

## (구두-2)

### 고려인삼으로부터 Peroxidase 유전자의 Cloning 및 Activity

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#### ABSTRACT

A peroxidase[E.C.1.11.1.7] is very important enzymes,e.g., as preventive antioxidants. The function is connected with growth and specialization of plant. It makes from the peroxidase and other product to save itself When a plant have been under stress of environment . A class III peroxidase cDNA was isolated from the flower bud of *Panax ginseng* C.A. Meyer and named *PgPrx3*. The *PgPrx3* is an ORF(open reading frame) of 1,065 bp and a amino acid of 355 residue. Used BioEdit software to compare the *PgPrx3* amino acid sequence with other plants which have already known a result of identity was *Spinacia oleracea*(70%), *Vigna angularis*(71%), *Nicotiana tabacum*(69%) and *Linum usitatissimum* (65%). The peroxidase of *Vigna angularis* has high homology relationship with ginseng. For that reason, the *PgPrx3* is a member of class III peroxidase family.

Key word : class III peroxidase , *Panax ginseng* .

#### 연구목적

Peroxidase는 세포의 성장과 분화를 조절하는 중요한 효소로 알려져 있으며, indole-3-acetic acid의 산화(Welinder 1985), 환원형 pyridoxal과 관련된 화합물의 산화(Van Huystee 1987), lignification 및 병원체에 대한 방어 (Laulan et al. 1985) 등의 기능을 가지고 있다. 본연구는 만병통치라 할 수 있는 생약(정후섭,1979, 이종철 등, 1986)으로 불리우는 고려인삼에서 peroxidase 유전자를 cloning하여 재도입함으로서 peroxidase의 activity를 조절함으로서 항 stress 내성 인삼을 생산하고자 수행하였다.

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결과

고려인삼 flower bud에서 mRNA를 분리하여 cDNA library를 제작하고 EST 분석한 결과, 인삼 flower bud의 cDNA library로부터 한 개의 full length cDNA를 확보할 수 있었다. 인삼 peroxidase유전자 *PgPrx3*는 길이가 1,192bp 이고 1,065bp의 open reading frame을 가지고 있었다. 단백질 번역부위(open reading frame)가 1번째 염기 ATG 코돈으로 시작되어 1065번째의 TAA 코돈으로 종결되었으며 355개의 아미노산으로 구성되었다(Fig.1).

Fig. 1 . A cDNA and deduced amino acid sequence of *PgPrx3* isolated from panax ginseng. The putative polyadenylation signal is underlined. The asterisk is indicated the stop codon.

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Peroxidase3	STLTS-1S1L77777S	LISLLLYTHLEWSIAAT-Y-PDDEPPLAIDP-DPDPYKQ	58
Spinacia oleracea	ATAGC---FPPLVLSI-LICLGS-----	CGCTTGTTCGTTTGTGTTTGTGTTGCGTTCGTTG	59
Vigna angularis	SISSESSAALSVLSSV-LILTSVINCVALADPDTT	ATGTTTGTGTTGCGTTCGTTGCGTTCGTTGCGTTC	60
Nicotiana tabacum	SITLSSAASLLLIL-WWYFQT-----	TAACGTTGTTGCGTTCGTTGCGTTCGTTGCGTTC	55
Linum usitatissimum	PISSR-WVLLTIALSAVLFAST-----	TAACTTGTGTTGCGTTCGTTGCGTTCGTTGCGTTC	54
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Peroxidase3	IXXIX-1S1L77777S	IXXIX-1S1L77777S	117
Spinacia oleracea	WQVQCSLTLAQLGLLHED-FPVCGTCSWLDGAGS-----	WQVQCSLTLAQLGLLHED-FPVCGTCSWLDGAGS-----	117
Vigna angularis	XXVXQSD-----LAMMILNLLHED-FPVCGTCSWLDGAGS-----	XXVXQSD-----LAMMILNLLHED-FPVCGTCSWLDGAGS-----	119
Nicotiana tabacum	COVPPDQ-1S1L77777S	COVPPDQ-1S1L77777S	114
Linum usitatissimum	XVXVPPDQ-1S1L77777S	XVXVPPDQ-1S1L77777S	114
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Peroxidase3	1S1L77777S	1S1L77777S	177
Spinacia oleracea	DPDPAAPL-1S1L77777S	DPDPAAPL-1S1L77777S	171
Vigna angularis	TRIGGLERSCSPCPTT1S1L77777S	TRIGGLERSCSPCPTT1S1L77777S	174
Nicotiana tabacum	ISPELDPDCCVPSDIT1S1L77777S	ISPELDPDCCVPSDIT1S1L77777S	174
Linum usitatissimum	DPLAIPAKCPCPDKP1S1L77777S	DPLAIPAKCPCPDKP1S1L77777S	174
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Peroxidase3	1S1L77777S	1S1L77777S	237
Spinacia oleracea	PFPSGCCD-1S1L77777S	PFPSGCCD-1S1L77777S	231
Vigna angularis	PFPSGCCD-1S1L77777S	PFPSGCCD-1S1L77777S	230
Nicotiana tabacum	PFPSGCCD-1S1L77777S	PFPSGCCD-1S1L77777S	234
Linum usitatissimum	PFPSGCCD-1S1L77777S	PFPSGCCD-1S1L77777S	234
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Peroxidase3	1S1L77777S	1S1L77777S	297
Spinacia oleracea	DPICPDTTDD-1S1L77777S	DPICPDTTDD-1S1L77777S	291
Vigna angularis	DPICPDTTDD-1S1L77777S	DPICPDTTDD-1S1L77777S	290
Nicotiana tabacum	DPICPDTTDD-1S1L77777S	DPICPDTTDD-1S1L77777S	294
Linum usitatissimum	DPICPDTTDD-1S1L77777S	DPICPDTTDD-1S1L77777S	293
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Peroxidase3	1S1L77777S	1S1L77777S	351
Spinacia oleracea	DPDPAAPL-1S1L77777S	DPDPAAPL-1S1L77777S	348
Vigna angularis	DPDPAAPL-1S1L77777S	DPDPAAPL-1S1L77777S	348
Nicotiana tabacum	DPDPAAPL-1S1L77777S	DPDPAAPL-1S1L77777S	351
Linum usitatissimum	DPDPAAPL-1S1L77777S	DPDPAAPL-1S1L77777S	351
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Peroxidase3	LG7-354		
Spinacia oleracea	SQF-351		
Vigna angularis	IM-357		
Nicotiana tabacum	SKT-354		
Linum usitatissimum	ACER-355		

Fig. 2 . Comparison of the amino acid sequence of panax ginseng PgPrx3 with, Spinacia oleracea, Linum usitatissimum, Mercurialis annua,icotianatabacum.Amino acid sequences were aligned using the CLUSTALW program.