Towards the assembly of the sugarcane genome

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Knowing the DNA sequence of the sugarcane genome should aid genetic breeding programs in obtaining genotypes with higher energy yields and better resistance to biotic and abiotic stresses. However, its highly polyploid and aneuploid nature poses difficulties for current assembly algorithms. Sorghum is the closest diploid species to sugarcane and its genome sequence was recently published, enabling the use of a comparative assembly approach that may facilitate efforts in obtaining a first sugarcane genome. Based on published information about the similarities and differences of both genomes, we simulated macro chromosome rearrangements starting from the publicly available sorghum genome sequence and constructed a synthetic sugarcane genome, from which we obtained a data set of DNA fragment reads that would be acquired from projected third-generation sequencing technologies having reads around length 1000 and an error rate of 10^-5. AMOS, the comparative assembler used, was able to provide a diploid-like assembly of the synthetic genome, but did not distinguish well the multiple copies of the same chromosome. We are currently working to build a comparative assembler than can both handle the high polyploidy/aneuploidy case, and also work with higher error rates.

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