Construction of Integrated High-density Genetic Linkage Map in ‘Whangkeumbae’ (Pyrus pyrifolia) × ‘Minibae’ (P. hybrid)

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Microarray has been used for genotyping of single nucleotide polymorphisms (SNPs) in diverse crops. Axiom 70K Pear SNP array has been developed for genetic study in pear (Pyrus spp.). The present study was performed to construct high-density genetic linkage map using Axiom 70K Pear SNP array. The Axiom 70K Pear SNP array was applied to 182 F1 individuals from a cross between ‘Whangkeumbae’ (P. pyrifolia) and ‘Minibae’ (P. hybrid). The 8,662 array-SNPs were detected and used for construction of genetic linkage map. For the construction of high-density genetic linkage map, genotyping-by-sequencing (GBS)-SNP, insertion/deletion (InDel), and simple sequence repeat (SSR) markers developed in previous study were also used. Linkage analysis was performed using MapChart 5.0. MapChart was used to visualize genetic linkage map. Genetic linkage map consisted of 1,197 markers, including 454 array-SNP, 710 GBS-SNP, 17 InDel, and 16 SSR markers. The genetic linkage map covered genetic distance of 2,298 centi-Morgan (cM), with an average marker density of 1.9 cM. The number of markers on linkage group (LG) varied from 50 (LG13) to 106 (LG13). The genetic distance ranged from 97.8 (LG4) to 190.9 cM (LG11). In comparison with previously constructed based genetic linkage map based on GBS-SNP markers, genetic distance was increased and average distance between markers got denser. This integrated map could provide physical location of mapped markers and would be useful tool for identification of quantitative trait loci.