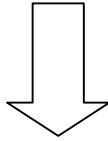
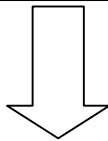


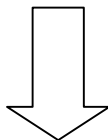
Step 1. Select DNA of parents and six individuals of the cross, exhibiting much morphologic difference among them



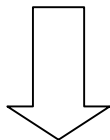
Step 2. Choose 96 SSR primer pairs to amplify the 8 DNA samples above. Each pair of primers can amplify only a single locus in the apple genome according to the published references



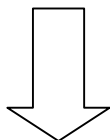
Step 3. Identify and choose these primers that can amplify two alleles in each parent presenting the segregation style of 'abxcd'



Step 4. Select a few identified 'abxcd'-style primer pairs, whose amplicons were mapped in the different linkage groups in the apple genome according to the published references, to amplify all DNA of the F<sub>1</sub> progenies and parents of the cross



Step 5. Identify the potential triploid plants, whose SSR alleles have the segregation pattern of 'abc' or 'abd'



Step 6. Select more co-dominant markers and use cytological methods to make a confirmation test on the potential triploid seedlings identified above