IDT7-118 | Assessment of rice (Oryza sativa L.) for drought tolerance with SSR markers

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Drought remains a major constraint in rice (*Oryza sativa* L.) for productivity in rainfed environments, leading to huge economic loss. Molecular marker technology helps in identifying genomic regions influencing the response of yield and its components to water deficits, which will aid in our understanding the genetics of drought tolerance and development of more drought-tolerant cultivars. Investigation was carried out in rain out shelter at Birsa Agricultural University, Ranchi, Jharkhand with the aim to identify superior F3 segregants having drought-tolerant QTLs, from 100 randomly selected segregants of a cross between drought-tolerant (DT) parent *Birsa Gora* 102 and drought-susceptible (DS) parent BPT 5204. Check parents *Vandana* (DT) and IR 20 (DS) were used. Plant height, panicle length, number of tillers, number of effective tillers, grains per panicle, panicle weight, seed yield per plant and test weight were the traits under investigation. Seventeen segregants were identified as superior, with yield higher than 7.03 g/plant. The parents were analyzed with 19 SSR markers, out of which 14 markers were found to be polymorphic. These polymorphic markers were used to analyze the randomly selected segregants. None of the segregants were found to be homozygous at entire 14 loci. Seventeen identified segregants were found to have the drought tolerant QTLs. The genomic regions flanked by the polymorphic markers have been reported to be associated with several drought resistance component traits. Hence, the segregants identified in the early generation can be advanced further to develop drought tolerant cultivar.

IDT7-119 | Effect of drought stress on antioxidant enzymes activity and gene expression and physiological response in Wheat (*Triticum aestivum* L.)

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Antioxidant enzyme activities and gene expression patterns were investigated in the leaf of wheat (*Triticum aestivum* L.) under drought stress. Two drought-tolerant genotypes (C306 and AKAW2712) and two drought consitiun genetypes (HD2687

AKAW3713) and two drought-tolerant genotypes (CS06 and AKAW3713) and two drought-sensitive genotypes (HD2687 and PBW343) were subjected to medium (75% of field capacity) and severe stress (45% of field capacity) for 10 days at tillering and anthesis stages. The drought treatment resulted in reduction in thousand grain weight and grain yield. The genotypic variations in drought tolerance were found to have a significant effect on physiological traits. Malondialdehyde content increased while the relative water content and chlorophyll index decreased significantly in all the genotypes in severe drought stress. The transcript level of copper/zinc superoxide dismutase

(Cu/Zn SOD) and Peroxidase (POX) was significantly higher at day 10 in C306, compared to well watered condition. The highest increase in transcript level of *manganese-superoxide dismutase* was observed at the 10th day of severe stress in C306 (42.8%) as compared with control condition, and significantly decreased in HD2687 at 1d and 10d. The highest decrease was found in the transcript level of Fe-SOD at day 10 in C306 (38.7%). The enzyme activities of SOD and POX were more in drought-tolerant genotypes. CAT activity decreased in the tolerant genotypes but increased in sensitive ones at 10 day of severe stress anthesis stage. The genotype level information on drought stress responses can be useful for breeding programs to create drought resistant varieties.