Contribution of Non-Allelic Homologues to Transgressive Segregation in Genomic Content: Significance and Possible Applications in Breeding

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We have shown previously that inbred maize lines (haplotypes) can differ from one another by the presence and absence of hundreds of phylogenetically conserved and expressed genes (PAVs). An analysis of two of the IBM recombinant inbred lines (RILs) relative to their inbred parents (B73 and Mo17) revealed the presence of several hundred apparently *de novo* copy number variants (CNVs). These changes in genome content were validated via both PCR and whole exome-array capture-and-sequencing experiments. 185 genomic regions, which overlap with 38 high-confidence genes, exhibited apparently *de novo* copy number variation (CNV) in these two RILs and in many instances the same *de novo* CNV events were observed in multiple RILs. Further analyses revealed that these recurrent *de novo* CNVs were caused by segregation of single-copy homologous sequences that are located in non-allelic positions in the two parental inbreds. The F_1 individuals will be hemizygous for each of these non-allelic homologs but F_2, or RIL, genotypes will contain zero, one or two copies of these sequences. The segregation of non-allelic homologs (SNH) provides a mechanism to explain the recurrent origin of (apparently) *de novo* CNV in offspring relative to their parents. The segregation of non-allelic homologs also provides the potential for transgressive phenotypes in recombinant individuals. Indeed, statistical associations between phenotypic QTL and genomic losses were observed for two of 14 tested pairs of non-allelic homologs.