**Genomic and epigenomic underpinnings of a novel and non-parental**

**stress-adaptive phenotype created by transgressive segregation**

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The classic genetic phenomenon of transgressive segregation offers a powerful strategy to create novel phenotypes beyond what is typically achieved by the conventional phenotype-to-gene selection in introgression breeding. In this study, we used a well-investigated recombinant inbred population (F9) of rice derived from two genetically diverse and contrasting parents, i.e., IR29 (indica-subgroup) x Pokkali (aus-subgroup), as a model system to understand the impact of recombination under mild genomic shock to the epigenomic landscape of a transgressive recombinant with superior tolerance to hyper-salinity stress than the tolerant parent. Our integrative profiling of recombinant genomes, methylomes, heterochromatin profiles (Topographically Associating Domains, TADs), and transcriptomes across the comparative panel revealed that the phenotypic novelty of the hyper-salinity super-tolerant transgressive progeny is associated with several peculiar features of the genome and epigenome. Using IR8 and N22 as biparental references, we have revealed that the rare transgressive segregant was a product of extensive recombination under moderate genomic shock, which led to a significant downsizing of the recombinant genome caused by the shedding of repetitive elements and transposons. Shedding was largely responsible for the extreme hypomethylation of the transgressive recombinant genome, peculiarity in the CHH context. One important consequence of the extreme hypomethylation of the downsized transgressive recombinant genome was a novel chromatin signature characterized by increased TAD segmentation across the genome. All these changes in the epigenome created a uniquely non-parental spatio-temporal transcriptome signature with direct functional significance to the novel stress-adaptive phenotype of the transgressive recombinant.

Keywords: Transgressive segregation, genome shock, genome size, genomics, epigenome, methylome, heterochromatin, TADs, retrotransposons