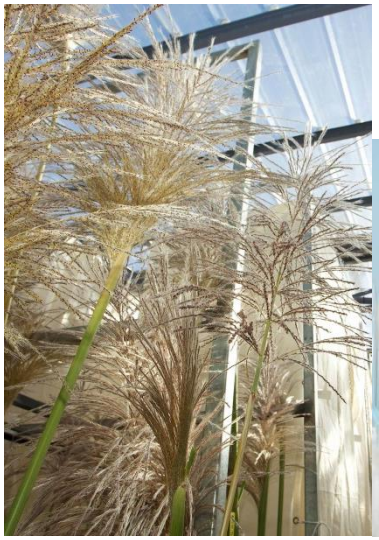
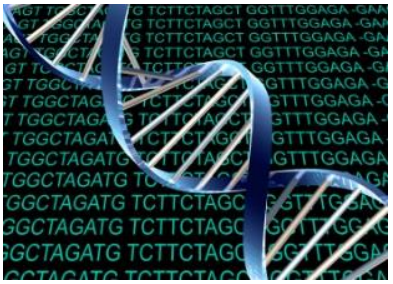
11th GERMPLASM & BREEDING

8th MOLECULAR BIOLOGY

ISSCT WORKSHOP

Saint-Gilles Réunion Island / 1–5 June 2015





« Pushing the frontiers of sugarcane improvement »

ABSTRACT

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ORGANIZATION

SUMMARY

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GENOME-WIDE ASSOCIATION STUDIES (GWAS) IN SUGARCANE CONTEXT: EXPERIENCE FROM A CASE STUDY AND QUESTIONS ABOUT WAYS OF OPTIMIZATION OF GWAS

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A Genome-Wide Association Study (GWAS) was undertaken to prospect for sources of resistance to Sugarcane yellow leaf virus (SCYLV) transmitted by aphid vectors. To this end, a panel of 189 sugarcane cultivars representative of the breeding germplasm was fingerprinted with 3,949 DArT and AFLP markers and was phenotyped for SCYLV infection in leaves and stalks under natural disease pressure prevalent in Guadeloupe in two repeated trials in two crop cycles. Mixed linear models including co-factors representing population structure fixed effects and pairwise family random relatedness effects provided an efficient control of the risk of inflated type-I error at a genome-wide level. Six independent markers were significantly detected in association with SCYLV resistance phenotype. Among them, two DArT markers were detected repeatedly across the GWAS exercises based on the different disease resistance parameters. These two markers could be blasted on *Sorghum bicolor* genome and candidate genes potentially involved in plant-aphid or plant-virus interactions were localized in the vicinity of sorghum homologs of sugarcane markers. The low frequency of all markers in the panel (8-20%) combined with a high virus incidence mean reflects (1) the absence of selection in breeding programs due to the recent spread of the disease and (2) a probable scarcity of sources of resistance available in modern sugarcane germplasm. All markers explained individually between 9 and 14% of the disease variation of the cultivar panel. The cumulative effects on disease resistance variation of the six detected markers were estimated with stepwise multiple regression models. Depending on trials and resistance parameters considered, between three and five markers were captured in multiple regressions. They explained a maximum of one third of disease resistance variation in the panel. Development of efficient marker-assisted breeding applications will depend on the ability to detect robust associations more or less numerous in GWAS experiments. Our work represents a case study illustrating questions we should paid attention for when designing GWAS experiments to optimize statistical power of association tests. Our presentation will review several considerations relative to statistical power including size and structure of mapping population, efforts invested in phenotyping, methodology of association tests, presumable architecture of target traits and marker technology so far available in sugarcane context.