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Deciphering molecular origin and functional impact of structural variation in maize through genome sequences comparison and integrative analysis of genetic variation, transcriptome and phenotype data.

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Structural variation (SV) is a major driver of plant adaptation and genome evolution. It originates from transposable element insertion, as well as gene Copy Number (CNV) and Presence/Absence Variation (PAV). Maize is a crop species with a complex genome, and exhibits extensive SV among lines, as well as strong phenotypic differences. It is therefore a good model to explore the diverse molecular mechanisms leading to SV, and to investigate to what extent SV impacts phenotypic variation. Finally, the geographical origin of the different maize inbred lines is well described, allowing for linking SV to environmental adaptation.
Here, we present whole genome assemblies from seven European and American maize lines of various geographical origins and phenotypes, and with contrasted genome size. This dataset allows unprecedented genome-wide comparisons and characterization of maize SV with high sequence accuracy, thus offering the opportunity to evaluate the prevalence of the molecular mechanisms underlying these variations and to characterize the features responsible for genome size variation.
These seven maize lines together with B73 were cultivated under contrasted water conditions in the PHENOARCH phenotyping platform allowing precise characterization of growth and development together with precise measurements of environmental conditions. Thirteen different organs harvested at various developmental stages have been used for RNA-seq-based transcriptome analysis. This massive dataset will be used to evidence the possible role of SVs in quantitative responses to water deficit as well as the impact of SVs in gene regulation networks. Overall, this work will provide insights on the molecular origins and functional consequences of SV.

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