Development of a SNP genotyping panel for detecting polymorphisms in *Oryza glaberrima*/*O. sativa* interspecific crosses

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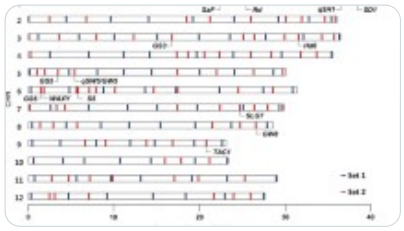
Abstract

Oryza glaberrima accessions harbor genes for tolerance to abiotic stresses such as mineral deficiency in problem soils. This genetic potential could be exploited in interspecific crosses with *Oryza sativa*, as in the case of the 'New Rice for Africa' (NERICA) varieties; however, to attain this goal it would be desirable to develop a high-throughput marker system to specifically detect *O. glaberrima* introgressions in an *O. sativa* background. Therefore, a single nucleotide polymorphism (SNP) genotyping analysis of an *O. glaberrima* accession (CG14) with two *O. sativa* lines (WAB56-104 and WAB181-18) was performed on a genome-

wide basis. Comparison of CG14 and the WAB lines resulted in a set of 9,523 polymorphic SNPs which would be suitable to detect *O. glaberrima* introgressions in upland NERICAs. In addition, a set of 1,540 polymorphic SNPs between *O. glaberrima* versus *O. sativa* was identified. A subset of SNPs which were evenly distributed in the genome was then used to design a flexible and cost-effective SNP genotyping panel using the Competitive Allele-Specific PCR technology (KASP). This SNP genotyping panel consists of 2,015 SNPs successfully converted into KASP markers, providing 745 polymorphic SNPs for the parents *O. glaberrima* CG14/*O. sativa* WAB56-104 (upland NERICA), and 752 for *O. glaberrima* TOG5681/*O. sativa* IR64 (lowland NERICA). KASP markers were successfully validated by mapping *O. glaberrima* introgressions in NERICA-derived breeding lines. This new SNP genotyping panel will be useful in modern breeding applications such as QTL mapping and/or marker-assisted selection.



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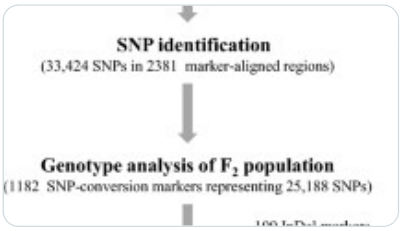

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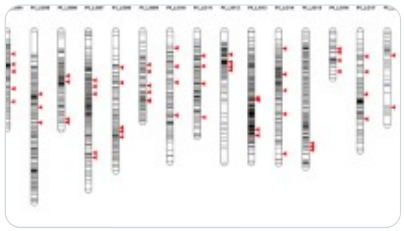

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Electronic supplementary material

Below is the link to the electronic supplementary material.

10681_2014_1183_MOESM1_ESM.xls

Online resource 1—Table S1. The complete list of 44 K SNP genotyping data. A SNP genotyping analysis of *O. glaberrima* (CG14) and *O. sativa* (WAB56-104, WAB181-18, IR74)

was performed on a genome-wide basis using the 44 K SNP Affymetrix genotyping array. (XLS 15683 kb)

10681_2014_1183_MOESM2_ESM.doc

Online resource 2—Fig. S1. Distribution of polymorphic SNPs between *O. glaberrima* CG14 and six *O. sativa* accessions. (DOC 55 kb)

10681_2014_1183_MOESM3_ESM.xls

Online resource 3—Table S2. The complete list of SNP—KASP markers. A set of selected SNPs were successfully converted into KASP markers. The genotyping data for the parents of upland and lowland NERICAs (*O. glaberrima* and *O. sativa*) is presented. (XLS 443 kb)

10681_2014_1183_MOESM4_ESM.xlsx

Online resource 4—Table S3. KASP data for N10W3/4 lines.The N10W3 and N10W4 are two BC_1F_4 sister lines derived from a NERICA10 × WAB56-104 backcross used for mapping *O. glaberrima* introgressions. (XLSX 220 kb)

10681_2014_1183_MOESM5_ESM.xlsx

Online resource 5—Table S4. Flanking region for each SNP—KASP marker. The physical position and the flanking region of each KASP marker is provided. The SNP is represented as [x/y], where x and y indicate the allele. (XLSX 180 kb)

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