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REGIONAL VARIABILITY IN PHASEOLUS VULGARIS L. (II)
 SEED CHARACTER FREQUENCIES IN TRANSYLVANIA

A.T. SZABÓ

Abstract

SZABÓ T.A., 1985, Regional variability in Phaseolus vulgaris L. (II.) Seed character frequencies in Transylvania Not. bot. hort. agrobot. Cluj., IV, 21-28. Attempt was made to evaluate gene frequencies using seed characters registered in Phaseolus vulgaris, cultivated in traditional multicropping (Zea + Phaseolus + Cucurbita) in a sample territory in Transylvania (Romania). The highest frequencies were found in the case of characters determined mostly by Y, T, D, and st gene group (according to PRAEKEN 1972); mottled seed coat and violet colour was relatively rare. The short and spherical forms are more frequent, as the long or compressed, with the notable exception of white compressed types. Our knowledge in Phaseolus genetics allowed only a first approach in a very restricted number of characters.

Key words: Phaseolus, seed characters, germplasm

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In order to manipulate the huge amount of variability accumulated during the collection, study and conservation of genetic resources, a method was proposed for the evidence of different genes and gene groups preserved in gene banks (BLIXT and WILLIAMS 1982). This paper is a first attempt to apply the proposal for a limited number of seed characters in the case of Phaseolus vulgaris L. The samples collected, examined and preserved are mixtures of different genotypes cultivated traditionally in a multicropping system (Zea mays + Phaseolus vulgaris + Cucurbita spp.) on small plots and gardens in Transylvania (Romania). In these mixtures the different genotypes are not perfectly isolated; hybridisation occurs, selection and microevolution acts.

Material and method

The occurrence (frequency) and participation in harvest (abundance) of different seed characters in randomly collected samples of *Phaseolus vulgaris* L. were analyzed. Sampling process and sampled territory was similar to that described by SZABÓ and DANKANITS (1978). Eight seed coat characters and two seed form characters (length index, flatness index) were considered. The genes influencing the examined seed coat characters were symbolized according to PRAKKE (1972); for the seed form the index described by SCHERMANN (1966) was used, with the modification that the lower values indicate the shortest and the roundest seeds. A character was considered present in the sample, if it was phenotypically detectable. In the case of samples large enough this approach may have a good informative value regarding the character frequencies on a given territory.

The collected samples were separated per phenotypes, measured and weighed separately, frequency and abundance values were calculated. The data regarding every sample were registered on BOBOTROE punched cards and preserved in the data bank of the germplasm resource laboratory. For the technical assistance, the kind help of Ilona SIMÓ is greatly acknowledged.

Results

From 27 seed samples cultivated in multicropping in 8 different localities 200 different phenotypes were identified (Tab. 1.).

Results regarding the frequency and abundance of phenotypically detectable seed characters (genes or gene groups) are included in table 2. and 3. Data regarding the seed length index and flatness index are included in tables 4-7.

Tab.1.

Collection sites and number of samples

Collection site	Number of samples		Total
	B u l k e d	I n d i v i d u a l	
Macáu	1	17	17
Mera	1	16	16
Girbáu	1	15	15
Mera	1	12	12
Mera	1	11	11
Macáu, Vlaha (Vl.)	4	9	36
Macáu, Viştea, Tureni, Vl.	4	8	32
Macáu, Viştea	3	6	18
Berind, Girbáu, Tureni, Vl.	5	5	25
Mera	2	4	8
Chioag, Macáu	2	3	6
Chioag	2	2	4
Total	27	108	200

Samples were bulked originally by the local farmers and cultivated in this stage in field. The most individual seed types were found in a single sample in Macáu (17). From the 27 samples analyzed, with a total weight of 4572 gr 200 individual types were separated, and the most types were present in more than one sample. Seeds of undoubtedly hybrid origin were found in 13 samples.

Tab. 2.

The number and frequency (%) of the different seed coat characters designated with gene symbols used by PRAKKE (1972) in the samples of *Phaseolus vulgaris* analyzed

Sample nr.	Gene symbols								
	Y	T	D	Cst	Pst	Bst	m	V	X
1.	10	10	9	5	0	0	0	0	0
2.	7	7	11	3	3	3	0	1	1
3.	11	11	9	1	1	1	1	0	1
4.	12	3	11	2	5	2	0	0	1
5.	5	5	7	2	3	0	2	0	0
6.	9	6	4	2	1	0	0	0	1
7.	4	5	2	2	1	0	7	0	1
8.	3	5	3	0	3	0	0	0	0
9.	8	5	5	1	1	0	0	0	0
10.	6	2	4	3	1	0	1	1	1
11.	6	4	5	1	1	3	1	0	1
12.	7	4	4	1	1	1	2	0	1
13.	8	4	4	2	1	1	0	0	0
14.	5	4	2	0	1	1	1	0	1
15.	4	4	1	0	1	1	0	0	0
16.	2	2	3	0	0	4	1	0	1
17.	5	2	2	1	2	0	0	0	0
18.	4	2	1	1	0	0	0	1	0
19.	2	5	0	0	0	0	0	0	0
20.	4	2	2	0	2	0	1	0	0
21.	4	3	1	1	0	0	1	0	1
22.	4	1	3	2	0	1	0	0	0
23.	4	2	2	2	0	0	0	0	1
24.	3	2	2	1	0	0	0	0	0
25.	2	1	2	0	2	0	0	0	1
26.	2	2	1	0	1	0	0	0	0
27.	2	2	0	0	0	0	0	0	0
Total	143	106	100	33	33	18	18	3	13
%	66,2	49,1	46,3	15,3	15,3	8,3	8,3	1,2	6,4

One character, expressed here by a gene symbol, was present in different character combinations and in different phenotypes (sub-samples), which is reflected in total number and in frequency (%) values too.

The frequency of Y gene is the highest, followed by characters determined perhaps by genes symbolized with T and D. The st gene group is also relatively frequent in the bulked samples (red, black and brown stripes) The mottled seed coat (m) and the violet seed coat colour (V) is relatively rare. Hybridisation was registered with a frequency of about 6 %.

Tab. 3.

The abundancy expressed by the weight (g) of seeds with a given character (gene symbols as in table 2)

Sample nr.	Gene symbols								
	Y	T	D	C st	F st	B st	m	V	X
1.	128	228	149	141	0	0	0	0	0
2.	61	168	71	92	24	46	0	0	10
3.	203	139	202	10	18	17	5	3	18
4.	417	410	76	180	85	71	0	0	21
5.	169	134	169	85	29	0	11	0	0
6.	115	40	78	33	4	0	0	0	12
7.	212	10	40	157	3	0	7	0	19
8.	20	45	63	0	22	0	0	0	0
9.	84	74	15	61	11	0	0	0	0
10.	128	62	70	51	7	0	17	17	11
11.	157	190	13	100	39	105	39	0	16
12.	78	53	37	30	12	12	16	0	4
13.	92	29	63	20	4	4	0	0	0
14.	67	38	49	0	18	18	8	0	14
15.	56	11	63	0	11	11	0	0	0
16.	23	28	9	0	0	30	0	0	3
17.	90	63	25	60	5	0	0	0	0
18.	356	130	224	130	0	0	0	2	0
19.	5	0	99	0	0	0	0	0	0
20.	51	18	34	0	20	0	14	0	0
21.	19	7	12	7	0	0	69	0	7
22.	59	47	12	44	0	3	0	0	0
23.	44	30	14	30	0	0	0	0	0
24.	233	229	39	194	20	0	0	0	0
25.	258	258	48	0	219	0	0	0	0
26.	6	28	6	0	23	0	0	0	0
27.	54	0	54	0	0	0	0	0	0
Total	3185	2469	1734	1425	554	317	191	22	138
%	70,3	54,5	37,9	31,2	12,1	6,9	4,2	0,5	3,2

In respect of the seed form expressed by seed index (Tab. 4. and 5. - length index; Tab. 6. and 7. - flatness), the short seeded forms are more common (50,6 % short seed vs. 18,1% long seed) and the thick, spherical forms are more frequent as the strongly compressed (69,2 % vs. 12,6 %).

Tab. 4.

The number and frequency (%) of different seed length index values in the samples examined

Sample nr.	Seed length index categories						
	0,5	1,0	1,4	1,7	2,0	2,3	2,6
1.	0	0	6	9	1	0	0
2.	0	1	8	6	1	0	0
3.	0	3	4	4	2	1	0
4.	2	4	2	4	0	0	0
5.	0	1	5	1	3	0	1
6.	0	2	3	2	2	0	0
7.	0	3	1	1	4	0	0
10.	0	1	3	3	1	0	0
11.	0	1	4	0	3	0	0
12.	0	4	1	2	1	0	0
14.	0	0	1	1	2	0	0
15.	0	1	2	3	1	0	0
16.	0	3	1	1	1	0	0
18.	0	0	2	1	1	1	0
19.	0	3	11	1	0	1	0
20.	0	1	2	1	1	0	0
21.	0	1	1	1	1	1	0
22.	0	2	0	2	0	0	0
23.	0	1	1	2	0	0	0
24.	0	1	1	0	0	0	0
25.	0	0	0	3	0	0	0
26.	0	0	0	2	1	0	0
27.	0	0	0	2	0	0	0
Total	2	33	49	52	26	3	1
%	1,2	19,9	29,5	31,3	15,7	1,8	0,6

Total number of samples measured: 166

In the case of seed form no clear-cut differences were found between the frequency and abundancy values.

Tab. 5.

The abundancy expressed by the weight (g) of seeds of different phenotypes with the same seed length index values

Sample nr.	Seed length index categories						
	0,5	1,0	1,4	1,7	2,0	2,3	2,6
1.	0	0	73	406	21	0	0
2.	0	7	141	73	2	0	0
3.	0	62	82	59	41	4	0
4.	145	170	17	100	0	0	0
5.	0	22	89	12	79	0	18
6.	0	31	19	56	9	0	0
7.	0	13	4	3	231	0	0
10.	0	5	58	30	57	0	0
11.	0	100	58	0	52	0	0
12.	0	51	8	27	4	0	0
14.	0	0	4	45	26	0	0
15.	0	2	17	44	11	0	0
16.	0	29	5	2	3	0	0
18.	0	0	132	214	0	10	0
19.	0	92	3	0	4	0	0
20.	0	21	30	13	4	0	0
21.	0	2	6	7	69	4	0
22.	0	34	0	25	0	0	0
23.	0	27	3	14	0	0	0
24.	0	35	4	0	0	0	0
25.	0	0	267	0	0	0	0
26.	0	0	0	24	5	0	0
27.	0	0	0	54	0	0	0
Total	145	703	753	1457	618	18	18
%	3,9	18,8	20,2	39,5	16,6	0,5	0,5

Tab. 6.

The number and frequency (%) of different flattness index categories

Sample nr.	Flattness index categories						
	0,7	1,0	1,2	1,4	1,6	1,8	2,0
1.	0	5	7	2	2	1	0
2.	0	6	5	4	0	1	0
3.	0	4	6	0	1	2	1
4.	0	3	3	5	0	2	0
5.	1	3	4	2	1	0	0
6.	0	1	4	2	1	0	0
7.	0	2	5	1	0	1	0
10.	0	2	6	0	0	0	0

Tab. 6.
(continued)

Sample nr.	Flattness index categories						
	0,7	1,0	1,2	1,4	1,6	1,8	2,0
11.	0	3	4	1	0	0	0
12.	0	2	4	1	0	1	0
14.	0	0	3	2	1	0	0
15.	0	1	3	1	0	1	0
16.	0	2	3	1	0	0	0
18.	0	1	2	0	1	0	0
19.	0	0	4	1	0	0	0
20.	0	2	2	1	0	0	0
21.	0	1	3	1	0	0	0
22.	0	0	2	1	0	1	0
23.	0	0	2	1	1	0	0
24.	0	0	1	1	0	0	0
25.	0	0	1	2	0	0	0
26.	0	1	1	0	1	0	0
27.	0	0	1	0	1	0	0
Total	1	38	76	30	10	10	1
%	0,6	22,9	45,8	18,1	6,0	6,0	0,6

Tab. 7.

The abundancy expressed by the weight (g) of seeds of different phenotypes with the same flattness index values

Sample nr.	Flattness index categories						
	0,7	1,0	1,2	1,4	1,4	1,8	2,0
1.	0	82	173	17	28	27	0
2.	0	91	64	52	0	0	0
3.	0	99	86	0	5	27	30
4.	0	83	235	95	0	28	0
5.	89	75	101	14	12	8	0
6.	0	3	50	36	26	0	0
7.	0	7	219	19	0	3	0
10.	0	51	99	0	0	0	0
11.	0	48	147	3	0	0	0
12.	0	37	26	10	0	17	0
14.	0	47	24	4	0	0	0
15.	0	2	55	10	0	7	0
16.	0	9	28	2	0	0	0
18.	0	10	132	0	214	0	0
19.	0	0	93	6	0	0	0
20.	0	18	34	16	0	0	0
21.	0	6	13	69	0	0	0
22.	0	0	16	31	0	12	0
23.	0	0	30	6	8	0	0
24.	0	0	35	4	0	0	0
25.	0	0	210	57	0	0	0
26.	0	0	1	0	23	0	0
27.	0	5	50	0	4	0	0
Total	89	626	1944	471	324	129	30
%	2,4	17,2	53,4	12,9	8,9	3,5	0,8

If the abundance values, calculated according to the total weight of a given type in a bulk sample, are compared with the correspondent frequency values, it may be established that the T gene is more frequent than abundant and the Cst gene is more abundant, than frequent. In the case of other genes in the analyzed samples no clear differences were found between the frequency and abundance values.

Rezumat

SZABÓ T. A., 1985, Variabilitatea la Phaseolus vulgaris L. (II.) Frecvența unor caractere ale seminței în Transilvania (în engleză), Not. bot. hort. agrobot., Cluj., XV.21 - 28. Se prezintă analiza frecvenței unor caractere ale seminței la 27 de probe mixte, provenite din 8 localități din Transilvania. Probele au fost recoltate din culturi mixte de porumb-fasole-dovleac (Zea-Phaseolus-Cucurbita) tradiționale în zona cercetată. Frecvența cea mai ridicată a fost înregistrată în cazul caracterelor determinate mai ales de genele Y, T, D și grupa st (conform PRAKKEN 1972). Semințele de formă sferică sînt mai frecvente, decît cele alungite sau comprimate cu excepția tipului alb comprimat preferat în cultură intercalată. Lucrarea reprezintă o primă încercare de aplicarea practică a principiilor enunțate de BLIXT și WILLIAMS (1982), în cazul unui număr restrîns de caractere seminale la Phaseolus.

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KITAIBELIA VITIFOLIA WILLD. - EINE NEUE SUBSPONTANE PFLANZE IN FLORA VON CLUJ-NAPOCA

I. PETRIDEAN

Abstract:

PETRIDEAN I., 1985, Kitaibelia vitifolia Willd. - eine neue subspontane Pflanze in Flora von Cluj-Napoca (Kitaibelia vitifolia Willd. - a new subspontaneous species in the flora of Cluj-Napoca) Not. bot. hort. agrobot., Cluj., XV, 29-32. Kitaibelia vitifolia Willd. has not so far been registered either in the flora of Cluj-Napoca or in the Romanian flora. In the autumn 1984, on the border of a pine forest, near a new constructed town quarter, herbarium specimens and seeds of this species were collected. This ruderalized, bushy habitat is perhaps the first, where Kitaibelia grew spontaneously in Transylvania.

Key words: Kitaibelia vitifolia, floristics, chorology

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Die mehr als 1000 Arten aus der ungefähr 80 Gattungen der Familie Malvaceae sind meistens weit verbreitet in verschiedenen Kontinenten (HEYWOOD, Ed., 1970). Kitaibelia vitifolia Willd. 1799 aus der Tribus Malopene ist eine bemerkenswerte Ausnahme: sie hat eine sehr enge Verbreitung als endemische Pflanze in Nord-West und Mittel Jugoslawien (Slavonien, Serbien). Interessant ist aber die langsame Verbreitung dieser Art als Zierpflanze in Kultur und auch als subspontane Wildpflanze. Kitaibelia fehlt aus der chorologische Bearbeitung der westeuropäischen Flora (MEUSEL et al. 1978).

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