F251

Statistical Analysis of Arabidopsis T-DNA-flanking Sequences

Hyung Seok Choi[P], Sunghwa Choe[C]

School of Biological Sciences, College of Natural Science NS70, Seoul National University, Seoul 151-747

Agrobacterium-mediated T-DNA transformation of plant genome has been instrumental in tagging and subsequent isolation of genes important in a plant life cycle. Underlying hypothesis of using T-DNA in plant functional genomics is that the T-DNA insertion occurs randomly in plant genomes. To test this hypothesis, we analyzed the T-DNA flanking sequences isolated by and available in the Salk Institute Genomic Analysis Laboratory (SIGnAl) database. Examining the data of 29,084 Arabidopsis genes containing insertion information of approximately 120,000 T-DNA insert lines and functional annotations of the genes revealed that 70% of the 29,084 genes have at least one T-DNA insert, whereas 8760 genes are still left without an insert. This is quite surprising, because statistically the 120,000 lines should cover more than 95% of the genes with an insertion. This result led us to further analyze if the T-DNA insertion events truly take place randomly in the genome. Arabidopsis genome consists of 56.8 Mb (48.4%) of genic region and 60.5 Mb (51.6%) of intergenic region. Mappingthe T-DNA insertion lines to the genome showed that 55% of the 120,000 T-DNA lines landed on the genic region, and 45% was assigned to intergenic regions. Nonparametric correlation tests indeed revealed that T-DNA insertion events occurred preferentially in the genic regions. Interestingly, the gene At2g25610 annotated as a putative vacuolar ATP synthase proteolipid subunit possess as many as 622 T-DNA inserts, again, suggesting a preferred T-DNA insertion region in the genome.

F252

벼 글루탐산 탈탄산효소 유전자의 클로닝 및 GABA 생산 능력이 증진된 벼 계통 개발 전략

오석홍[P], 이인태[1], 최원규[1], 박명렬[2], 윤성중[2]

[P1]우석대학교 생명공학부, 전주 565-701; [2]전북대학교 생물자원과학부, 전주 561-756

GABA(-aminobutyric acid) 고함유 쌀 생산 전략의 일환으로 글루탐산을 GABA로 전환하는 벼 (*Oryza sativa* L.) 글루탐산 탈탄산효소(glutamate decarboxylase, GAD) 유전자 (OsGAD, OsGAD1, OsGAD2)를 벼 뿌리 cDNA libraries와 현미에서 추출한 RNA로부터 분리하였다. 뉴클레오티드 서열분석 결과 OsGAD 클론은 505개 아미노산을 코딩하는 하나의 open reading frame (ORF)을 포함하는 총 1,712 bp로 구성 되어 있었다. OsGAD ORF로부터 얻어진 505개 아미노산 서열은 OsGAD1과는 67.7%, OsGAD2와는 61.9% 서열 동질성을 보였다. 이들 유전자를 대장균용 발현 벡터인 pVUCH와 pKK388 플라스미드에 클로닝하여 발현시킨 후 효소활성을 측정하여 본 결과 모두 글루탐산 탈탄산효소 활성을 보였고, 칼슘과 칼모듈린에 의하여 그 활성화 정도가 달라짐을 알 수 있었다. 또한 벼 형질전환체를 생산하기 위하여 rice endosperm-specific promoter를 클로닝하였고, 이 promoter와 OsGAD, OsGAD1, OsGAD2 유전자가 각각 삽입된 재조합 벡터를 제작 하고 있다. 이 재조합 발현 벡터를 이용하여 GABA 생산 능력이 증진된 벼 계통을 개발할 계획이다. (This work was supported by Korea Research Foundation Grant, KRF-2002-042-F00005).

F253

AtBAT1 (Binding Ability to Telomeric DNA), a Novel Telomeric-repeat Binding Protein of *Arabidopsis*, Binds to Both Human and Plant Telomeric Repeats

Won-Kyung Lee[P], Moo Gak Hwang[1], Kyunghye KIM[1], Myeon Haeng Cho[C]

Department of Biology, Yonsei University, Seoul 120-749

Telomeres are nucleoprotein complexes at the physical ends of linear eukaryotic chromosomes for a protective cap. There are several genes in *Arabidopsis thaliana* known to encode plant telomere binding proteins. We have recently identified AtBAT1 containing a single Myb domain similar to those in AtTBP1 and hTRF1. Despite its sequence similarity, its Myb domain is located at its N terminus and Histone H1/H5-like domain is located at the center of the AtBAT1, which shows similar protein architecture to that of hTRF1. Northern blot analysis indicated that *AtBAT1*gene is expressed ubiquitously in *A. thaliana* and transiently expressed the GFP-fused AtBAT1 was found mainly in the nucleus of onion epidermal cells. To elucidate DNA binding property of AtBAT1, we have expressed the Myb domain of AtBAT1 in *E. coli*. Expressed GST-fused Myb domain was capable of binding specifically to the double-stranded plant telomeric DNA ([TTTAGGG]n). However, it showed much higher binding affinity to human telomeric DNA ([TTAGGG]n). These data suggest that *AtBAT1*encodes a putative plant telomere binding protein(TBP) which constitutes telomere structure. Furthermore, as it also binds to human telomeric repeats with higher affinity, itis a novel protein with distinct properties distinguished from those of known AtTBPs. Possible role of AtBAT1 in *Arabidopsis*will be discussed. [Supported by grant from KRF (2002-015-DP0415)]

F254

Identification and Characterization of Antiviral Peptide in Various Potato Cultivars

Hongxian Li[P], Hyeonsook Cheong[C], Yoonkyung Park[1], Haktae Lim[2]

[PC]Department of Genetic Engineering, Chosun University, Kwangju 501-759; [1]Research center for Proteineous Materials and Department of Pharmacology, School of Medicine, Chosun University, Kwangju 501-759; [2]Kangwon National University, Chuncheon 200-701

PLRV (Potato Leafroll Virus), PVX (Potato Virus X), PVY (Potato Virus Y) are major viral pathogen in potato(*Solanum tuberosum*) diseases. We infected PVX and PVY onto wounded potato leaves because the physical barrier of the cell wall had been breached by injury, thereby acilitating entry of the virus. Virus infected plants using sap-inoculation(virus ample with 0.1M phosphate buffer) method showed various symptoms including mosaic, yellowing, necrosis, mottle, vein clearing, vein bending or changeless-ness etc. We have used Enzyme-Linked Immunosorbent Assay and PCR for virus detection and screening for virus-resistant potato cultivars from 13 potato species including *Golden, Early, Winter, Purple, Alchip*. We selected new virus-resistant potatoes in which we assume that there are antiviral peptides or antibacterial peptides among expressing changelessness symptom potatoes. To minimize the damage ofpotato viruses, CA(1-8)-MA(1-12), PMAP-23, SMAP-29, HP (2-20) and analogous peptides can be applied to sensitive to virus infected potato cultivars. Those peptides can be overproduced by transformation to the plants to get virus-resistant potatoes.