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Linkage Disequilibrium Mapping And Tagging In Sugarcane

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Linkage disequilibrium (LD) in crops, established by domestication and early breeding, can be a valuable basis for mapping the genome. We have assessed LD in sugarcane (*Saccharum* spp), characterized by one of the most complex crop genomes, with its high ploidy level (>8) and chromosome number (>100) as well as its interspecific origin. Using AFLP markers, we surveyed 1,537 polymorphisms among 72 modern sugarcane cultivars. We exploited information from available genetic maps to determine a relevant statistical threshold that discriminates marker associations due to linkage from other associations. LD is very common among closely linked markers and steadily decreases within a 0–30 cM window. Many instances of linked markers cannot be recognized due to the confounding effect of polyploidy. However, LD within a sample of cultivars appears as efficient as linkage analysis within a controlled progeny in terms of assigning markers to cosegregation groups. Saturating the genome coverage remains a challenge, but applying LD-based mapping within breeding programs will considerably speed up the localization of genes controlling important traits by making use of phenotypic information produced in the course of selection. One validation and application was developed in a region bearing a gene (*Bru1*) that confers resistance to brown rust, which is under map-based cloning. The markers found to surround *Bru1* within a 12 cM window were surveyed in 405 international sugarcane cultivars that were also phenotyped for rust resistance in Réunion Island or Guadeloupe Island. All the markers display

massive LD with rust resistance. The Bru1 haplotype is present in 87 % of the resistant cultivars. The other resistant cultivars represent alternative sources of resistance to the rust pathogen.