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### Characterization Of The Bru1 (Brown Rust Resistance) Locus; Distribution In Modern Sugarcane Cultivars

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The genome of modern sugarcane cultivars is highly polyploid, aneuploid, of interspecific origin, and contains 10 Gb of DNA. Its size and complexity represent a major challenge for the isolation of agronomically important genes. A durable major rust resistance gene (Bru1) identified in the cultivar R570 is the focus of a map-based cloning approach. To overcome constraints associated with high polyploidy, we developed genomic strategies including diploid/polyploid syntenic shuttle mapping with two model diploid species (sorghum and rice) and haplotype-specific chromosome walking. Their applications allowed us (i) to develop a high-resolution map including markers at 0.28 and 0.14 cM on both sides and 13 markers cosegregating with Bru1 and (ii) to develop a physical map of the target haplotype that still includes two gaps at this stage due to the discovery of an insertion specific to this haplotype. Several BAC clones representing different hom(oe)ologous haplotypes were sequenced. Their sequences are used to continue the characterization of this resistance locus. Several markers surrounding Bru1 in R570 were surveyed in 405 international cultivars that were phenotyped for rust resistance in Réunion or Guadeloupe Island. The results revealed that Bru1 is present in most of the resistant cultivars. Only 13% of them did not display the Bru1 haplotype. They represent alternative sources of resistance to the rust pathogen. Two of the PCR

markers developed in the course of this mapping are in perfect linkage disequilibrium with Bru1 and thus can be used as diagnostic for the presence of Bru1 in modern sugarcane cultivars.