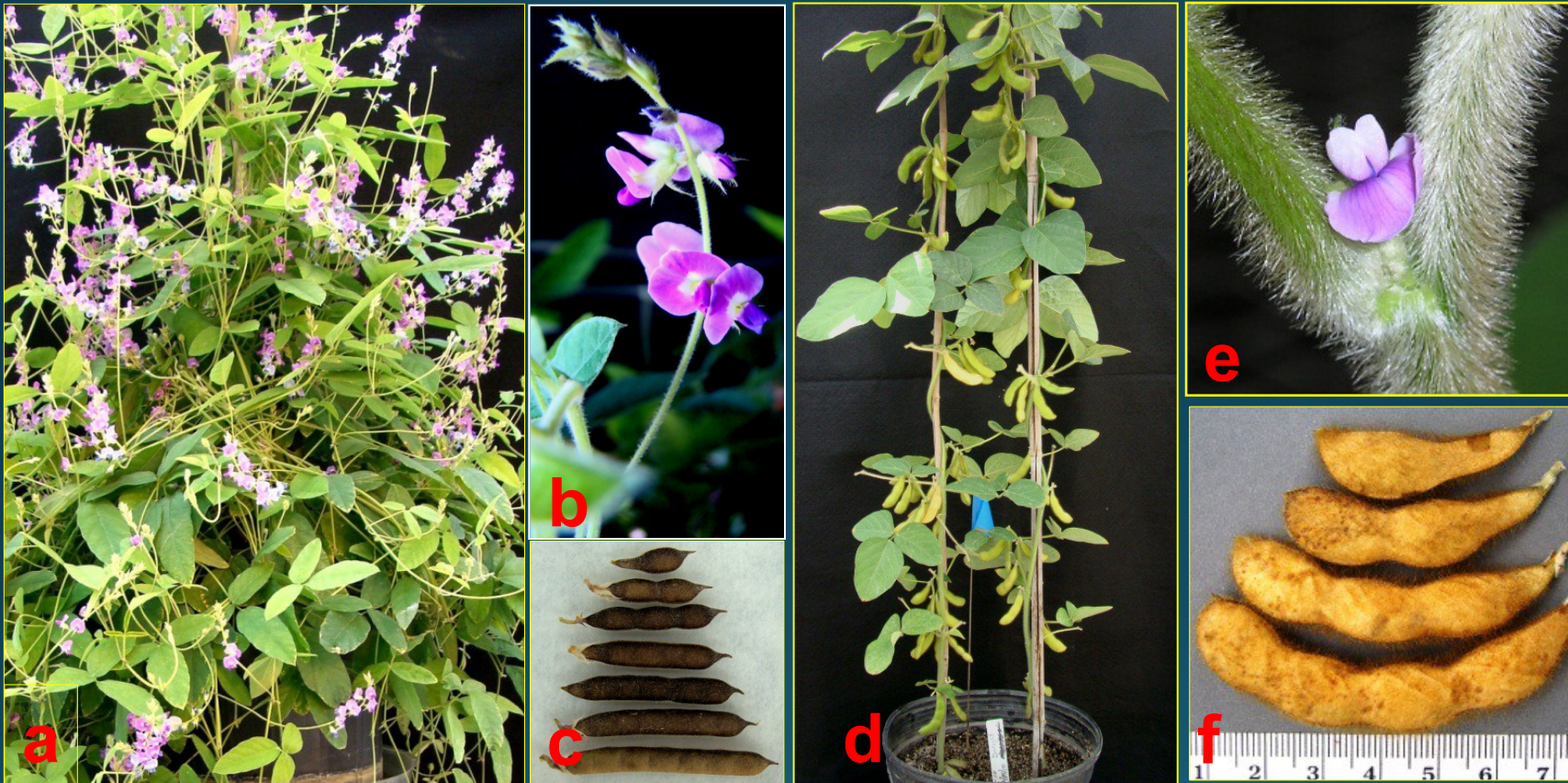


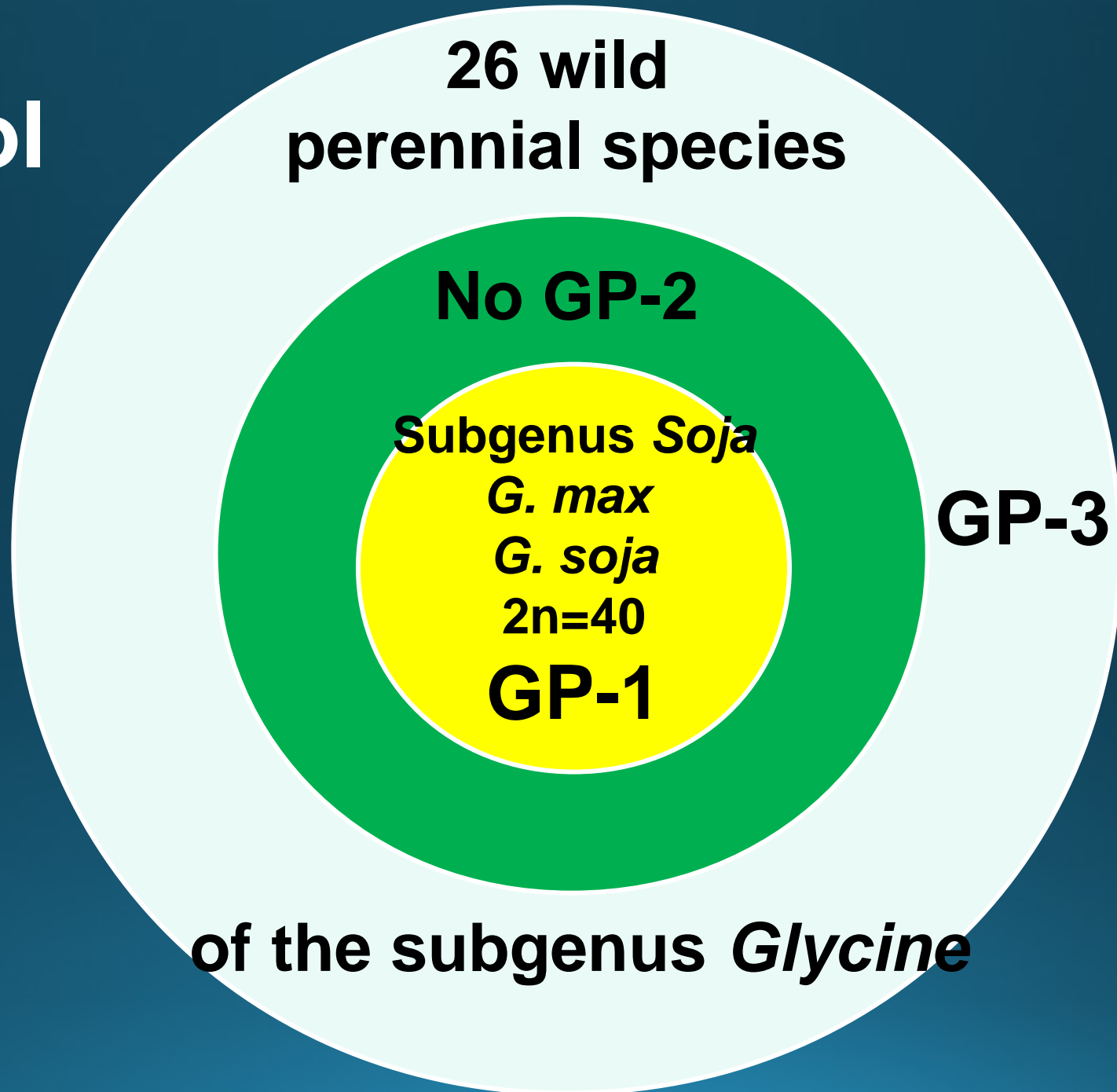
Methodology to exploit *Glycine tomentella* for broadening the genetic base of modern soybean

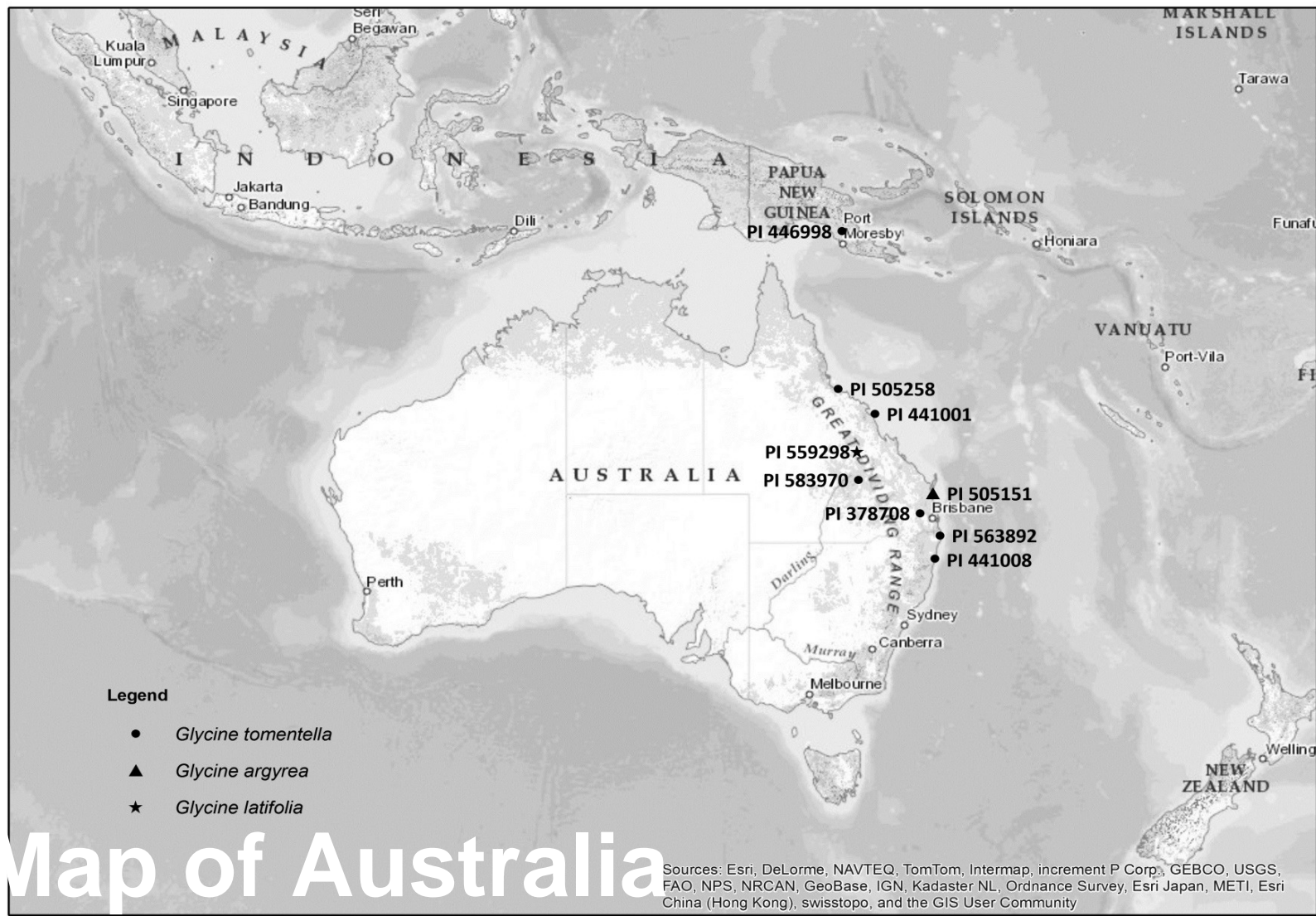
Ram Singh and Randall Nelson
USDA-ARS, Department of Crop Sciences,
University of Illinois, Urbana



***Glycine tomentella* PI 441001, $2n = 78$ *Glycine max* cv. Dwight, $2n = 40$**

**Gene pool
of the
soybean**





Map of Australia

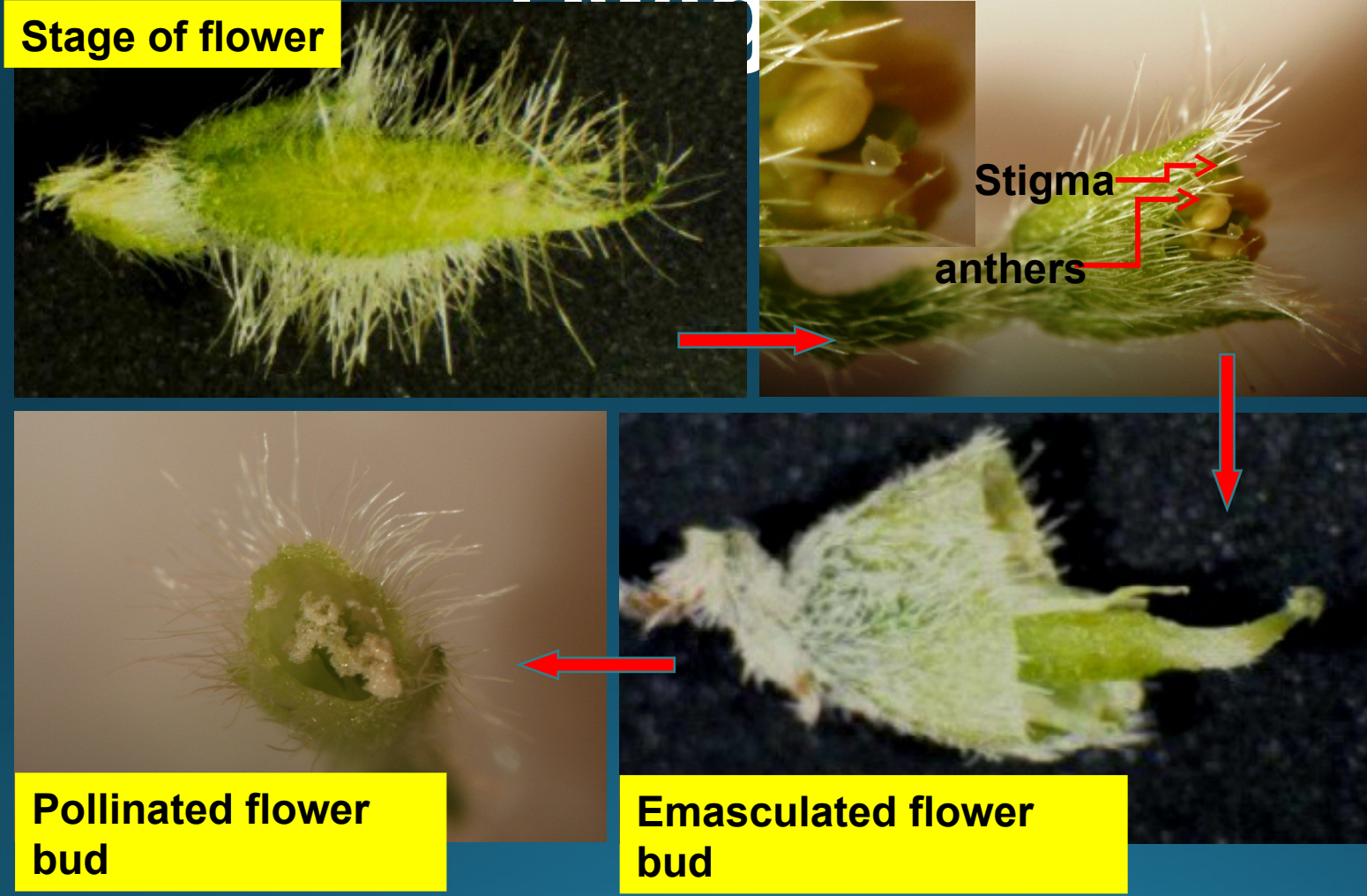
Sources: Esri, DeLorme, NAVTEQ, TomTom, Intermap, increment P Corp., GEBCO, USGS, FAO, NPS, NRCAN, GeoBase, IGN, Kadaster NL, Ordnance Survey, Esri Japan, METI, Esri China (Hong Kong), swisstopo, and the GIS User Community

Initial Intersubgeneric Hybridization between soybean and *Glycine tomentella*

- i. Dwight ($2n = 40$) x PI 441001
- ii. PI 441001 ($2n = 78$) x Dwight
- iii. Ina ($2n = 40$) x PI 441001
- iv. Macon ($2n = 40$) x PI 441001
- v. Williams 82 ($2n = 40$) x PI 441001
- vi. IA3010 ($2n = 40$) x PI 441001
- vii. Dwight x PI 441008
- viii. Dwight x PI 441001 x PI 441008

Hybridization in soybean cv.

Dwight



Growth hormone solution

GA3 = 100mg

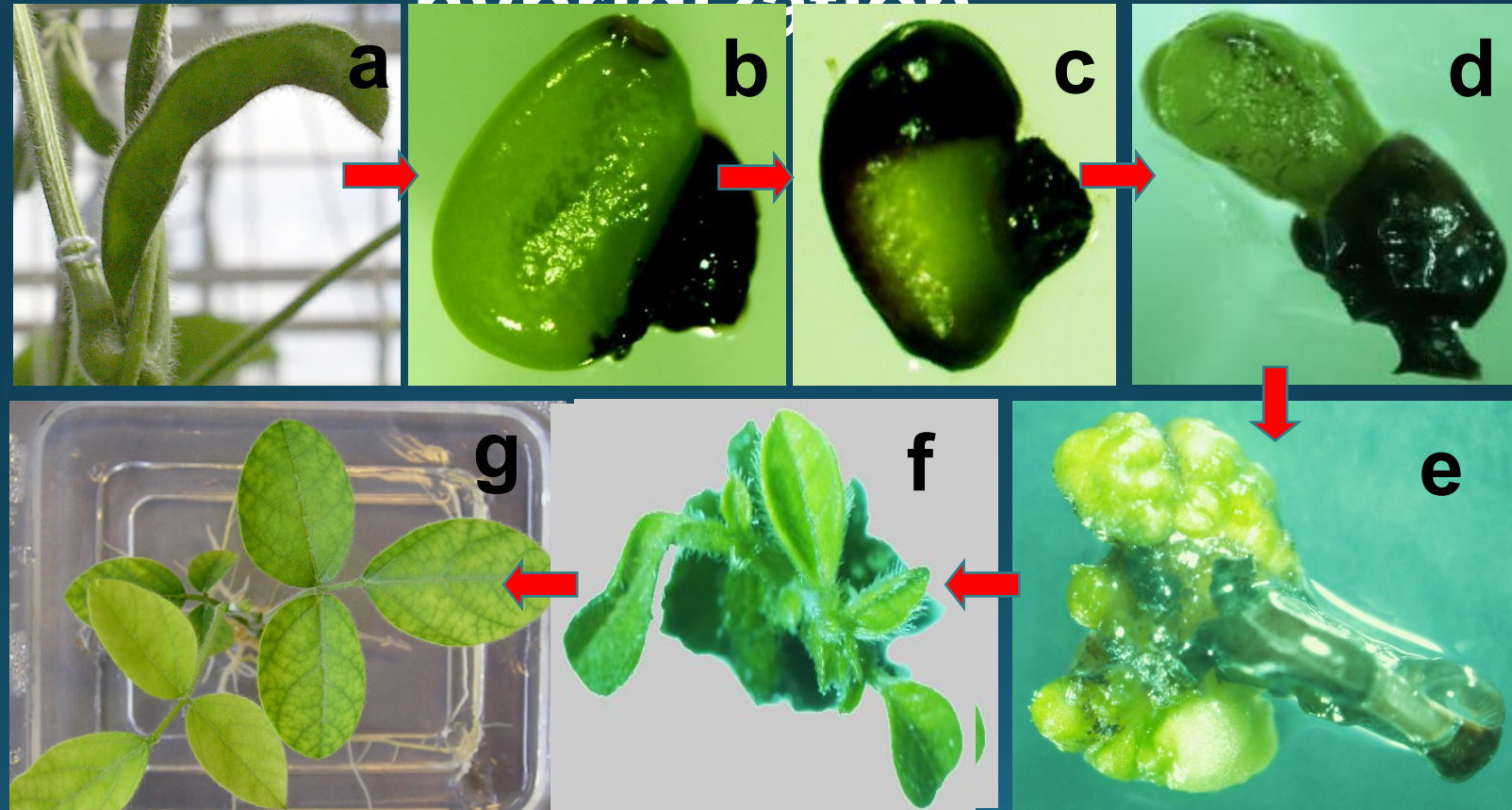
NAA = 25mg

Kinetin = 5mg

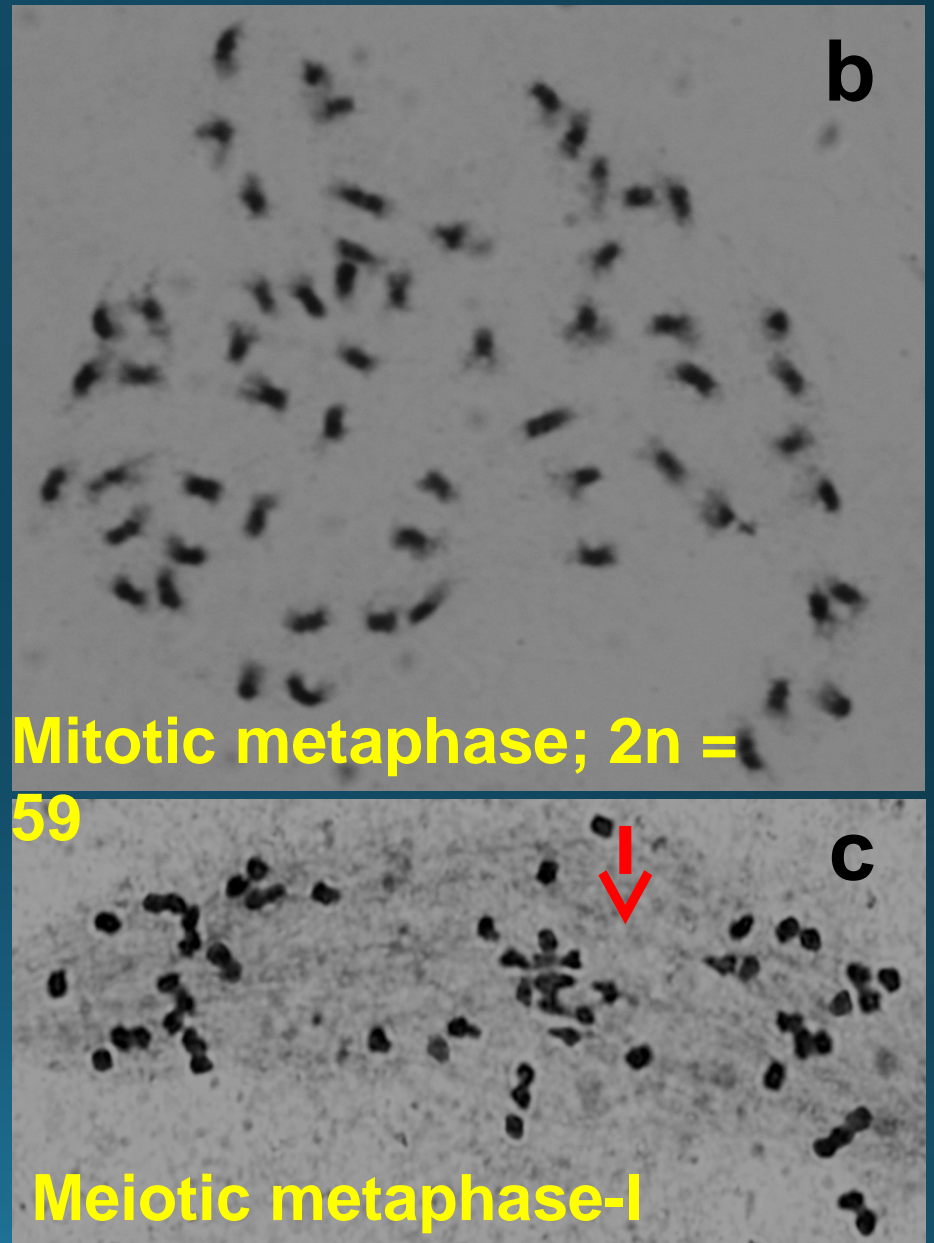
Distilled water = 1000ml

Methodology for generating fertile plants between Dwight and PI 441001 hybridization

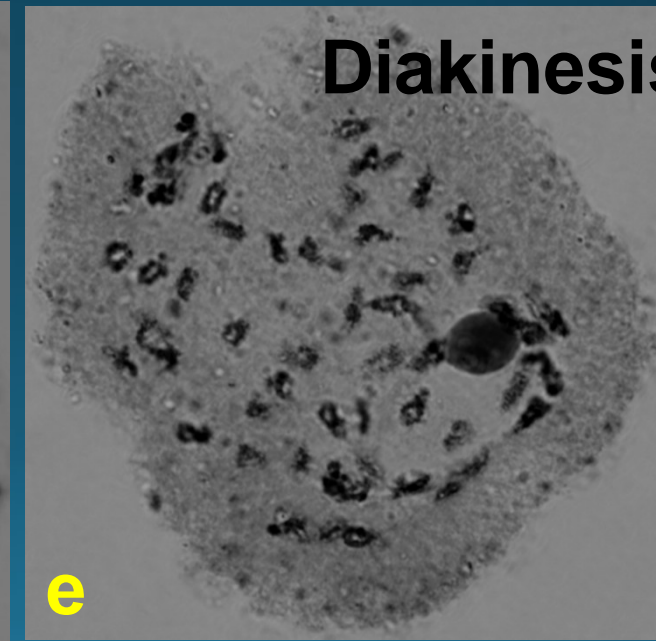
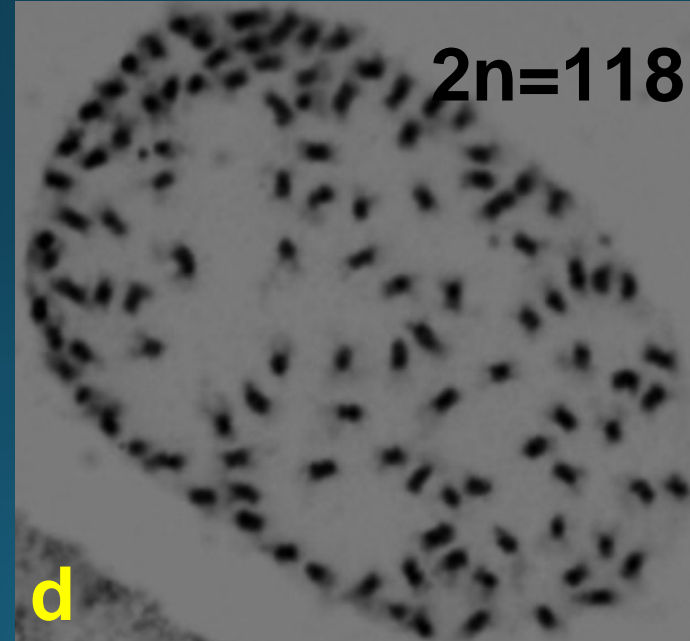
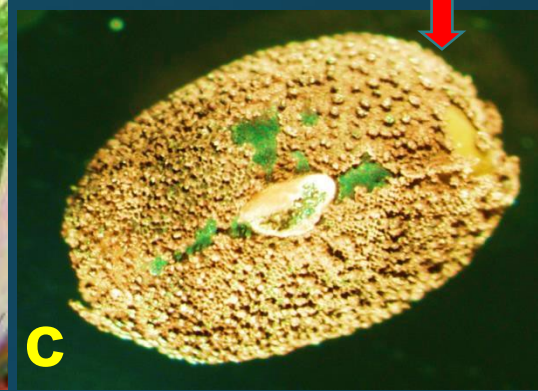
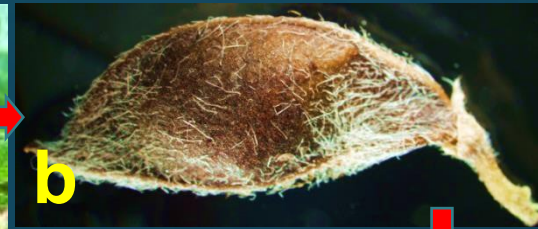
Immature
hybrid
Seed rescue



F1 plant
in
greenhouse

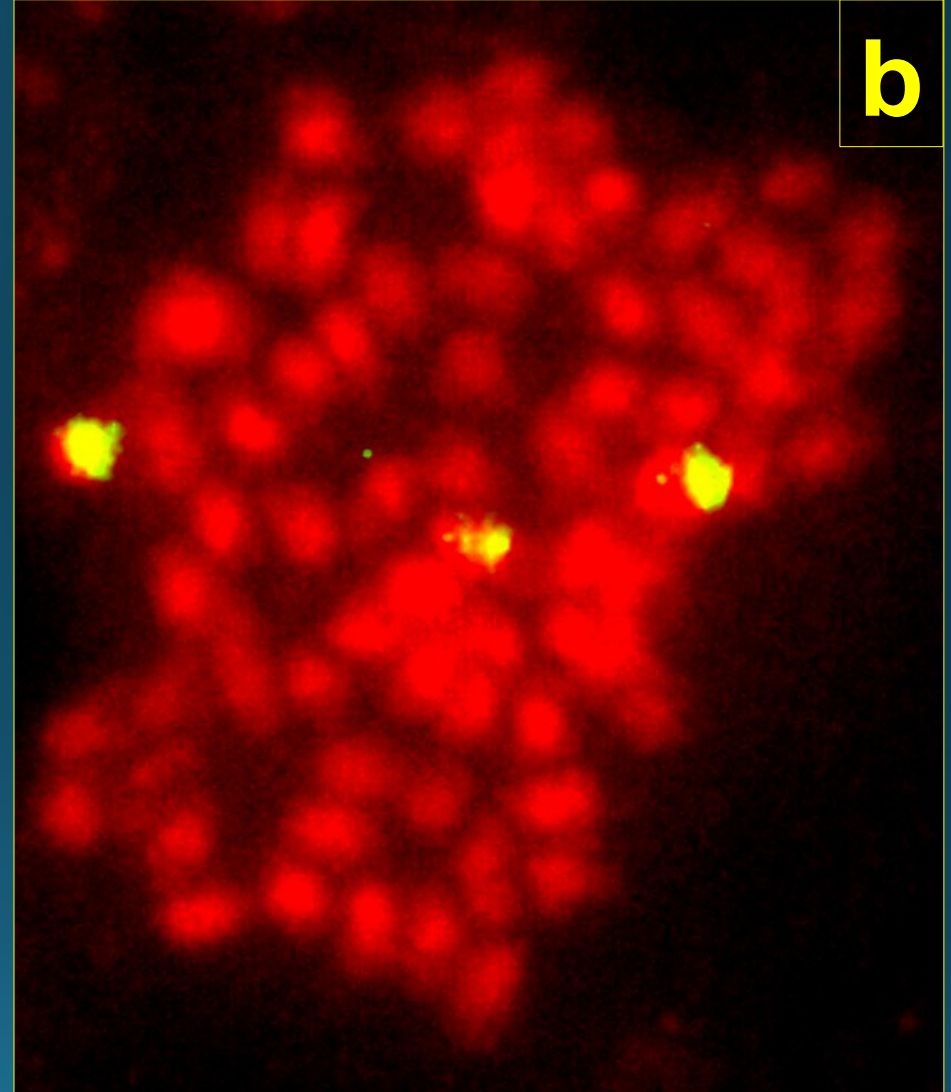


Production of amphidiploid

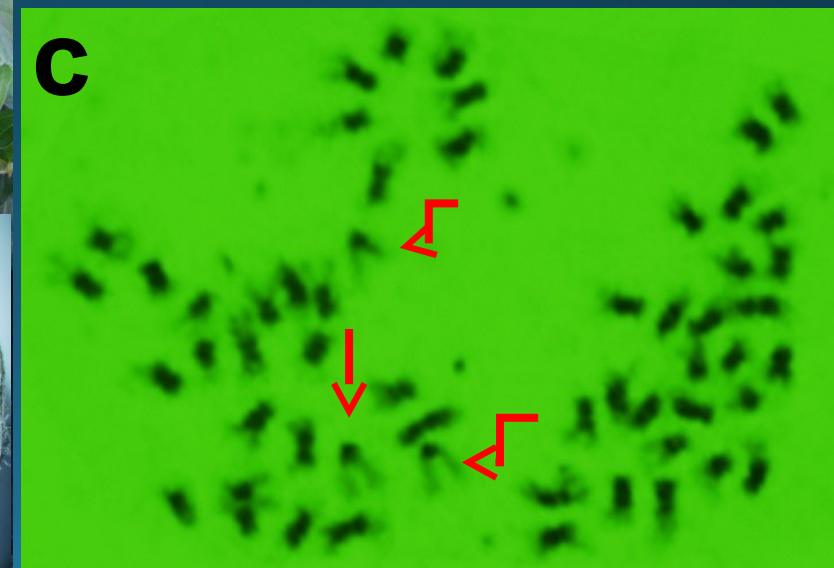


**a; BC1
plant**

**b; FISH of
BC1 plant**



BC2F1 plants



BC3F1 plants



07H6-3
 $2n = 41$



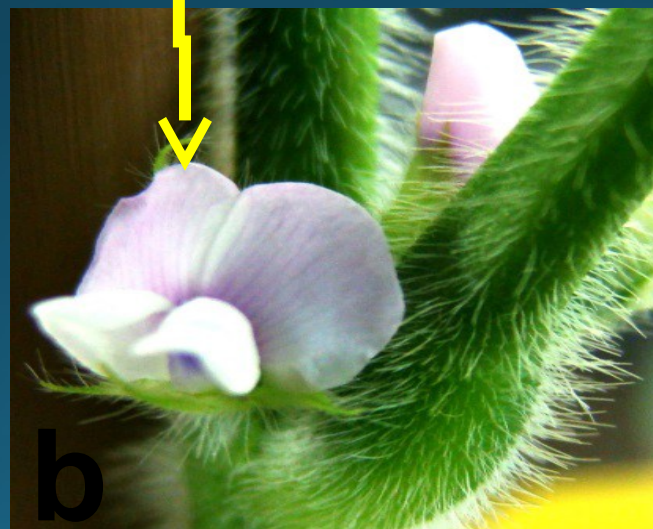
07H6-21
 $2n = 41$



07H5-8
 $2n = 41$



Progeny of 07H6-3
(BC3F2)



White flower allele test

			Observed	Expected	Obs.- Exp.	(Obs.- Exp) ²	(Obs.- Exp) ² /Ex p.
		Ratio 9:7					
14ST2 x PI 548631 (Williams) <i>w1</i>	Purple	9	159	156.375	2.625	6.89	0.044
	White	7	119	121.625	-2.625	6.89	0.056
	Total	16	278			Sum = 2 Value	0.10
14ST2x PI 547685 (Harosoy) <i>w1</i>	Purple	9	110	110.25	-0.25	0.06	0.00
	White	7	86	85.75	0.25	0.06	0.00
	Total	16	196			Sum = 2 Value	0.00
14ST2x PI 547657 (Clark) <i>w4</i>	White	567					



G. max cv. Dwight
 $2n = 40$

x

G. tomentella, PI 441001
 $2n = 78$

F1; $2n = 59$

Colchicine treatment



Amphidiploid
 $2n = 118$

x

Dwight
 $2n = 40$



BC1, $2n = 79$ x

Dwight
 $2n = 40$



BC2
2n = 55-59



X



BC3
2n = 40 to 49

X



BC4-BC6;
F2-4
2n = 40-42

X



Dwight
2n = 40

Dwight
2n = 40

Dwight
2n =
40

Isolation of possible 39 MAALs and 39 DAALs and derived modified soybean (2n = 40) lines in *G. max* cytoplasm

G. tomentella, PI 441001
2n = 78

G. max cv. Dwight
2n = 40

x



F1; 2n = 59

Colchicine treatment



Amphidiploid
2n = 118

Dwight
2n = 40

x



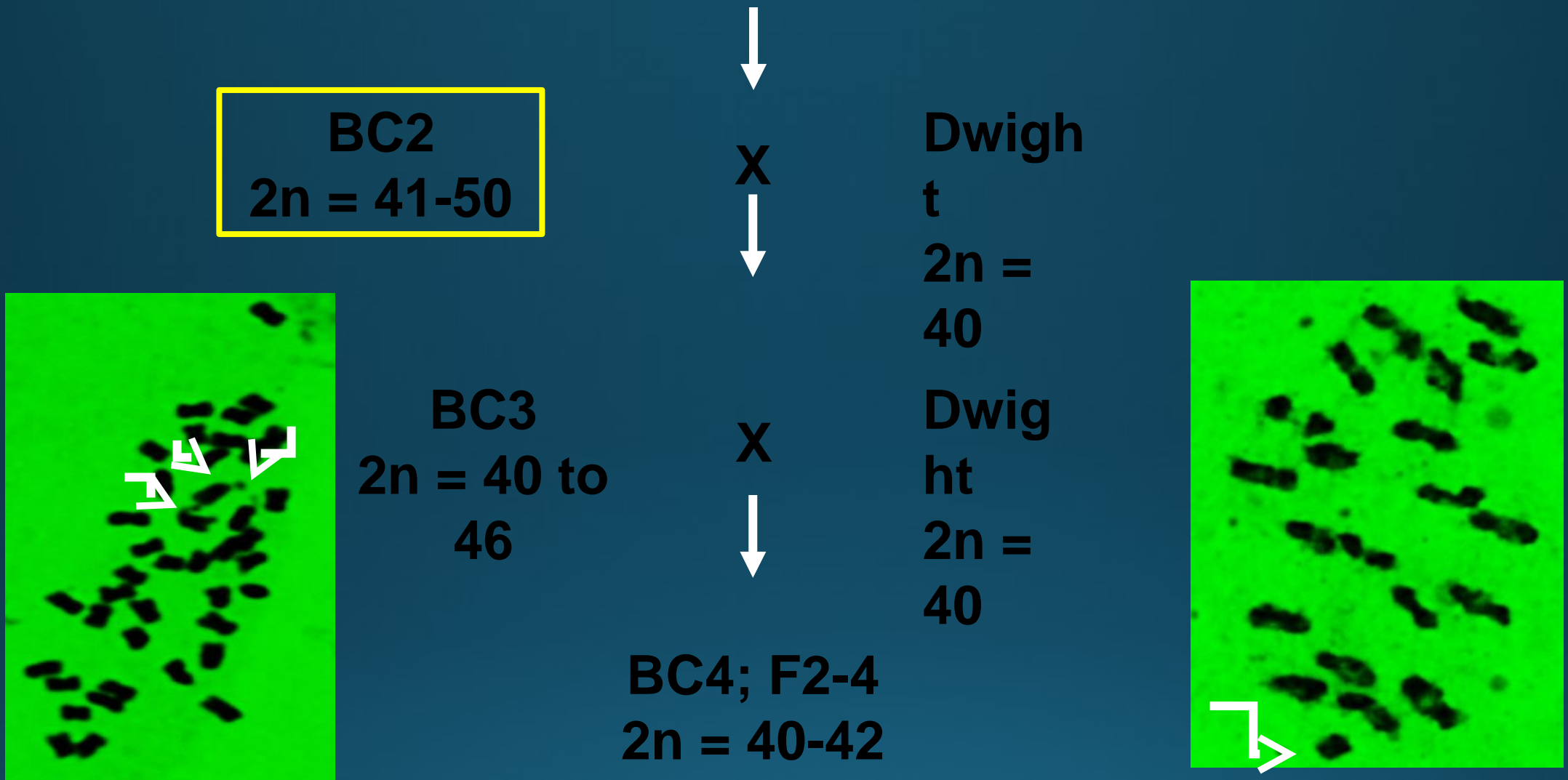
BC1,
2n = 79

x



Dwight
2n = 40





Isolation of possible 39 MAALs and 39 DAALs and derived modified soybean (2n = 40) lines in *G. tomentella* cytoplasm

Number of lines from greenhouse to field since(2008)

Year	Lines	BC2 plants
2008	286	2
2009	574	3
2010	691	5
2011	6,000	10
2012	1,696	14 (tom + max)
2013	853	8 (mostly tom)
2014	702	13 (tom + max)
2015	608	10 (mostly tom)

From test tube (2003) to field (2008 → 2015)



Screening of derived lines from Dwight x PI 441001 and PI 441001 x

- ★ **Dwight cytoplasm**
- ★ **Soybean rust**
- ★ **Phytophthora root rot**
- ★ **Soybean cyst nematode**
- ★ **Tolerance to salt**
- ★ **Higher yield**
- ★ **Early to late maturity**
- ★ **High protein**

Acknowledgements

- * G. Hartman (USDA\ARS): Soybean rust screening
- * D. Walker (USDA\ARS): Soybean rust screening
- * A. Akperley (UIUC; graduate student): Yield test
- * S. Wang (UIUC; graduate student): Progenies of $2n=42$ and protein content
- * J. Ma (UIUC; graduate student): Phytophthora root rot screening
- * G. Battu (UIUC; post-doc.): FISH and GISH
- * P. Brown (UIUC): Sequencing
- * T. Niblack (OSU): SCN screening
- * R. Yusuf (UIUC): Greenhouse work
- * Many undergraduate students: Culture maintenance

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- ★ **Illinois Soybean Association**

Thank you!