in 3564 genes distinguished the low and high bulks of Hd, T and TGW traits; however, only 611 non-synonymous SNPs in 447 genes were involved in KEGG pathways. Among these non-synonymous SNPs, only six SNPs in the sequences of LOC107275952, LOC4334529, LOC4326177, LOC107275432, LOC4335790 and LOC107273425 genes were associated with H, T and TGW traits. These genes participated in the following KEGG pathways: abscisic-acid biosynthesis, carotenoid biosynthesis, starch and sucrose metabolism, and cytokinin biosynthesis. Analysis of candidate genes using 9, 10, and 5 genes associated with Hd, T, and TGW traits showed 2, 2, and 3 non-synonymous variations in the sequence of Hd3a and Ehd2 from the group of Hd genes (no KEGG pathway); D10 and D53 from the group of T genes (strigolactones biosynthetic pathway), and Gni1a and GIF1 from the group of TGW genes (cytokinin biosynthetic pathway, and starch and sucrose metabolism pathway), respectively. The results of this study provides significant TAVs for subsequent applications in rice breeding programmes.

Conflicts of Interest: The authors declare no conflict of interest.

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