CHARACTERIZATION OF NPR1 ANKYRIN DOMAIN FROM

CHILLI PEPPER (*Capsicum annuum* L.) var Lotanbar

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BACKGROUND

Pepper Yellow Leaf Curl Disease Caused by Gemini-Virus



- Decrease of yield can reach up to 100%
- No effective control so far.
 High genetic variation.
 Transmitted by Whitefly













Genes Expressing During Gemini Virus Infection in Ca.



The PR genes Are More Expressed

ID	GENE NAME		Fold-chang	e
	Oxidative response	R / S	S / M	R / M
Pepper28784	CAT	0.94	3.67	3.48
Pepper25924	ANN4	1.07	7.42	7.98
Pepper30410	ANN1	1.11	4.26	4.74
Pepper28222	GST1	1.08	4.82	5.24
	Pathogenesis-related	protein		
Pepper00302	PR-5	0.97	25.05	24.37
Pepper27140	PR-1	1.25	14.22	17.89
Pepper31625	PR-1	1.11	16.08	17.89
	Ethylene and jasmoni	c acid		
Pepper01276	ACC	0.98	2.02	1.99
Pepper00009	EIN3	1.18	0.48	0.57
Pepper26071	OPR1	0.90	2.76	2.51
Pepper31749	LOX1	0.99	3.48	3.47
Pepper32274	HEL	1.08	2.25	2.43
Pepper32368	b-Chi	1.04	39.59	41.35
	Others			
Pepper05849	RRP1	0.96	69.59	66.96



Source: Góngora-Castillo et al. (2012)

Why NPR1?



Source: Mukhtar, et al. (2009)

NPR1 Regulation in Plant Defense System

(C) SAR



Source: Mukhtar, et al., (2013)

Protein-Protein Interaction During GV Infection

Identity	Function	Selection criteria	Reference
Group B (promote earlier infection)			
Bearskin 2 (BRN2)	Transcription	Phloem over-expression	[89]
Importin alpha isoform 4 (IMPA-4)	Transport	CP interaction	[71]
Lactoylglutathione lyase (GLO1)	Stress	C3 Interaction	Hericourt et al. (in preparation)
Replication protein A32 (RPA32/RPA2)	DNA metabolism	Rep interaction	[32]
Dehydration responsive 21 (RD21)	Stress	V2 interaction	Hericourt et al. (in preparation)
RING-type E3 ubiquitin ligase (RHF2A)	Protein modification	Transactived by TrAP/C2	[82]
Ubiquitin activating enzyme (UBA1)	Protein modification	TrAP/C2 Interaction	Hericourt et al. (in preparation)
Group C (delay, reduce or prevent the infection)			
4-coumarate:CoA ligase (AT4CL1)	Metabolism	Phloem over-expression	[89]
Allene oxide cyclase (AOC1)	Metabolism	Phloem over-expression	[82]
Barely any meristem 1 (BAM1)	Protein modification	C4 interaction	Hericourt et al. (in preparation)
Coatomer delta subunit (<i>deltaCOP</i>)	Protein transport	C3 interaction	Hericourt et al. (in preparation)
COP9 signalosome subunit 3 (CSN3)	Protein modification	Cellular process	[90]
Geminivirus Rep A-binding (GRAB2)	Transcription	Rep interaction	[29]
Heat shock protein cognate 70 (HSC70)	Protein modification	Phloem over-expression	[82]
Nuclear acetyltransferase (NSI)	Signal transduction	NSP Interaction	[31]
Patatin-like protein 2 (PLP2)	Stress	Phloem over-expression	[82]
Shaggy-related kinase kappa (<i>SK4-1/SKK</i>)	Protein modification	C4 interaction	Hericourt et al. (in preparation)
SKP1-like 2 (ASK2)	Protein modification	Transactived by TrAP/C2	[9]

Source : Lozano-Dura´n ,et al, (2011)

Protein-Protein Interaction In Plant





MATERIALS AND METHODS

Materials and Methods







Domain Structure of NPR1 *Capsicum annum* var. Zunla



DOMAIN

NPR1 Structure of Capsicum annum var.Zunla

NPR1					
Access No.	DQ648785.1				
Size of NPR1 mRNA	2,191 bp				
Start Location in Chromosome 7	112,610,515				
End Location in Chromosome 7	112,636,367				
Size of NPR1 Genome	25,852 bp				
Exon Fragment 1	112,610,515 112,611,427 (912 bp)				
Exon Fragment 2	112,632,267 112,633,014 (747 bp)				
Exon Fragment 3	112,634,512 112,634,712 (200 bp)				
Exon Fragment 4	112,635,955 112,636,367 (412 bp)				

Specific Primers for NPR1 Gene

Primer ID	Sequence (5' - 3')	Length (nt)	Size of PCR product (bp)
Outer Forward	TTCCCCCTTTGCAGAGACAC	20	0000
Outer Reverse	CCTGCACCCACTTTGAGCTT	20	2626
Inner Forward	AACAAAGCTGCAGCAGACGA	20	607
Inner Reverse	CGCCTGCCATAGCAAGAGAT	20	687

RESULTS AND DISCUSSION



Cloning of NPR1 Fragment



Sequence Analysis

Bownload - GenBank Graphics

Capsicum annuum cultivar Zunla-1 chromosome 7, Pepper Zunla 1 Ref_v1.0, whole genome shotgun sequence Sequence ID: <u>NC 029983.1</u> Length: 222112641 Number of Matches: 1

Carrye 1	: 112032323 to	112032909 G	The states	Y NEXLI	Chread	
Score		Expect	Identities	Gaps	Strand	
1166.0	ofts(631)	0.0	641/645(99%)	4/645(0%)	Plus/ Plus	
Feature	regulatory pr	rotein NPR1	>			
Query	11	CTGTTGC	-ACATTTGTGGT-AAGCA	TGTGAGAGATTGCT	TTCAAGCTGCATTGAGATTA	67
Sbjet	112632325	CTGTTGCAR	AACATTTGTGGTAAAGCA	TGTGAGAGATTGCT	TTCAAGCTGCATTGAGATTA	112632384
Query	68	TTGTCAAGI	ICTAATGTTGATATTATA	ACCCTTGATAAGGC	TTTGCCTAATGACATCGTAA	127
Sbjct	112632385	TTGTCAAG	ICTAATGTTGATATTATA	ACCCTTGATAAGGC	TTTGCCTAATGACATCGTAA	112632444
Query	128	AACAAATTA	ACTGATTCACGCACTGAA	CTTGATCTACAAGG	GCCTGTAAACCATGGTTTTC	187
Sbjet	112632445	AACAAATTA	ACTGATTCACGCACTGAA	CTTGATCTACAAGG	GCCTGTAAACCATGGTTTTC	112632504
Query	188	CTGATAAAG	CATGTTAAGAGGATACAT	AGGGCATTAGACTC	TGATGATGTTGAATTACTAA	247
Sbjet	112632505	CTGATAAAO	CATGTTAAGAGGATACAT	AGGGCATTAGACTC	TGATGATGTTGAATTACTAA	112632564
Query	248	GGATGTTG	CTTAAAGAGGGGGCATACT	ACTCTAGATGATGC	GTATGCTCTCCACTATGCTG	307
Sbjet	112632565	GGATGTTG	CTTAAAGAGGGGGCATACT	ACTCTAGATGATGC	GTATGCTCTCCACTATGCTG	112632624
Query	308	TAGCATATI	IGCGATGCAAAGACTACA	TCAGAACTTTTAGA	TCTTGCACTTGCTGATGTTA	367
Sbjet	112632625	TAGCATATI	IGCGATGCAAAGACTACA	TCAGAACTTTTAGA	TCTTGCACTTGCTGATGTTA	112632684
Query	368	ATCACCAA	AATCCTAGAGGATACACG	GTGCTTCATGTTGC	TGCCATGAGAAAAGAGCCTA	427
Sbjct	112632685	ATCACCAA	AATCCTAGAGGATACACG	GTGCTTCATGTTGC	TGCCATGAGAAAAGAGCCTA	112632744
Query	428	AAATTATAG	STGTCCCTTTTAACCAAA	GGAGCTAGACCTTC	TGACCTGACATCCGATGGCA	487
Sbjet	112632745	AAATTATAG	TGTCCCTTTTAACCAAA	GGAGCTAGACCTTC	TGACCTGACATCCGATGGCA	112632804
Query	488	GAAAAGCAG	CTTCAAATTGCAAAGAGG	CGCACTAGGCTTGT	GGATTTTATTAAGTCTACAG	547
Sbjct	112632805	GAAAAGCAG	CTTCAAATTGCAAAGAGG	CGCACTAGGCTTGT	GGATTTTATTAAGTCTACAG	112632864
Query	548	AGGAAGGA	AAATCTGCTCCAAAGGAT	CGGTTATGCATTGA	GATTCTAGAGCAAGCAGAAA	607
Sbjet	112632865	AGGAAGGA	AAATCTGCTCCAAAGGAT	CGGTTATGCATTGA	GATTCTAGAGCAAGCAGAAA	112632924
Query	608	GAAGAGAT	CCACTACTTGGAGAAGCT	TCAGTATCTCTTGC	-ATGG 651	
Shict	112632925	GAAGAGATO	CACTACTTCCACAACCT	TCAGTATCTCTTCC	TATCC 112632969	

BLAST: 99% homology with NPR1 *Capsicum annum*

Domain Analysis of CbNPR1-Fragment.



NPR1 *Ankyrin Domain* Capsicum annum var. Lotanbar – *Arabidopsis thaliana*

	10	20	30	40	50	
NP 176610.1 regulatory protein	ACMKLLDRCKEI	IVKSNVDMVS	LEKSLPEELV	KEIIDRRKELG	LEVPKVK	
Lotanbar NPR1 Ankyrin Domain	ACERLLSSCIET	TVKSNVDTTT	I.DKAT.PNDTV	KOTTDSRTEL	TOGPVNHGFP	
Clustal Consensus	** •** * **	******	* • * • * * • • • *	*.* * * * **	* * * •	
Clustal consensus	•••••		••••••••	· · · · · · · ·		
NP_176610.1 regulatory protein Lotanbar_NPR1_Ankyrin Domain Clustal Consensus	110 ATDLLKLDLADV TSELLDLALADV :::**.*	120 NHRNPRGYTV NHQNPRGYTV	130 ••• ••• LHVAAMRKEP LHVAAMRKEP ********	140 	150 . ASASEATLEGR ARPSDLTSDGR *: * : **	
NP_176610.1 regulatory protein Lotanbar NPR1 Ankyrin Domain	210 . VPPSFAVAADE ASVSLAWGGBT					
Clustal Consonsus	4.4					
Clustal Consensus	•• ••• ••					
CbNPR1 1 ACERI	LSSCIEIIVKS	NVDIITLDK	ALPNDIVK	DITDSRTELI	DLOGPVNH	50
	1 1 - 1 1 1 1 1		: [] . : : []		. : . .	
AtNPR1 1 ACMKI	LDRCKEIIVKS	NVDMVSLEK	SLPEELVK	EIIDRRKELO	SLEVPK	48
CbNPR1 51 GFPD	HVKRIHRALDS	DDVELLRML	LKEGHTTL	DDAYALHYAN	AYCDAKT	100
	11:1:111	= = = =	111-11-1	. :	:-	
AtNPRI 49VKP	HVSNVHKALDS	DDIELVKLL	LKEDHTNL	DDACALHFA	AYCNVKT	96
CbNPR1 101 TSELI	DLALADVNHQN	PRGYTVLHV	AAMRKEPK	IIVSLLTKGA	ARPSDLTS	150
	- - :	<mark>.</mark> .	1111111	: : -	:- -	
AtNPR1 97 ATDLI	KLDLADVNHRN	PRGYTVL <mark>H</mark> V	AAMRKEPQI	LILSLLEKGA	ASASEATL	146
CbNPR1 151 DGRKA	LQIAKRRTRLV	DFIKSTEEG	KSAPKDRL	CIEILEQAER	RRDPLLGE	200
: . AtNPR1 147 EGRT2	. :. LMIARQATMAV	ECNNIPEQC	.:. . KHSLKGRL	CVEILEQEDR	REQIPRD	196
CbNPR1 201 ASVSI	A 206					
AtNPR1 197 VPPSE	A 202					

Cys216 and His334 are marked by blue and green color, respectively. The Ankyrin domain is underlined.

Secondary and Tertiary structure NPR1 Ankyrin Domain



C. annuum var Lotanbar (7 helices)





DNA-A like Genome of Pathogenic and Mild Isolate of GV



Jamsari, et al., (2013)

Jamsari, et al., (2016)

Protein Modelling of C1 (Rep) Protein from PSS14 –TD21



PepYLClpsV-14 Pathogenic PepYLCWSV/TD21 Mild Isolate

Docking of Ankyrin with C1 PSSWS vs TDWS



Predicted Docking Between Ankyrin with Pathogenic and Mild Replicase Protein







- 1. CaL-NPR1 ankyrin domain shares 78.1% similarity with AtNPR1, suggested that CaL-NPR1 gene is predicted to be homologous with Arabidopsis AtNPR1.
- 2. The conserved residue of Cys216 and His334 are suggested that they may have similar in structural conformation and related with Pathogenesis Related Protein.
- 3. Docking simulation with two different in pathogenic level indicated that Resistancy against GV might be related with interaction between GV-Rep protein with Ankyrin domain.

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Integrated Biological Sciences for Human Welfare

Dear Mr/Mrs Jamsari

Jember, April 20th 2017

On behalf of The 2nd ICOLIB committee, it is our pleasure to inform you that your paper entitled: **"CHARACTERIZATION OF NPR1 ANKYRIN DOMAIN FROM CHILLI PEPPER (***Capsicum annuum* **L.)**" has been accepted to be presented in Plenary Session of The 2nd ICOLIB 2017. You are requested to submit the full paper trough "Online paper Submission" in the ICOLIB homepage by June 30 2017 and to arrange the payment (Invoice is attached). Please follow the guidelines as mentioned in our website: <u>http://icolib.unej.ac.id</u>

To those DAAD alumni, please fill the alumni DAAD form which can be downloaded at http://icolib.unej.ac.id/?page_id=466 *)

We look forward to having you participate in this upcoming seminar and present your work.

Sincerely,

Purwatiningsih, Ph.D

Chairwoman of The 2nd Internasional Conference of Life Science and Biotechnology

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