

## Variation Block Browser for Functional Crops

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### [Introduction]

In genomics era, genetic assisted breeding is more effective tool, which improves the crops cultivation from different environmental factors and prevent from revenue loss. Cross breeding of different phenotypes is resulted with new cultivars by the DNA recombination. Those, Cultivars are evolved with low levels of genetic diversity in specific genome loci with high recombination rate. Those regions are filled with high dense of nucleotide variations, these regions are called as “Variation Blocks” (VB). These variations blocks are highly interlinked with the phenotypes.

### [Materials and Methods]

In this study, we established barcode system approach based on insertions/deletions (InDel) markers for Cucumber (*Cucumis sativus*) as model system. Firstly, 564 VBs were mined by analyzing whole genome data of two Cucumber cultivars (CS11 and CS12) for transferability to VB-specific InDel markers. Secondly, 51,376 putative InDels in the VB regions were identified for the development of Cucumber barcode system. In addition, the changing of the VBs in a chromosomal level can be quickly identified due to investigation of the reshuffling pattern of the Cucumber cultivars.

### [Results and Discussion]

This browser is more useful for detecting the recombinant loci and trait associated marker, which are more effective for agricultural traits and to identify agronomical important genes, which could use for gene cloning applications. Moreover, VB browser facilitate genome wide VB visualizations using genome browsers. VB browsers is publicly available as Cropsquare (<http://cropsquare.net/index.do>).

### [사사]

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