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REGULAR ARTICLE

Evaluation of genotypic and genetic variances of quantitative traits in pea (*Pisum sativum* L.)

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ABSTRACT

A new approach has been applied for identification of the changes in gene spectra, in accordance with the graphic model of Hayman, which allows making a comparison of varieties, presented in the graphics, as well as, a new method for interpretation of the change in location of certain varieties, with respect to given signs, at different environmental limits. In the genetic control of the characteristics of plant weight and seed weight per plant, a major role plays gene over-domination. The results obtained indicate a possibility of assessment of field peas genotypes by genetic-physiological systems in different environmental limits. No universal donor has been established between hybrids for attraction and adaptability. From selection point of view, of interest are the hybrids №11 (E.F.B.33 × Mir) with respect to green biomass (forage)and №12 (E.F.B.33 × Pleven 10), and with respect to seed №9 (Pleven 10 × E.F.B.33). Assessment of the source material, according to genetic-physiological systems, allows, with a higher degree of probability, to select an appropriate genotype, which exceeds the parental forms, in terms of productivity and ecological stability, and also to accelerate the process of creating new pea varieties.

Keywords: Additivity; Dominance; Epistasis; Heritability; Heterosis

INTRODUCTION

Prior to creation of the ecological-genetic model for organization of the quantitative trait, a number of researchers denied the possibility for development of rapid assessment methods (without testing the progeny) of the breeding material of individual genotypes, in accordance with their phenotype, with respect to quantitative traits. The task for identifying the genotype through phenotype has the purpose to find in the initial population, in accordance with phenotype traits correlating with the genotypic value of the individual or in accordance with markers, that unique plant or seed, which progeny will have high productivity and combinative value (Kocherina, 2007; Kocherina and Dragavtsev, 2007).

According to Dragavtsev, the solution of identification task of the genotype in accordance with phenotype will reveal opportunities to enhance the efficiency of selection up to 1000 times. With the present existing labor-intensive methods for gene identification in the traditional breeding from 10 000 best initial plants, only about 2 to 5 valuable genotypes are finally realized. It is, therefore, necessary to search for the links between the knowledge of genetic determination of the quantitative trait and the identification of selection-valuable genotypes in accordance with phenotype (Dragavtsev et al., 1984; Dragavtsev, 1988).

All known contemporary breeding technologies have two "bottlenecks", which significantly limit their efficiency: lack of methods for rapid and reliable detection of individual genotypes in accordance with phenotype (identification of genotype by means of phenotype) in the earlier stages of breeding, lack of scientific methods for selection of the parent couples at hybridization and methods for prediction of transgressions and heteroses (Dragavtsev, 1995).

With the currently used breeding technologies, only 0.001% of genotypes, which the breeder works with, at selection of individuals in F_2; they can reach application for cultivar registration. But during this stage of breeding, around 90% of the resources needed for variety creation are spent. Therefore, solving the problem of achieving reliable identification of genotype by phenotype will increase

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breeding efficiency up to 1000 times. It is commonly accepted that the selection of parents for hybridization in cross-pollinated crops should be based on knowledge of the genetics of quantitative and qualitative traits. The object of attention for the breeder are usually quantitative traits, related to productivity and yields, which arise at high organization levels from cellular level to the level of agrophytocenosis. It is considered that more than 80% of all final yields in plant production are determined by emergent properties of the organisms. Nowadays, there are methods for identification of genotype by phenotype for the quantitative traits, which opens up new prospects before quantitative genetics and selection (Drozdov et al., 2014).

In the ecologo-genetical model for organization of the quantitative trait, the term "module" is postulated. The module is a result of multiplicative inheritance of two component traits, whose product gives a resulting trait. Yield per unit area is a final product, whose formation can be represented by a pyramid of modules. Modules can be defined, which are presented as time spans in the ontogenesis. In the light of these notions, the influence of environment comes down to a change of limiting factors in critical for the organogenesis or productive process phases of growth and development. The ecologo-genetical model and the fundamental consequences resulting from it are presented in detail by Dragavtsev (Dragavtsev and Dyakov, 1998; Dragavtsev, 2000).

It is the change of limiting factors of the environment in critical phases of organogenesis that leads to a change of the spectrum of loci, determining the quantitative trait in plants. In other words, in those cases, there is a change in the genetic formula of the quantitative trait Dragavtsev (1995). There are still insufficient genetic studies, analyzing the nature of module inheritance, their formation and links in the pyramid of modules (Skuridin and Koval, 2002).

According to Dragavtsev (1984), at the contemporary level of development of the genetics of quantitative trait in plants, quantitative traits such as grain yield or biomass should be studied, considering the modular organization of quantitative trait, as well as, the pyramid of modules, which determine their phenotype manifestation. It is necessary, the character of inheritance of the modules associated with the yield formation to be studied, in relation with the study of genetic homeostasis.

Objective of the study: identification of the genotype by phenotype through application of the method of orthogonal regressions. An attempt has been made for transition from a selection, based on the concepts of "gene-trait", to a selection of genetic-physiological systems.

MATERIALS AND METHODS

An experimental study was conducted from 2009 to 2011 at the Second Experimental Field of the Institute of Forage Crops, Pleven (43.41°N, 24.61°E), situated in the central part of the Danube hilly plain. The experiment was set up as a complete block design with two replications during the winter of 2010/2011. The parental forms (P_1 and P_2) and the first hybrid generation (12 F_1) were sown according to a scheme (P_1, F_1, P_2), with a plot size of 2 m × 1 m, at a row spacing of 20 cm, at two distances: within a row of 5 cm (dense sowing) and within a row of 10 cm (rare sowing) and plot to plot distance of 0.70 m. The seeds were sown by hand at a depth of 5 cm. All the agronomy practices during the trial were ordinary and officially approved by the Institute of Forage Crops. The hybridisation was done by hand in 2009.

The following field pea (*Pisum sativum* L.) cultivars (Table 1) were used as the parental components: spring-sown cultivar Kerpo and three autumn-sown cultivars namely Pleven 10, Mir and EFB33.The hybridisation included all direct and reciprocal crosses which is a full diallel scheme. From each genotype in P1, P2 and F1 a sample of 20 plants was used for analysing the following quantitative traits: seed weight per plant (g) and plant weight (g). The plants are harvested at two phenological stages of plant development – full pod formation and maturity stage.

Table 1: Pea parental components used in the research

Genotypes	Kerpo	Mir	Pleven 10	E.F.B.33
Distinctive features				
Origin	Bulgaria	Bulgaria	Bulgaria	Germany
Subspecies	Sativum	Arvense	Arvense	Arvense
Plant type	Mean	Long	Long	Long
Flower color	white	Purple	Purple	Purple
Hilum color	white	Black	Black	Black
Anthocyanin pigmentation	Absent	Present	Present	Present
Leaf type	Normal	Normal	Normal	Normal
Plant height, cm	71	219	224	198
Height to first pod, cm	52	118	118	101
Number of pods per plant	6.88	25.73	22.88	27.83
Number of seeds per plant	28.60	115.80	107.70	113.13
Number of seeds per pod	4.14	4.51	4.72	4.06
Seed weight per plant, g	6.58	12.75	12.95	9.25
Fertile nodes per plant	3.56	13.33	11.85	14.42
1000 seeds mass, g	232.29	108.70	118.48	82.70

The diallel analysis of variance (ANOVA) graphical analysis (Wr/Vr; Wr^/Vr) by Hayman is based on the variance-covariance matrix (Vr-Wr). where: "a" is primarily additive effects; "b" is primarily dominance effects; "b_1" is mean deviation of F_1's from their mid-parental value; "b_2" is variation of deviation of F1's from their mid-parent value over arrays; "b_3" is that part of dominance variation unique to each F1; "c" is average maternal or cytoplasmic effect of each parental line; "d" is reciprocal differences not ascribable to "c". The mean square of casual deviations of initial data on ANOVA analysis of diallel crosses was used for estimating σe^2. Estimating includes the values of the following genetical parameters: "D" are additive gene effects (additive variance); "H1" and "H2" are dominance gene effects (dominance variance 1 and dominance variance 2); "F" is covariance of additive and non-additive effects in all the arrays that has a positive or negative sign depending on whether dominant genes or recessive genes are more. When F>0 predominate dominant alleles, when F<0 – the recessive ones, when F=0 – the alleles are equal represented. In addition, "h2" is dominance effect as the algebraic sum over all loci in heterozygous phases in all cases; "Hbs" is heritability for diallel in a broad sense; "Hns" is heritability for diallel in a narrow sense; H1/D is average degree of dominance in experimental material; H2/4H1 is a measure of the average value ($p_i q_i$) of all the polymorphic loci exhibiting dominance ($di \neq 0$); h2/H2 is the number of groups of genes which control the character and exhibit dominance; and ((4DH1)½+F)/(4DH1)½-F)) is proportion of dominant and recessive genes in the parents. The conclusions from the Wr. Vr graph are: 1) Wr is related to Vr by a straight regression line of unit slope in the absence of non-allelic interaction and with independent distribution of genes among the parents; 2) The distance between the origin and the point where the regression line cuts the Wr-axis provides a measure of the average degree of dominance; 3) $D > H_1$ (partial dominance) when the intercept is positive; D = H1 (complete dominance) when line passes through the origin; D < H1 (over dominance) when intercept is negative; and no dominance when the regression line touches the parabola limit.

In the modular organization of the quantitative trait, the resulting trait could be considered as componential in other following module. For example: component trait 1 × component trait 2 = resulting trait (Dragavtsev, 1995).

The orthogonal regression was described by Kramer (Dragavtsev, 1995): If "φ" is the angle of orthogonal regression, then "x_i" is an individual (or mean) value the character "x_i", "x" is a mean value of all the individuals within the variety (or the mean of the average values of the varieties when calculating the genotypic regression), "μ" – the average value of the trait of all individuals in the population.

$$tg2\varphi = \frac{2\mu_{11}}{\mu_{20} - \mu_{02}}$$

$$\mu_{20} = \frac{1}{n-1}\sum_{i=1}^{n}(x_i - \bar{x})^2$$

$$\mu_{02} = \frac{1}{n-1}\sum_{i=1}^{n}(y_i - \bar{y})^2$$

$$\mu_{11} = \frac{1}{n-1}\sum_{i=1}^{n}(x_i - \bar{x})(y_i - \bar{y})^2$$

The parameters of axes of the orthogonal regression are given by:

$$y - \bar{y} = \frac{2\mu_{11}}{(\mu_{20} - \mu_{02}) \pm \sqrt{(\mu_{20} - \mu_{02})^2 + \mu_{11}}}(x - \bar{x})$$

Where the sign "-" corresponds to the longer axis of the ellipse of dispersion, "y_i" is an individual (or mean) value the character "y_i", "y" is a mean value of all the individuals within the variety.

$$a = \frac{c}{\frac{1}{2}\left(\frac{1}{\mu_{20}} + \frac{1}{\mu_{02}}\right) \pm \sqrt{\frac{1}{4}\left(-\frac{1}{\mu_{20}} + \frac{1}{\mu_{02}}\right)^2 - \frac{1 - r^2}{\mu_{20}\mu_{02}}}}$$

Where 'r' is the coefficient of correlation, 'c' - the constant (c = 2 with P = 5%), 'a'- the initial ordinate.

The essence of the phenomenon becomes clear, when examining the contrariety in a two dimensional coordinate system with two traits – a selection trait (ST) and a background trait (BT). In this system the so-called orthogonal regressions are used, wherefrom, the method bears the name "method of orthogonal regression". These regressions are different from those commonly used in applied regression analysis, which are always two – A × B and B × A. The orthogonal regression is always a single one – this is the major axis of the ellipse of scattering or the geometrical locus of the points (a straight line), the sum of squares of the distances, from which empirical points of scattering is minimal. For example, if on a graphic, points of measurements of individual plants are indicated, noises (or deviations) arise, which disappear when on the graphic, average values of 50-100 individual measurements of the trait are indicated. The crossed-out co-variances represent the removed noises (deviations), as average dimensions are situated on the graphics. The coordinate system ST-BT (Selection-Background Trait) allows for the genotype of

the individual organism through phenotype to be identified. Therefore, the relative size of the influence of the genotype and the environment are assessed quantitatively in a scale from actual measurements of the trait. By contrast with the methods for genetic analysis of traits, a study of 7 genetic-physiological systems is suggested to be made.

The obtained data have been analysed according to Hayman (1954a), while the genetical properties of the parental components have been determined according to the graphical method by Hayman (1954a, 1954b), using the software DIALL (Ukai, 1989).

RESULTS AND DISCUSSION

Everyone dealing with applied genetics and plant breeding needs to know the genetical structure of a specific trait in concrete material that is, what genetical effects prevail, the number of the polymorphic loci, how the alleles are shared and so on. Such information gives opportunity of including novel cultivars in hybridisation designs and breeding programmes. The theoretical base of diallel analysis of the additive-dominant model according to Hayman is founded upon the following presumptions: the investigated genotypes are diploid and homozyguous, every locus can be in two allelic positions, no exhibition of epistatic effects, no difference in inheritance in reciprocal crosses and independently distribution of the genes between the parents (Hayman, 1954a; 1954b).

Diallel ANOVA

The components of the genetical variation were established with the disperssion analysis of the traits in the tested field pea genotypes (Table 2). The analysis of variance revealed highly significant differences among the progeny, indicating that the parents were diverse in regard to the studied traits. In the diallel ANOVA all the genetic effects were significant without "a" for D; "b_1" for B, G and H; "b_2" for D; b_3 for A, B, C, D G, H; d for D and H. Dominant gene effects prevailed in a majority of the traits in F_1 generation.

Wr/Vr analysis

The estimate of the components of genetical variation for the different quantitative traits in forage pea is given in Table 3. One is the number of the group of genes controlling this trait and exhibiting dominance (h_2/H_2) in both densities. The ratio $H_2/4H_1$ can be done by concluding that plus and minus alleles are distributed in a non-uniform way between parental forms, with the exception of E and F. The ratio of $((4DH_1)^{1/2} + F)/(4DH_1)^{1/2} - F))$showed a prevalent dominant gene effect for all traits.

In all tested traits, the coefficient of inheritance in a broad sense (Hbs) has a greater value than that in a narrow sense (Hns). A relatively high coefficient of inheritance in the narrow sense is established at technical maturity in a dense stand for both traits, as well as, in full lower pods in diluted stand. The low value of the coefficient of inheritance in a narrow sense presupposes great influence of weather conditions on the inheritance of the trait and conducting an effective selection for desired traits in later hybrid generations (F_3-F_4), when the effects of domination and epistasis decrease and increase the homozygosity.

In Fig. 1a and c the results are shown of graphical diallel analysis according to the model of Hayman for trait plant weight in diluted and dense stand at the phenological stage of full lower pods. The chart shows that the dependence Wr/Vr is a straight line with single slope, which lies inside the limiting parabola.

Table 2: Analysis of variance (ANOVA) for combining ability of the field pea hybrids traits in f_1 generation (by Hayman)

Sourse	df	Full pod formation				Maturity stage			
		Rare sowing		dense sowing		Rare sowing		Dense sowing	
		a	b	c	d	e	f	g	h
Replication	1	30.75	4290.16	0.38	45.84	263.34**	81.60**	3.64	7.90
a	3	11503.08**	535.77*	2802.58**	232.95	2336.48**	886.78**	591.40**	122.62**
b	6	21200.75**	677.06*	4424.01**	258.82*	5446.53**	1389.63**	614.82**	136.17**
b1	1	16008.92**	45.49	6180.86**	798.68**	6898.65**	1426.81**	60.48	12.69
b2	3	36874.22**	997.79**	6646.97**	72.81	6308.70**	657.02**	1182.66**	265.82**
b3	2	286.45	511.74	211.16	267.91	7477.22**	2469.94**	40.23	3.44
c	3	19048.66**	1695.18**	6996.47**	1209.22**	480.12**	1025.02**	240.00**	159.37**
d	3	15.823.90**	1778.48**	32.76**	129.47	5414.41**	1799.77**	223.98*	15.91
Error	15	269.61	159.36	70.91	81.58	17.44	7.22	62.78	14.27
S.E P1-P2		480.89	57.10	43.30	6.81	5.06	6.10	5.89	0.89
S.E. - F1		24.78	9.35	23.29	52.38	10.39	1.82	32.85	8.88
Total	31								

*Significant at 5% level; ** significant at 1% level. full pod formation - rare sowing a: Plant weight (g.); b: Seeds weight from plant (g.); - dense sowing; c: Plant weight (g.); d - seeds weight from plant (g.); maturity stage - rare sowing e: Plant weight (g.); f: Seeds weight from plant (g.); - dense sowing g: Plant weight (g.); h: seeds weight from plant (g.)

Table 3: Estimates of components of variation for different quantitative traits in field pea cultivars

Genetic parameters	Full Pod Formation				Maturity Stage			
	Rare Sowing		Dense Sowing		Rare Sowing		Dense Sowing	
	a	b	c	d	e	f	g	h
D	580.48	4449.89	19984.76	49.341	171.250	84.125	94.881	21.214
H_1	713.92	6003.75	30117	426.276	4968.779	1340.321	347.104	84.781
H_2	519.81	4366.63	20969.55	358.157	4517.910	1247.086	239.068	59.752
F	689.48	5400.43	26352.32	109.640	−427.029	−114.854	−132.060	−35.750
D-H_1	−133.44	−1553.86	−10132.24	−376.936	−4797.529	−1256.196	−252.224	−63.567
h_2/H_2	0.490	0.050	0.831	0.835	0.570	0.429	0.093	0.060
H_1/D	1.230	1.349	1.507	2.939	5.387	3.992	1.913	1.999
$H_2/4H_1$	0.182	0.182	0.174	0.210	0.227	0.232	0.172	0.176
$((4DH_1)^{1/2}+F)/ ((4DH_1)^{1/2} -F))$	1.002	1.0002	1.0004	2.215	0.624	0.707	0.466	0.406
Hns	0.16	0.23	0.21	0.04	0.31	0.31	0.73	0.72
Hbs	0.68	0.97	0.98	0.94	0.99	0.98	0.97	0.91

Full pod formation - rare sowing a: Plant weight (g.); b: Seeds weight from plant (g.); - dense sowing c: Plant weight (g.); d: Seeds weight from plant (g.); maturity stage - rare sowing e: Plant weight (g.); f: Seeds weight from plant (g.); - dense sowing g: Plant weight (g.); h: Seeds weight from plant (g.)

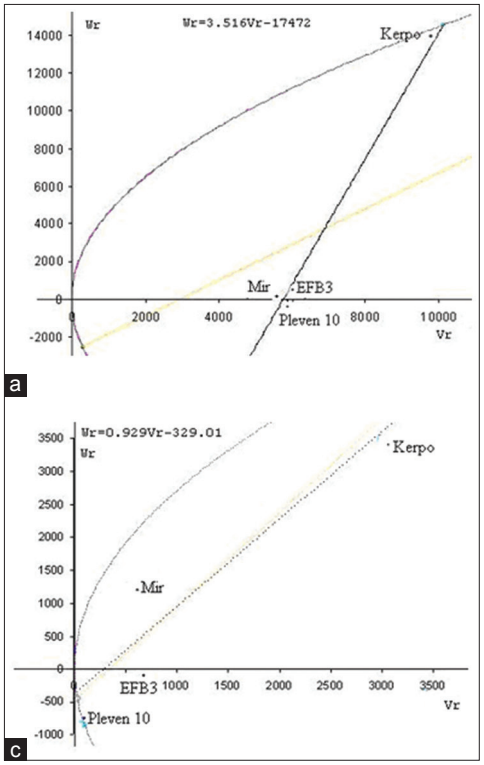

Fig 1. (a and c). Graphical analysis of the field pea hybrids traits in F1 generation-full pod formation - rare sowing "a" - plant weight (g); - dense sowing "c" - plant weight (g).

The regression line, around which points (varieties) are situated, depending on the values of variance (Vr) and covariance (Wr) and in both densities, intersects the coordinate system of the chart below zero, on the negative side and shows over-domination of the genes in the inheritance of the trait. Growing conditions have not affected the genetic control of the trait, but have an impact on the places of individual varieties in the graphics. When changing the limit of environment (in compressed stand) varieties Mir, Pleven 10 and EFB33 are shifted substantially to the vertical axis of the coordinate system, while Kerpo variety relatively preserves its position to the far-right in the recessive zone.

For the trait of seed weight per plant (Fig. 2b and d) quite a different reaction especially of varieties EFB33 and Kerpo was found. In conditions of competition (compressed stand) variety Kerpo appears on the dominant side of the graphic, and variety EFB33, which has the highest dispersion values, falls within the recessive zone. In comfortable conditions (diluted stand) these varieties swapped their places in the graphics. Only Mir variety retains its position in both growing environments. This indicates that different genotypes have different genetic structures, which determine the expression of each trait. The phenomenon is known as predetermination of the genetic formula of the trait when there is a change in the environmental conditions.

At stage of technological maturity (Fig. 3e and g) at a diluted stand, it makes an impression that varieties Pleven 10 and Kerpo take very close place in the beginning of the coordinate system, which is an indication for strong action of dominant alleles determining the trait. Parental components Mir and EFB33 are located to the far right of the graphics in the recessive zone, indicating that they possess gene systems, differing from the other varieties, regarding the trait of plant weight. When placed in a competitive environment (compression of the stand), the varieties significantly change their position in the graphics, as with Pleven 10 and Kerpo varieties recessive genes take part in the manifestation of the trait, and with Mir and Kerpo – dominant gene systems. Therefore, when changing the limiting factors of the environment of the varieties, specific gene systems determining the genetic variability of the trait are manifested. At the same phenological stage (Fig. 4f and h) regarding the trait of seed weight at a diluted

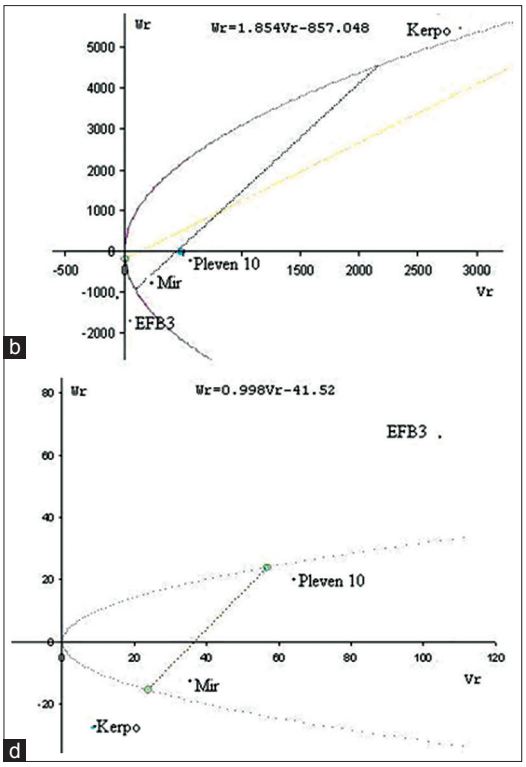

Fig 2. (b and d). Graphical analysis of the field pea hybrids traits in F1 generation-full pod formation - rare sowing "b" - seed weight per plant (g); - dense sowing "d" - seed weight per plant (g).

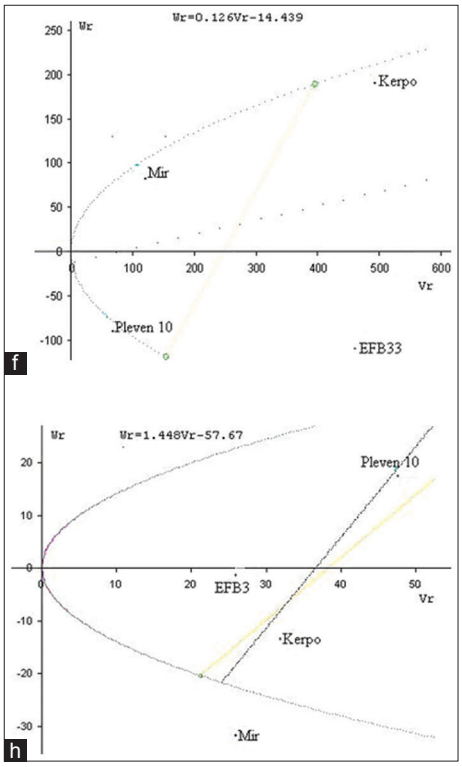

Fig 4. (f and h). Graphical analysis of the field pea hybrids traits in F1 generation-maturity stage - rare sowing "f" - seed weight per plant (g); - dense sowing "h" - seed weight per plant (g).

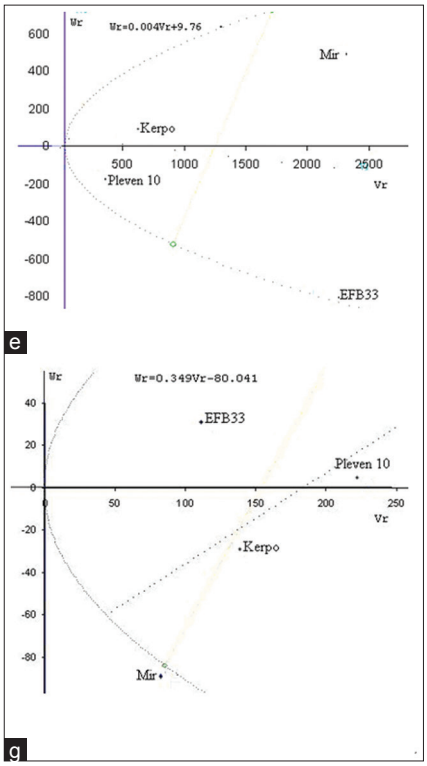

Fig 3. (e and g). Graphical analysis of the field pea hybrids traits in F1 generation-maturity stage - rare sowing "e" - plant weight (g); - dense sowing "g" - plant weight (g).

stand Pleven 10 variety again occupies a place close to the vertical axis. In comparison with the trait of plant weight, it has been established that the inheritance of these traits is similar and is determined by dominant genes. The behavior of the Kerpo variety and its position in the graphics show that the expression of the trait is under the influence of recessive genes. In conditions of a compressed stand, all varieties shift their position to right in the recessive zone of the graph.

The joint examination of the influence of environment limits and the analysis of the adaptive properties of varieties allow for their shifting along the line of regression to be explained. The genetic analysis according to Hayman allows establishment of genetic parameters of a population important for the breeding. However, the prognostic capability of the methods of Hayman and Griffing is now being questioned (Kocherina, 2009).

The model of ecologo-genetic organization of complex quantitative traits for productivity

In Fig. 5 (a and b) it can be seen that the tested varieties and hybrids differ in the stability of their genetic systems, when changing the limits of the environment at the phenological phase of full lower pods. If in the figure a genotype with maximum values regarding attraction is found and another

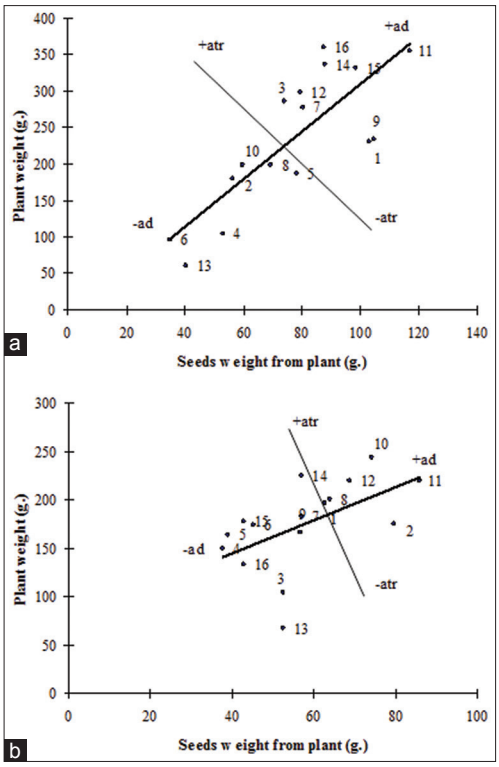

Fig 5. (a and b). Distribution of mean values of hybrid genotypesfull pod formation: a - rare sowing; b - dense sowing; 1 - P_1 (Mir); 2 - P_2 (Pleven 10); 3 - P_3 (E.F.B.33); 4 - P_4 Kerpo); 5 - $P_1 \times P_2$; 6 - $P_1 \times P_3$; 7 - $P_1 \times P_4$; 8 - $P_2 \times P_1$; 9 - $P_2 \times P_3$; 10 - $P_2 \times P_4$; 11 - $P_3 \times P_1$; 12 - $P_3 \times P_2$; 13 - $P_3 \times P_4$; 14 - $P_4 \times P_1$; 15 - $P_4 \times P_2$; 16 - $P_4 \times P_3$.

one having maximal values for adaptability, then, they are the most appropriate of the studied genotypes as parental components in combined selection. From their hybrids in the second generation transgressive forms can be obtained, combining in the most appropriate way genes for attraction and adaptability. According to Dragavtsev and Dyakov (1998) if you find parents with such qualities, it is very important to have information about how genes additively interact for attraction and adaptability in these genotypes.

The situation with the F1 hybrid (№11 and №12), occupying a positive part regarding adaptability, is retained in both sowing densities (Fig. 5, a and b). The position of the majority of hybrids and varieties is substantially changed at deterioration of the cenotic environment. Stable position in the negative part occupy genotypes №4 and №13. Variety №1 in a diluted stand is on the verge of negative adaptability.

Fig. 6c shows that the hybrid №9 demonstrates the highest values with respect to the tested traits at technical maturity. For its maximum adaptability and relatively good attractiveness, it can be assumed that it has good genes for adaptability and attraction with regard to the plant weigh and seed weight per plant. Variety №3, as well as, hybrids №15 and №16 are shifted to the negative part of the line for adaptability, which is an indication that the genetic control on the adaptability is redefined unfavorable in the higher crop density for these genotypes. At this phenological stage in a diluted stand, a favorite that shows a significant positive attraction and to be a donor of genes for strong attraction cannot be defined. Regarding the genetic change in attraction of the pea genotypes a strong polymorphism (the points are scattered on the positive and negative line of regression) can be detected, which indicates a good prospect for selection improving.

When studying the behavior of hybrids in a compressed stand (Fig. 6d) it is observed that hybrids №12, №5, №7 and №8 fall into the quadrant, which is characterized by positive adaptability and attraction. It can therefore be assumed that their genomes under certain conditions may manifest genes determining the strengthening of these traits. Stable but with negative adaptability are hybrids №2, №4 and №13.

Analysis of the data shows that genotypes №6, №7, №11 and №15 are ecologically stable donors of attraction, although they are situated very close to the regression line. The positive part of orthogonal regression identifies the changes with respect to adaptability. It can be seen that the scope of volatility in adaptability exceeds the scope in attraction.

It has been established that in both phenological stages (in a compressed stand) stability exhibits hybrid №12, occupying the positive line in the graphics above orthogonal regression. The same hybrid exhibits a good combination of genes for adaptability and attraction (fast movement of plastic substances) in case of deterioration of the conditions.

Thus, through graphical representation the donor may be determined characteristic for each genotype with respect to adaptability and attraction (Ismoilov, 2006). Dragavtsev et al. (1984) consider that for the phenotypic manifestation of a quantitative trait of a genotype, situated in different conditions, determining significance may have absolutely different genes.

In their studies Dragavtsev and Dyakov (1982) and Mikhailenko and Dragavtsev (2013) substantiate a new theory, revealing an opportunity for identification of plant genotypes in the early stages of selection by phenotypes. Data have been obtained in support of this new scientific viewpoint, which gives greater opportunities for a significant improvement of selection efficiency (Dragavtsev, 1995). The authors reveal a phenomenal multi-directional displacement of the genetic and ecological

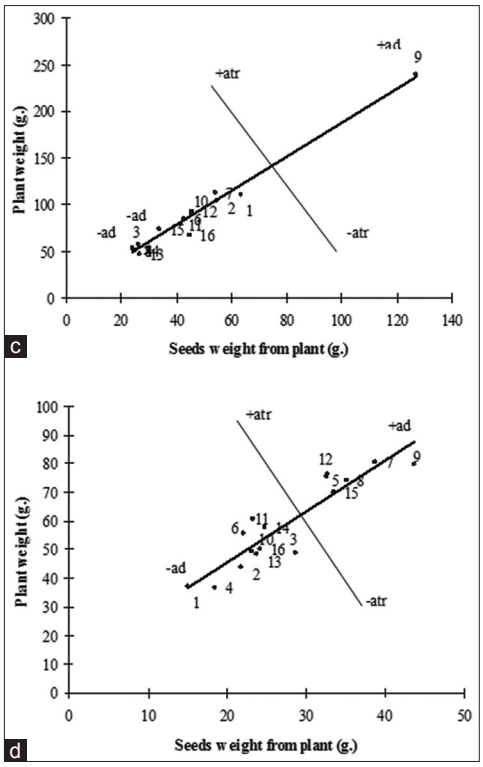

Fig 6. (c and d). Distribution of mean values of hybrid genotypes maturity stage: c - rare sowing; d- dense sowing 1 - P_1 (Mir); 2 - P_2 (Pleven 10); 3 - P_3 (E.F.B.33); 4 - P_4 Kerpo); 5 - $P_1 \times P_2$; 6 - $P_1 \times P_3$; 7 - $P_1 \times P_4$; 8 - $P_2 \times P_1$; 9 - $P_2 \times P_3$; 10 - $P_2 \times P_4$; 11 - $P_3 \times P_1$; 12 - $P_3 \times P_2$; 13 - $P_3 \times P_4$; 14 - $P_4 \times P_1$; 15 - $P_4 \times P_2$; 16 - $P_4 \times P_3$

dispersion of a quantitative trait of an individual organism under change of limiting conditions of environment. An opportunity has been disclosed for the extent, in which variation of the trait is due to genetic or environmental reasons (change of environmental limits), to be estimated quantitatively (Dragavtsev and Kocherina, 2006).

CONCLUSIONS

A new approach has been applied for identification of the changes in gene spectra according to the graphic model of Hayman, which allows a comparison of varieties, located in the graphics, as well as, a new method of interpretation of the location change of certain varieties, with regard to given signs in different limits of the environment, has been used. In the genetic control of the plant weight and seed weight per plant traits, a major role plays the over-dominance of genes. Exhibited dominant alleles were found in Mir and Pleven 10 varieties at pod formation stage for both traits in both growing environments. At technical maturity, when changing the limits of the environment, an action has been established of different gene systems with the varieties in the manifestation of the traits. The cultivar Kerpo exhibited recessive alleles for all the traits.

The results obtained indicate a possibility of assessment of pea genotypes by genetic-physiological systems in different environmental limits. A universal donor between hybrids for attraction and adaptability has not been established. The evaluation of source material through genetic- physiological systems allows with a high probability for an appropriate genotype to be selected, which exceeds the parental forms, regarding to productivity and environmental stability, but also to accelerate the process of development of new pea varieties.

Author's contributions

Natalia Georgieva and Valentin Kosev wrote the manuscript. Valentin Kosev conceived carried outof the statisticall analysis. Natalia Georgieva a revised and approved the manuscript. All authorsread and approved the final manuscript.

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