

Discovery of Genes for Stress Resistance in Mungbean (*Vigna radiata*)

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Abstracts

Mungbean is a socio-economically important legume crop in Asia. It is generally grown in rotation with cereal crops such as rice, maize, and wheat. However, the average seed yield of mungbean is low, being only about 900 kg per hectare, due to biotic and abiotic stresses including bruchid (*Callosobruchus analis*, *Callosobruchus chinensis* and *Callosobruchus maculatus*) infestation, powdery mildew (PM) disease caused by *Erysiphe polygoni*, Cercospora leaf spot (CLS) disease caused by *Cercospora canescens*, yellow mosaic disease (YMD) caused by *Mungbean Yellow Mosaic Virus (MYMV)* and *Mungbean Yellow Mosaic Indian Virus (MYMIV)*, calcareous soil (iron deficiency chlorosis), and soil salinity. These stresses are believed to be exacerbated by climate change, threatening food security. Marker-assisted breeding (MAB) and genomics-assisted breeding (GAB) are promising approaches to efficiently and rapidly develop new crop cultivars with improved yield, quality, and resistance to biotic and abiotic stresses. Although mungbean was among the first legume crops subjected to genomics studies three decades ago, progress in genomics research for this crop has been very slow due to a lack of genomic resources. Additionally, there are only a few laboratories/institutes that consistently and continuously work on genomics and molecular breeding of mungbean. However, in recent years, quantitative trait loci (QTL) controlling bruchid resistance, PM resistance, CLS resistance, YMD resistance, calcareous soil tolerance, and salt tolerance have been identified by high-resolution mapping and/or genome-wide association studies. In addition, candidate genes controlling these stresses have been identified: *VrPGIP1* and *VrPGIP2* encoding polygalacturonase inhibitors for bruchid resistance, *VrMLO12* encoding Mildew Locus O 12 protein and *VrRPP13L* encoding *Peronospora parasitica* 13-like protein for PM resistance, *VrTAF5* encoding TATA-binding-protein-associated factor 5 and *VrRLP12* encoding receptor-like protein 12 for CLS resistance, *VrYSL3* encoding yellow stripe-like3 protein for calcareous soil tolerance, and *VrCYBDMG1* encoding a cytochrome b561 domain-containing protein. Tightly linked and/or functional markers have been developed for these genes for MAB of mungbean and are being used in the development of stress-resistant mungbean cultivars.

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Mungbean

- Short-duration legume crop (60-75 days)
- Widely grown in Asia with production area of 7.5-8.0 Mha (India 5.0 Mha, Myanmar 1.0 Mha, China 0.8 Mha)
- Direct consumption and processed foods
- Low seed yield (<900 kg/ha)

Important stresses causing low mungbean yield

Inheritance of stress resistance in mungbean

Stress	Resistant germplasm	No. of loci	H ² (%)	References
Powdery mildew	V4718 and RUM5	2-3	>80	Reddy (1994) Chankaew et al. (2013)
Cercospora leaf spot	V4718 and V2817	1-2	>80	Chankaew et al. (2011)
Bruchids	V2709, V2802, V1128 and V2817	1 (Br)	>95	Somta et al. (2007) Chotechung et al. (2016)
Calcareous soil	NM10-12	1	>60	Srinives et al. (2010) Prathet et al. (2012)
Yellow mosaic virus	NM92 and BARI moong 1	1-2	>75	Malik et al. (1992) Alam et al. (2014)
Salinity	CPI 100834	1	45%	Deeroum et al. (2024)

Genome sequence of mungbean and insights into evolution within *Vigna* species

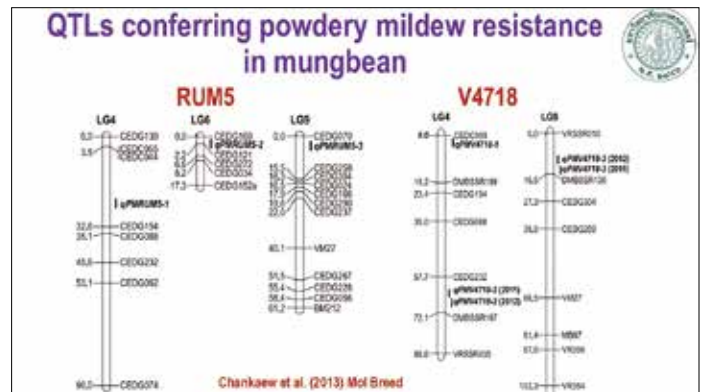
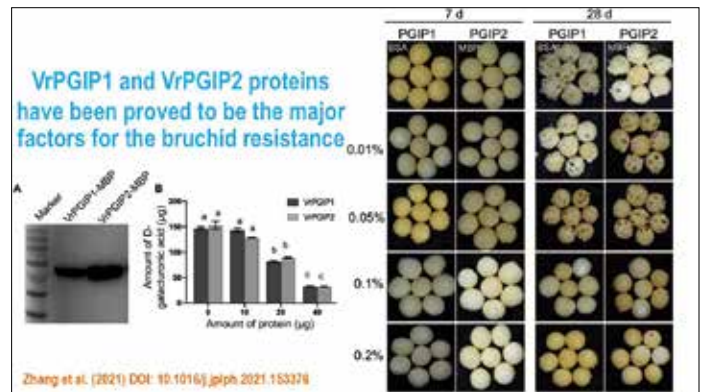
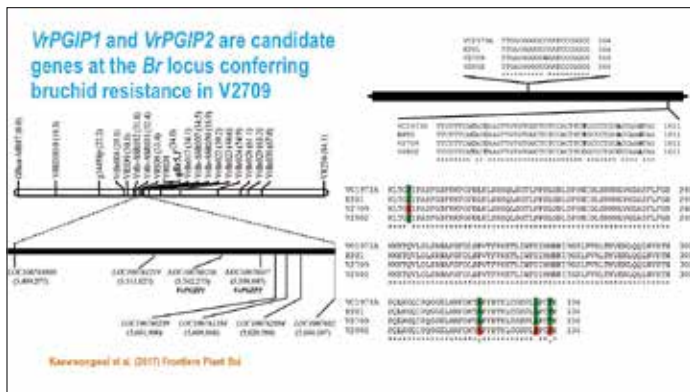
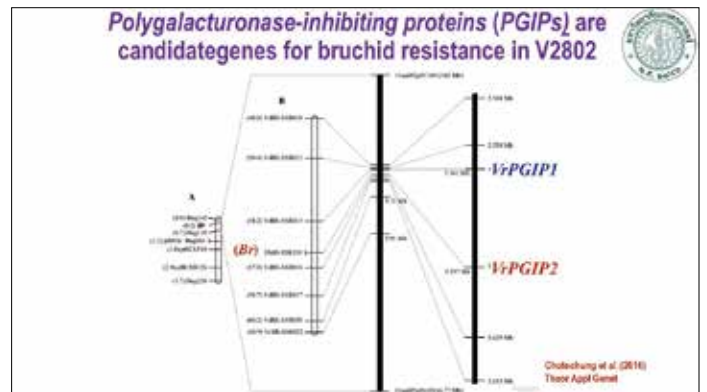
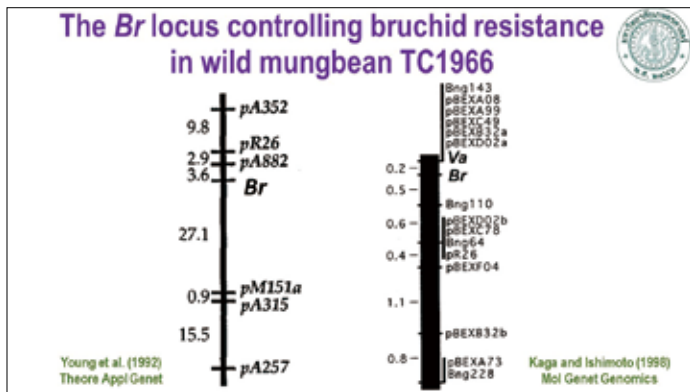
A near-complete genome sequence of mungbean (*Vigna radiata* L.) provides key insights into the modern breeding program

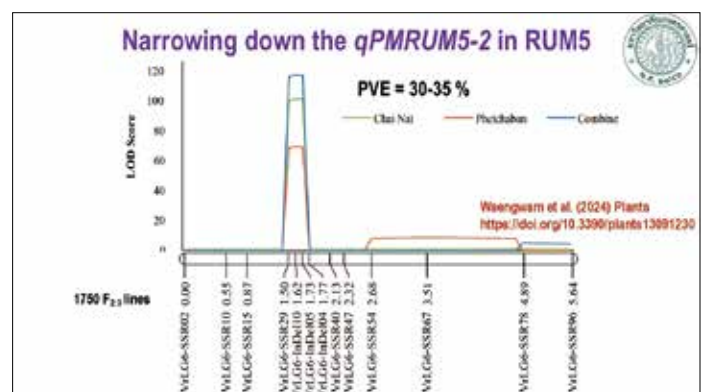
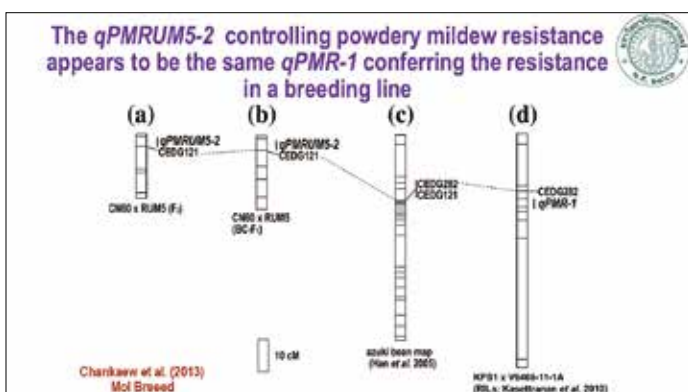
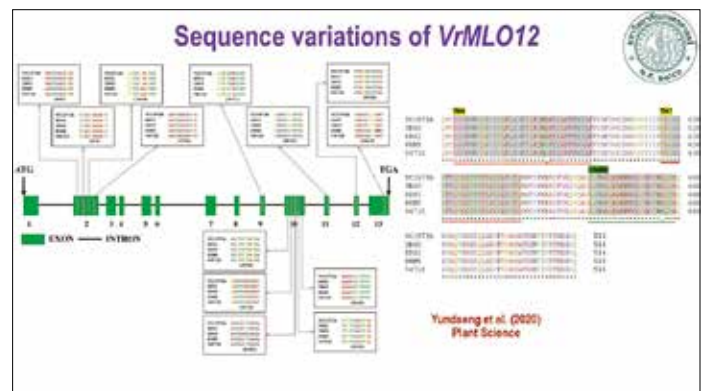
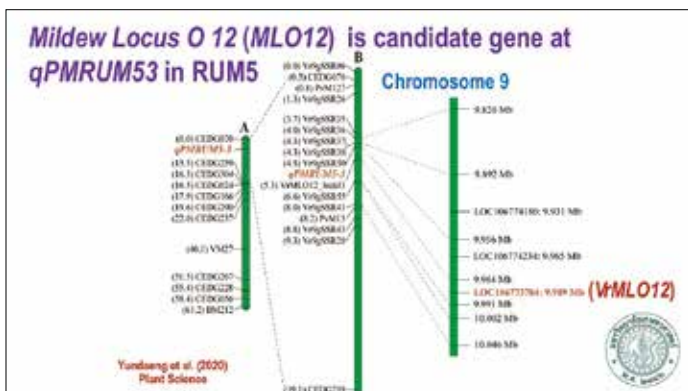
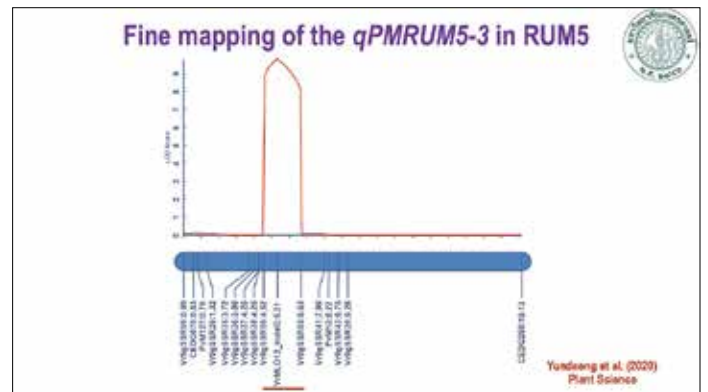
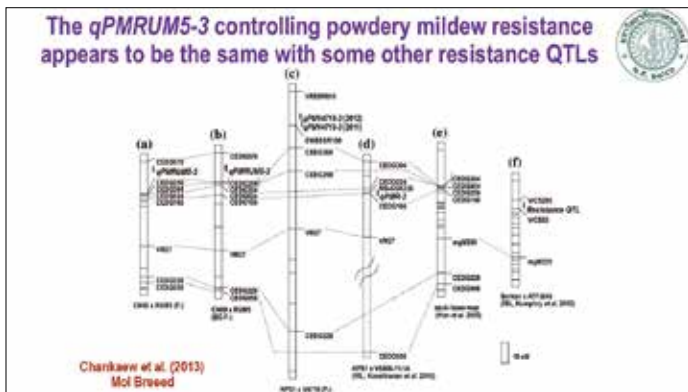
The improved genome of VC1973A was released in 2021

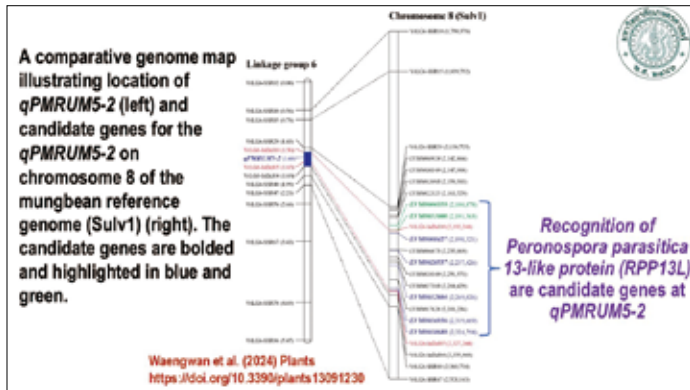
The first genome sequence of mungbean (VC1973A) was released 2014

Bruchids (Seed weevil)

Callosobruchus chinensis *Callosobruchus maculatus*



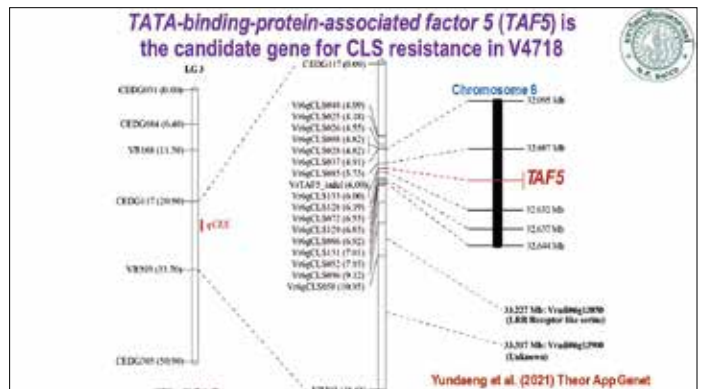
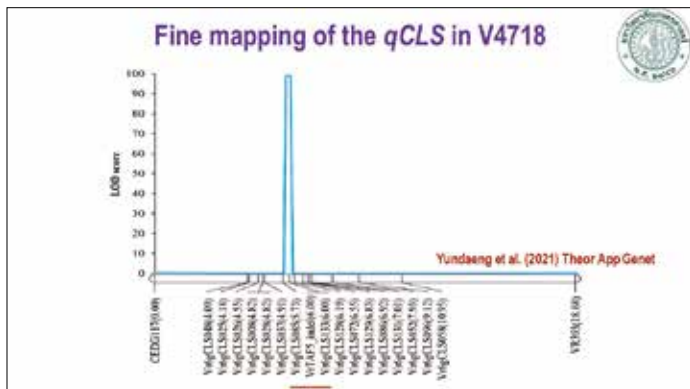
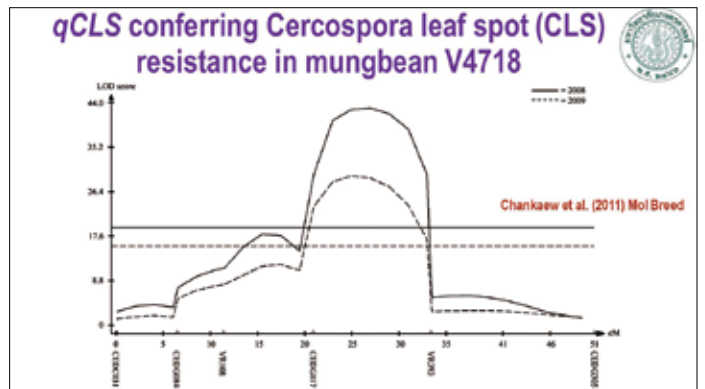


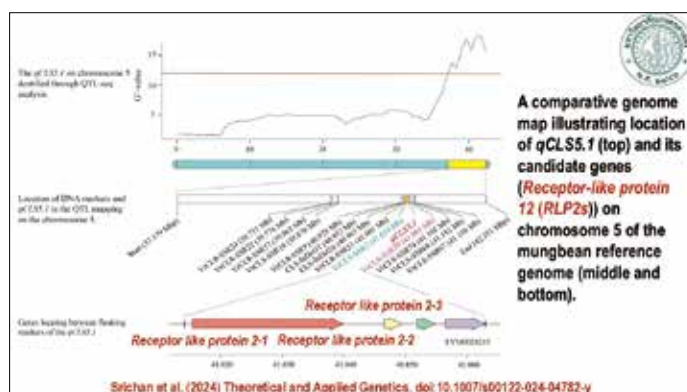
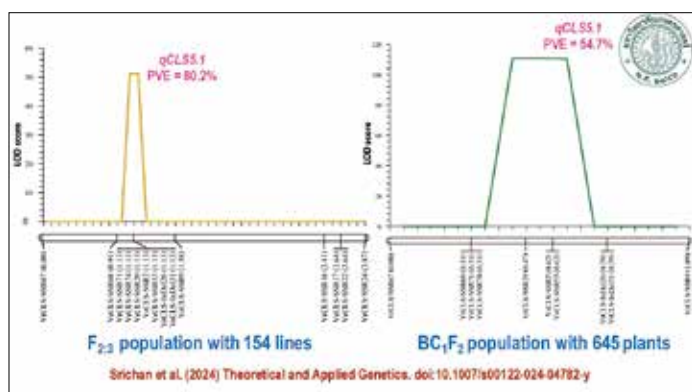
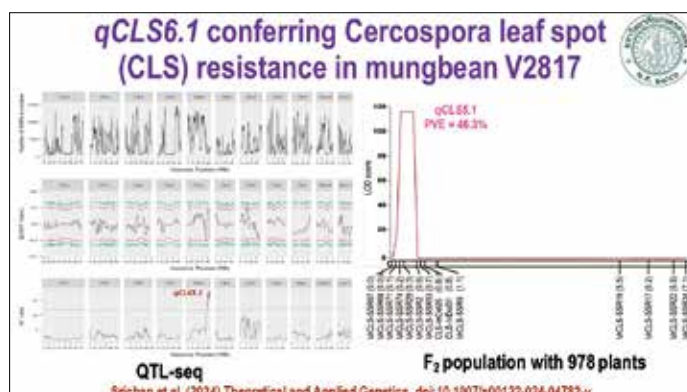
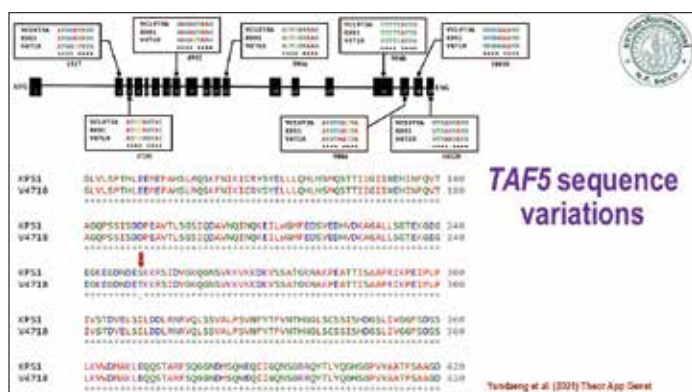


Single nucleotide polymorphisms (SNP) identified between Chai Nat 60 (CN60) and RUM5 in *RPP13L* genes locating in and nearby the *qPMRUM5-2* region

Gene	No. of SNPs	Types of SNPs
<i>EVM0031008</i> (<i>VrRPP13L-2</i>)	151	nonsynonymous SNP (102), synonymous SNP (46), and splicing-relevant SNP (3)
<i>EVM0008427</i> (<i>VrRPP13L-3</i>)	229 and 5	nonsynonymous SNP (158) and synonymous SNP (71)
<i>EVM0028537</i> (<i>VrRPP13L-4</i>)	51 and 8	nonsynonymous SNP (31), synonymous SNP (18) and stop-gain SNP (2)
<i>EVM0032804</i> (<i>VrRPP13L-5</i>)	77 and 1	nonsynonymous SNP (52), synonymous SNP (22), and stop-gain SNP (3)
<i>EVM0016936</i> (<i>VrRPP13L-6</i>)	35 and 2	nonsynonymous SNP (21), synonymous SNP (11), and stop-gain SNP (3)
<i>EVM0018588</i> (<i>VrRPP13L-7</i>)	25 and 10	nonsynonymous SNP (16) and synonymous SNP (9)

Waengwan et al. (2024) Plants. <https://doi.org/10.3390/plants13091230>



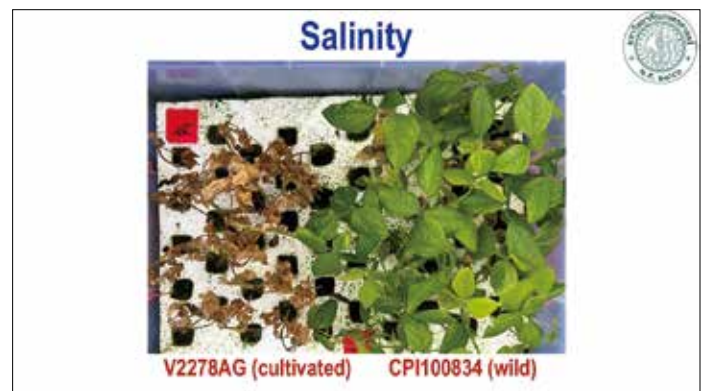
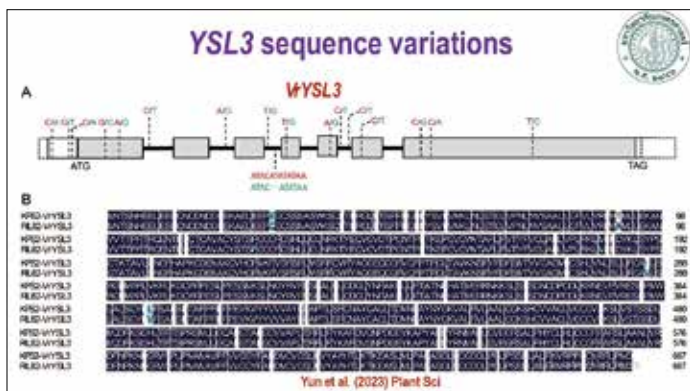
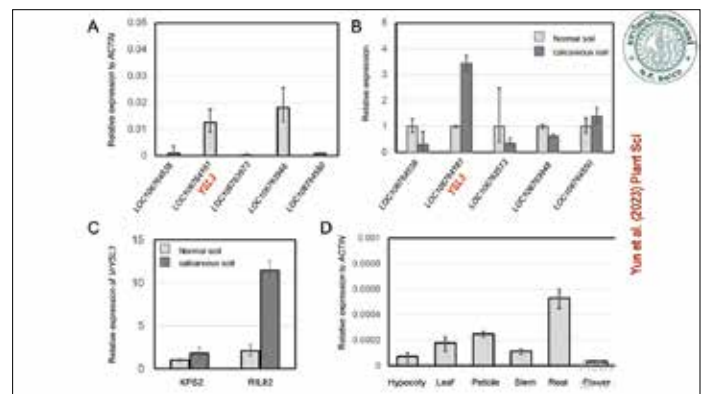
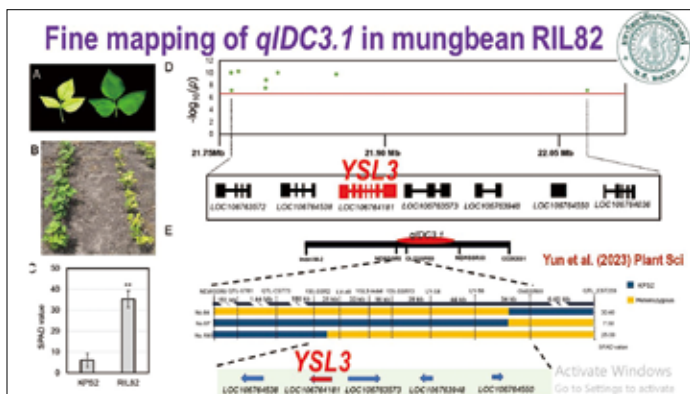
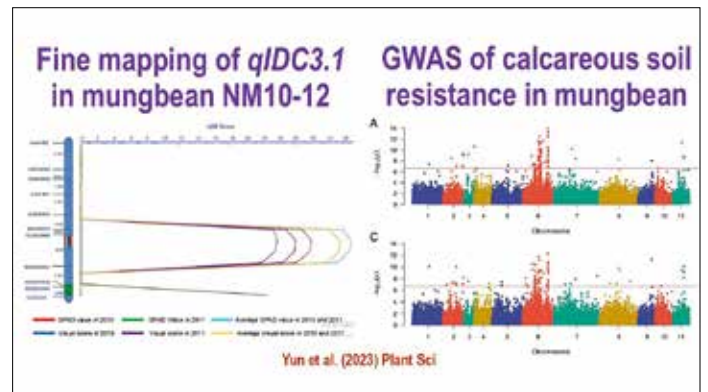
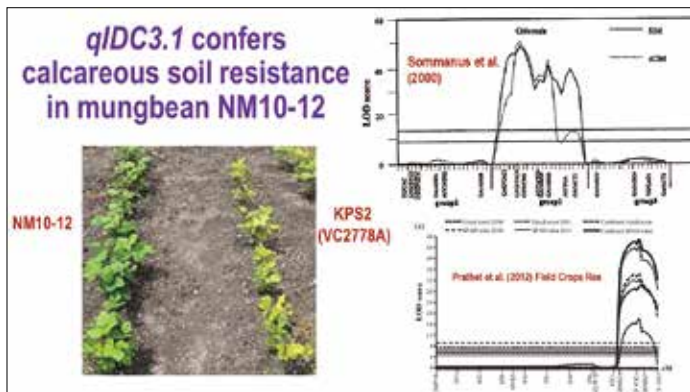


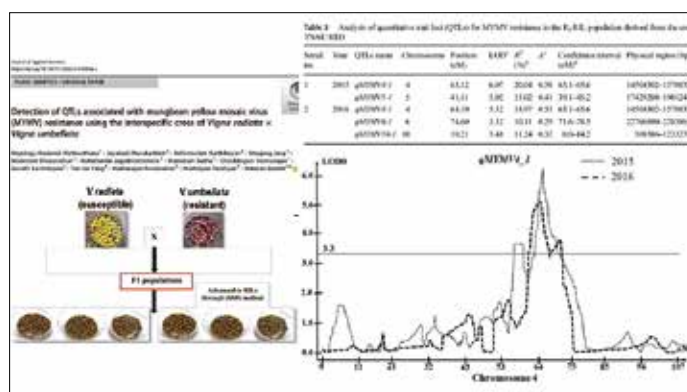
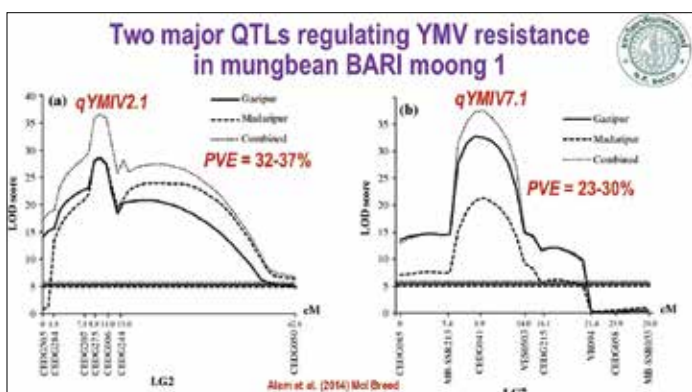
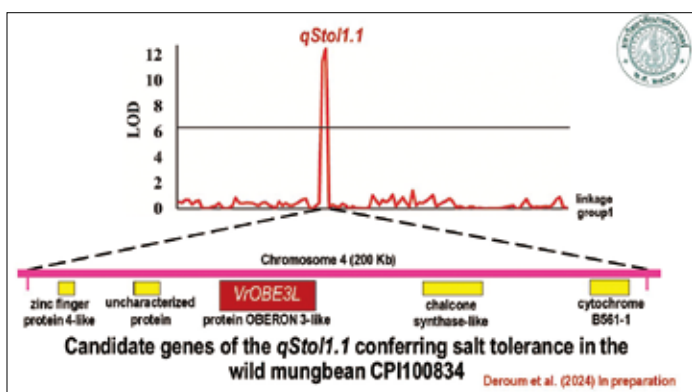
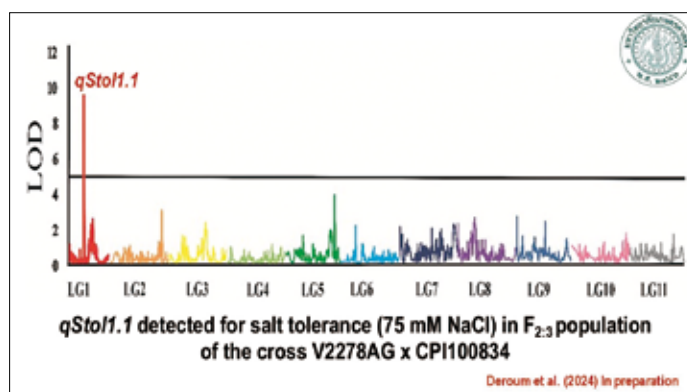
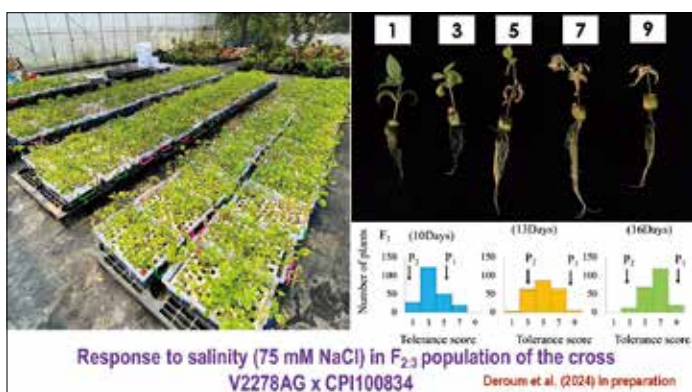
Single nucleotide polymorphisms (SNPs) and insertions/deletions (InDels) identified between V1197 and V2817 in candidate genes of the qCLS.1

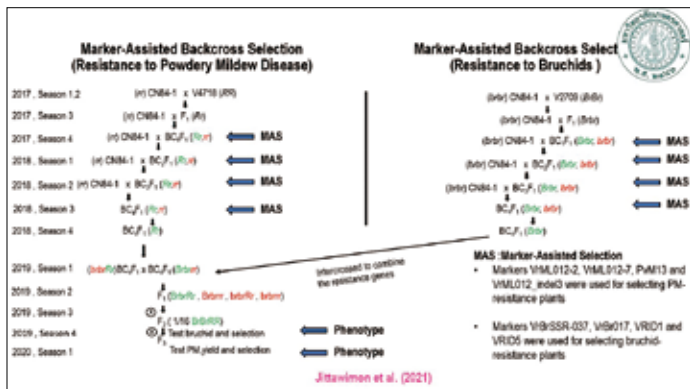
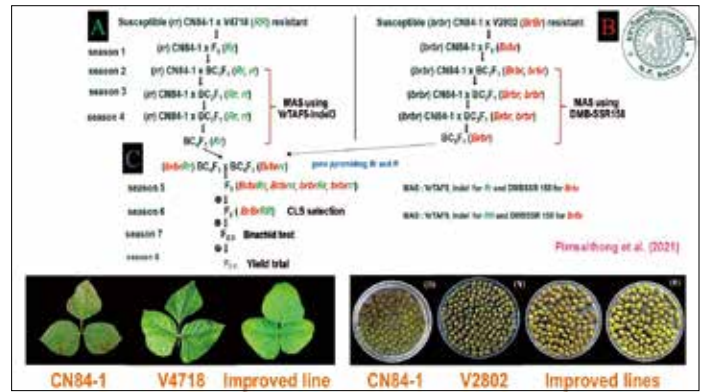
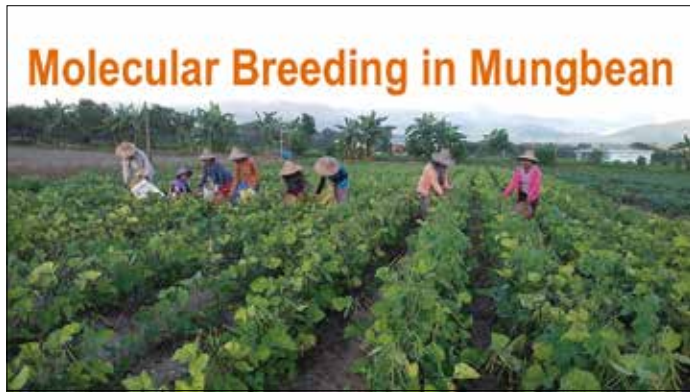
Gene	Number of SNPs and InDels	Types of mutations
VrRLP2-1	131	nonsynonymous SNP (83), synonymous SNP (35), stop-gain SNP (2) and frameshift mutation (3)
VrRLP2-2	145	nonsynonymous SNP (97), synonymous SNP (47) and non-frameshift mutation (1)
VrRLP2-3	118	nonsynonymous SNP (83), synonymous SNP (33) and stop-gain SNP (2)

Seichan et al. (2024) *Theoretical and Applied Genetics*. doi: 10.1007/s00122-024-04782-y









Mungbean improved lines developed by MAS

Lines	PDS	AUDPC		D50F (Days)	D90M (Days)	Height (cm)	100SOW (g)	Seeds per pod	Yield (t/ha)
		Bottom leaves	Whole plants						
KUML2017A-12	7.00	101.33	61.93	41.67	69.00	36.57	7.46	11.75	258.56
KUML2017A-22	24.00	99.13	59.64	42.00	68.67	37.54	7.30	12.00	202.91
KUML2017A-40	22.00	104.67	62.90	41.67	69.00	39.13	7.78	12.17	235.28
KUML2017A-88	7.00	106.70	60.17	40.87	68.00	38.93	7.78	11.88	223.68
KUML2017A-104	10.00	81.66	55.61	42.33	69.00	38.21	7.92	11.75	226.30
KUML2017A-106	21.00	108.83	63.48	42.67	70.33	38.09	7.72	11.75	231.23
CN84-1 (RP)	81.68	131.69	79.77	43.00	69.33	36.48	7.58	11.93	181.62
V2709 (DP)	1.97	119.40	74.46	39.33	60.00	27.66	3.40	11.18	147.75
V4718 (DP)	93.68	17.20	12.29	39.67	68.00	31.33	3.26	12.21	241.27

PDS = % damaged seeds caused by bruchids, AUDPS = area under the disease progress stairs, D50F = days to 50% flowering, D90M = days to 90% pod maturity, 100SOW = 100-seed weight.

Jitawimol et al. (2021)

Conclusions

- Most of biotic and abiotic stress resistance in mungbean is controlled by single major QTL
- *VrPGIP1* and *VrPGIP2*, *VrMLO12* and *VrRPP13Ls*, *VrTAF5* and *VrRLPs*, *VrYSL3*, and *VrOBE3L* are candidate genes for resistance to bruchid, powdery mildew, CLS, calcareous soil, and salinity, respectively, in mungbean

Images showing mungbean seeds, sprouts, and various food products like mungbean flour and fried mungbean.

Logos of the Program Management Unit for Human Resources & Institutional Development, Research and Innovation (PMU-B); Jiangsu Agricultural Science Academy (JAAS); National Science and Technology Development Agency (NSTDA); Seoul National University; and National Agriculture and Food Research Organization (NARO).



