Abstract:
Peach (Prunus persica) is the model species of the Rosaceae family with an estimated genome size of 265 Mb. Among all the Prunus (almond, apricot, cherry and plum), peach has low levels of genetic variability due to lack of a functional self-incompatibility system. This limits the current peach breeding to prolonged shelf life, fruit quality and disease resistance. One way to enrich the peach genome would be to introgress the novel alleles from wild and cultivated Prunus species. For this we started the approach Marker Assisted Introgression (MAI), for introgression of alleles from almond “(Texas)” into peach “(Earlygold)” in a short time frame of 9-10 years. A initial survey of genetic analysis was done using the prIL (pre-introgression line) set with low number of almond introgressions, where some interesting almond alleles providing powdery mildew disease resistance and red fresh color were identified. We are developing a introgression line (IL) collection of almond genomic fragments in the peach genome background. Currently we have a collection of individuals with 2 introgressions covering the almond genome, and two sets of lines with one introgression in heterozygosis and homozygosis covering 87% and 60% of the almond genome, respectively. Although, there were some major problems encountered that delayed the progress of the IL collection, like cytoplasmic male sterility (forced us to change the direction of crossing leading to an additional generation) and the embryo rescue process, as a consequence of the use of an early peach, the IL collection is now ready to be used and become a resource for genetic analysis in Prunus and as a tool to breed improved peach cultivars. The main characteristics of the IL collection and the results with several characters of simple genetic inheritance will be discussed.