



# **Soybean Nested Association Mapping**

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# Outline

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- Background on nested association mapping (NAM).
- Maize NAM effort.
- Population development.
- Planned experiments.
- Expected outcomes.
- Cooperators.

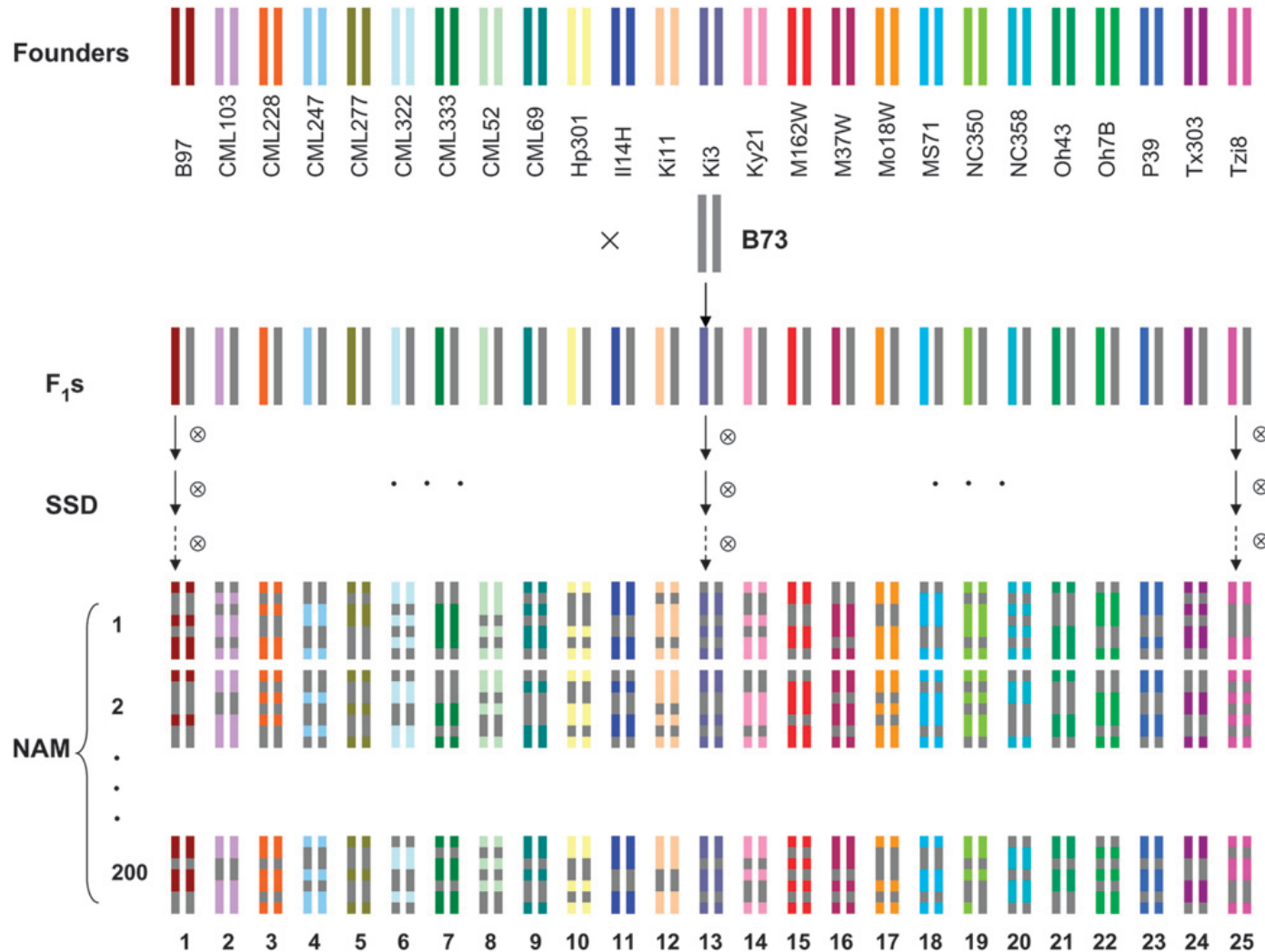
# Nested Association Mapping

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- Nested association mapping (NAM) combines advantages of linkage and association mapping.
  - Linkage mapping - Advantage of power in identifying QTL but disadvantage of poor map resolution.
  - Association mapping – Advantage of high map resolution but disadvantage of poor power in identifying QTL.



# Structure of Maize NAM



From Yu et al. Genetics 178:539-551.

# Maize NAM

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- 39 QTL were mapped for days to silking.
- Not able to map QTL controlling yield. because the parents were too diverse.
- Increasing marker density.
  - 50 million SNPs on parents.
- Expect to map QTL to haplotypes.

# SoyNAM

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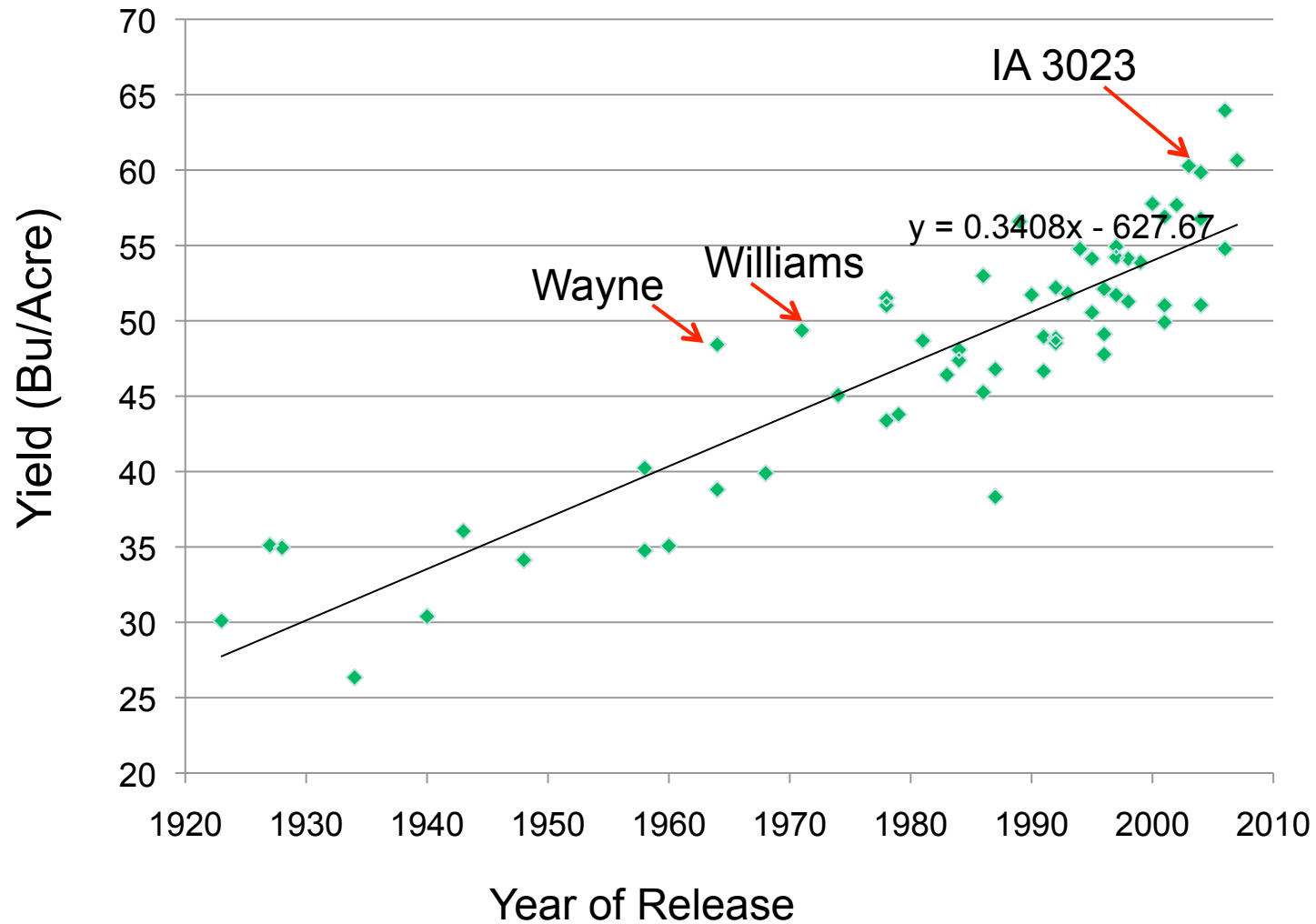
- Objective is to map QTL that control seed yield, agronomic traits, and seed composition in soybean germplasm to haplotypes (intervals that average 150 kb).
  - Provide information on allelic diversity for QTL controlling agronomic traits across a wide range of germplasm including elite and exotic sources.
  - Make it possible to predict what QTL alleles are in lines and select alleles through marker-assisted selection.

# SoyNAM

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- Populations being developed so that all lines will be MG III.
- Developing 40 populations by crossing 40 parents to the ISU cultivar IA3023.
  - Each population will include 140 lines for a total of 5,600 lines.
  - Populations are being selected for maturity during inbreeding.
- Should have power to detect  $> 0.95$  QTL with effects as low as 3%.

# MG III Yield Across Environments in 2010







# SoyNAM Parents

- 40 Parents include:
  - 17 high yielding parents from 8 states.
  - 15 lines with diverse ancestry from R. Nelson's program.
  - 8 plant introductions.

Parent	Origin	Parent	Origin
<b>4J105-3-4</b>	Purdue Univ.	<b>LG94-1128</b>	USDA-ARS
<b>5M20-2-5-2</b>	Purdue Univ.	<b>LG94-1906</b>	USDA-ARS
<b>CL0J095-4-6</b>	Purdue Univ.	<b>LG97-7012</b>	USDA-ARS
<b>CL0J173-6-8</b>	Purdue Univ.	<b>LG98-1605</b>	USDA-ARS
<b>HS6-3976</b>	Ohio State	<b>Magellan</b>	Univ. of Missouri
<b>LD00-3309</b>	Univ. of Illinois	<b>Maverick</b>	Univ. of Missouri
<b>LD01-5907</b>	Univ. of Illinois	<b>NE3001</b>	Univ. of Nebraska
<b>LD02-4485</b>	Univ. of Illinois	<b>Prohio</b>	Ohio State Univ.
<b>LD02-9050</b>	Univ. of Illinois	<b>S06-13640</b>	Univ. of Missouri
<b>LG03-2979</b>	USDA-ARS	<b>Skylla</b>	Mich. State Univ.
<b>LG03-3191</b>	USDA-ARS	<b>TN05-3027</b>	Univ. of Tenn.
<b>LG00-3372</b>	USDA-ARS	<b>U03-100612</b>	Univ. of Nebraska
<b>LG04-4717</b>	USDA-ARS	<b>PI 398.881</b>	South Korea
<b>LG04-6000</b>	USDA-ARS	<b>PI 427.136</b>	South Korea
<b>LG05-4292</b>	USDA-ARS	<b>PI 437.169B</b>	Russia
<b>LG05-4317</b>	USDA-ARS	<b>PI 438.164B</b>	China
<b>LG05-4464</b>	USDA-ARS	<b>PI 518.751</b>	Serbia
<b>LG05-4832</b>	USDA-ARS	<b>PI 561.370</b>	China
<b>LG90-2550</b>	USDA-ARS	<b>PI 404.188A</b>	China
<b>LG92-1255</b>	USDA-ARS	<b>PI 574.486</b>	China

# SoyNAM Genotyping

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- Parents of the populations being tested with 50,000 SNP markers.
- Requesting funding to resequence the 41 parents to identify millions of SNPs.
- Lines in populations will be tested with 1,536 SNP markers.
- The millions of SNPs can be projected to lines in the populations

# Phenotyping

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- 70 of the 140 lines/population will be available for testing in 2011 (2,800 lines).
  - Tests planned for Illinois and Nebraska.
- 140 lines/population will be available for yield testing in 2012 and 2013 across more locations (5,600 lines).
- Test lines for seed yield, maturity, plant height, lodging, and seed protein and oil content.

# Phenotyping

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- Commitments have been made to grow plots in 2012 and 2013 (assuming funding approved).

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Cooperator	State	Institution	Annual no. of plots
Stella Kantartzis	Illinois	Southern Illinois Univ. Univ. of Illinois and	2,000
Brian Diers and Randall Nelson	Illinois	USDA-ARS	5,600
Bill Beavis	Iowa	Iowa State Univ.	5,600
William Schapaugh	Kansas	Kansas State Univ.	4,000
Dechun Wang	Michigan	Michigan State Univ.	1,000
Grover Shannon	Missouri	Univ. of Missouri	1,000
George Graef and James Specht	Nebraska	Univ. of Nebraska	5,600
Leah McHale	Ohio	Ohio State Univ.	2,000
Rouf Mian	Ohio	USDA-ARS	2,000
Total			28,800

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# Conclusions

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- A set of 40 NAM populations are being developed.
- Field testing will be initiated in 2011 and continue through 2013.
- Working on securing funding for resequencing parents and phenotyping.
- These populations will be a resource for mapping QTL controlling other traits.

# Acknowledgements

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- Funding from the United Soybean Board has supported the population development, marker testing and initial field tes

