

## Patterns of thousand-seed weight inheritance in $F_1$ and $F_2$ pea hybrids

F. A. Davletov<sup>1✉</sup>, K. P. Gaynullina<sup>1,2</sup>, A. V. Pleshkov<sup>1</sup>

<sup>1</sup> Bashkir Research Institute of Agriculture – Subdivision of the Ufa Federal Research Centre of the Russian Academy of Sciences, Ufa, Russia

<sup>2</sup> Institute of biochemistry and genetics – Subdivision of the Ufa Federal Research Centre of the Russian Academy of Sciences, Ufa, Russia

✉ E-mail: davletovfa@mail.ru

**Abstract.** The research aim is to study the inheritance of a thousand-seed weight trait by  $F_1$  and  $F_2$  hybrids peas. **Research methods.** The study was conducted at the Chishminskiy plant breeding center of the Bashkir Research Institute – the Subdivision of the Russian Science Academy, located in the Cis-Ural steppe zone, in 2017–2019. The paper describes hybridization with two parental pairs, reciprocal crosses, and resulting pea hybrids. Five varieties were analyzed: Shikhan, Chishminskiy 75, Chishminskiy 80, Chishminskiy 95, Melkosemyanny 2. The resulting seeds were divided into groups: large, medium-large, medium, medium-small, small. The standard deviation ( $\sigma$ ), the coefficient of variation ( $V_c$ , %), heritability estimate ( $H^2$ ), and the degree of dominance ( $h_p$ ) were determined. Statistical data were analyzed in Microsoft Office Excel 2010 using Statistica 7.0. **Results.** As a result of the conducted experiments,  $F_1$  hybrid peas showed lower thousand-seed weight than the large-seeded parent plants. Whereupon, the large-seeded genotype of a mother plant had a greater effect on the manifestation of this trait in hybrids.  $F_2$  hybrid peas expressed a thousand-seed weight trait in an intermediate fashion. However, the average values of this trait were much lower than in  $F_1$  hybrids. The coefficient of variation  $V_c$  in  $F_2$  plants was 24.3–33.3%, the degree of dominance  $h_p$  was 0.20–0.32 (incomplete dominance of the trait). **Scientific novelty.** The inheritance of a thousand-seed weight in regional varieties that distinctly differ on this trait and in hybrids obtained by crossing was studied for the first time in conditions of the Republic of Bashkortostan. New large-seeded and small-seeded sources for pea breeding were identified.

**Keywords:** peas, breeding, crossing, hybrid, thousand-seed weight, seed size, heritability estimate, degree of dominance.

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### Introduction

The selection of new varieties is of primary importance in ensuring increased productivity of pea grains [1, p. 604], [2, p. 21]. Currently, intervarietal hybridization plays the most important role among other plant breeding methods as remote hybridization, physical and chemical mutagenesis, experimental polyploidy, and the use of cell, tissue, and organ cultures [3, p. 145].

However, it has some limitations in creating high yielding, readily producible varieties adaptive to local conditions. The way hybrids inherit quantitative traits, and the degree parent genotypes influence their manifestation, are not well understood [4, pp. 21–22]; [5, p. 947], [6, p. 208]. This paper presents the results of research on specific aspects of this problem.

The target is to study the inheritance of a seed size trait (thousand-seed weight) in pea hybrids, and the degree parent plants affect its expression.

### Methods

The experiments were conducted at the Chishminskiy plant breeding center of the Bashkir Research Institute – the Subdivision of the Russian Academy of Sciences, in 2017–2019.

Five pea varieties (Shikhan, Chishminskiy 75, Chishminskiy 80, Chishminskiy 95, Melkosemyanny 2) were used as a material to analyze the way a seed size trait is inherited.

Plant crossing was performed according to the scheme: Shikhan  $\times$  Melkosemyanny 2, Chishminskiy 75  $\times$  Melkosemyanny 2, Chishminskiy 80  $\times$  Melkosemyanny 2, Chishminskiy 95  $\times$  Melkosemyanny 2. Backcrossings were carried out as well.

First- and second-generation hybrids were sown using an SKS-6-10 seeder. The predecessor is winter rye. Farming methods are generally accepted for the zone. The area of plant alimentation is  $20 \times 5$  cm. The plot size was determined by the seed presence. Hybrids were planted next to their parent forms.

The inheritance of the seed size trait was studied on  $F_1$  and  $F_2$  hybrids. Bundles of hybrid swarms were selected for analysis. Seeds were weighed on laboratory scales. As a result of weighting, seeds were divided into groups according to their sizes, shown in table 1.

The analysis involved finding standard deviation ( $\sigma$ ), the coefficient of variation ( $V_c$ , %), heritability estimate ( $H^2$ ), and the degree of dominance ( $h_p$ ). Statistical processing of data resulted from field experiments was conducted following the generally accepted method of B. A. Dospekhov. It was done with the Statistica 10.0 and Microsoft Office Excel 2010 software packages. Each indicator was handled in terms of the mean value ( $M$ ), standard error ( $\pm SEM$ ), and confidence interval ( $t_{0.05} \times SEM$ ).

### Results

Little is understood on the inheritance of a thousand-seed weight trait, although some studies are devoted to this problem. In 1912, while crossing small-seeded pea samples with large-seeded ones, Tschermak found an intermediate character of a thousand-seed weight inheritance in  $F_1$  and a large variety in size in  $F_2$ . The ratio of small seeds to all other transitional types was 1:264, close to the 1:255 tetrahybrid segregation model. Based on this, the Austrian scientist concluded that the small-seeded parent form used in crosses had four recessive genes responsible for the formation of small seeds, the large-seeded parent form had four dominant genes, and the intermediate forms are the result of a combination of recessive and dominant genes [7, p.18], [8, pp. 401–402], [9, p. 64]. Subsequently, Wellensiek used  $Sg_1$ ,  $Sg_2$ ,  $Sg_3$ ,  $Sg_4$  symbols in 1925, and Yarnell applied  $S_1$ ,  $S_2$ ,  $S_3$ ,  $S_4$  signs in 1964 [7, p. 19], [10, p. 15], [11, p. 23].

In 1969–1970 V. H. Khangildin and V. V. Khangildin, using the Sewall Wright formula, calculated the smallest possible number of non-allelic genes responsible for varietal differences in seed size. Dispersion analysis of the thousand-seed weight in varieties with different seed sizes and their hybrids showed that large-seeded varieties differ from Melkosemyanny 2 variety in the presence of two dominant gene alleles [7, p. 19; 11, p.23]. Melkosemyanny 2 variety (thousand-seed weight is 80–110 g) has five recessive seed size genes. Large-seeded pea varieties have 4–5 dominant genes involved in the formation of high weight of 1000 seeds. Seed size is mostly determined by the internal genetic potential of the variety and the conditions of its cultivation [12, p. 63], [13, p. 7], [14, pp. 71–72].

The literature indicates that first-generation hybrids are characterized by an intermediate manifestation of the trait with a bias towards the parent form with larger seeds when crossing samples that distinctly differ in a thousand-seed weight. In the second filial generation, there is trait segregation with a predominance of plants with intermediate values of a thousand-seed weight [15, pp. 36–37], [16, p.607].

In our experiments,  $F_1$  hybrids from direct and reverse (reciprocal) crossing being significantly different in the thousand-seed weight were characterized by intermediate values of this trait with a bias towards the large-seeded parent form. However, their thousand-seed weight was lower. Thus, hybrids from large-seeded varieties of mother plants had lower the thousand-seed weight by an average of 15.4%. Hybrid offspring from large-seeded varieties of father plants were 19.8% inferior to them (table 2).

As the experiment results show, the manifestation of the thousand-seed weight trait in  $F_1$  pea hybrids is mostly influenced by the genotype of a large-seeded variety, regardless of whether it is used as a mother or father form. However, it should be noted that in our studies, the manifestation of this trait in pea hybrids was greater when a large-seeded variety was of a mother form.

In our studies,  $F_2$  hybrid offspring were characterized by lower average weight values of 1000 seeds than  $F_1$  hybrid offspring (table 3).

Thus, the obtained data are consistent with the opinion of other researchers regarding the intermediate inheritance of the studied trait in hybrids (fig. 1).

In our experiments, the coefficient of variation in the parent varieties ranged from 6.5 to 12.3%. In the hybrid combinations of the second generation, this indicator varied in the range of 24.3–33.3%. A sharp increase in the coefficient of variation in  $F_2$  hybrids indicates that in addition to environmental factors, there is genotypic segregation making hereditary variability 87–95%. The dominance degree  $h_p = 0.20$ – $0.32$  demonstrates incomplete dominance of the thousand-seed weight trait.

Table 1  
Classification of pea seeds by their size

Seed size class	Weight of 1 seed, g	Weight of 1000 seeds, g
I. Large	0.280–0.300	280–300
II. Semi-large	0.250–0.279	250–279
III. Medium	0.160–0.249	160–249
IV. Semi-small	0.130–0.159	130–159
V. Small	0.090–0.129	90–129

Table 2  
Thousand-seed weight in  $F_1$  pea hybrids and their parents (2017)

Number of hybrids, pcs	Weight of 1000 seeds, g			Deviation of the weight of 1000 seeds in a hybrid relative to the best parent	
	Mother plant	$F_1$ hybrid	Father plant	Absolute value, $\pm$ g	Relative value, $\pm$ %
Direct crosses					
4	253 $\pm$ 5.0	214 $\pm$ 3.8	105 $\pm$ 2.8	–39	–15.4
Reciprocal crosses					
4	105 $\pm$ 2.3	203 $\pm$ 3.5	253 $\pm$ 5.0	–50	–19.8

Table 3  
Thousand-seed frequency distribution  $F_2$  pea hybrids and their parents (2018)

Varieties and hybrids	Number of seeds assigned to the size class, pcs					Weight of 1000 seeds, g
	I	II	III	IV	V	
Direct crosses						
Shikhan	352	605	43	0	0	270 ± 14.6
Shikhan × Melkosemyannyy 2	67	256	370	243	64	206 ± 7.8
Melkosemyannyy 2	0	0	9	840	151	110 ± 8.6
Chishminskiy 75	0	89	859	52	0	220 ± 9.0
Chishminskiy 75 × Melkosemyannyy 2	0	8	240	504	248	180 ± 3.8
Melkosemyannyy 2	0	0	9	840	151	110 ± 8.6
Chishminskiy 80	105	599	296	0	0	256 ± 10.0
Chishminskiy 80 × Melkosemyannyy 2	57	260	470	182	31	206 ± 7.8
Melkosemyannyy 2	0	0	9	840	151	110 ± 8.6
Chishminskiy 95	250	602	148	0	0	263 ± 10.0
Chishminskiy 95 × Melkosemyannyy 2	63	250	375	250	62	206 ± 8.0
Melkosemyannyy 2	0	0	9	840	151	110 ± 8.6
Reciprocal crosses						
Melkosemyannyy 2	0	0	9	840	151	110 ± 8.6
Melkosemyannyy × Shikhan	60	260	373	233	74	201 ± 9.4
Shikhan	352	605	43	0	0	270 ± 14.6
Melkosemyannyy 2	0	0	9	840	151	110 ± 8.6
Melkosemyannyy 2 × Chishminskiy 75	0	13	234	491	262	173 ± 7.8
Chishminskiy 75	0	89	859	52	0	220 ± 9.0
Melkosemyannyy 2	0	0	9	840	151	110 ± 8.6
Melkosemyannyy 2 × Chishminskiy 80	70	245	459	192	34	211 ± 9.0
Chishminskiy 80	105	599	296	0	0	256 ± 10.0
Melkosemyannyy 2	0	0	9	840	151	110 ± 8.6
Melkosemyannyy 2 × Chishminskiy 95	72	266	361	255	46	217 ± 9.8
Chishminskiy 95	250	602	148	0	0	263 ± 10.0

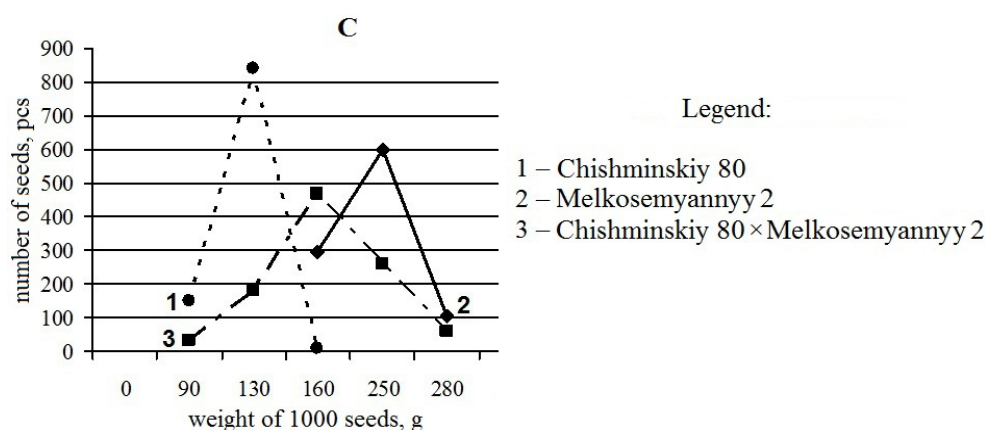


Fig. 1. Seed size frequency distribution in  $F_2$  pea hybrids and their parents

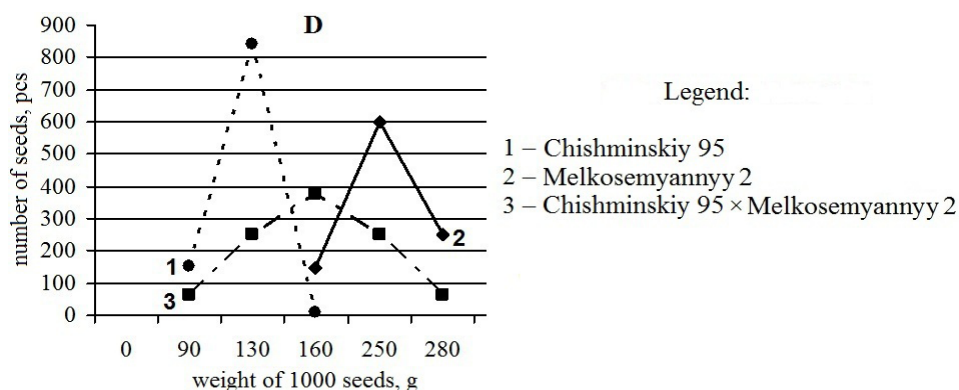


Fig. 2. Pea seeds of different sizes

On the whole, the conducted study showed that crossing local medium- and large-seeded pea varieties Shikhan, Chishminskiy 75, Chishminskiy 80, Chishminskiy 95 with a contrasting small-seeded Melkosemyanny 2 resulted in intermediate inheritance of the studied trait in the first generation of hybrids.

In the second generation, the trait was split, and the proportion of small-seeded hybrids with 4-5 recessive genes in their genotype ranged from 3.1 to 6.4%. However, there were identified valuable small-seeded  $F_2$  hybrids. The analysis of the hybrid population from a direct crossing of the medium-seeded Chishminskiy 75 and Melkosemyanny 2 varieties resulted in 8 medium-large, 240 medium, 504 medium-small, 248 small-seeded samples (fig. 2). Moreover, small-seeded and medium-small-seeded hybrids being of interest for breeding purposes were found with a frequency of 24.8 and 50.4%, respectively.

Reciprocal  $F_2$  hybrids by seed size (weight of 1000 seeds) occupied an intermediate position between parent plants with a bias towards the best variety and slightly differed from  $F_2$  hybrids of the direct crossing.

Studying regularities in the inheritance of quantitative traits involved in the formation of pea productivity will improve the efficiency of selection in segregated hybrid swarms. This knowledge is essential when planning crossings, selection of parent pairs, the choice of the breeding methodology. The seed size trait, developed by polymeric genes, can vary greatly depending on the growing conditions. The given study showed that the calculation of the heritability coefficients and variability makes it possible to predict the manifestation of the desired genotypes when crossing varieties characterized by different seed sizes. It resulted in new large- and small-seeded sources for pea breeding, which are being evaluated in the breeding nursery.

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**Authors's information:**

Firzinat A. Davletov<sup>1</sup>, doctor of agricultural sciences, chief of the laboratory of selection and seed-growing of pulse crops, ORCID 0000-0002-7421-869X, AuthorID 782015; +7 960 383-67-44, [davletovfa@mail.ru](mailto:davletovfa@mail.ru)

Karina P. Gaynullina<sup>1, 2</sup>, candidate of biological sciences, senior researcher of the laboratory of selection and seed-growing of pulse crops<sup>1</sup>, senior researcher of the laboratory of plant genomics<sup>2</sup>, ORCID 0000-0001-6246-1214, AuthorID 783611; +7 989 953-15-00, [karina28021985@yandex.ru](mailto:karina28021985@yandex.ru)

Aleksandr V. Pleshkov<sup>1</sup>, agronomist of the laboratory of selection and seed-growing of pulse crops, ORCID 0000-0002-5513-2065, AuthorID 1039895; +7 917 344-04-50, [gam303@yandex.ru](mailto:gam303@yandex.ru)

<sup>1</sup> Bashkir Research Institute of Agriculture – Subdivision of the Ufa Federal Research Centre of the Russian Academy of Sciences, Ufa, Russia

<sup>2</sup> Institute of biochemistry and genetics – Subdivision of the Ufa Federal Research Centre of the Russian Academy of Sciences, Ufa, Russia