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**The integration of genomics approaches for lettuce (*Lactuca sativa* L.) improvements on the disease resistances and other agronomic qualities.**

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**Abstract**

The aim of this research is to improve Korean lettuce varieties in terms of Fusarium wilt, bolting under hot weather and nutritional function applying genomics approaches. To find related gene/molecular markers, we selected 96 lettuce varieties which are popular in domestic fresh vegetable markets. To construct frame works of the genomic approaches, we exploited GBS(Genotyping by Sequencing) and found total 61,407 SNPs from lettuce whole genomes (MAF>0.02). We observed that Three SNPs array per 100kb of lettuce genome. Average LD decay is expected to expand up to 3.9M(million)bp. Thus, we concluded that about 104 SNPs exist within a LD, which is sufficient to use GWAS(Genome-wide Association Study) to explore the useful gene/molecular markers. In addition, we optimized mass screening method to evaluate disease resistance levels against *Fusarium wilt* and are testing the bolting sensitivity during summer growing season for those lettuce allele mining set.

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