P5

Strategy of mitochondria transformation and mass production of mitochondrial lipid transfer protein as for prospective antifungal agents in plant

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Our group successfully isolated and characterized mitochondrial specific genes which are designated to *Cdf*s (mitochondrial transfer protein, CDF). The new mitochondrial targeting vector (pMTCG) for this research constructed using the a TPI (Triose-phosphate isomerase) promoter and transcriptionally fused two genes (*Cdf*3 and GFP genes). With this information, we are sure that both genes are expressed in the mitochondria under the one TPI promoter in yeast. As for plant mitochondria transformation, a new mitochondria targeted vector (pTA7002 vector) was constructed. In this vector, *Cdf*3 and GFP genes are transcriptionally fused and driven by a DEX gene which is a inducible promoter by dextran. This is another evidence that artificial operon with *Cdf* and GFP in plant tissues can be expressed and secreted in a mitochondrium correctly. In conclusion, two types of eukaryotic mitochodrial vectors (pMTCG and PTA7002) are constructed both either with constitutive or inducible promoter and transcriptioanlly fused structural genes (from *Cdf*3 and GFP) which are correctly and efficiently expression in a both yeast and plant. With this information, over one genes can be expressed artificially at the same time which will be very useful for several antibody protein production in one mitochondrium.

P6

Development of CpG Island Search Tool

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CpG is the pair of nucleotide C and G, appearing successively, in this order, along one DNA strand. It is known that due to biochemical consideration CpG is relatively rare in most DNA sequences. However, in particular subsequences, which are a few hundred to a few thousand nucleotides long, the couple CpG is more frequent. These subsequences, called CpG islands, are known to appear in biologically more significant parts of the genome. The ability to identify CpG islands along a chromosome will therefore help us spot its more significant regions of interest, such as the promoters or 'start' regions of many genes. In this context, I developed CpG island search tool of which graphical user interface may facilitate end-users to pinpoint CpG islands on genomic DNA sequences. Even though a sliding 200 base pair window algorithm was used for this tool according to the criteria of CpG islands described by Gardiner-Garden and Frommer, two more parameters - the number of CpGs in the 200 bp (and the value of the gap between adjacent CpG islands - were added to implement this tool. Graphical user interface enables end-users to change the default parameter values into the ones tailored to their analysis intent.