DEVELOPMENT AND MOLECULAR CHARACTERIZATIONOF A RICE MAPPING POPULATIONFOR BLAST RESISTANCE

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THE RESEARCH

Blast, caused by the fungus *Magnaportheoryzae*, is themost damaging disease in rice.The use of resistance genes in crop breeding programshas been the major, and most sustainable,means for disease control.

To identify new resistance genesor alleles to be introduced in breeding lines, a mapping population was developed crossing BRS Esmeralda, an upland cultivar, and Três Marias, a Brazilian landrace internationally recognized as blast resistant. The population was advanced until F_7, using the single seed descent (SSD) method. The 99 recombinant inbred lines (RIL) were genotyped following a double enzyme genotype by sequencing (GBS) approach. The NGSEP (Next Generation Sequencing Experience Platform) pipeline was used to analyze the data.

OUTSTANDING RESULTS

After data filtering, 12,929 SNVs, 973 biallelicindels, 688 biallelic STRs and 199 complex variants were obtained, keeping only variants in non-repetitive regions of the rice reference genome, genotyped in at least half of the population, with minimum genotype quality of 30 and minor allele frequency (MAF) over 0.05. Close to 80% of these variants had an expected segregation pattern with MAF above 0.2. The overall percentage of missing data was 15% and missing data was generally well distributed across samples. Heterozygosity rates were on average 2.19%, with only one sibling having more than 5% heterozygosity and 1,005 variants (6.8%) having an observed heterozygosity (OH) above 0.05.

Further filtering, keeping variants with at least 80 individuals genotyped, MAF greater than 0.2 and OH below 0.05, reduced the number of variants to 7,805, but also reduced the percentage of missing data to 5.9%. These selected variants account for an average density of 19.5 variants/Mbp, which should be good enough to perform association mapping. This density is generally uniform across the genome having only 19 windows of 1Mbp represented by up to one variant. Filtering based on OH reduced the average heterozygosity rate per sample to 1.6%, but interestingly the heterozygosity increased for 13 samples, going over 5% for two samples.

Analysis of linkage disequilibrium (LD) decay revealed that LD reached background values over 4Mbp, which is expected for a biparental population. Based on this result, we performed LD-based imputation of the 5.9% missing data.

In the next step, association between genotypic and phenotypic data(blast evaluation) will be tested to identify regions associated with blast resistance in rice.

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