

## *Session 4: Disease management and plant resistance*

### **4.5 Genetic mapping of sugarcane resistance to smut through bi-parental segregation and associations among modern cultivars**

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Breeding for smut resistance is efficient because this trait is fairly heritable but it requires complicated screenings. Moreover, the genetic control of smut resistance is still unknown. With the objective to identify the mendelian factors involved in sugarcane resistance to smut, two strategies have been implemented (1) QTL mapping in a bi-parental progeny derived from a cross between a resistant cultivar 'R 570' and a highly susceptible clone 'MQ 76/53', evaluated in Reunion island for resistance to smut (2) Association study in a population of cultivars, evaluated in Burkina Faso for resistance to smut. The genetic maps of the two parents of the bi-parental progeny, 'R 570' and 'MQ 76/53', were constructed using a population of 198 progeny. A total of 1666 polymorphic markers were produced using 37 AFLP primer pairs combinations, 46 SSRs and 9 RFLP probes. Linkage analysis allowed the construction of 86 cosegregation groups for 'R 570' and 105 cosegregation groups for 'MQ 76/53' encompassing 424 and 536 single dose markers respectively. The cumulative length of 'R 570' map was 3144 cM. The cumulative length of 'MQ 76/53' map was 4329 cM. Field trials and greenhouse trials using different inoculation methods were conducted in order to characterize the resistance of the 198 progeny clones from the bi-parental population. The distribution of disease scores observed in all those trials was highly unbalanced toward the resistant parent indicating the segregation of multiple dominant resistance factors. A QTL detection was performed using the 1666 available markers allowing the identification of a few genomic zones with small effects. The structure of linkage disequilibrium in the population of 74 cultivars was investigated using 1626 AFLP markers, among which 408 have known positions on 'R 570' genetic map. This analysis confirmed that linkage disequilibrium in sugarcane extends over distances of tenth of centiMorgans but drops sharply for distances over 5 cM. This order of magnitude makes genome-wide association studies achievable in sugarcane. The association study performed in the population of 74 cultivars (constituted of two subpopulations, one highly susceptible to smut and the other highly resistant to smut) revealed interesting haplotypes associated with resistance. Two QTLs have been detected through both approaches. The progress obtained toward a better understanding of the genetic determinism of sugarcane resistance to smut is modest. The potential of association studies in sugarcane appeared interesting although much more markers and an extended population would have to be used to make the most of it.