



Category: Plant Genomics

Genome-wide comparative analysis of three local aromatic rice lines revealed novel markers

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Abstract

Rice is the primary source of dietary energy for half of the World population, and 90% of them are present in developing countries in Asia. We have sequenced three local rice varieties Chenga, Tulai-panji, Kalonunia and compared with *Oryza sativa cv. Nipponbare*, *Oryza sativa cv. 93-11* and *Oryza sativa cv. Kasalath*. 30X paired end 2 X 100 bp reads were generated for each of the 3 samples on Illumina HiSeq 4000, next generation sequencing platform. The raw data was subjected to pre-processing and aligned with *reference genomes* individually. The SNPs/INDELs were identified for each of the 3 local rice varieties with the each reference genome. A total of 0.15, 0.34 and 0.57 million SNPs and 10863, 11435 and 21841 INDELs were identified in Chenga, compared to *Oryza sativa cv. Nipponbare*, *Oryza sativa cv. 93-11* and *Oryza sativa cv. Kasalath*, respectively. In Tulai-panji, 0.23, 0.76 and 0.71 SNPs as well as 12854, 18987 and 22901 INDELs were identified when compared to *MSU7*, *93-11* and *Kasalath assemblies respectively*. Analysis of Kalonunia data revealed 0.24, 0.58 and 0.54 SNPs and 10775, 14281 and 16657 INDELs against 3 reference genomes as above. We investigated for homozygous polymorphic markers between Chenga (Non aromatic) and Tulai-panji (Aromatic), and found 38,471 SNPs at read depth of 10. Similarly, comparative analysis between Chenga (Non aromatic) and Kalonunia (Aromatic) 130,376 homozygous polymorphic markers which can be explored for mapping novel alleles associated with aroma.

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