

**DISENTANGLING THE GENOME WIDE CONTRIBUTE OF STRUCTURAL VARIATIONS TO DROUGHT STRESS RESISTANCE IN THE MODEL SPECIES ORYZA SATIVA**

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Although it has been demonstrated that the actions of Transposable Elements (TEs) – i.e. insertions/deletions/inversions etc. can be triggered by a wide array of stresses in plants, very little is known about their role in stress response regulatory networks, and how their movement is influenced by selection during local adaptation, speciation, domestication and breeding. To better understand the interplay between these actions (i.e. structural variations – SVs), and stress responses in plants we studied the role played by SVs in both progressive and intermittent vegetative-stage drought tolerance in rice. To achieve this goal, we long-read resequenced 180 domestic rice accessions representing the 15 major subpopulations of *O. sativa*, maximizing both genetic diversity and the tolerance variation to drought stress. Comparison of each accession to the *O. sativa* vg. japonica cv. Nipponbare reference genome led to the identification of ten of thousand SVs that totaled to an average of 33.70 Mb per genome. About 85% of the SVs content originated from TE activity with LTR-retrotransposons and MITEs being the major components. The variability observed was greater between varieties belonging to different major groups than between those

within these groups. The distribution of SVs across accessions followed the subpopulation structure for rice. To find evidence of associations between SVs and response to stress, extensive phenotype data in field experiments from drought stress was collected for each accession. Transcriptome data are produced as well. This entire dataset will be further interrogated for evidence of associations between TE-PAPs, gene expression, and phenotypes on a genome-wide scale to understand the molecular mechanism underlying drought tolerance in *O. sativa* for precision breeding.