

# CONSTRUCTION BI-PARENTAL GENETIC LINKAGE MAP IN SUGARCANE

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Molecular markers have been used to develop genetic maps in crops to improve our understanding of genome structure, localize and identify genes of agronomic importance. In polyploidy organisms, the genetic mapping became possible through the segregation analyses of the markers in a single dose (SDM). The map were construction using a F1 segregation population, which consists in a 220 progeny, originated from a bi-parental cross between the elite clone IACSP95-3018 as the female parent is a promising clone used as parent in the breeding program and the variety IACSP93-3046 as the male parent has high levels of sucrose, good tillering, erect stool habit, recommended to mechanical harvest and prone environments, both from the Sugarcane Breeding Program from Instituto Agrônomico de Campinas. In total were used 84 EST-SSR were development for our group obtained the Brazilian EST database, the Sugarcane EST Project (SUCEST) all available in the public domain, 35 genomic SSR and 15 amplified fragment length polymorphism (AFLP) combining two restriction enzyme (*EcoRI* and *MseI*) with polymerase chain reaction (PCR). Of the total, 958 polymorphic markers were generated with 549 (57,31%) segregating in SDM (1:1 and 3:1) that were used for to construct the linkage map using OneMap. Out of these SDM 340 (62%) were linkage in 96 linkage groups (LG) and were regrouped into 13 putative homology groups (HG) based on markers derived from the same SSR loci. The full coverage map was 3877 cM suggesting the use of a higher number of molecular markers and other doses (double, triple and higher doses) in order to obtain a better map saturation.

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