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Genome dynamics of the recently duplicated regions in soybean [*Glycine max* (L.) Merr.]

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A single recessive gene, *rxp*, on linkage group (LG) D2 controls bacterial leaf pustule resistance in soybean. We identified two homoeologous contigs (GmA and GmA') composed of five bacterial artificial chromosomes (BACs) during the selection of BAC clones around *Rxp* region. With the RIL population from the cross of Pureunkong and Jinpumkong 2, SNP genotyping was able to locate GmA' approximately 1.9 cM away from Satt684 on LG A1. Based on information in the Soybean Breeders Toolbox, and our results, parts of LG A1 and LG D2 share duplicated regions. Alignment and annotation revealed that many homoeologous regions contained kinases and proteins related to signal transduction pathway. Interestingly, inserted sequences from GmA and GmA' had homology with transposase and integrase. Estimation of evolutionary events revealed that speciation of soybean from *Medicago* and the recent divergence of two soybean homoeologous regions occurred at 24 and 5 million years ago, respectively. In distribution of the gene duplication as a function of K_s, the first secondary peak (mode K_s = 0.10 to 0.15) followed by two smaller bulges were displayed between soybean homologous regions. Thus, soybean genome is a diploidized paleopolyploid.
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Characterizations of inclusion body induced by CMV 3a expressed in *E. coli*

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Inclusion bodies occur naturally in prokaryotic cells, but are particularly common when foreign proteins are overproduced in bacterial systems. This study indicates that the plant disease virus protein CMV 3a (cucumber mosaic virus movement protein) forms perfect inclusion bodies in *E.coli* via the expression of recombinant proteins, and the results of confocal laser scanning showed that expressed inclusion bodies with fluorescent protein GFP are localized within *E.coli* at two poles at different rates. Via continuous cell division, these *E.coli* evidence biofilm-like forms and evidence characteristics such as profound resistance against external environmental stressors. These results indicated that inclusion bodies might cause non-toxic effects in the cellular metabolism of bacterial cells. We assessed the effects of the overexpression of a cucumber mosaic virus movement protein (CMV 3a) in cells via confocal laser scanning, in order to assess the generality of this finding. *E. coli* forms aggregates, such as biofilms, in order to help with adaptation and protection against environmental stresses. The tendency for cell-to-cell attachment was increased significantly. Bacteria are capable of communicating between themselves and unifying their metabolic functions, which can, as a result,be greater than those of each individual cell.[this study was supported by a Grant from the BioGreen 21 program (20070301034019) from the Rural Development Administration in Korea]