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Genome-wide identification of InDel markers from imported Rice varieties

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[Introduction]
Rice, being a staple food crop for over one third of the world's population, has become a potential target for many dishonest traders and stakeholders for mixing with low grade, low cost grains/products and low nutritious adulterants to fetch profits with least efforts.

[Materials and Methods]
Single nucleotide and insertion-deletion (InDel) polymorphisms have been widely used as DNA markers, not only in plant breeding but also to identify various traits in rice. Recently, next-generation sequencing (NGS) has produced deep sequences that allow genome-wide detection of these molecular markers. These polymorphisms can potentially be used to develop high-accuracy polymerase chain reaction (PCR)-based markers. PCR based techniques are the rapid and successful method to purge the problem of adulteration at commercial level.

[Results and Discussion]
Here, we reported genome-wide analysis of InDel markers from of 39 commercially imported Japonica and Indica rice varieties from China, Australia, America, Thailand and India. In order to do highly accurate analysis, all above imported rice varieties has been sequenced at approximately 30x genome coverage using Illumina HiSeq 2500. An average of 10.6GB clean reads per sample was produced and ~98.3% of the reads could be mapped to the rice genome reference IRGSP 1.0. After a series of filtering we selected 114 unique InDel markers for validation. The validation results were compared with Hwayoung cultivar. The results revealed that, these InDel markers can be used for rice authentication and traceability, and other applications in molecular breeding.

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