Oral Communication Abstract – 7.08

A HIGH RESOLUTION INTRA-SPECIFIC LINKAGE MAP OF PEPPER (*CAPSICUM ANNUUM* L.) BASED ON RILs AND IDENTIFICATION OF THE MOST INFORMATIVE INDIVIDUALS

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Capsicum annuum, RILs, intra-specific linkage map, selective genotyping

Cultivated *Capsicum* species (*Solanaceae*) are diploid with a total number of 24 chromosomes (2n=2x=24). The haploid DNA content was estimated to 2.76 pg and the genome size to 2702-3420 Mbp per haploid genome. Several pepper linkage maps have been constructed by using *C. annuum* intra-specific crosses as well as inter-specific crosses between *C. annuum* and *C. chinense* or *C. annuum* and *C. frutescens.*. Inter-specific progenies allow the detection of higher level of polymorphisms, facilitating map construction and alignment compared to intra-specific progenies; however, low fertility, segregation distortion, and major structural rearrangements limit reliability of linkage analysis and its use for breeding purposes. An integrated map based on the pooled data from six distinct intra- and inter-specific progenies and consisting of 2262 markers covering 1832 cM was developed (Paran *et al*. 2004*, Molecular Breeding* 13:251-261). Map integration improved the marker density and genome coverage. However, the confidence in marker relative position and order remained low because of a weak integration of progeny specific markers, particularly between intra- and interspecific maps.

Here we report on the construction of a high resolution intra-specific linkage map of pepper (*C. annuum* L.) using a population of 297 recombinant inbred lines (RILs: F5). The parents were the large fruited inbred line "Yolo Wonder" and the hot pepper line "Criollo de Morelos 334" that is used by breeders as a source of resistance to multiple diseases. A set of 597 molecular markers (507 AFLPs, 40 SSRs, 18 RFLPs, 20 SSAPs, 12 STSs) were used to generate the map; by using thresholds of LOD>8 and r<10 cM, 499 were assigned to forty nine linkage groups of which 14 large groups, including from 10 to 60 markers, and 35 small groups, including from 2 to 9 markers. The map covered 1857 cM with an average map distance of 5.71 cM. Twenty-three linkage groups, which comprise 409 markers (68%) and cover 1553 cM, were assigned to the twelve haploid pepper chromosomes, by alignment with previous maps; twenty-six linkage groups, covering 308 cM, remained unassigned. The chromosome framework map was constituted of 251 markers with a high order confidence (LOD>4) and an average map distance of 6.18 cM. By applying the MapPop software (Brown and Vision 2000, http://www.bio.unc.edu/faculty/vision/lab/mappop/) subsets of 141 and 93 individuals were identified as being the most informative for future mapping studies and phenotypic tests. The subsets were tested for QTL mapping accuracy of three traits: (i) Lfw (logarithm of fruit weight), (ii) Axl (plant axis length) and (iii) Rec (receptivity) which is a

component of resistance to *Phytophthora capsici.* Only for Rec, the same major effect QTL at the same position was detected when 141 or 93 individuals were tested instead of 293. On the contrary, the number of QTLs for Lfw decreased from 9 to 3 and for Axl from 5 to 1, when the number of individuals included in the analysis decreased from 293 to 141 and to 93. In every case, this resulted from a decrease in the LOD score values of QTLs when reducing the population size whereas the determination (R^2) values remained stable or even increased. The present results show that MapPop software represents an alternative strategy to identify representative subsets of individuals useful for mapping studies but, as expected, by increasing the number of individuals in analysis, a higher level of accuracy is observed.