Sugarcane transcriptome. A landmark in plant genomics in the tropics

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In the last 10 years, when a vast array of genomic tools became available, new opportunities have been opened to explore complex plant biological systems. This is the case of sugarcane, an important cash crop of the tropics that is cultivated for its stalks, which accumulate sucrose. It contributes with 60% of the raw sugar production and in some countries, like Brazil, part of its biomass is also used for the production of ethanol. Sugarcane became an important crop when geneticists crossed Saccharum officinarum, a high-sugar species, to Saccharum spontaneum, a wild and vigorous relative (Berd ing and Roach, 1987). Progress in sugarcane genetics, however, has been slow because of its genomic complexity, characterized by a high level of ploidy (Sreenivasan, et al., 1987). The modern sugarcane hybrids present 2n = 100 to 130 chromosomes derived from a combination of S. officinarum (2n = 80 chromosomes) and S. spontaneum (2n = 40 to 128 chromosomes) (Butterfield et al., 2001; D’Hont and Glaszmann, 2001). Because of the different basic chromosome sets of S. officinarum and S. spontaneum, the hybrid genome presents complex chromosome organization and recombination events (Grivet et al., 1996; Ming et al., 1998). However, despite the high level of ploidy, the monoploid genome sizes of S. officinarum and S. spontaneum are around 930 and 750 Mbp, respectively (D’Hont and Glaszmann, 2001), a value comparable to that of sorghum (~760 Mbp) and about twice that of rice (~430 Mbp).

The understanding of the complex genome of sugarcane will benefit from a number of discoveries on other cereals, including the high chromosome synergy between grasses (Freeling, 2001), the availability of high density maps for sorghum and maize and the completion of genome sequence of rice. However, additional genomic resources will be necessary to reach this goal, some of which are now beginning to become available. For example, a sugarcane Bacterial Artificial Chromosome (BAC) library of more than 100,000 clones has been constructed (Tomkins et al., 1999) and will be necessary to reach this goal, some of which are now beginning to become available. For example, a sugarcane Bacterial Artificial Chromosome (BAC) library of more than 100,000 clones has been constructed (Tomkins et al., 1999) and will be of tremendous value for the construction of a physical map and to extend the comparison with other grasses. Recently several projects aiming at sequencing sugarcane ESTs related to signal transduction, plant development, biotic and abiotic stress, gene regulation, transposable elements, polymorphism analysis, organelle constitution and a miscellaneous of topics related to plant metabolism.

I believe that this collection of articles will be a highly valuable resource for the plant biology community to extend investigation on sugarcane and related grasses such as maize, sorghum and rice.

REFERENCES


