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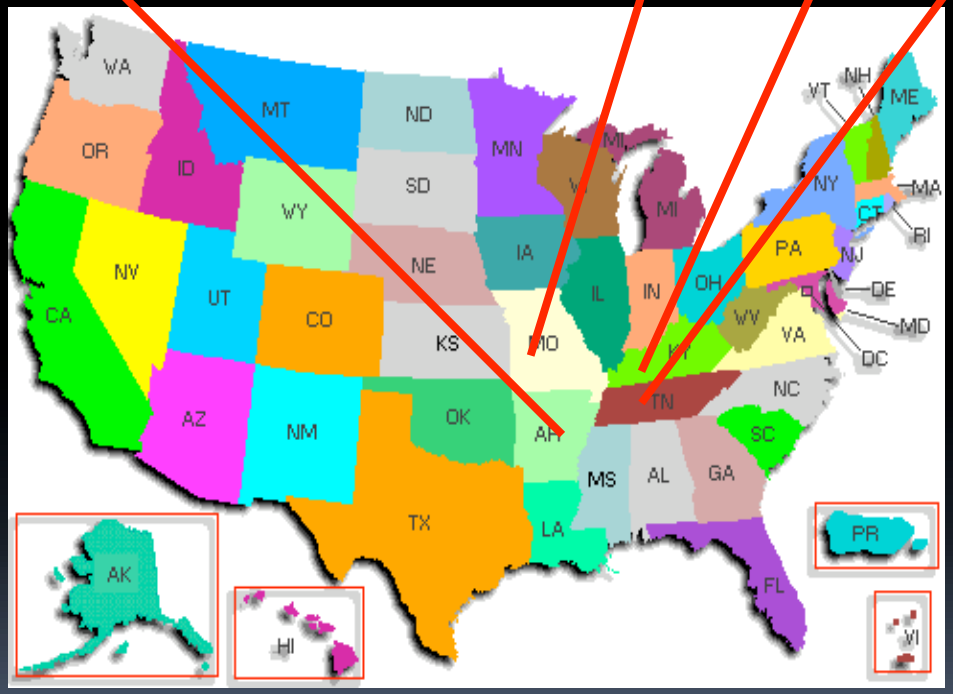
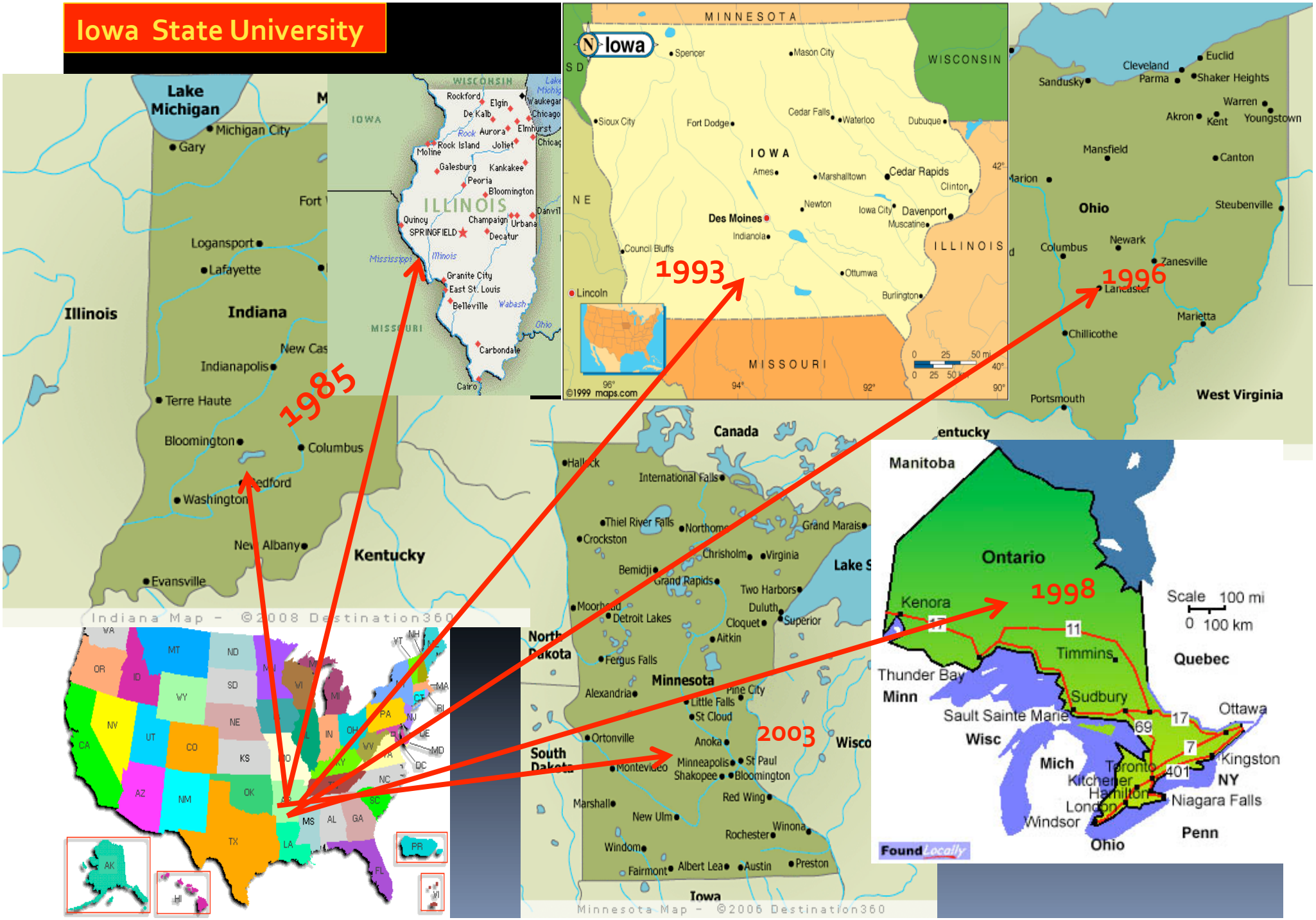
1971 - Arkansas

1984 - Missouri, Kentucky, Tennessee

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Lake Michigan
Michigan City
Gary
Logansport
Lafayette
Illinois
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Indianapolis
Terre Haute
Bloomington
Columbus
Washington
Evansville
Kentucky
1985
WISCONSIN
IOWA
ILLINOIS
MISSOURI
Rockford
Elgin
De Kalb
Aurora
Rock Island
Joliet
Moline
Galesburg
Kankakee
Peoria
Bloomington
Quincy
Champaign
Urbana
SPRINGFIELD
Decatur
Granite City
East St. Louis
Belleville
Carbondale
Cairo
MINNESOTA
Iowa
Spencer
Mason City
Sioux City
Fort Dodge
Cedar Falls
Waterloo
Dubuque
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Thiel River Falls
Crookston
Grand Marais
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Bemidji
Grand Rapids
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Duluth
Moorhead
Detroit Lakes
Cloquet
Superior
Aitkin
North Dakota
Fergus Falls
Minnesota
Alexandria
Pine City
Little Falls
St Cloud
Ortonville
Anoka
Minneapolis
St Paul
Shakopee
Bloomington
South Dakota
Montevideo
Red Wing
Marshall
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Winona
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Austin
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Minnesota Map - ©2006 Destination360
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Thunder Bay
Minn
Sudbury
Ottawa
Sault Sainte Marie
Wisc
Mich
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Hamilton
Niagara Falls
London
Windsor
Penn
Ohio
FoundLocally
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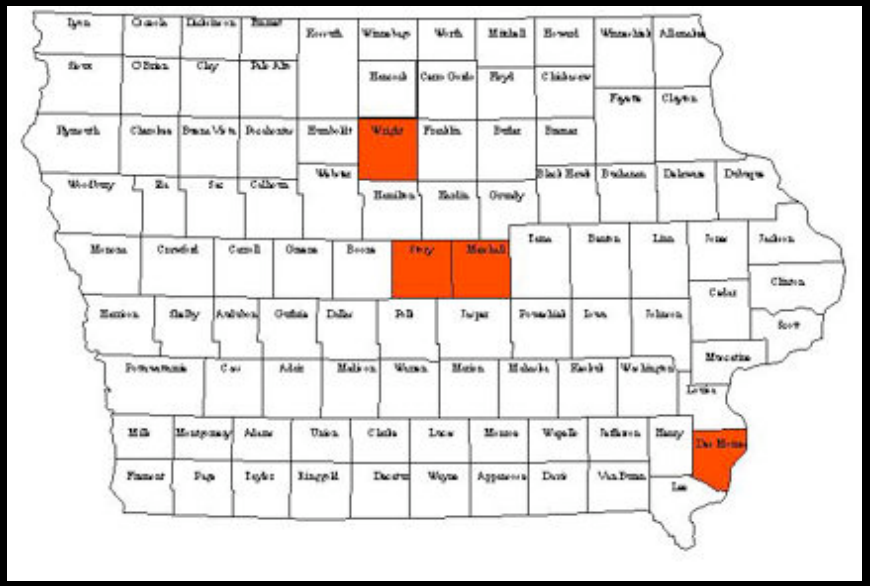

1994 SDS in Iowa

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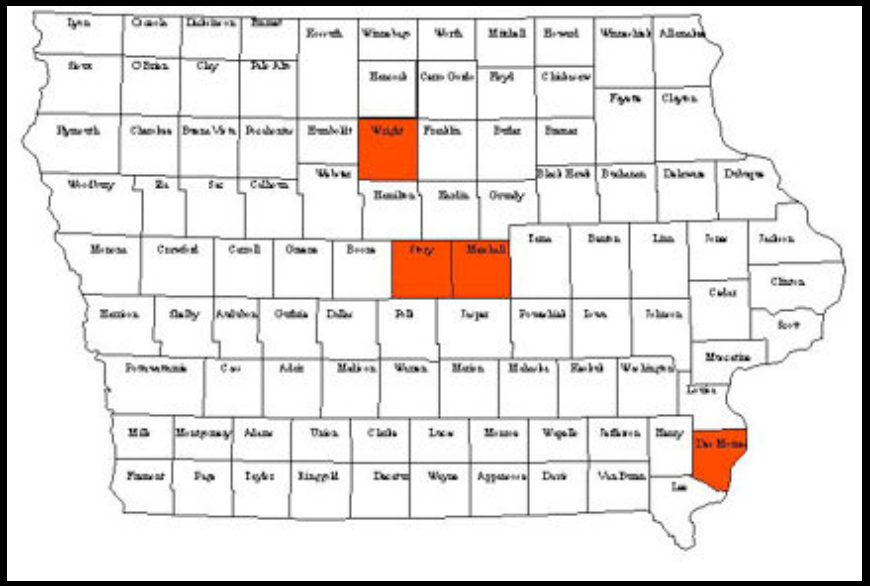
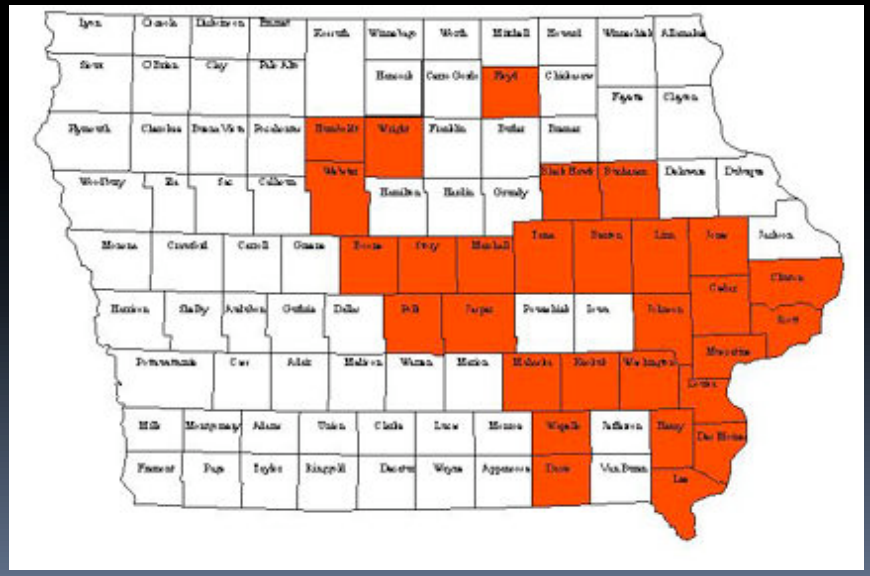
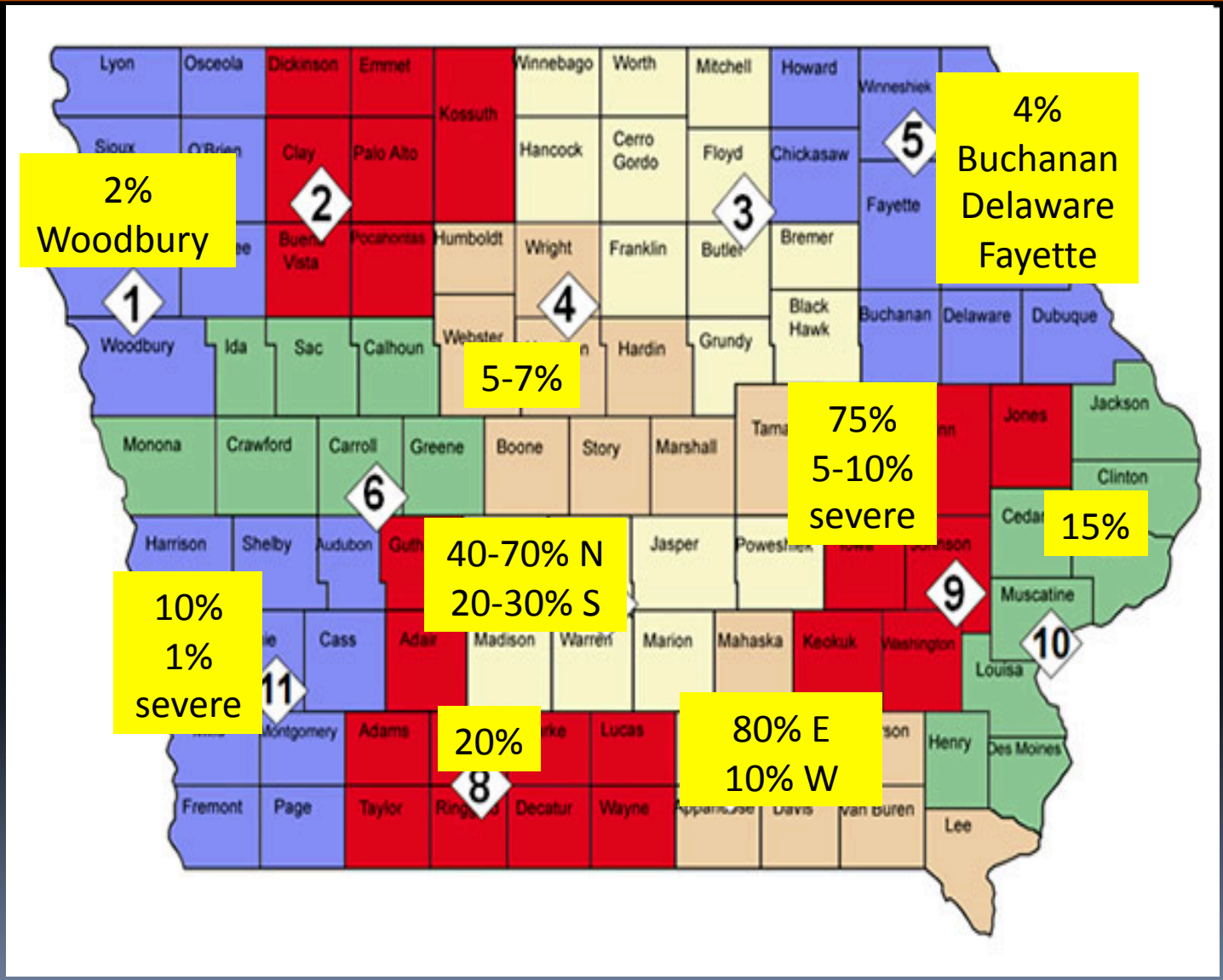


1994 SDS in Iowa



1998 SDS in Iowa

SDS Estimates in 2009



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SDS – Fungal disease caused by *Fusarium virguliforme*

BREEDING EFFORTS TO IMPROVE SDS RESISTANCE IN SOYBEAN

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Rationale for Breeding efforts

Relate to the plant

- Rapid spread of disease in soybean production areas
- Limited
  - number of genetic sources of resistance
  - knowledge of inheritance of resistance

Relate to the pathogen

- Screening tools amenable to differentiate small phenotypic effects
- Detailed genetic work to facilitate breeding resistance work in soybean

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Breeding efforts

- Several groups are developing populations by crossing R x S genotypes
- Some are using screening data and molecular information to select for resistance
- At ISU, we still cross R x S, and also starting to develop populations by crossing R x R genotypes

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Sources of SDS resistance

Breeding at ISU

- LS98-0582
- LS99-2235
- LS94-3207
- Ripley

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Sources of SDS resistance
Breeding at ISU

LS98-0582
LS99-2235
LS94-3207

- Ripley

	Disease Index				
	2004				
	IA	IA	Can	IL	IL
AR10SDS	**1**	**9**	**1**	**1**	**16**
MN 1606 SP (Res)	2	0	1	0	8
Venus RR (Res)	0	0	0	15	4
5171 RR (Susc)	4	8	0	15	20
	2005				
AR10SDS	**0**		**14**	**0**	**0**
MN 1606 SP (Res)	0		26	0	0
Venus (Res)	0		15	0	0
5171 RR (Susc)	0		19	2	20
	2007				
AR10SDS		**2 (MN)**	**1 (IL)**	**0**	**0**
MN1606 SP (Res)		10	0	0	0
Venus (Res)					
5171 RR (Susc)		20	8	4	17

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The molecular information available

Population	# of QTL	Chromosomes
Essex x Forrest	9	13, 16, 6, 20, 13
Pyramid x Douglas	3	3,6,18
Hartwig x Flyer	2	18,8
Ripley x Spencer	3	4,17,19
PI567374 x Omaha	2	17, 20

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Simultaneous work on

- I. Breeding for germplasm releases
  - Germplasm release - spring 2010
  - Searching for the proper combination of yield, SDS and MG for Iowa
- II. Considering interactions
  - SDS and SCN
  - SDS and BSR
- III. Research
  - modifications to the screening method (Luckew & Leandro)
  - new screening methods - toxin use (Bhattacharyya's lab)
  - molecular marker development
  - search for new genes

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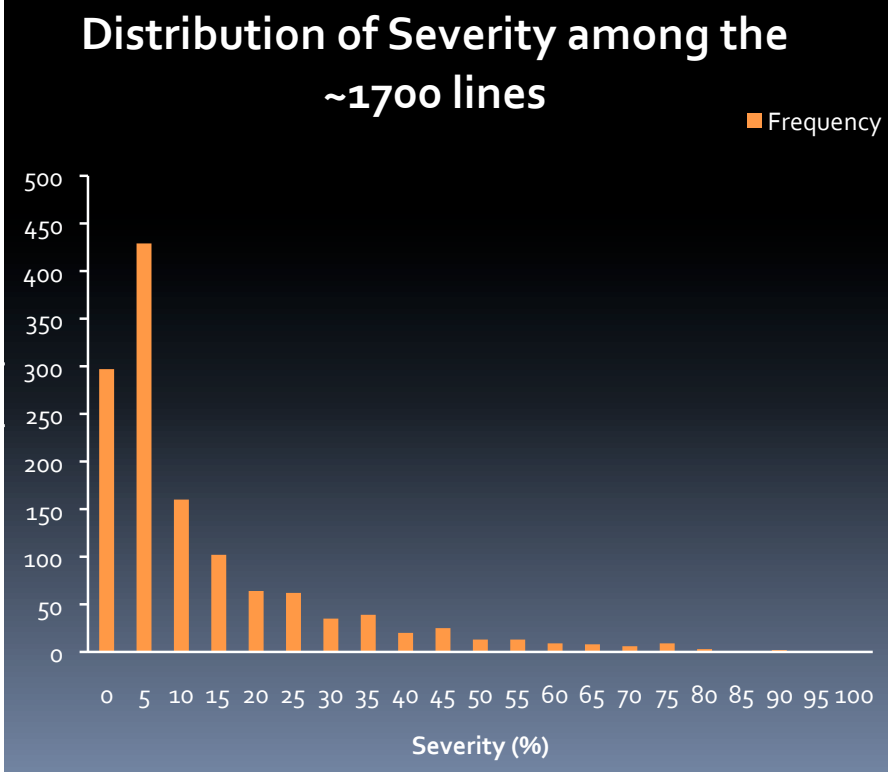
- Find the number of QTLs that will confer adequate resistance
- Screen ~1700 lines for differing SDS resistance
  - Using the classic screening method



- The second screening method
  - Toxin assay using cultured filtrate
    - Mont-1 isolate
    - Plants with intact roots immersed in diluted toxin
    - Ten genotypes

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Details of Inbred Soybean Lines

Population Name	Susceptible parent	Resistant parent	No. of Populations	No. of Subpopulations
AX19286	A95-684043	LS94-3207	11	391
AX19287	A95-684043	LS98-0582	10	435
AX19288	A95-684043	LS99-2235	1	392
AX19289	IA1006	LS94-3207	4	446
AX19290	IA1006	LS98-0582	3	471
AX19291	IA1006	LS99-2235	1	85
AX19294	IA2050	LS94-3207	8	461

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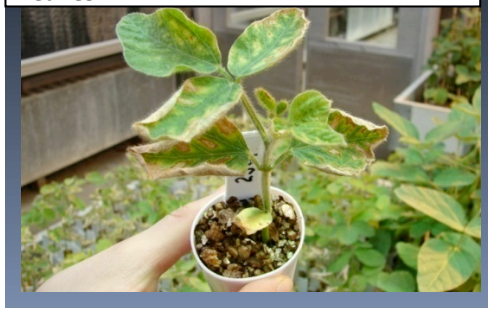
Screening of AX19286 subpopulations

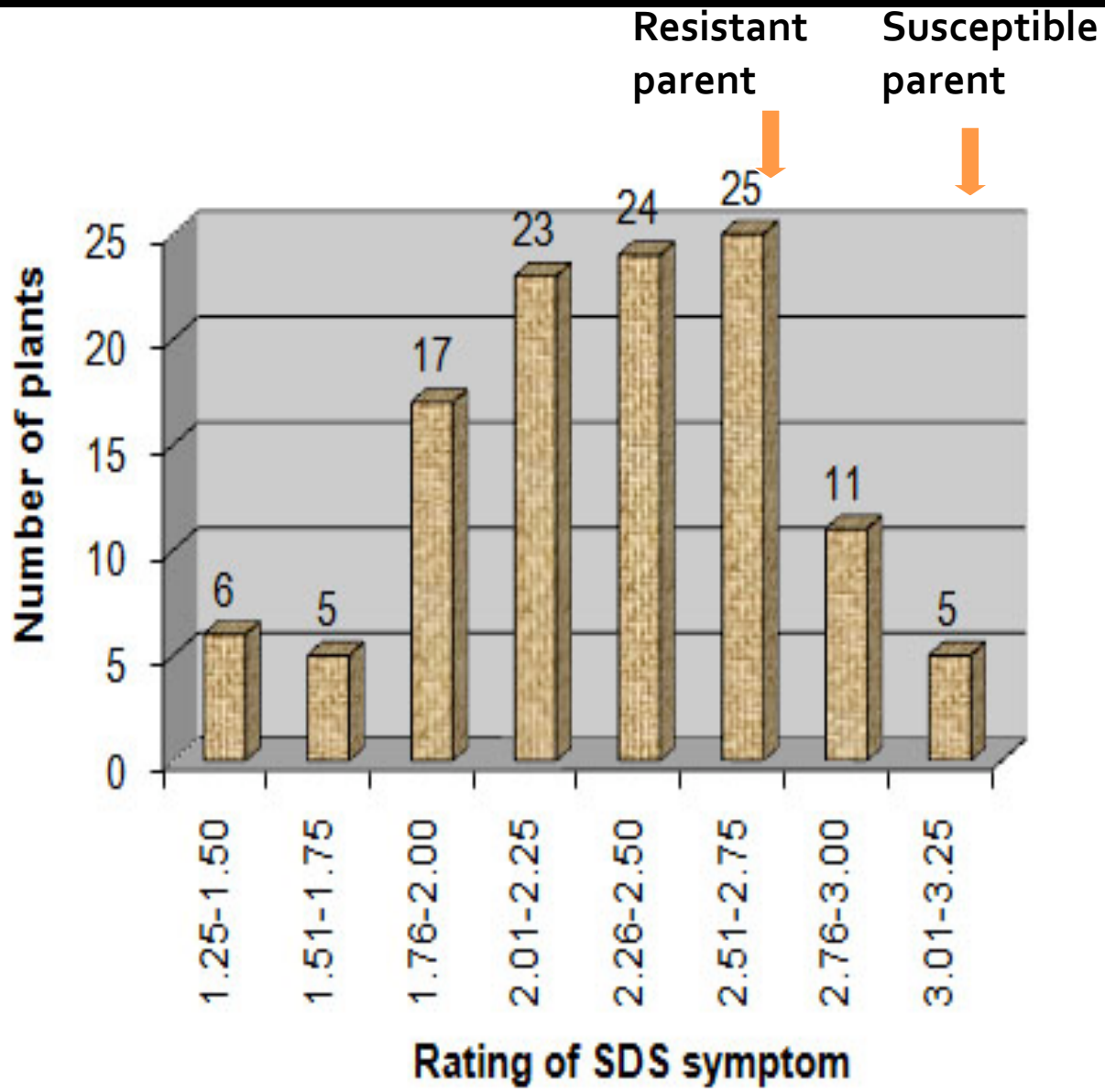
2 slight chlorotic flecks/ blotches

3 Leaf with inter-veinal chlororsis

4 - necrosis + chlorosis

5 extended Necrosis + cupping of leaves





V3 stages of plants scored

Therefore,

- The work is undergoing in several breeding labs, with interesting results
- Important work is underway on the pathogen
- Screening techniques are modified and new ones are under development, serving phenotyping efforts, better and more efficiently
- Lines in early maturity groups are and will be available for breeding for disease resistance.
- And, the collective work continuous