

# I - D. Evaluation of Wild Perennial *Glycine* Species and Crosses For Resistance to *Phakopsora*

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## WILD PERENNIAL *GLYCINE* GERM PLASM

The genus *Glycine* Willd. currently is divided into two subgenera, *Glycine* and *Soja* (Moench) F.J. Herm. (Table 1). The subgenus *soja* includes the cultivated soybean, *G. max* (L.) Merr, and the wild soybean, *G. soja* Sieb. and Zucc. Both species are annual, diploid with  $2n=40$ , and hybridized readily. The soybean grows only under cultivation while *G. soja* grows wild in China, Japan, Korea, Taiwan and Russia. *Glycine max* and *G. soja* form the primary gene pool for the cultivated soybean (10). Evidence from several sources, including morphology, cytogenetics, seed proteins, phytoalexins, restriction endonuclease fragment analysis of mitochondrial DNA, ribosomal RNA, and chloroplast DNA supports the hypothesis that *G. soja* is the wild ancestor of the soybean (7, 8, 13, 15, 19).

In 1976, the subgenus *Glycine* contained six wild perennial species, that is, *Glycine canescens*, *G. clandestina*, *G. falcata*, *G. latrobeana*, *G. tabacina* and *G. tomentella*. At present, the subgenus consists of 16 wild perennial species (Table 1). The increase in the number of species in the subgenus *Glycine* is due to both extensive plant exploration by me and my Australian colleagues as well as classical taxonomic studies conducted by Mary Tindale, National Herbarium of New South Wales, Sydney, Australia (24, 25, 27, 28).

Utilization of wild species for improvement of their cultivated counterparts is steadily increasing in various crops (9, 17, 21-23). Exploitation of the wild progenitors is a reasonable approach since a cultigen (e.g. the soybean) and its wild progenitor (*G. soja*) are genetically members of the same species and gene transfer between them is a relatively easy task. Use of other wild species,

such as those belonging to the secondary or tertiary gene pools of the cultigen (10), is much more difficult since various types of isolating mechanisms that prevent gene flow between different biological units must be overcome. On the other hand, because of genetic remoteness and unique selection pressures on these wild species in comparison with the cultigen, there is a good possibility that they possess variation in economically valuable characteristics that may be missing in the cultivated germ plasm.

Investigations of wild perennial *Glycine* species related to the soybean were restricted in the past by the lack of experimental material. Prior to 1979, about 68 wild perennial *Glycine* accessions were maintained as part of the USDA soybean germ plasm collection (Table 2). *Glycine latrobeana* was not represented in the collection. For *Glycine canescens* and *G. falcata* there were one or two accessions, respectively.

In 1977, I initiated a major plant exploration effort to introduce wild perennial *Glycine* germ plasm into the U.S. for the express purpose of carrying out biosystematic and cytogenetic investigations. Thus far, plant exploration trips have been undertaken by me or by colleagues to Australia, Papua New Guinea, the Philippines, Taiwan, Pescadores Islands (Taiwan), Marianas, Tonga, Fiji, Ryukyu Islands (Japan), Vanuatu (New Hebrides), and New Caledonia. In 1996, Tony Brown and Jim Grace, CSIRO/Canberra, and I hope to explore the central arid zone of Australia for perennial *Glycine* species. At present, the collection has 888 accessions with representatives of all taxa (Table 2). In September 1987, the USDA and the University of Illinois at Urbana-Champaign signed a cooperative

Table 1. List of species in the genus *Glycine* Wilid., three letter code, 2n, standard (P1), genome symbols and distribution.

Species	Code	2n	Standard	Genome	Distribution	
		Subgenus	<i>Glycine</i>			
<i>G. albicans</i> Tind. and Craven	ALB	40	—	—	Australia	
<i>G. arenaria</i> Tind.	ARE	40	505204	—	Australia	
<i>G. argyrea</i> Tind.	ARG	40	505151	A <sub>2</sub> A <sub>2</sub>	Australia	
<i>G. canescens</i> F. J. Herm	CAN	40	440932	AA	Australia	
<i>G. clandestina</i> Wendl.	CLA	40	440948	A <sub>1</sub> A <sub>1</sub>	Australia	
<i>G. curvata</i> Tind.	CUR	40	505166	C <sub>1</sub> C <sub>1</sub>	Australia	
<i>G. cyrtoloba</i> Tind.	CYR	40	440963	CC	Australia	
<i>G. falcata</i> Benth.	FAL	40	505179	FF	Australia	
<i>G. hirticaulis</i> Tind. and Craven	HIR	40,80	—	—	Australia	
<i>G. lactovirens</i> Tind. and Cravens	LAC	40	—	—	Australia	
<i>G. latifolia</i> (Benth.) Newell and Hymowitz	LAT	40	378709	B <sub>1</sub> B <sub>1</sub>	Australia	
<i>G. latrobeana</i> (Meissn.) Benth.	LTR	40	483196	A <sub>3</sub> A <sub>3</sub>	Australia	
<i>G. microphylla</i> (Benth.) Tind.	MIC	40	440956	BB	Australia	
<i>G. pindanica</i> Tind. and Craven	PIN	40	—	—	Australia	
<i>G. tabacina</i> (Labill.) Benth.	TAB	40	373990	B <sub>2</sub> B <sub>2</sub>	Australia	
		80	—	Complex <sup>1</sup>	Australia, West Central South Pacific Islands	
<i>G. tomentella</i> Hayata	TOM	38	440998	EE	Australia	
		40	—	DD <sup>2</sup>	Australia, Papua New Guinea	
		78	—	Complex <sup>3</sup>	Australia, Papua New Guinea	
		80	—	Complex <sup>4</sup>	Australia, Papua New Guinea, The Philippines, Taiwan	
Subgenus <i>Soja</i> (Moench) F. J. Herm.						
<i>G. soja</i> Sieb. and Zucc.		SOJ	40		GG	China, Russia, Taiwan, Japan, Korea (wild soybean)
<i>G. max</i> (L.) Merrill		MAX	40		GG	Cultigen (soybean)

<sup>1</sup> Allopolyploids (A and B genome) and segmental allopolyploids (B genome)

<sup>2</sup> At least three groups

<sup>3</sup> Allopolyploids (D and E, A and E, or any other unknown combination)

<sup>4</sup> Allopolyploids (A and D genomes, or any other unknown combination)

agreement. The wild perennial *Glycine* collection maintained at the UIUC became part of the U.S. plant germ plasm system. In addition, CSIRO/Canberra maintains a large collection of wild perennial *Glycine* species. The numbering systems of both collections, that is, the Australian G numbers and the U.S. PI and IL

numbers are coordinated. Thus research publications listing wild perennial accessions reported in methods and materials sections can be converted quite easily from the Australian accession identification system to the U.S. accession identification system and vice versa.

Table 2. The U.S. wild perennial *Glycine* collection, 1979 and 1995.

Species	2n no.	Number of Accessions	
		1979	1995
<i>G. albican</i>	40	0	2
<i>G. arenaria</i>	40	0	3
<i>G. argyrea</i>	40	0	3
<i>G. canescens</i>	40	1	81
<i>G. clandestina</i>	40	14	138
<i>G. curvata</i>	40	0	6
<i>G. cyrtoloba</i>	40	0	28
<i>G. fatcata</i>	40	20	14
<i>G. hirticaulis</i>	40	0	1
<i>G. hirticaulis</i>	80	0	1
<i>G. lactovirens</i>	40	0	2
<i>G. tactifolia</i>	40	0	46
<i>G. latrobeana</i>	40	0	12
<i>G. microphylla</i>	40	0	32
<i>G. pindanica</i>	40	0	5
<i>G. tabacina</i>	40	0	14
<i>G. tabacina</i>	80	0	131
<i>G. tabacina</i>	?	28	90
<i>G. tomentella</i>	38	0	22
<i>G. tomentella</i>	40	0	57
<i>G. tomentella</i>	78	0	55
<i>G. tomentella</i>	80	0	53
<i>G. tomentella</i>	?	23	92
Total accessions		68	888

#### SCREENING FOR RESISTANCE TO PHAKOPSORA

Singh *et al.* (20) reported, that under field conditions in India, accessions of *Glycine tabacina* and *G. tomentella* were resistant to soybean rust. I believe that this is the first paper reporting resistance to soybean rust within the subgenus *Glycine*.

In Australia (2, 5, 6, 16) and in the U.S. (12), the potential use of wild perennial *Glycine* species in plant improvement programs was discussed. The wild perennial *Glycine* represent a potentially rich source of germ plasm for soybean breeders. Yet, these species have been relatively little studied or exploited in plant breeding programs.

The 1988 Asian Vegetable Research and Development Center (AVRDC) Progress Report (1) revealed that 100 wild perennial *Glycine* accessions from Australia were screened for resistance to soybean rust in Taiwan. High levels of resistance were exhibited by accessions of *G. argyrea*, *G.*

*clandestina*, *G. tabacina* (2n=80) and *G. tomentella* (2n=40, 80),

In 1992, Hartman *et al.* (11) reported that over a 3-year period, 294 accessions representing 12 perennial *Glycine* species were screened for resistance to *P. pachyrhizi* at AVRDC in Taiwan. Resistant or moderately resistant accessions to soybean rust were identified within accessions of *G. argyrea*, *G. canescens*, *G. clandestina*, *G. latifolia*, *G. microphylla*, *G. tabacina* and *G. tomentella*.

#### GENETICS OF RESISTANCE TO PHAKOPSORA

Thus far, all genetic studies of resistance of wild perennial *Glycine* species to soybean rust have been conducted in the laboratory of Jeremy Burdon, CSIRO/Canberra. Burdon (3) reported on the phenotypic and genetic patterns of resistance to soybean rust within two populations of *Glycine canescens*. In both populations, resistance was conditioned by single dominant genes. Burdon estimated that the two populations contained a minimum of 10 to 12 resistance genes. In another experiment, Burdon (3) demonstrated that single resistance

genes were detected in six out of seven host *G. canescens* lines. In the seventh line, two independently inherited genes for resistance were present. Intercrossing showed that some of these resistance genes were inherited independently.

Jarozz and Burdon (14) studied resistance to *P. pachyrhizi* within a population of *Glycine argyrea*. Four phenotypic patterns of resistance and susceptibility to nine races of the pathogen were found among 49 plants of a *Glycine argyrea* population. Genetic analysis suggested that the most common phenotypic patterns were determined by two alleles at a single locus. These results contrasted with those studies conducted with *Glycine canescens*. Burdon postulated, "that *G. argyrea*'s relatively high rate of outcrossing and the apparent prevalence of forms of resistance which delay the development of the pathogen may have contributed to the small number of major resistance genes in this population."

Schoen *et al.* (18) studied the resistance of *Glycine tomentella* to soybean rust in relation to ploidy level and geographic distribution. Results from crosses between accessions with tetraploids indicate that in the aneuploid form (2n=78) resistance to *P. pachyrhizi* was under the control of a single dominant gene whereas in the tetraploids (2n=80) resistance was controlled by two or three gene loci. The investigator located two regions of susceptibility. The highest proportion of susceptible accessions of *G. tomentella* occurs in the Kimberley Plateau region of Western Australia and the Northern Territory, and another region of susceptibility is found in the Townville/Cairns region of Queensland.

Backcross derived fertile plants from soy bean and *G. tomentella* intersubgeneric hybrids were

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reported by Singh *et al.* (21). At present, progeny are being screened by A. Brown, CSIRO/Canberra, to determine if the resistance of *G. tomentella* to soybean rust has been transferred into the cultivated soybean.

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