Genetic diversity in *Melanaphis sacchari* and host-plant resistance in sugarcane

Samuel Nibouche, Hélène Delatte, Bernard Reynaud, Laurent Costet
**Melanaphis sacchari** (Zehnter)

pest of sorghum (feeding damages) and sugarcane (virus vection, ScYLV)

mostly anholocyclic, with known holocycle in Mexico (Peña-Martínez et al. 2016), India (David & Sandhu 1976), China (Zhang & Zhong 1983)

considered by Blackman & Eastop (1990) as a species complex = *M. sacchari* (Zehnter) and *M. sorghi* (Theobald)
Genetic diversity worldwide, 2002-2009

- 1333 specimens
- 57 samples, 42 localities, 15 countries
- Two main host plants
- 10 SSR loci
- 658 bp sequence of the mitochondrial COI gene

- S. bicolor
- Saccharum sp.
- S. bicolor subsp. verticilliflorum
- S. halepense
- P. glaucum
Clonal diversity and COI sequence variation

- 36 Multi Locus Genotypes (MLG)
- Low clonal richness
  - $R_{MLG} = 0.36$
- No sexual reproduction
  - Genepop: $P_{sex} < 0.01$
- 5 Multilocus Lineages (MLL)
- very low COI variation
Geographic distribution of clonal lineages
Genetic diversity on Réunion, 2009-2010

- 855 specimens
- 31 samples
- two host plants
- 10 SSR loci

- 13 MLG, all belonging to MLL-C
  - 8 new ones
- Low clonal richness
  - RMLG = 0.40
  - Identical to the worldwide value

Saccharum sp.

S. bicolor subsp. Verticilliflorum
Distribution of MLGs on Réunion
Host plant specialisation of the three most common MLGs

Field prevalence

Artificial transfert experiments
Exploration of the genotypic diversity of SCA resistance in sugarcane germplasm

- Field trial, 3 years
- 181 sugarcane cultivars
- Alpha-lattice design
- Between plots susceptible spreader cv.
- % infested leaves
  - 20 leaves / plot
  - Each 14 days (7 – 12 counts / year)
Exploration of the genotypic diversity of SCA resistance in sugarcane germplasm

- Significant genotypic diversity
  - 22 resistant cv.
  - 20 susceptible cv.
- Good fiability of the indexation method
  - $H^2 = 0.75$
- Spatial heterogeneity of infestations controlled by the alpha lattice
  - No spatial correlation of model residuals
- Resistance to SCA reduced ScYLV incidence
  - 51% vs. 98%
Genome wide association study

- Searching for QTL for aphid resistance

- Method
  - 181 cultivars / field phenotyping
  - 3,327 molecular markers (AFLP, DArT, SSR)
  - GLM and MLM controlling spurious effects of genetic structure or family relatedness among cultivars

- Result
  - Several QTLs detected for traits of interest (yield components, resistance to diseases)
  - But zero QTL identified for aphid resistance
Resistance to SCA in the sugarcane cv. R575

- R365 (resistant) vs. MQ76/53 (susceptible)

Field comparison

Potted plantlet infestation
antixenosis on potted plantlets

antibiosis on excised leaves

- $r_m$ on *M. sacchari*
  - R365 = 0.058
  - MQ76/53 = 0.206

- $r_m$ on *Rhopalosiphum maidis*
  - R365 = - 0.094
  - MQ76/53 = 0.140
Analysis of feeding behavior with Electrical penetration graph (EPG)
Comparison of feeding behavior

- Passive ingestion in phloem
- Salivation in phloem
- Non probing
- Others
Perspectives

- To resolve the taxonomic ambiguity between *sacchari* and *sorghi*
  - morphometry
  - sequencing other genes (ITS, EF1-alpha, COII...)

- To analyse the evolution of the genetic diversity in the current outbreaks on sorghum in US, Central America and Caribbean
  - host shift or invasion?