

## S2-12

### COMPLEXITIES OF CHROMOSOME LANDING IN A HIGHLY POLYPLOID, ANEUPLOID, INTERSPECIFIC GENOME: TOWARDS MAP-BASED CLONING OF A RESISTANCE GENE (BRU1) IN SUGARCANE (2N=CA 115)

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The genome of modern sugarcane cultivars is highly polyploid (~12x), 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. We have undertaken the first attempt to isolate a gene from sugarcane by map-based cloning, targeting a durable major rust resistance gene (Bru1). To overcome constraints associated with high polyploidy, we developed strategies including diploid/polyploid syntenic shuttle mapping with model diploid species (sorghum and rice) and haplotype-specific chromosome walking. These strategies allowed us to develop a high-resolution genetic map including 17 markers in an interval of 0.42 cM comprising Bru1 and to build 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. BAC clones representing seven different hom(oe)ologous haplotypes have been sequenced. These sequences are being used to complete the physical map of the target haplotype.

Keywords: sugarcane, resistance gene, diploid/polyploid syntenic, map-based cloning