Mérida Session III (MSIII)

MSIII.1 E. Ritter: Comparative linkage mapping in three guava mapping populations and construction of an integrated reference map in guava

Comparative linkage mapping in three guava mapping populations and construction of an integrated reference map in guava

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Individual and combined parental linkage maps have been constructed in three mapping populations (Enana x N6, Enana x Suprema Roja, and Enana x Belic L-207) based on AFLP and SSR markers. Between 100 and 120

AFLP primer combinations (PCs) were analysed in each population, generating between 700 and 1100 segregating AFLP fragments. The distribution of parent-specific and common markers indicated that Enana is slightly less heterozygous than the other parents and that all parents share a considerable gene pool. In addition, between 50 and 200 SSR PCs were analysed for linkage mapping in the populations. Polymorphic DNA fragments were scored for presence and absence. Linkage analysis between marker fragments, estimation of recombination frequencies, and determination of linear order between linked loci including multipoint linkage analysis were performed with the MAPRF program. Firstly, linkage groups were constructed based on fragments specific to either parent in each population. Linked fragments were arranged into linkage groups using a minimum, commonly accepted LOD threshold of 3.0 between consecutive markers. In all mapping population 11 linkage groups (LGs) corresponding to the 11 chromosomes of the haploid guava genome were obtained. Based on the available SSR markers a combined parental linkage map of each mapping population was produced using mainly as anchor points allelic SSR fragments but also some common fragments having recombination values of zero with individual markers from both parents. These combined maps contain between 500 and 1000 markers and have lengths of 1500 to 2200cM each. Individual linkage groups vary between 150 and 240 cM in length and contain between 35 and over 100 markers each. Finally, an integrated guava reference linkage map was established by combining the maps derived from the three mapping populations. For this purpose these maps were aligned und unified on the basis of co-dominant SSR and common AFLP markers which were placed onto the available linkage maps. In this way we obtained one integrated guava reference map with a high marker density of more than 1500 markers.