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## **Experimental Validation of Genomic Selection in Sugarcane**

Date: Monday, January 14, 2013

Room: Grand Exhibit Hall

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Sugarcane cultivars (*Saccharum* spp.) are interspecific hybrids characterized by highly heterozygous and polyploid genome. Genomic selection (GS) approach is believed to be well suited for complex traits by including all markers in prediction models. Our objective was to test the GS approach in a complex polyploid crop. Predictions of genetic values were carried out on two independent panels, each composed of 167 cultivars and breeding materials covering the worldwide diversity. Accessions were genotyped using 1499 DArT. Phenotyping was carried out in Reunion for one panel and in Guadeloupe for the other one. We considered ten traits relative to sugar and fiber contents, digestibility and composition of the bagasse, plant morphology and disease resistances. We used seven predictive models: Bayesian Regression, Bayesian LASSO, Ridge-regression, BayesA, BayesB, Reproducing Kernel Hilbert Space and Partial Least Square Regression. Accuracies of predictions were assessed through correlations between observed and predicted genetic values, firstly by using a cross-validation within each panel, and secondly by using a cross-validation between panels. Accuracies of predictions were of similar value between the seven GS models for a given trait, while differences were observed among traits. Depending on the trait considered, the average GS accuracy values related to within-panel prediction ranged from 0.29 to 0.61 in the Reunion panel and from 0.13 to 0.5 in the Guadeloupe panel. GS accuracy values based on cross-validations between the two independent panels ranged from 0.13 (smut resistance) to 0.55 (brix). This study represents the first validation of GS approach in sugarcane with experimental data.