

**EXPERIMENTAL ASSESSMENT OF THE ACCURACY OF GENOMIC SELECTION
IN SUGARCANE**

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Sugarcane cultivars are interspecific hybrids with an aneuploid, highly heterozygous polyploid genome. The complexity of the sugarcane genome is the main obstacle to the use of marker assisted selection in sugarcane breeding. Given the promising results of recent studies of plant genomic selection, we explored the feasibility of genomic selection in this complex polyploid crop. Genetic values were predicted in two independent panels, each composed of 167 accessions representing sugarcane genetic diversity worldwide. Accessions were genotyped with 1499 DArT markers. One panel was phenotyped in Reunion Island and the other in Guadeloupe. Ten traits concerning sugar and bagasse contents, digestibility and composition of the bagasse, plant morphology and disease resistance were used. We used four statistical predictive models: bayesian LASSO, ridge regression, reproducing kernel Hilbert space and partial least square regression. The accuracy of the predictions was assessed through the correlation between observed and predicted genetic values by cross-validation within each panel and between the two panels. We observed equivalent accuracy among the four predictive models for a given trait, and marked differences were observed among traits. Depending on the trait concerned, within-panel cross validation yielded median correlations ranging from 0.29 to 0.62 in the Reunion Island panel and from 0.11 to 0.5 in the Guadeloupe panel. Cross validation between panels yielded correlations ranging from 0.13 for smut resistance to 0.55 for brix. This level of correlations is promising for future implementations. Our results provide the first validation of genomic selection in sugarcane.

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