

Examination of Pungency Characteristics in Pepper by 'Option 1' Approach

Seung In Yi¹, Choong Jae Lee², Eun Hee So¹, Yong Sham Kwon¹, Byung Dong Kim²

¹Variety Testing Division, National Seed Management Office, Suwon 443-400, Korea.

²Department of Plant Science, College of Agriculture and Life Sciences, and Center for Plant Molecular Genetics and Breeding Research, Seoul National University, Seoul 151-921, Korea.

NSMO www.seed.co.kr

- No. 1 vegetable crop in Korea

- Seed: 30 million US\$ (2005)
- Product: 1.5 billion US\$ (2004)

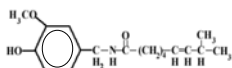
- No. of registered variety for marketing

: 1,132 (include duplicates)

- DUS testing in 2006

- 1st year: candidate var. 20, comparing var. 14
- 2nd year: candidate var. 24, comparing var. 17
- 3rd year: candidate var. 2, comparing var. 1

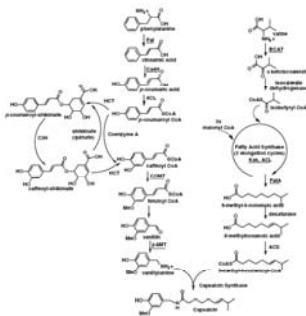
- Pungency is the most important trait in pepper
- Two types of pepper(*Capsicum annuum* L.)
 - chili pepper: hot
 - sweet pepper(paprika, bell pepper): non-hot
- Pungency level is proportion to the content of capsaicinoids



Chemical structure of capsaicin(C10)

- **Taste test:** quick and cost effective but give some pain to tester
 - TG/76/8(pepper): characteristic No. 45 (absent or present)
- **HPLC:** accurate but cost demanding with special equipments
- Scoville Heat Unit (Dilution test, Chile Pepper Institute, New Mexico State University), GC

Condensation of head and tail: phenylpropanoid metabolism (head, left) and fatty acid synthesis (tail, right)



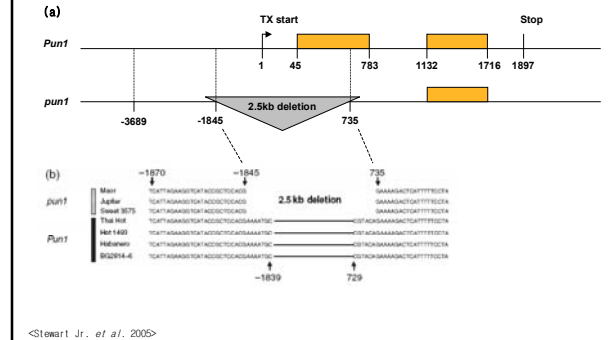
- Two factors for pungency phenotype

- genetics: qualitative and quantitative type
- environment: water potential, temperature...
- genotype-by-environment

- A single dominant gene, *Pun1(C)*

- *Pun1/Pun*, *Pun1/pun1* : pungent
- *pun1/pun1*: non-pungent

- **Mapping data** (Kim *et al.* 2001)
 - Co-localization of SB2-66 with *Pun1* locus : co-segregation with pungency
 - A candidate gene for Capsacin synthase
- **Genome structure and expression** (Stewart Jr. *et al.* 2005)
 - Presence/absence of a deletion in recessive/dominant allele
 - Transcript and protein expression is placenta specific and regulated with fruit development
- ❖ ***Pun1* locus in pepper encodes a pupative acyltransferase(AT3)**

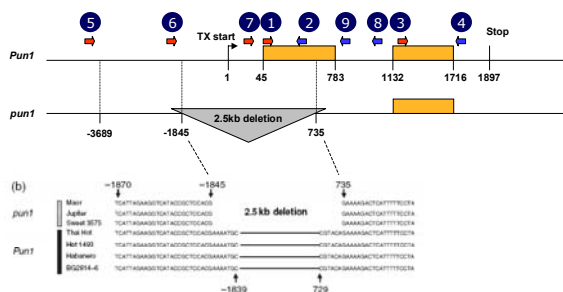


- **Pungency in Pepper: a single dominant gene *Pun1/Pun*, pungent; *pun1/pun1*, non-pungent**
- **Identification of *Pun1(C)* locus on Ch. 2 = AT3, a putative acyltransferase**
- **Presence of available marker system ?**

Possible Option 1 model ???

Primer name	Oligo nucleotide sequence	Tm (°C)	Size (nt)
CSF1	5'- ATG GCT TTT GCA TTA CCA TCA - 3'	54.4	21
CSR2	5'- CCT TCA CAA TTA TTC GCC CA -3'	55.2	20
CSF3	5'- CCA ACA AGG GCA GAA GTT GT -3'	53.8	20
CSR4	5'- TCA AAC ACC ACA AAA GAC TTG G -3'	54.0	22
BF5	5'- CCA TGA CCA CAT CAT TTT GG -3'	53.0	20
BF6	5'- GAA AGA TCC GAC CTC GTC AA -3'	53.7	20
BF7	5'- GGG GTT GGG TAG AGG TTG TT -3'	54.0	20
BR8	5'- TGA CAC CAA TAA GTG GAG TGC T -3'	53.4	22
BR9	5'- GAC AAA CAA TAA TGG ACG ATG G -3'	53.2	22

<Lee *et al.* 2005>



- **136 accessions mostly covered by DUS testing**
- **Pungency type:**
 - Ripened red fruit for spice
 - Young green fruit for fresh consumption or processing: 13
 - Ornamental type (inbred): 2
 - Self-pollinated varieties: 9
- **Non-pungency type:**
 - Sweet pepper: 10

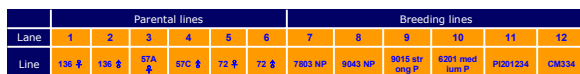
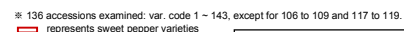
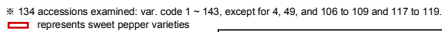


1[LDS14] 2[LDS12] 3[LDS34] 4[LDS58] 5[LDS68]



in pepper varieties by LDS markers

* Size deviation of DNA fragment is < 10 bp



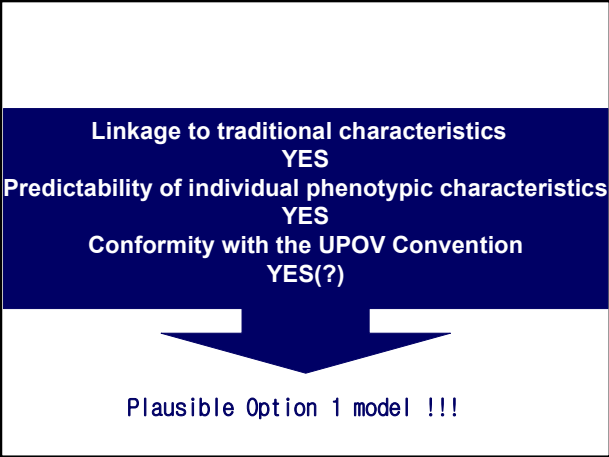
1) CAN, candidate variety; CO, comparing variety
2) 1, ≤ 0 ; 2, 0-0.2; 3, 0.2-0.45; 4, 0.45-0.75; 5, 0.75-1.55; 6, 1.55-2.55; 7, >2.55
3) P, pungency; NP, non-pungency; P(H), heterozygote with pungency; ND, not determined
4) **Bolds** indicate sweet pepper varieties

Pungency	Taste testing	Molecular marker detection
phenotyping	examiner, environments, and genotype	genotype
weak	present (9)	present (9)
very weak (environment and/or genotype)	absent (1)	present (9)
late expression	absent (1)	present (9)

2006								2005							
Test #	Variety code	Type ¹	Capasaicinoid (mg/g, dw)	Note ²	Capasaicinoid (mg/g, dw)	Note ²	LDS59 marker ³	Test #	Variety code	Type ¹	Capasaicinoid (mg/g, dw)	Note ²	Capasaicinoid (mg/g, dw)	Note ²	LDS59 marker ³
35	054	CAN	0.08	2	0.39	3	P	57	...	CO	0.23	3	N/D	N/D	N/D
36	095	CO	0.53	4	0.80	4	P	58	136	CO	0.17	2	N/D	N/D	P(H)
37	055	CAN	0.09	2	0.00	1	P	59	079	CAN	0.63	4	0.95	5	P
38	067	CAN	0.45	3	0.63	4	P	60	080	CO	2.93	7	4.51	7	P
39	080	CO	0.00	1	0.00	2	P	61	081	CAN	0.19	2	0.27	3	P
40	098	CAN	1.09	5	1.01	5	P	62	082	CO	1.20	5	1.29	5	P
41	069	CAN	0.54	4	0.87	5	P	63	085	CAN	0.25	3	0.34	3	P
42	063	CAN	0.88	4	1.56	6	P	64	086	CO	1.60	6	1.69	6	P
43	025	CO	0.98	5	1.38	5	P	65	084	CAN	0.22	3	0.43	3	P
44	031	CAN	0.48	4	0.53	4	P	66	088	CAN	0.18	2	0.36	3	P
45	056	CAN	1.60	6	1.20	5	P	67	040	CO	0.08	2	0.00	1	P
46	059	CO	0.00	1	0.28	3	P	68	089	CAN	0.74	4	0.88	5	P
47	057	CAN	0.73	4	0.79	5	P(H)	69	090	CO	1.28	5	1.19	5	P
48	055	CAN	0.08	2	0.32	3	P(H)	70	091	CAN	0.42	3	0.39	3	P
49	018	CO	0.25	3	0.32	3	P	71	025	CO	0.78	5	1.38	5	P
50	072	CAN	0.08	2	0.28	3	P(H)	72	092	CAN	0.22	3	0.40	3	P
51	002	CO	0.46	4	0.65	4	P	73	110	CAN	0.60	1	0.00	1	NP
52	074	CAN	2.97	7	2.90	7	P	74	111	CO	0.00	1	0.00	1	NP
53	075	CAN	0.20	2	0.00	1	P	75	112	CAN	0.00	1	0.00	1	NP
54	076	CAN	1.43	5	2.31	6	P	76	113	CO	0.00	1	0.00	1	NP
55	077	CO	1.40	5	1.98	5	P	77	114	CAN	0.00	1	0.00	1	NP
56	079	CAN	0.07	2	0.37	3	P	78	115	CO	0.00	1	0.00	1	NP

1) CAN, candidate variety; CO, compound variety.
2) 1, < 0.2; 0-2, 0.2-0.45; 3, 0.45-0.75; 5, 0.75-1.55; 6, 1.55-2.55; 7, > 2.55
3) P, pungency; NP, non-pungency; P(H), heterozygote with pungency; ND, not determined

1) CAN, candidate variety; CO, comparing variety
2) 1, ≤0; 2, 0-0.2; 3, 0.2-0.45; 4, 0.45-0.75; 5, 0.75-1.55; 6, 1.55-2.55; 7, >2.55
3) P, pungency; NP, non-pungency; P(H), heterozygote with pungency; ND, not determined



- To test wider variety sets (ex. foreign varieties) and variety group
- Segregation analysis on F₂ population for heterozygote type
- To test this system among UPOV Members