GENETIC LINKAGE MAP IN SUGARCANE USING SNPS

Marconi, T.G.[1]; Rodrigues, R.[3]; Mollinari, M.[3]; Margarido, G.R.A.[3]; Vicentini, R.[1]; Souza, G.M.[5], Henry, R.J.[2]; Pinto, L.R.[6], Garcia, A.A.F.[3], Souza, A.P.[1,4]

[1]Centro de Biologia Molecular e Engenharia Genética (CBMEG), Universidade Estadual de Campinas (UNICAMP), Brazil; [2]Centre for Plant Conservation Genetics, Southern Cross University, Australia.; [3]Departamento de Genética, Escola Superior de Agricultura Luiz de Queiroz (ESALQ), Universidade de São Paulo (USP), Brazil; [4]Departamento de Biologia Vegetal, Instituto de Biologia, Universidade Estadual de Campinas (UNICAMP), Brazil; [5]Instituto de Química, Universidade de São Paulo (USP), Brazil; [6]Centro Avançado de Pesquisa Tecnológica do Agronegócio de Cana, IAC/Apta, Brazil.

Sugarcane is one of the most important crops in tropical countries. It's estimated for Brazil a production of 625 million tons in 2010/2011, a total area of 8 million hectare with an average production of 78 ton/ha. Despite the efforts of the breeding programs, obtaining an improved variety with agronomic traits is a long and laborious process that can take up to 15 years. The development of molecular markers and the construction of genetic maps can help understand the genetic architecture introducing new strategies into breeding programs in order to accelerate the development of new varieties. With advances in molecular technologies, the SNP markers have been widely used because they are the most abundant source of variation in the genome and useful for constructing genetic maps with high resolution, facilitating the identification of QTLs. This study developed and analyzed SNP markers from expressed sequences from SUCEST database and the SNPs were genotyped using the mass spectrometry platform Sequenom®. We selected 2908 sequences with differential expression, the software QualitySNP was used to discover the SNPs and the MassArray Assaydesign® to design the primers, it was possible to develop 943 SNPs. The markers were genotyped in a mapping population derived from a bi-parental cross of commercial varieties, IACSP 95-3018 as female parent and male parent as IACSP 93-3046, and the progeny of 220 individuals. Of the total, 790 (84%) SNPs were successfully amplified and tested for segregation showing single, double, triple and higher doses in the progeny. We used a previous genetic map constructed with SSRs to incorporate 31 new SNPs. Newly segregation ratio 1:2:1 could be incorporated to the genetic map. Since they are much more informative than single dose markers, there were some reallocations and repositioning of the markers on the previous map, resulting in a better coverage and resolution.

Supported by: FAPESP AND CNPQ

Excluído: Bundock, P.[2];

Excluído: of sugarcane

Excluído: of sugarcane

Excluído: derived

Excluído: ratio

Excluído:

Excluído: generating

Formatado: Inglês (EUA)