

# Mapping quantitative trait loci (QTL) for seed traits in sunflower

**Bing Yue, Jinguo Hu**

Department of Plant Sciences, NDSU, Fargo, ND  
Sunflower Unit, NCSL, USDA-ARS, Fargo, ND

# Why seed traits?



## Confection (non-oil) vs. oilseed sunflower

gray or white with stripes,

larger seed size

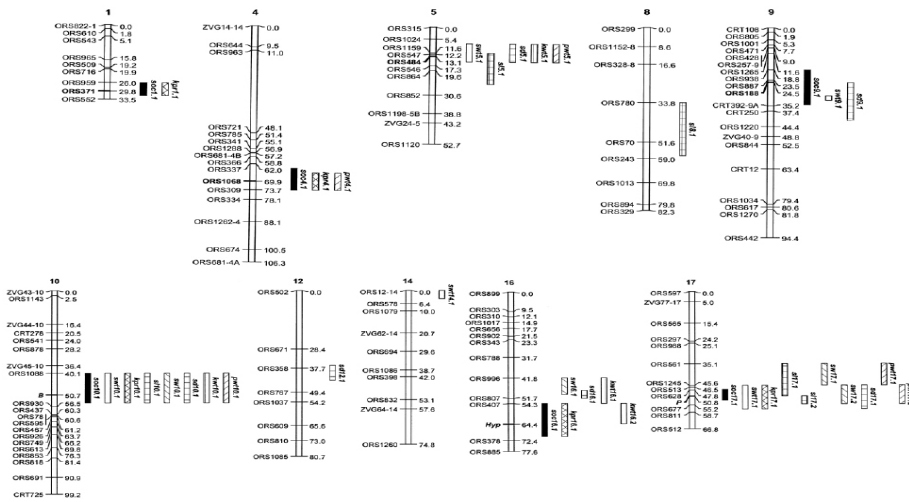
lower kernel-to-pericarp weight ratios (easily shelled)

**Seed traits are typical quantitative traits, controlled by multiple genes. Thus the genetic basis of seed traits is complex and has seldom been studied in sunflower.**

**Hull color** are controlled by pigments in three layers (Miller and Fick, 1997). These two loci, *Hyp* and *P*, have been mapped (Leon et al. 1996; Tang et al. 2006).

**QTL mapping** for the other seed traits was only conducted in two studies in sunflower:

- Burke et al. (2002) firstly identified 14 QTL for seed weight, seed length and seed width.
- Tang et al. (2006) detected 40 QTL for 8 seed traits.



# QTL analysis

(estimating the Number, effects and locations of the genes controlling quantitative trait using phenotyping, genotyping data by computer software)

**In this study**, QTL mapping for 12 seed traits was conducted.

## Experimental design:

HA89 × LSS (confection line)



F<sub>1</sub> (2006)



F<sub>2</sub> Greenhouse (2006)

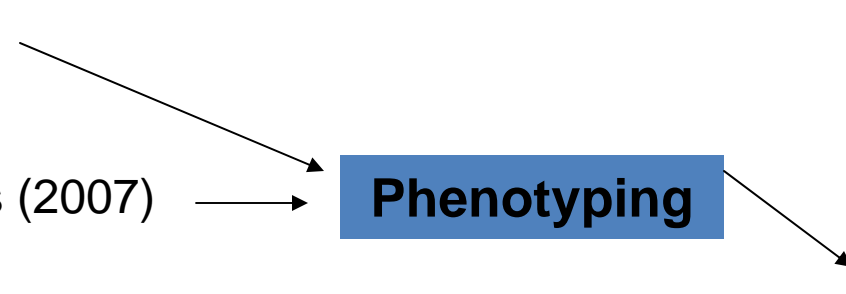


F<sub>2:3</sub> Field two replicates (2007)

Phenotyping

DNA extraction, genotyping

QTL mapping



# Materials and Methods



LSS

HA89

**F<sub>1</sub> hybrid** crossing from two distinguishing parents



**F<sub>2</sub> population**, Greenhouse,

Winter, 2006, Two gallon pots, one plant/pot



**F<sub>2:3</sub> families**, field, 2007,

two replicates, randomized

## Traits and measurements

### Sampling:

Ten seeds from each  $F_2$  individual

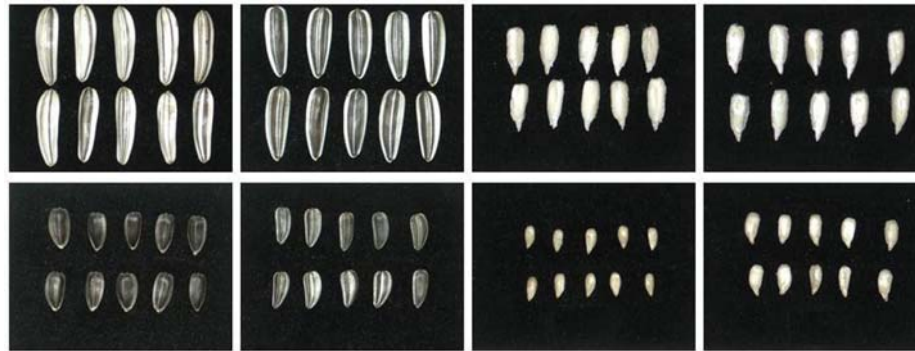
Twenty to thirty seeds from each  $F_{2:3}$  family (two seeds per head)

### Seed traits including:

- 100-seed weight (SWT, g)
  - 100-kernel weight (KWT, g)
  - stripe (STR, 0=totally dark, to 3=white with the least stripe)
  - seed length (SL, cm)
  - seed width (SW, cm)
  - kernel length (KL, cm)
  - kernel width (KW, cm)
  - seed vertical asymmetry (SVA)
  - kernel vertical asymmetry (KVA)
  - seed length to width ratio (SLW, %)
  - kernel length to width ratio (KLW, %)
  - kernel to seed weight ratio (KSR, %)
- Weighted**
- Visually scored**
- Software:**  
**TomatoAnalyzer version 1.2**  
**Brewer et al. 2006**
- Calculated**

# TomatoAnalyzer was developed for analysis tomato fruit shape

Getting images at first



TomatoAnalyzer - seed L019

File Edit View Analyze Settings Help

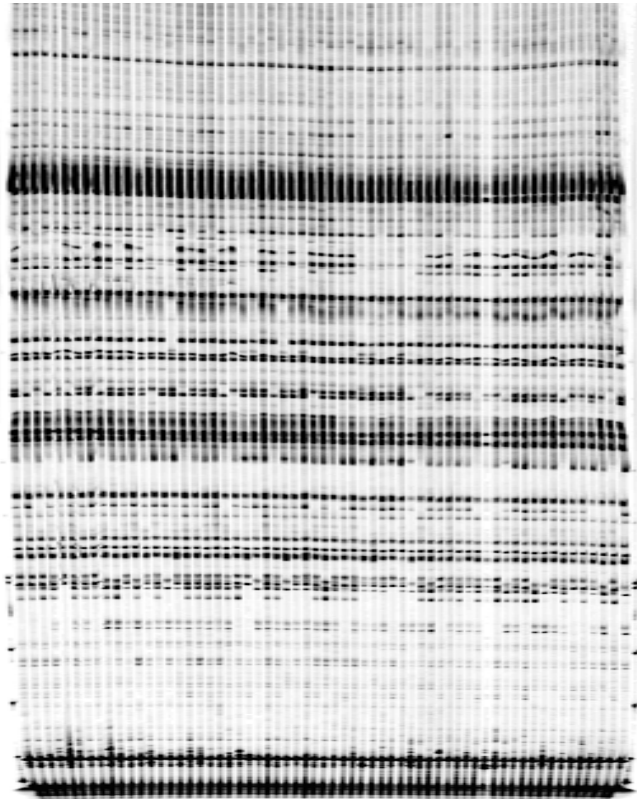
Open Image Save Fruit Export Data Fit size Analyze Revise

#	Perimeter	Area	Width Mid-height	Width Widest	Height Mid-w
01	1320.0925	77806....	188.0000	196.0000	531.0000
02	1431.0042	10016....	215.0000	222.0000	570.0000
03	1370.7199	95771....	204.0000	212.0000	544.0000
04	1404.8864	90563....	191.0000	203.0000	554.0000
05	1351.6560	83982....	191.0000	201.0000	519.0000
06	1422.4844	84919....	193.0000	202.0000	544.0000
07	1460.5433	10569....	219.0000	231.0000	563.0000

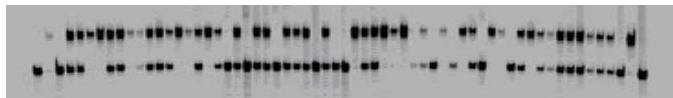
Adjusting rotation and boundary

Automatically getting data

# Genotyping, map construction and QTL analysis



TRAP (Target region amplification polymorphism, Hu and Vick, 2003)



SSR (Simple sequence repeat, Tang et al, 2002)

## Map construction and QTL analysis

### Mapmaker/EXP 3.0

(Lander et al. 1989) (LOD>4.5).

### Mapmaker/QTL1.1

(Lander and Botstein 1989; Lincoln et al. 1993).



# Results

## The performance of these traits in the parents and population

Traits	HA89	LSS	Means	Range
SL	1.1/1.1 <sup>b</sup>	3.1*/2.2*	1.6/1.7	(0.9-2.2)/(1.2-2.5)
SW	0.6/0.5	0.7/0.6	0.6/0.6	(0.3-0.8)/(0.5-0.9)
KL	-/0.8	-/1.4*	1.2/1.2	(0.7-1.4)/(0.9-1.5)
KW	-/0.5	-/0.4	0.5/0.5	(0.3-0.6)/(0.4-0.6)
SLW	2.0/2.0	4.6*/3.8*	2.8/2.8	(2.0-4.1)/(2.2-4.5)
KLW	-/1.9	-/3.5**	2.6/2.7	(2.1-3.2)/(2.1-3.5)
SWT	-/6.1	-/12.3*	8.7/10.7	(2.9-14.8)/(5.7-21.3)
KWT	-/4.6	-/6.4*	6.2/6.6	(2.4-10.0)/(4.0-11.2)
KSR	-/75.9**	-/51.7	72.8/62.1	(56.2-87.3)/(48.4-77.0)
STR	0.0/0.0	3.0**/3.0**	1.7/1.5	(0-3)/(0-3)
SVA	-/2.3	-/7.0*	5.3/5.2	(2.2-9.8)/(3.2-9.6)
KVA	-/2.8	-/4.7*	4.9/3.5	(1.7-9.3)/(1.9-5.9)

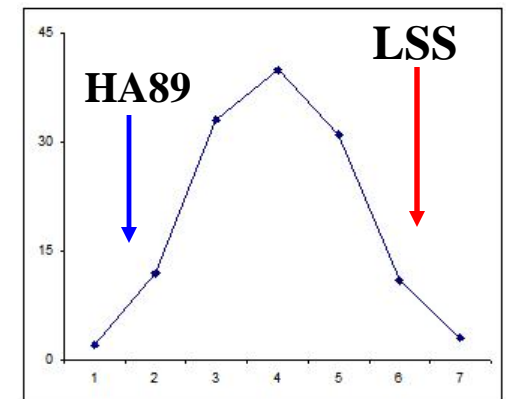
**Two parents:**

**Seed (kernel) length, weight, vertical symmetry, length to width ratios, and stripe**

**Kernel to seed weight ratio**

**In population:**

**In general, these traits were fit to normal distribution, and transgressive segregation was observed for most of traits.**



## Correlations among the seed traits in the population

	SL	SW	KL	KW	SLW	KLW	SWT	KWT	KSR	STR	SA	KA
SW	0.57 <sup>a</sup>											
	0.55											
KL	0.86	0.66										
	0.86	0.55										
KW	0.44	0.89	0.61									
	0.35	0.88	0.46									
SLW	0.51	-0.40	0.22	-0.51								
	0.64	-0.28	0.49	-0.40								
SKW	0.42	-0.31	0.38	-0.50	0.85							
	0.55	-0.25	0.59	-0.44	0.87							
SWT	0.70	0.84	0.82	0.80	NS	NS						
	0.78	0.87	0.79	0.70	NS	NS						
KWT	0.61	0.83	0.80	0.85	-0.24	NS	0.96					
	0.67	0.81	0.80	0.78	NS	NS	0.91					
KSR	-0.61	-0.47	-0.48	-0.23	NS	-0.25	-0.55	-0.32				
	-0.56	-0.48	-0.35	NS	-0.21	-0.24	-0.59	-0.22				
STR	NS	NS	0.26	NS	NS	NS	0.26	NS	-0.41			
	NS	NS	NS	NS	NS	0.22	NS	NS	-0.46			
SVA	0.42	NS	0.35	NS	0.34	0.27	NS	NS	NS	NS		
	0.57	0.30	0.45	NS	0.35	0.29	0.36	0.28	-0.32	NS		
KVA	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	0.52
	0.24	NS	0.28	NS	NS	NS	NS	NS	NS	NS	NS	0.43

**The traits of seed (kernel) length, width, weight highly intercorrelated ( $0.46 < r < 0.96$ )**

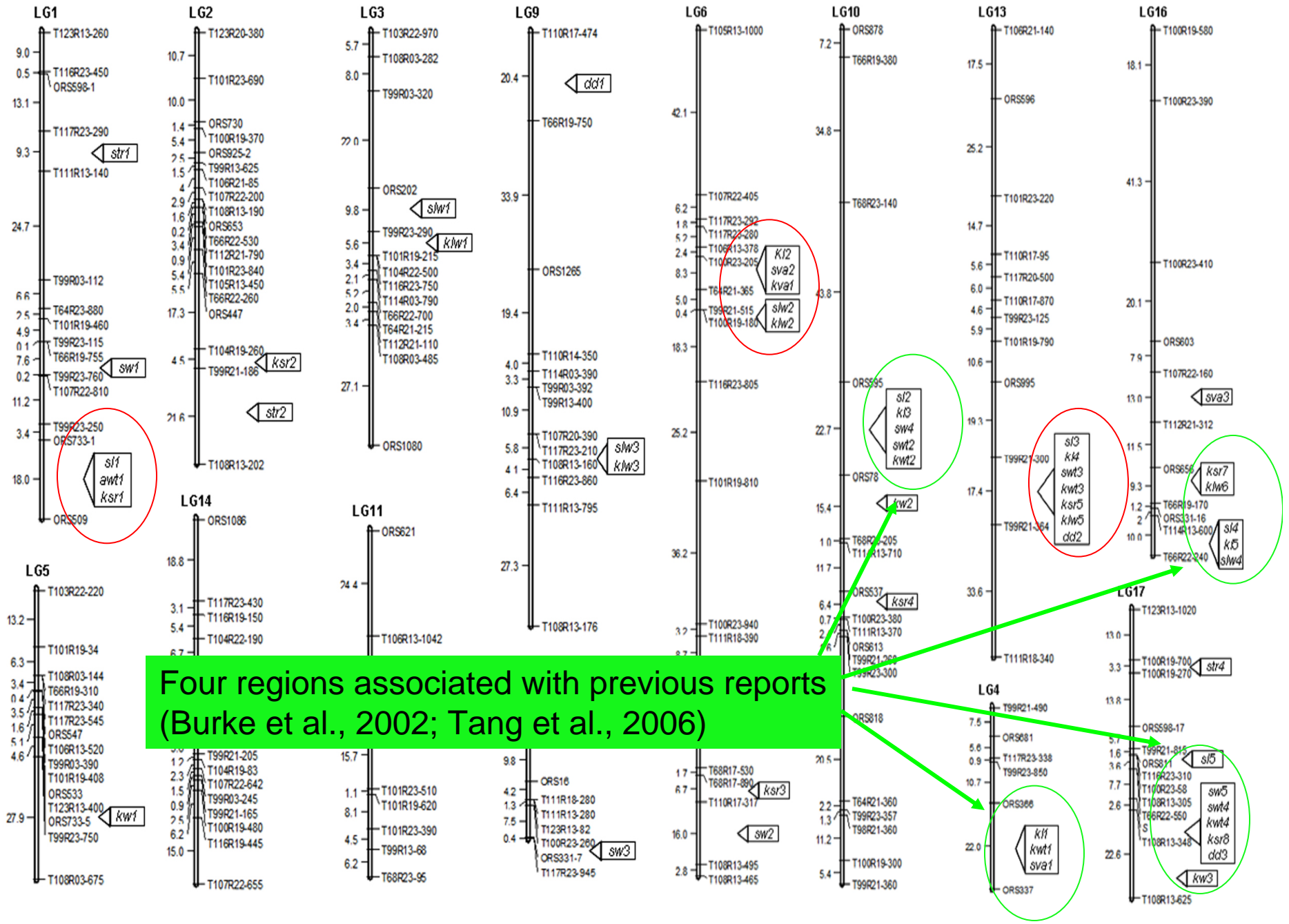
**Kernel to seed weight ratio negatively correlated to the other traits**

## **Map construction and QTL mapping**

**165 TRAP, 44 SSR markers, 17 linkage groups, spanning a total distance of 1784.3 cM.**

**For TRAP marker, each PCR reaction averagely generated 9.6 polymorphic markers; TRAP is more efficient in linkage map construction than other DNA marker techniques.**

**Totally 52 QTL for 12 seed traits were detected, and 60% of the QTL were identified in two tests.**

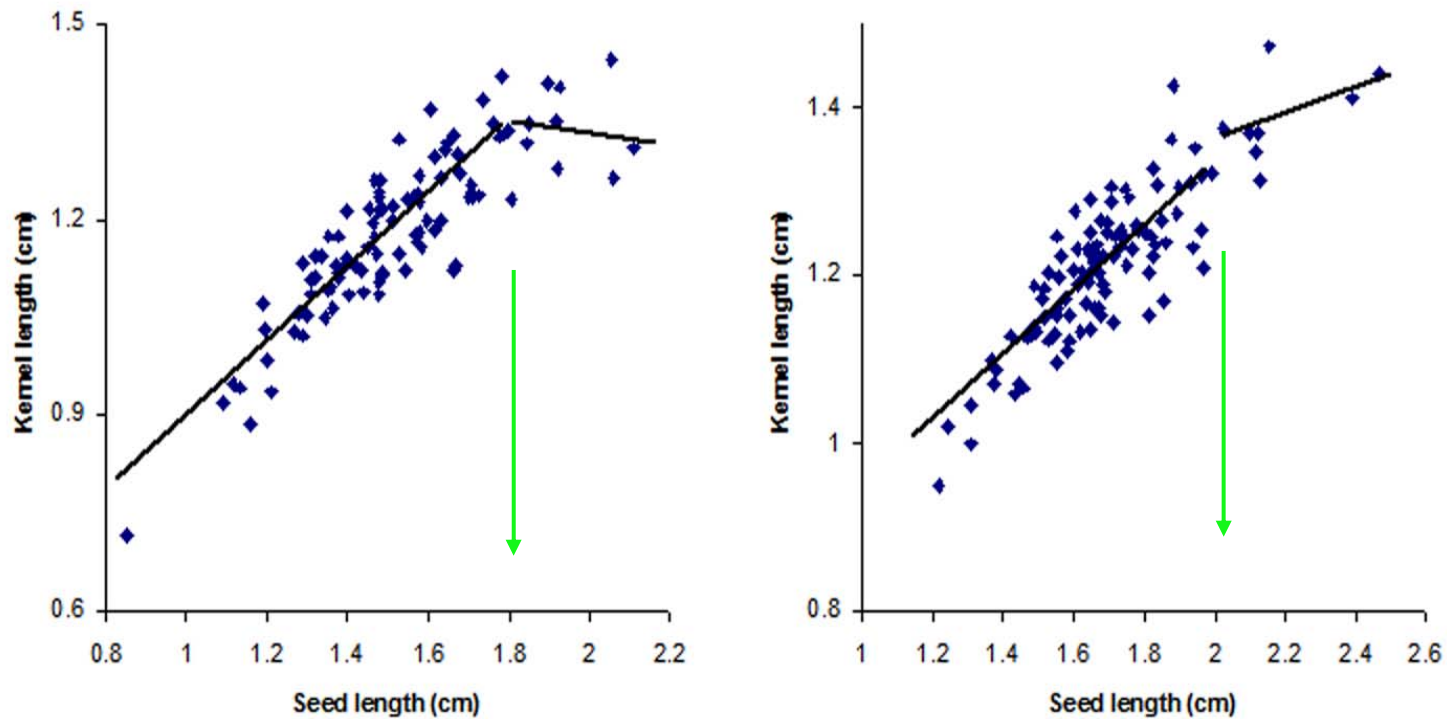


Map and the QTL, QTL clustered in seven chromosomal regions

## **LONG SEEDS $\neq$ LONG KERNEL ?**

**The kernel length was not increasing with the seed length >1.8 cm in greenhouse and 2.0 cm in field.**

**Genetic basis of kernel length is more complex.**

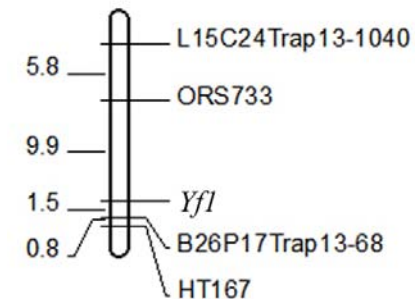
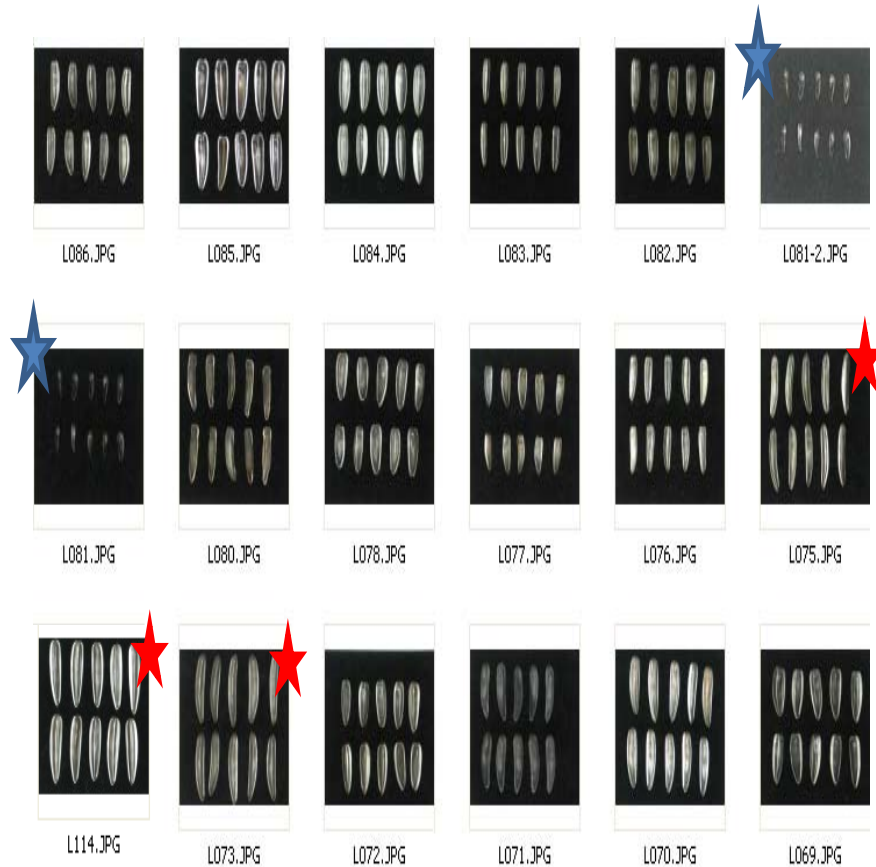


**Scatter plots of seed length against kernel length in greenhouse (left) and field (right) conditions**

## **Conclusion:**

- A linkage map containing 165 TRAP and 44 SSR markers was constructed.**
- A total of 52 QTL for seed traits were detected, each of the QTL explained <30% of the phenotypic variation, suggesting these traits were controlled by multiple genes.**
- The majority of the QTL for confection seed traits (seed or kernel size, kernel-to-seed weight ratio) were located in seven regions, and four of them were co-located with previous reports.**
- In confection sunflower breeding: seed length < 2.0 cm**

# Working Plan in 2008



•Advancing some lines with large seeds size ★

•Advancing some lines with pale ray flower and genetic studies

# Acknowledgement

- **Dr. Brady Vick,**                      **Research Leader**  
• **Dr. Jinguo Hu,**                      **Supervisor**
  
- **Ping Wang,**  
• **Angelia Hogness,**  
• **Wenge Yuan,**                      **Weeding, watering, harvesting**
  
- **Jerry Miller,**  
• **Dale**                                      **Make cross**
  
- **Lisa Brown,**  
• **Leonard Cook,**  
• **Marjorier Olson,**  
• **Theresa Gross,**  
• **Bruce Goren,**                      **Insects inspection, mouse trap, harvesting**
  
- **Financial supported by a grant from the National Sunflower Association (Project number 07-P07).**





谢谢大家!

Thank you!