

IDT9-083 | Marker-assisted stacking of QTLs/genes for drought, blast and BLB into popular rice variety– Lalat

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Achieving the desired increase in rice production to feed the growing population faces severe constraints due to varying climate patterns. In shallow, rainfed lowland ecosystems, drought, blast and bacterial blight are considered major constraints affecting rice yield. *Lalat* is a medium-duration, high-yielding, long slender grain variety rice, having resistance to gall midge, brown plant hopper, stem borer and sheath rot. But it is highly susceptible to drought, blast and bacterial blight. The present study aims to improve *Lalat* variety with introgression of major QTLs for grain yield under drought ($qDTY_{11}$, $qDTY_{37}$, $qDTY_{121}$), broad-spectrum blast resistance gene (*Pi9*) and durable bacterial blight resistance genes (*xa5*, *xa13*, *Xa21*). Different donors were

used to combine the target traits by utilizing a complex crossing scheme. F_5 s were tested for the presence of target genes/QTLs by gene-specific markers for gene or peak, as well as flanking markers in case of QTLs. At F_2 level, three-way strategies were adopted to develop double haploids with the required gene combinations, identify F_3 lines with homozygous and heterozygous gene combinations, as well as attempt backcrosses using *Lalat* as recipient and donor line with gene combinations. Several lines with the target traits combining good agronomic performance were selected at F_3 stage. F_3 double haploid lines as well as BC_1F_1 lines are being advanced to develop breeding lines with appropriate combination of genes.

IDT9-084 | Identification and validation of insertion–deletion polymorphisms in pigeonpea

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Completely sequenced plant genomes provide scope for designing a large number of genome wide insertion–deletion (InDel) markers, which are useful in various aspects of crop breeding and genetic analysis. With the objective of developing InDel markers from pigeonpea genome, the re-sequencing data of eight MAGIC parental lines were used to identify InDels using Dindel software. As a result, a total of 102,181 InDels were identified. Of these 70,158 InDels were found unique. The higher number of InDels were found in intergenic (43%) followed by upstream (26%) and downstream (24%) regions. A total of 6.93% of InDels were found in the genic region. Out of 70,158 InDels, 2,426 (1,032 insertions and 1,394 deletions) with ≥ 20 bp size among different parental lines were selected. Average distribution of selected 2,426 InDels was found 220 InDels/LG with maximum number of InDels on CcLG11 (385 InDels) and minimum number of In-

Dels on CcLG05 (70 InDels). A set of 293 InDels could assess genetic diversity and establish phylogenetic relationships among 16 parental lines of different mapping populations. Validation of these primer pairs on parental lines of different mapping population resulted in higher amplification success rate ($\geq 83\%$) with almost 52.04% polymorphism rate among parental lines on 3% agarose gel. The number of alleles per locus ranged from 2 to 9 with an average of 3.8 alleles. Further, to track the genome of parents in complex funnel crossing scheme of pigeonpea MAGIC population at 28-two way, 14-four way and 7-eighth way stages, we have identified unique InDel primers for each of the 8 MAGIC parents. The result showed that InDel markers with their high polymorphic potential in comparison to SSR markers would be preferred candidate markers in various marker-based applications in pigeonpea genetics and breeding.