

## Geographical Patterns of Morphological Variation in Soybean Germplasm

**Mun Sup Yoon\*<sup>†</sup>, Jong Woong Ahn\*\*, Sei Joon Park\*\*\*, Hyung Jin Baek\*,  
Nam Kyu Park\* and Young Deok Rho\*\*\*\***

\*National Institute of Agricultural Science and Technology, RDA, Suwon 441-707, Korea

\*\*Research Management Bureau, RDA, Suwon 441-707, Korea

\*\*\*National Crop Experiment Station, RDA, Suwon 441-100, Korea

\*\*\*\*Dept. of Agronomy, Kyung Hee Univ., Suwon 449-701, Korea

**ABSTRACT:** A total of 1,830 soybean collections were grown in the field and characterized for 10 morphological traits to determine the diversity and relationship within and among geographical regions. Phenotypic variation was found within all regions for most characters. The Shannon-Weaver diversity index ranged from 0.49 to 0.62 across regions, and 0.09 to 1.00 across characters. Canonical discriminant analysis and clustering of the canonical means delineated 3 regional clusters: (i) Kyunggi, Chungchong, Kangwon, Chulla, and Kyungsang; (ii) Heilongjiang; and (iii) Jilin, Manchuria, central China, south China, Others (China), Hokkaido, Honshu, and Others (Japan).

**Keywords :** *glycine max*, morphological trait, diversity index, canonical discriminant analysis.

The determination of the extent of phenotypic and genotypic diversity in germplasm collection provide indications of redundancies or omissions and can aid in managing collection. The information on diversity analysis also, could be used to devise a core collection. Further, easily observable morphological traits are generally used to characterize genetic resources (Perry & McIntosh, 1991). In order to determine the distribution of diversity in germplasm, phenotypic and genotypic variation within and between countries and regions of origin have been examined for several crop species including: soybean (Perry & McIntosh, 1991); rice (Holcomb *et al.*, 1977); durum wheat (Jain *et al.*, 1975); and barley (Tolbert *et al.*, 1979). The study aimed to describe the extent of geographical diversities and relationships and obtain a basic information to make a soybean core collection.

### MATERIALS AND METHODS

A total of 1,830 accessions of soybean from three countries, Korea, China, and Japan, were chosen from the soy-

bean germplasm collection of Genetic Resources Division, Rural Development Administration, for analysis of geographical diversity and relationships (Table 1). Accessions from China and Japan, introduced from USDA, were

**Table 1.** Origin of soybean germplasm and number of accessions.

Country/Region	No. of accession (%)	Country/Region	No. of accession (%)
<b>Korea</b>	<b>944(100)</b>	<b>South China</b>	<b>18(2.5)</b>
Kyunggi	88 (9.3)	Shandong	
Kangwon	47 (5.0)	Jiangsu	
Chungchong	105(11.1)	Henan	
Chulla	244(25.8)	Hubei	
Kyungsang	460(48.7)	Zhejiang	
		Jiangxi	
		Others	74(10.3)
<b>China</b>	<b>716(100)</b>	<b>Japan</b>	<b>170(100)</b>
Heilongjiang	145(20.3)	Hokkaido	77(45.3)
Jilin	192(26.8)	Honshu	74(43.5)
Manchuria	203(28.4)	Others	19(11.2)
Central China	84(11.7)		
Liaoning			
Beijing			
Hebei			

**Table 2.** Descriptors, descriptor states, and score codes/units<sup>†</sup> used for characterization of soybean.

Characters
1. Stem termination : determinate(1), indeterminate(2)
2. Leaf shape : narrow(3), intermediate(5), broad(7)
3. Pubescence density : sparse(3), normal(5), dense(7)
4. Pubescence color : gray(1), brown(2)
5. Leaf size : small(3), medium(5), large(7)
6. Flower color : white(1), purple(2)
7. Mature pod color : tan(1), brown(2), black(3)
8. Seed coat color : yellow(1), green(2), green mixed(3), brown(4), brown mixed(5), black(6)
9. Hilum color : yellow(1), brown(2), black(3)
10. Maturity group : 00(below 108 days), 0(108~115 days)
I(116~123 days), II(124~131 days)
III(132~139 days), IV(140~147days)
V(148~155 days), VI(156~163 days)
VII(over 163 days)

<sup>†</sup>Descriptor score codes and units are in parentheses.

<sup>†</sup>Corresponding author: (Phone) +82-31-299-2793 (E-mail) msyoon@niast.go.kr

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**Table 3.** Phenotypic variation in 10 characters for soybean germplasm from 15 different local origins.

Character	KG K <sup>†</sup>	KW K	CC K	CL K	KS K	HJ C	JL C	MC C	CC C	SC C	OT C	HD J	HS J	OT J
<b>Stem termination</b>	%													
Determinate	98.7	97.9	99.1	95.3	96.1	98.0	93.8	97.0	97.6	88.9	98.6	89.6	93.2	94.7
Indeterminate	1.3	2.1	0.9	4.7	3.9	2.0	6.2	3.0	2.4	11.1	1.4	10.4	6.8	5.3
<b>Leaf shape</b>														
Narrow	1.3	2.1	0	0	0.7	2.8	0	0.5	0	0	8.1	1.3	2.7	0
Intermediate	1.3	0	0	2.4	1.1	18.6	2.6	4.0	4.8	5.6	5.4	5.2	5.4	5.3
Broad	97.4	97.9	100	97.6	98.3	78.6	97.4	95.5	95.2	94.4	86.5	93.5	91.9	94.7
<b>Pubescence density</b>														
Sparse	2.6	0	0	4.3	2.6	3.5	2.1	4.4	0	0	4.1	5.2	4.0	0
Normal	93.6	97.9	99.0	94.9	94.8	87.5	89.1	86.2	91.7	72.2	87.8	88.3	81.1	100
Dense	3.8	2.1	1.0	0.8	2.6	9.0	8.8	9.4	8.3	27.8	8.1	6.5	14.9	0
<b>Pubescence color</b>														
Gray	42.3	38.3	33.3	47.6	36.5	57.9	65.6	60.6	69.1	55.6	50.0	40.3	68.9	52.6
Brown	57.7	61.7	66.7	52.4	63.5	42.1	34.4	39.4	30.9	44.4	50.0	59.7	31.1	47.4
<b>Leaf size</b>														
Small	10.3	4.3	3.8	11.4	5.9	20.3	8.3	13.8	5.9	16.7	13.5	10.4	8.1	5.3
Medium	78.2	83.0	90.5	83.9	90.2	68.3	84.9	84.7	91.7	72.2	86.5	87.0	87.8	94.7
Large	11.5	12.8	5.7	4.7	3.9	1.4	6.8	1.5	2.4	11.1	0	2.6	4.1	0
<b>Flower color</b>														
White	44.9	44.7	30.5	33.5	21.3	20.7	58.3	46.3	47.6	50.0	51.4	37.7	50.0	42.1
Purple	55.1	55.3	69.5	66.5	78.7	79.3	41.7	53.7	52.4	50.0	48.6	62.3	50.0	57.9
<b>Mature pod color</b>														
Tan	25.6	10.6	15.2	26.0	20.0	5.5	6.3	6.4	11.9	27.8	9.5	10.4	16.2	10.5
Brown	65.4	55.3	78.1	64.0	63.0	80.0	89.0	86.2	78.6	72.2	82.4	84.4	83.8	89.5
Black	9.0	34.0	6.7	1.0	17.0	14.5	4.7	7.4	9.5	0	8.1	5.2	0	0
<b>Seed coat color</b>														
Yellow	42.3	31.9	38.1	52.4	40.2	82.8	95.3	91.1	91.7	83.3	90.5	72.3	89.2	73.7
Green	14.1	14.9	7.6	10.2	22.0	3.4	1.0	2.0	4.8	16.7	0	6.5	6.8	15.8
Green mixed	12.8	17.0	5.7	6.7	7.6	0	0	0	0	0	0	0	0	0
Brown	6.4	8.5	17.1	7.5	9.3	8.3	2.1	2.0	2.4	0	5.4	9.1	0	0
Brown mixed	0	4.3	0.9	0.8	1.0	0.7	0	0	0	0	1.4	0	0	0
Black	24.4	23.4	30.5	22.4	18.9	4.8	1.6	4.9	1.2	0	2.7	11.7	4.0	10.5
<b>Hilum color</b>														
Yellow	3.8	12.8	10.5	11.8	10.4	2.8	3.6	1.5	4.8	5.6	5.4	3.9	13.5	10.5
Brown	43.6	38.3	40.0	47.6	42.4	55.9	77.6	72.4	83.3	72.2	77.0	51.9	64.9	47.4
Black	52.6	48.9	49.5	40.6	47.2	41.4	18.8	26.1	11.9	22.2	17.6	44.2	21.6	42.1
<b>Maturity group</b>														
00	0	0	0	6.3	0.2	21.4	4.7	6.9	4.8	5.5	10.8	1.3	5.4	0
0	10.2	2.1	1.0	4.3	0.4	40.7	16.1	34.5	21.4	22.2	28.4	20.8	21.6	15.8
I	16.7	4.2	1.9	5.9	1.1	30.3	22.9	33.5	20.2	11.1	29.7	36.4	33.8	26.3
II	0	0	1.0	1.2	1.1	4.8	18.2	17.7	36.9	22.2	8.1	28.6	27.0	26.3
III	7.7	6.4	11.4	7.5	4.6	1.4	21.9	6.4	9.5	22.2	10.8	11.7	12.2	15.8
IV	15.4	31.9	31.4	16.5	16.7	1.4	10.9	1.0	5.9	0	8.1	0	0	15.8
V	12.8	6.4	9.5	14.2	18.0	0	5.2	0	1.2	5.5	1.4	1.3	0	0
VI	29.5	36.2	32.4	25.2	38.0	0	0	0	0	11.1	2.7	0	0	0
VII	7.7	12.8	11.4	18.9	19.8	0	0	0	0	0	0	0	0	0

<sup>†</sup>KGK-Kyunggi; KWK-Kangwon; CCK-Chungchong; CLK-Chulla; KSK-Kyungsang; HJC-Heilongjiang; JLC-Jilin; MCC-Manchuria; CCC-Central China; SCC-South China; OTC-Others (CHN); HDJ-Hokkaido; HSJ-Honshu; OTJ -Others (JPN).

selected based on information found in the United States Department of Agriculture (USDA) soybean germplasm collection inventory (Nelson, 1987). Korean accessions were collected all across the country in 1985.

All accessions were planted in the field of Genetic Resources Division, RDA, in Suwon, Korea in 1994 and

1995. Plants were scored or measured for 10 traits (Table 2) based on the Evaluation Descriptor of Plant Genetic Resources (RDA, 1986). The maturity groups were distinguished according to method of Kwon *et al.* (1974).

The diversity index ( $H'$ ) of Shannon and Weaver (1949) was used as a measure of phenotypic for each trait. The hier-

archical cluster analysis used the cluster procedure, unweighted pair-group method using group average (UPMGA) (SAS Institute, 1985).

## RESULTS and DISCUSSION

### Distribution of phenotypic classes

Table 3 showed differences among geographical regions in their distribution and range of variation for 10 characters. Stem termination of Japanese accessions showed more variation than the Korean and Chinese accessions. However, Hymowitz and Kaizuma (1979) reported that most of Korean and Japanese soybeans were determinate and Chi-

nese soybeans were indeterminate. Frequency of indeterminate characteristics was high in Kyungsang of Korea and south China of China, while Japanese accessions showed high frequency in accessions of high latitude such as, Hokkaido. Seed coat color was most variable in Korean regions. Leaf size was variable in all regions, and leaf shape was variable in Chinese and Japanese regions. The variation in maturity group was greatest for accessions from the five Korean regions. There is no distinct difference in maturity among accessions in Japanese region. Hymowitz and Kaizuma (1979) reported that the varieties of maturity groups 00 to VII are cultivated in Hokkaido, Japan. Also, maturity group 0 to X are cultivated in Southern regions such as, Shikoku, Kyushu, and Okinawa.

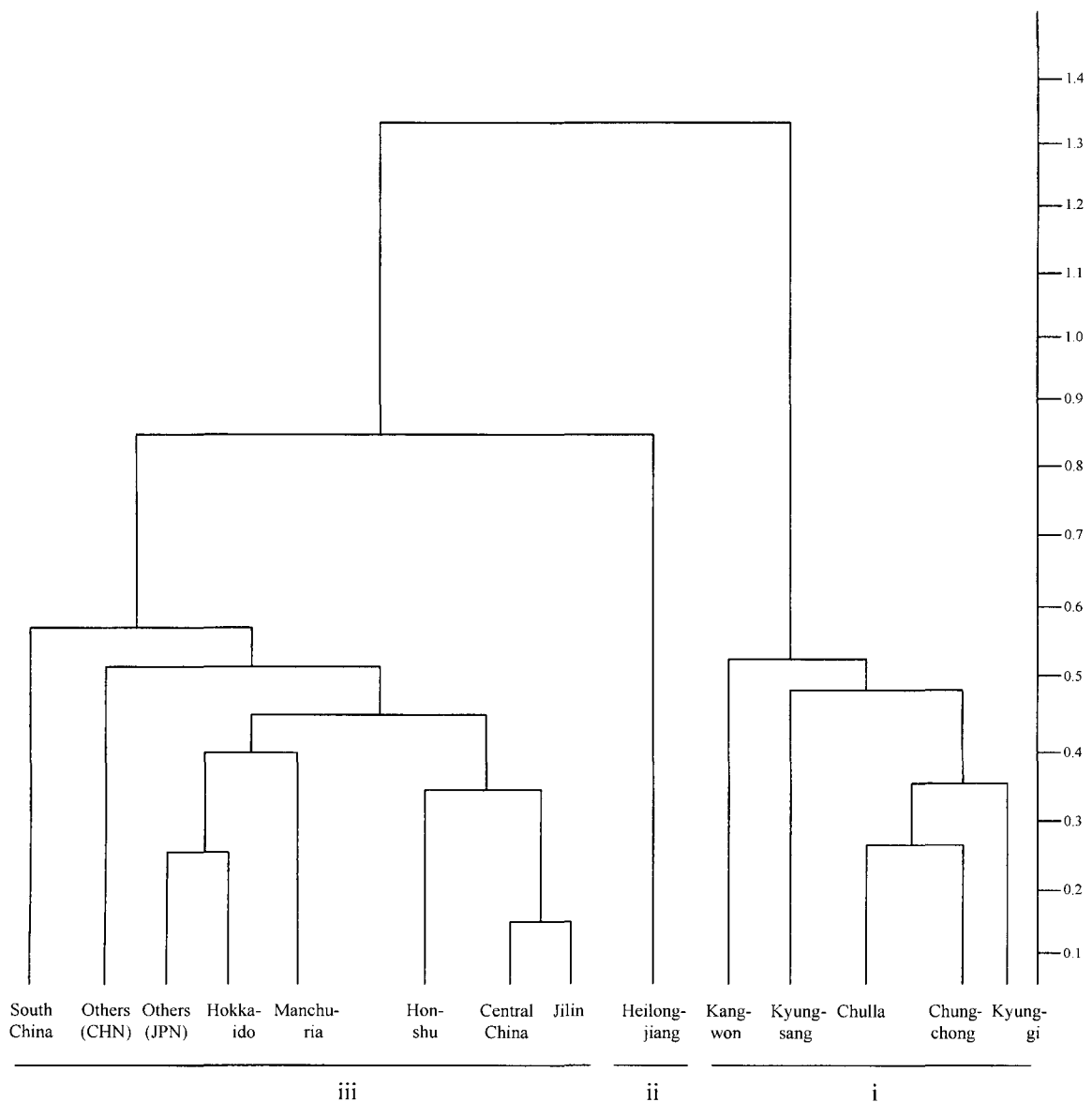


Fig. 1. Phenogram of phenotypic distances between geographic regions of origin computed with morphology of soybean.

### Diversity index

The Shannon-Weaver diversity index ( $H'$ ) was calculated to compare phenotypic diversity among characters and regions. This index is used in genetic resources studies as a convenient measure of both allelic richness and allelic evenness when using genetic data. But, because of the log transformation it is not readily interpretable in genetic terms (Brown & Weir, 1983). A low  $H'$  indicates extremely unbalanced frequency classes for an individual trait and lack of genetic diversity.

Estimates were made for each character and pooled across characters and regions for 10 traits (Table 3). The  $H'$  values for each trait ranged from 0.09 to 1.00 on average across all regions. The characters that had the highest  $H'$  were pubescence color. Leaf shape had the lowest value. The characters that had the highest  $H'$  in Korean accessions were different according to regions and they were flower color, seed coat color, and hilum color; leaf shape and leaf size in Chinese accessions; and stem termination, pubescence density, and pubescence color in Japanese accessions.

The regional ranges of diversity value in Korean, Chinese, and Japanese accessions were 0.53–0.62, 0.49–0.56, and 0.50–0.58, respectively. The diversity value of Korean accessions was generally greater than Chinese and Japanese accessions. The soybean first emerged as a domesticate in the eastern half of north China around the 11th century B.C. and was migrated to south China, Korea, Japan, and south East Asia at nearly same times (Hymowitz, 1970). However, because soybean in Korea was selected with more diverse usage such as, sauce bean, sprout bean, and soybean for cooking with rice than others, the high diversity was supposed to have been maintained in Korean collections. The highest  $H'$  values in the regional diversity value were acces-

sions from Kyunggi of Korean accessions, ones from central China and south China of Chinese accessions, and ones from Hokkaido of Japanese accessions.

### Canonical discriminant analysis

Canonical discriminant analysis was used to provide a reduced dimension model that would indicate measured differences among groups. The first canonical variable accounted for 87.6% of the total variation. Each additional canonical variable further reduced the total variation by 0.55% and 0.2%, respectively.

A hierarchical cluster analysis conducted on the means of the first eight canonical variables resulted in three clusters (Fig. 1). All accessions from Korea were grouped in cluster i. However, accessions from Kangwon, Korea in cluster i were not strongly related to other regions. Accessions from Heilongjiang formed cluster ii. All Chinese accessions except accessions from Heilongjiang and Japanese accessions were grouped in cluster iii. But, south China accessions in cluster formed weak cluster. Vavilov (1951) first determined that the primary center of diversity for soybean was northeast, central and south China, and Korea. Perry and McIntosh (1991) reported that the accessions in the USDA germplasm collection from Korea are more closely related to the accessions from Japan rather than ones from China. These results may happen according to genotype of their holdings, but were supported by SSR marker (Yoon *et al.*, 1998) and frequency of  $\beta$ -amylase isozyme (Yoon *et al.*, 2000) for same materials. Hymowitz and Kaizuma (1981) also suggested that accessions from Korea were divided into different regions because they were derived from different sources.

**Table 4.** Estimates of Shannon-Weaver diversity index ( $H'$ ) from morphological traits of soybean germplasm of different regional origins.

Trait	Region														Mean
	KG K <sup>†</sup>	KW K	CC K	CL K	KS K	HJ C	JL C	MC C	CC C	SC C	OT C	HD J	HS J	OT J	
Stem termination	0.10	0.15	0.07	0.27	0.24	0.14	0.34	0.19	0.16	0.50	0.11	0.48	0.36	0.30	0.24
Leaf shape	0.13	0.09	0.00	0.10	0.09	0.55	0.11	0.18	0.18	0.20	0.44	0.25	0.30	0.19	0.20
Pubescence density	0.26	0.09	0.05	0.20	0.22	0.41	0.36	0.44	0.26	0.54	0.41	0.40	0.53	0.00	0.30
Pubescence color	0.98	0.96	0.92	1.00	0.95	0.98	0.93	0.97	0.89	0.99	1.00	0.97	0.89	1.00	0.96
Leaf size	0.61	0.50	0.34	0.49	0.35	0.56	0.48	0.43	0.31	0.71	0.36	0.41	0.41	0.19	0.44
Flower color	0.99	0.99	0.89	0.92	0.75	0.74	0.98	1.00	1.00	1.00	1.00	0.96	1.00	0.99	0.94
Mature pod color	0.77	0.85	0.60	0.60	0.56	0.56	0.38	0.45	0.61	0.54	0.53	0.48	0.40	0.29	0.54
Seed coat color	0.79	0.91	0.80	0.74	0.83	0.37	0.13	0.22	0.21	0.25	0.23	0.49	0.23	0.44	0.47
Hilum color	0.75	0.89	0.87	0.88	0.87	0.72	0.57	0.59	0.50	0.67	0.60	0.75	0.80	0.87	0.73
Maturity group	0.84	0.71	0.74	0.89	0.72	0.60	0.83	0.66	0.73	0.83	0.80	0.64	0.67	0.70	0.74
Mean	0.62	0.61	0.53	0.61	0.56	0.56	0.51	0.51	0.49	0.62	0.55	0.58	0.56	0.50	0.56

<sup>†</sup>KGK-Kyunggi; KWK-Kangwon; CCK-Chungchong; CLK-Chulla; KSK-Kyungsang; HJC-Heilongjiang; JLC-Jilin; MCC-Manchuria; CCC-Central China; SCC-South China; OTC-Others (CHN); HDJ-Hokkaido; HSJ-Honshu; OTJ-Others (JPN).

**Table 5.** Phenotypic variation of 3 cluster groups formed from canonical variable analysis.

Character	Cluster		
	i	ii	iii
	-----%		
<b>Stem termination</b>			
Determinate	96.5	98.0	95.0
Indeterminate	3.5	2.0	5.0
<b>Leaf shape</b>			
Narrow	0.5	2.8	1.3
Intermediate	1.3	18.6	4.2
Broad	98.2	78.6	94.5
<b>Pubescence density</b>			
Sparse	2.7	3.5	3.1
Normal	95.3	87.5	87.4
Dense	2.0	9.0	9.5
<b>Pubescence color</b>			
Gray	39.7	57.9	60.2
Brown	60.3	42.1	39.8
<b>Leaf size</b>			
Small	7.4	20.3	10.4
Medium	87.2	68.3	86.2
Large	5.4	1.4	3.4
<b>Flower color</b>			
White	28.7	20.7	49.5
Purple	71.3	79.3	50.5
<b>Mature pod color</b>			
Tan	21.1	5.5	9.3
Brown	65.0	80.0	85.0
Black	13.9	14.5	5.7
<b>Seed coat color</b>			
Yellow	43.0	82.8	89.5
Green	16.2	3.4	3.5
Green mixed	8.1	0.0	0.0
Brown	9.4	8.3	2.8
Brown mixed	1.5	0.7	0.1
Black	21.8	4.8	4.1
<b>Hilum color</b>			
Yellow	10.4	2.8	4.6
Brown	43.4	55.9	71.9
Black	46.2	41.4	23.5
<b>Maturity group</b>			
00	1.7	21.4	5.5
0	2.4	40.7	24.2
I	3.9	30.3	28.5
II	0.9	4.8	21.4
III	6.5	1.4	12.9
IV	19.0	1.4	5.0
V	15.1	0.0	1.9
VI	33.2	0.0	0.3
VII	17.3	0.0	0.3

The morphological traits are summarized by cluster in Table 5. Accessions in cluster iii had more indeterminate than others at the stem termination. Broad leaf shape was most highest in cluster i, and narrow and intermediate leaf shape was most highest in cluster ii. Cluster ii had higher sparse at pubescence density than other clusters. Cluster i

had the most highest brown or tawny at pubescence color, and cluster ii had predominantly many small type at leaf size. Yellow seed coat color was higher in cluster iii than in other clusters, and colored seed coat was high in cluster i. Cluster i contained all maturity groups 00 to VII, and accessions of cluster i and ii had mostly maturity groups 00 to III with early maturity.

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