Bulgarian Journal of Agricultural Science, 31 (No 4) 2025, 731–740

Selection estimation of chaenomeles accessions

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Abstract

Georgieva, N., Kosev, V. & Mihova, T. (2025). Selection estimation of chaenomeles accessions. *Bulg. J. Agric. Sci., 31*(4), 731–740

The application of traditional methods in selection-genetic studies is necessary to be combined with new possibilities for estimation. In the present study, based on the application of the ecological-genetic model for organization of the quantitative trait, an attempt was made to determine the genotype of 15 chaenomeles accessions by their phenotype. The applied method makes it possible to increase the breeding process efficiency, and valuable genotypes to be recognized still at the initial stage of breeding, according to their phenotype. Parameters and coefficients that determine the adaptability and plasticity of the accessions in the Middle Balkan Mountains conditions were calculated. The results showed that A14 and A6 possess strong genes of the physiological system of adaptability in terms of productivity and yield. A13, A8, A3, and A11 are characterized by a weak but positive attractiveness. Accession A14 was distinguished by negative attractiveness regarding the vegetation period duration, and A6 had positive manifestations of genes for adaptability (good productivity) and attraction (long vegetation period). A7, A10, A5 and A13 were less productive, but can be used in combinative breeding to develop early-ripening forms. In decorative direction, with positive attraction and adaptability, suitable were A7 and A6 due to the increased number of flowers per bush. Accessions A1 and A2 showed good stability concerning flowers number per bud, and the same can be used as parental components in the decorative direction. The general adaptation index determined A14, A6 and A7 as highly adaptable genotypes. With high values of the coefficient of multiplicativity were A2, A3, A7 and A8 (5.13–3.62), and with good ecological plasticity – respectively, A13 (IEP = 10.3), A14 (IEP = 2.89), A6 (IEP = 1.72) and A17 (IEP = 1.19).

Keywords: chaenomeles; genotype; phenotype; productivity; decorative direction

Introduction

Chaenomeles is a relatively new orchard crop with good prospects for cultivation in Europe. It belongs to the family *Rosaceae* Juss., subfamily *Maloideae* C. Weber, genus *Chaenomeles* Lindl. It is grown as a valuable ornamental plant, and determined as one of the 15 most beautiful flowering shrubs with wide ecological plasticity. In Japan, the United States and European countries, a huge varietal diversity of chaenomeles has been created, numbering, according to various estimates, between 200 and 500 cultivars (Pilkevich, 2018). In recent decades, interest in this crop has been determined not only by its ornamental qualities, but also by the high biological value of the fruits (Kaufmane et al., 2021). In terms of biochemical composition, they are closer to lemon fruits, than to other pome species (apple, pear and quince), and are distinguished by a high and favorable content of organic acids, pectins, aromatic substances and biologically active compounds. It is found that fruits possess various pharmacological activities, such as antibacterial, anti-inflammatory, anti-diabetic, anti-tumor cell proliferation, anti-hyperglycemic, immunomodulatory, and antioxidant activities (Zhang et al., 2019). For modern fruit growing, chaenomeles is also valuable with other characteristics – good productivity, pest resistance and tolerance to unfavorable climatic conditions. The wide potential region of distribution, easy propagation and high economic efficiency, confirm the merits of chaenomeles as a crop (Fedulova and Shikovets, 2016; Milanova and Fedulova, 2018; Kurtto et al., 2018).

According to Kuklina et al. (2015) and Komar-Tyomnaya (2017, 2018), chaenomeles productivity is affected by: average daily air temperature and precipitation amount during the flowering period, average temperature during fruit formation, temperature and precipitation during setting and differentiation of generative buds for the next year's crop, as well as the rainfall during fruit ripening.

In order to optimize the breeding process and selection efficiency, methods for ecological and genetic assessment of crop adaptability were developed, agroclimatic models and models of plant ontogenetic adaptation were created (Lopatina and Dragavtseva, 2014). Currently, there is a traditional approach to identifying the genotype of an organism through its phenotype – testing its progeny. The frequency of occurrence of unique genotypes in the populations, is so low, and the populations are so voluminous, that the breeder, in the first breeding stages, has to reject up to 80-90% of the individuals of the cleavage population, according to their phenotypic manifestation. Thus, most valuable forms are irretrievably lost, which cannot be compensated by a more accurate evaluation in the subsequent breeding stages. The results of time-consuming, expensive and long-term progeny tests, have a number of disadvantages. They are influenced considerably by the presence of a cytoplasmic effect, ecological consequences of the environment on the quantitative traits of the progeny, intergenotypic competition, ecological diversity, etc. (Yakushev et al., 2015).

Currently, many geneticists and breeders use Hayman's (1954) method of diallelic analysis, or its simplified variants, for genetic analysis of plant quantitative traits. But the interpretation of the genetic parameters and graphs of Hayman (1954), built on the paradigm of the concepts of classical genetics of Mendel (1865), in most cases is not correct. All parameters and graphs of Hayman (1954), vary sensibly from one geographical point to another, and from year to year, i. e., there is no stable genetics of quantitative traits (Dragavtsev, 2019). According to Kuklina and Fedulova (2015), there are no stable donor characteristics of any genotype, regarding the quantitative trait against the background of various limiting factors of the environment. Therefore, all transgressions in terms of complex productive traits are ecologically dependent.

At the end of the last century, a new model for ecological-genetic control of the quantitative trait has published. According to it, when the limiting factor of the environment changes, the spectrum of genes, determining the level and genetic dispersion of the trait, also changes. It is an obvious fact, that it is impossible to describe real ecological and genetic organization of the complex quantitative trait in the language of Mendelian, biometric and molecular genetics. Any quantitative characteristic, subjected to the genotype-environment interaction, is a result of the interaction of gene products in plant cells with fluctuating environmental factors. The nature of development of the complex character of productivity, can only be understood by studying a system consisting of both gene products, and the specific dynamics of environmental limiting factors. A complete description of such a system is possible only through ecological genetics (Dragavtsev, 2009), based on which it is possible to develop a model, that predicts the chaenomeles productivity depending on the environmental conditions.

The aim of this research was an ecological-genetic estimation of chaenomeles accessions, and their reaction to the environmental conditions in the Middle Balkan Mountains region.

Material and Methods

The experimental activity was conducted during the period 2010–2012, at the Research Institute of Mountain Stockbreeding and Agriculture (Troyan), which is located in the Middle Balkan Mountains, at an altitude of 380 m. The object of study was a collection of 15 chaenomeles accessions, which are seed forms obtained from free pollination and possessing valuable decorative, medicinal and nutritional characteristics. Inter-row/intra-row spacings in the plantation was 2.5 m/1 m. The shrubs were grown in nonirrigated conditions, naturally grassed between rows, which were mowed several times depending on the rainfall during the vegetation. Pruning and fertilizing were not carried out.

The modular organization of quantitative traits was presented according to the model of Dragavtsev (2002). According to it, the genetic formula of a trait consists of multiple discretely manifesting, functionally related components of a single system. As a consequence of integrating the genetic system elements within the whole organism, the phenotype can represent as a realization of two hierarchies – structural and temporal. The module, as an elementary unit, describes the organization of the quantitative trait, which consists of three interrelated characteristics (two componential and one resulting). The module reflects all stages of realization of genetic formulas depending on the level of environmental factors during ontogenesis. In the modular organization, the resulting trait can be considered a component trait in another subsequent module. For example, component trait 1 × component trait 2 = resulting trait.

The coordinate system of selection trait-background trait (ST-BT) allows quickly, without changing the offspring, to identify the genotype of an organism by phenotype, i.e., to quickly obtain information on whether a given phenotypic value of a trait is determined by genetic systems, or represents a modification (i. e., it arose as a result of the influence of the microecological habitat niche of that individual). At the same time, the contribution of genotype and environment is quantified on a scale for trait measurement. Thus, for ecological deviations of a quantitative trait (modifications), and for deviations due to genetic causes, in certain systems of trait coordinates, there is a specific expression (multi-directionality of these deviations), which allows their clear distinction and quantification.

In addition, the following parameters were calculated: adaptability, based on the use of the multiplicative coefficient (KM) (according to the method of Dragavtsev, 1984); index of ecological plasticity (IEP) (according to the method of Gryaznov, 1996); fruiting index (ratio of fruit weight to number of inflorescences) (according to the method of Fesenko, 1983) and Taranenko and Yacishen, 2014). The method of Zhivotkov et al. (1994) was also applied. It is based on identifying the potential productivity and adaptability of a genotype, compared to the general adaptive response of the group of genotypes to environmental conditions.

All experimental data were statistically processed using the computer software MS Excel (2016), and Statgraphics Plus for Windows Version 2.1.

Results

The study period included three consecutive years, differing in meteorological terms. The region territory refers to the foothills of the temperate-continental climatic zone. The climate is characterized by great diversity due to the physical and geographical conditions of the area. It is mainly determined by the direct and strong influence of the Balkan Mountains, which affects both precipitation and temperatures. The average annual air temperature for the study period was 10.8°C (Table 1). Winter was moderately mild, with an average seasonal temperature of around 0°C. The initial date of sustainable retention of the average daily temperature above 5°C (when the vegetation period of plants begins) was the end of March, and the final date was the end of November. Due to the relatively higher altitude, the summer was not very hot, with the highest average day and night temperature during August (24.4°C). The precipitation regime had a continental character. The average annual amount of precipitation for the study period was 756.8 mm, and for the period with an average day and night temperature above 10 °C was 480 mm. Precipitation maxima and minima over the years varied, but as a whole, the most precipitation fell in May (106.6 mm), and the least in February (45.6 mm).

Orthogonal regression method. Identification of genotype by phenotype

The ecological-genetic approach implies (instead of carrying out a genetic analysis of traits), studying the genetic-physiological systems of the organism, through which appropriate (to achieve the research aim), genotypes can be

Table 1. Meteorological characteristic for the study period

Month/year	Temperature, ˚C				Precipitation, mm			
	2010	2011	2012	average	2010	2011	2012	average
January	-0.5	-0.2	-2.1	-0.9	40.7	22.5	124.5	62.6
February	1.7	-0.3	-5.4	-1.3	66.4	24.8	45.6	45.6
March	5.3	4.9	5.6	5.3	76.9	41.7	35.5	51.4
April	10.8	9.7	12.2	10.9	112.6	68.0	36.0	72.2
May	15.9	14.7	15.1	15.2	76.7	69.1	174	106.6
June	18.6	18.5	20.8	19.3	132.7	98.4	51.8	94.3
July	20.6	21	24.2	21.9	146.3	72.9	7.2	75.5
August	21.7	20.2	31.3	24.4	40.9	96.8	39.1	58.9
September	15.8	18.2	17.8	17.3	50.6	6.8	30.8	29.4
October	8.8	8.6	13.2	10.2	94.4	109.0	43.6	82.3
November	10.3	1.8	7.6	6.6	18.8	2.0	11.8	10.9
December	0.9	2.6	-0.4	1.0	88.0	34.3	79.1	67.1
Average annual temperature/ Annual amount of precipitation	10.8	10.0	11.7	10.8	945	646.3	679	756.8

identified and improved. This approach does not aim to model the dynamics of the huge number of genetic spectra, but to estimate the effect of these systems on the state of starting module (trait). Unlike methods of genetic analysis of traits, the orthogonal regression method offers the study of 7 genetic-physiological systems. The use of this method in breeding allows optimizing the selection of promising starting material, as well as potential parental forms for combinative breeding purposes. In the selection trait-background trait (ST-BT) system, the deviations of the points of individual genotypes from the positive regression line can use to identify genetic deviations, caused only by attraction genes, regardless of the magnitude and number of other effects, directed along the positive regression line.

If a trait with zero genetic variance is found in a given plant population, then the variation of that trait is only ecological. In case, when the genotype has a positive trait deviation compared to the population average, there is a plus-modification i. e., the genotype has fallen into the best microecological niche (background trait, BT). If the selection trait (ST) of the same genotype is displaced in a positive direction (plus) corresponding to the background trait, then this is a modification, and that genotype should not be selected. If in another genotype, BT is at the level of the average value for the population, and ST displaces to the positive side, then this is a recombination (or mutation) necessary for constructive breeding work.

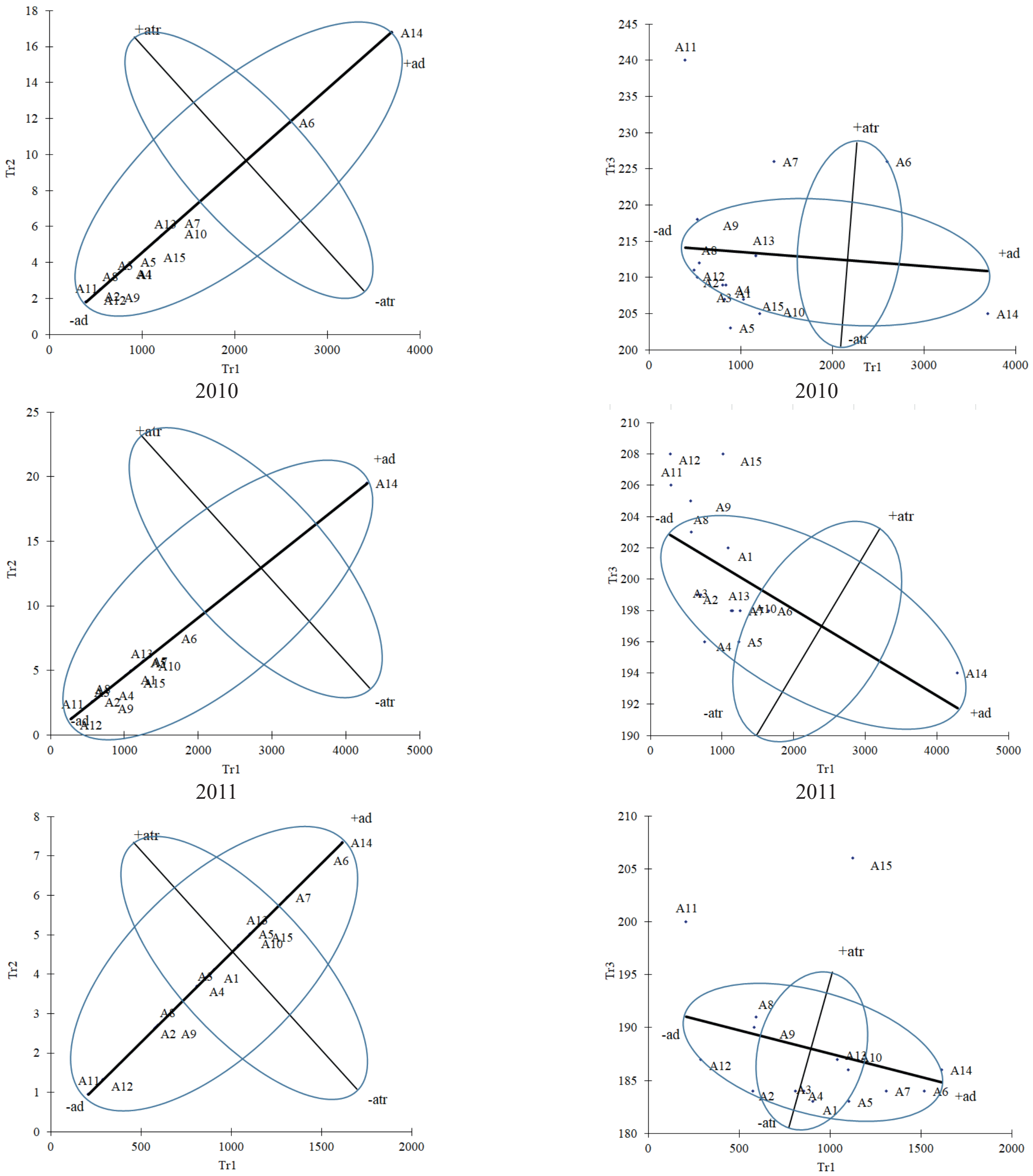
The presented graph (Figure 1) uses the so-called orthogonal regressions, where the name «orthogonal regression method» has come from. Orthogonal regression is always only one – it is the major axis of scatter ellipse or the geometric place of points (straight line). As a criterion for selection of valuable (in terms of breeding) accessions, the direction and magnitude of displacement of the genotypes along the coordinate system are used.

In the two-dimensional coordinate system, the used traits were fruit yield per da (ST), fruit productivity per plant (BT), and duration of vegetation period (BT). The graph for 2010, presents the location of the accessions in the coordinate system (in terms of yield and productivity) under favorable environmental conditions. Accessions A6, and especially A14, were high yielding and with positive adaptation. Their projections were in the quadrant, bounded by the positive part of adaptability and very close to the regression line with almost zero attractiveness. The remaining genotypes adaptively did not perform well, bearing in mind that their projections were close to the beginning of the coordinate system. The least adaptive were A11, A12 and A2. They did not respond positively when placed under favorable environmental conditions.

When the cenotic situation worsened in climatic terms in 2011, A14 was again adaptively most valuable. A14 did not change its placement compared to 2010, and remained in the same quadrant, indicating that it has “strong” genes for adaptability. In contrast, A6 moved to the quadrant with negative adaptation, where all other genotypes were also located which determines weaker adaptability. Accessions A13, A8, A3 and A11 were located in the negative part of the adaptability line, but unlike the other accessions, they had a weak, but positive attractiveness.

Of interest was the behavior of the chaenomeles genotypes in 2012, when the climatic conditions were not as restrictive as in the previous 2011. The phenomenon of “divergence” in the expression of the quantitative trait has been found under the influence of genetic and environmental causes. It can be formulated as follows: it is possible to quantitatively assess to what extent the deviation of a trait from the population mean was determined by its genotype, and to what extent by environmental factors. The essence of divergence consists in the fact that genetic and environmental deviations of quantitative traits become divergent when they are viewed in a two-dimensional coordinate system, built for two traits (ST and BT). In this particular case, if the fruit yield increased proportionally to the weight of the fruits per bush, then the slope of the regression line to the abscissa and ordinate of the coordinate system will be at an angle of 45˚. If the value of yield exceeds that of productivity (fruit weight per bush), then the line will be inclined to the abscissa in accordance with this excess. Under a moderate deterioration of the environmental conditions (less abiotic stress), a redefinition of the traits (fruit yield and productivity) was established. As demonstrated by the figure, A14 did not change its location in the coordinate system, which suggests that it was a donor with a broad genetic base regarding abiotic stress. The position of A6 resembled this one in 2010. This accession again moved into the positive quadrant of adaptability. Taking into account its good productive ability, A6 could be successfully grown under conditions of moderate abiotic stress. A7, A13, A5, A15 and A10 also moved to the same quadrant. Accessions A11 and A12 had a position close to the origin of the coordinate system. That was an indicator that the genetic control on adaptability, regarding fruit yield and productivity, was redetermined negatively at these environmental limits.

The orthogonal regression method (Figure 1), was also used to analyze the vegetation period duration – a parameter applied as a BT, and fruit yield was accepted again as ST. By analogy with quantitative traits, the vegetation period was also affected by the strength and duration of stress factors. One of the main directions in the chaenomeles breeding is the creation of highly productive forms with a shorter vegetation period. During the favorable year 2010, a significant number of accessions was located in the quadrant, bounded by the negative part of regression and orthogonal lines. They were characterized by negative adaptability and attraction. This group was dominated by genotypes with yields around or below the average, but all they had short vegetation. In this sense, they were not of particular breeding interest.



2010 2010

2011 2011

2012 2012

Tr1 – fruit yield/da, Tr2 – fruit weight/bush , Tr3 – duration of vegetation period

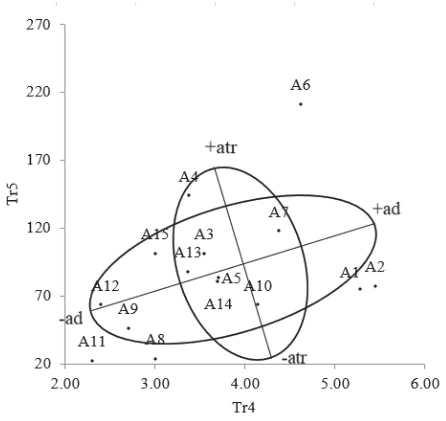
Fig. 1. Method of orthogonal regression for identification of genotype by phenotype in chaenomeles accessions (in direction of productivity)

Accession A14 was located in the lower right quadrant with positive adaptation (high fruit yield) and negative attractiveness (vegetation period shorter than the average for the studied group). In this case, it exhibited a good combination of genes for adaptability and attraction. It was characterized by positive manifestations of genes for adaptability and attraction. Its distance from the main abscissa shows that it had longer vegetation, but its good productivity gave it some advantage over the others.

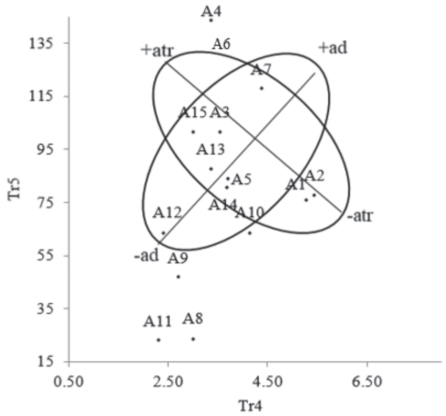
A11, A7, A9 and A13 were located in the quadrant with negative adaptability and positive attraction. In general, this group is characterized by low productivity and a longer vegetation period, especially pronounced in A11.

The drought in 2011 had a negative effect on both the yield and the longevity of the vegetation period. The data showed that compared to 2010, with few exceptions, a redefinition of the studied traits was observed in most chaenomeles genotypes. Accession A14 retained its high level of fruit yield, but now with positive attractiveness i.e., it has strong genes for attraction. A6 fell in the opposite (compared to the 2010) quadrant (in the negative part of adaptability and attraction). Its development under abiotic stress conditions, resulted in a shorter growing period and lower productivity, but it retained the second position after A14. In the same quadrant were A2, A3, A4, A5 and A10, which kept their position. Some of them were less productive, but they all had shorter vegetation. In the same year, the projections of points of A8, A12, A1, and A15 fell into the quadrant with positive attractiveness and negative adaptability i.e., they were not ecologically stable.

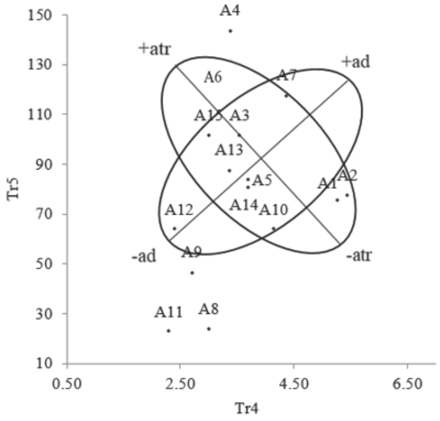
Under the deterioration of environmental conditions to a certain level, some genotypes reacted linearly, triggering physiological-genetic mechanisms to overcome the stress factor. A14 occupied an extremely right position at both environmental limits (2011, 2012), which is determined by its strong genes for adaptability. A positive displacement in this direction of the coordinate system was also found for A6, and its location was very close to A14. Accessions A7, A10, A5, and A13 were located in the same quadrant and may be of interest for combinative breeding to create new early-maturing forms of chaenomeles.



2010



2011



2012

Tr4 – number of flowers/bud, Tr5 – number of flowers/bush

Fig. 2. Method of orthogonal regression for identification of genotype by phenotype in chaenomeles accessions (in ornamental direction)

The method for express evaluation of the relationship between the genetic systems of attraction and adaptability, is based on the fact that the line of ecological regression of coordinate traits reflects the true (reference) reaction of two traits, to improvement or deterioration in the growing conditions of a given genotype. Each point on the graph is an expression of the average values of two traits. If the genotypic and environmental regression lines overlap each other, this indicates that there is no connection between the genetic systems of attraction and adaptability, and both „operate“ completely additively.

Chaenomeles is also widely used as an ornamental plant. Therefore, in the present study, an attempt was made to identify genotypes in this direction, as well as through the orthogonal regression method (Figure 2). It is notable that at different environmental limits, the regression and orthogonal lines had different slopes relative to the abscissa and ordinate axes of the coordinate system. If the genetic regression „tilts“ in a clockwise direction, this means that „economically useful“ genes (for example, determining an increased number of flowers per bush) for adaptability, are genetically related to „selectively undesirable“ genes (determining the development of a smaller number of flowers per bud) for attractiveness. If the genetic regression line “tilts” in a counter-clockwise direction, this means that the genes for attraction are in a favorable interaction with the genes for adaptability.

The characteristics “number of flowers/bud” and “number of flowers/bush”, which are background and selection trait respectively, were used as criteria for decorativeness. According to genotypes’ distribution in the coordinate system, it was established that A7 and A6 (regardless of the environmental conditions) were always located in the quadrant with positive attraction and adaptability. Depending on the abiotic stress strenght, they moved, but within the same quadrant. A6 can be defined as more attractive, and A7 as more stable, with stronger genes for adaptability when placed in stress conditions. When conditions are comfortable, A6 expressed genes that produce more flowers per bud and per bush. Accessions A1 and A2 also showed good adaptation and stability regarding number of flowers/bud and can be used as parental components for development of cultivars with decorative value.

Assessment of adaptability and plasticity

To identify the physiological-genetic systems that determine the fruit yield in chaenomeles and influence its growth, the most often used indices in breeding practice were calculated. Regarding the general adaptation index (Zhivotkov et al., 1994), the genotypes differed considerably, which indicates a high compensatory effect in some of them (Figure 3). The higher the index value, the more drought-tolerant and adaptable a cultivar is. In the conditions of the present study, accessions A14, A6 and A7 were distinguished with a high general adaptation index.

Of the productivity elements, the most closely related to the yield and highly dependent on the environmental conditions, are the fruiting index, fruit attractiveness and flowers number per plant. According to the fruiting index (Fesenko, 1983; Taranenko & Yacishen, 2014), the studied accessions differed essentially. The highest fruiting index was found at A14 (55) and A6 (29), and the lowest one – at A11, A12, A9, A8 and A7 (Figure 4).

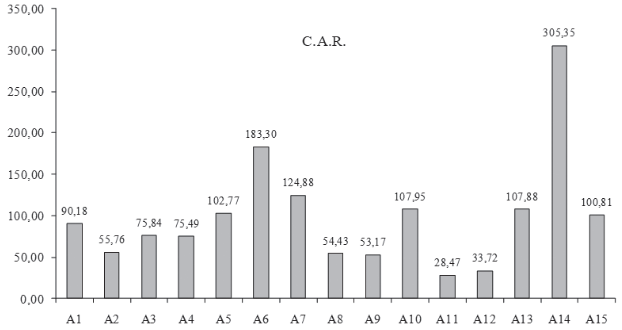


Fig. 3. Coefficient of general adaptive reaction (C.A.R.) in chaenomeles accessions

Regarding the coefficient of multiplicativity (KM), high values were demonstrated by accessions A2, A3, A7, and A8 (5.13–3.62) (Figure 5). In contrast, A11, A1 and A5 occupied the last positions, with the lowest values. The index of ecological plasticity (IEP) allows us to assess the plasticity of a given trait for a cultivar. At IEP > 1, the cultivar is defined as plastic. From the studied accessions, with high values of KM was characterized A13 (IEP = 10.3), whose coefficient was many times higher than the rest of the genotypes, followed by A14 (IEP = 2.89), A6 (IEP = 1.72), and A17 (IEP = 1.19). A11, A12, A2 and A3 showed a weaker adaptability. A8 and A9 can also be included in the same group. These data show the possibility of using index parameters in breeding programs through direct selection methods for yield increase and stabilization.

Discussion

According to Litun (1982), the experimental evaluation of the efficiency of traditional breeding by phenotype showed that out of 10 000 selected best plants, only one plant could be genetically valuable i.e., the accuracy of “recognizing” a genotype from its phenotype is 0.0001. In this case, the ran-

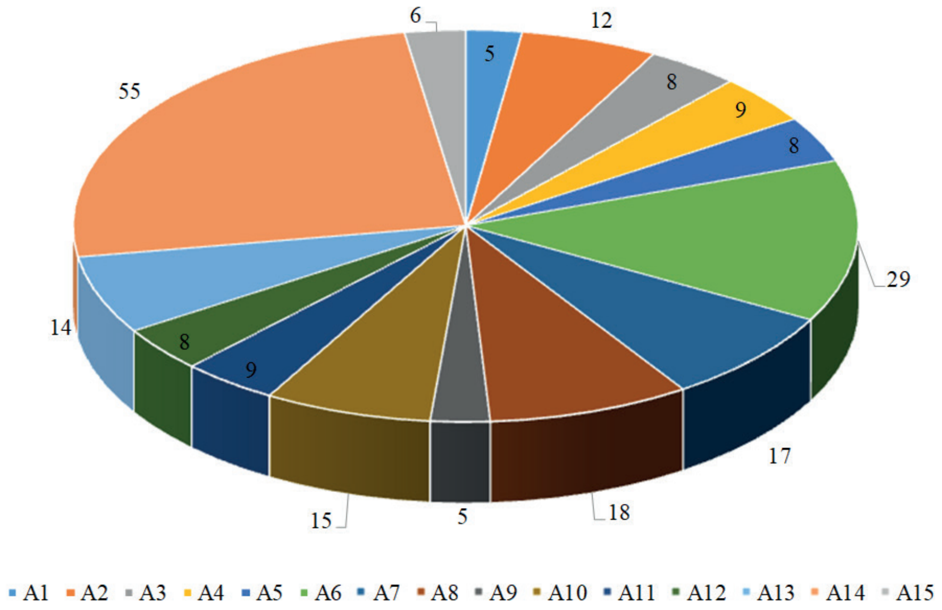


Fig. 4. Fruiting index in chaenomeles accessions

dom selection may be even more efficient than a selection of the best phenotypes. In contrast, other researchers (Dragavtsev et al., 1981), considered that the application of the method of orthogonal regressions (in theoretical and experimental aspects) rejects these claims, and creates the possibility of rapid (without changing generations) identification of the genotypic value of a given trait of the individual in the cleavage population, with an accuracy up to 1000 times greater than the accuracy of traditional visual "recognition" of a genetically valuable individual.

Kocherina and Dragavtsev (2007) stated that in the absence of reliable methods for identifying genotypes by their phenotype, most valuable forms are irretrievably lost, which cannot be compensated with more accurate assessments of the progenies in the next stages of the breeding process. The authors considered that traditional breeding methods, in principle, are difficult, expensive and require a long time to test the progenies, and their reliability is low. The study of the relationship between the genetic-physiological systems of adaptability and attraction of a genotype, and limiting components of the environment, allows a rational use of plant species and varieties. In particular, it allows the use of new approaches in fruit crop breeding based on revealing the mechanism of "genotype-environment" interaction, and selection of donors of adaptability.

The development of the principle of BT and the discovery of 7 genetic and physiological systems, which contribute to increased yield, gave rise to the principle of divergence („orthogonal" identification). That makes it possible to quickly identify the positive genetic contributions of each of 7 genetic and physiological systems of productivity, and to abandon the traditional low-efficiency visual breeding based on the phenotypic values of traits (Kocherina and Dragavtsev, 1998).

The phenomenon of divergence has also been found in other crops. In research with maize genotypes, Hristov et al. (2002) concluded that Dragavtsev and Diakov (1982), finding according to which the changes in quantitative traits under changing environmental limits are divergent, is of great practical interest. The authors noted that it is possible to measure phenotypic and genotypic variances in a two-dimensional system of trait coordinates without changing generations.

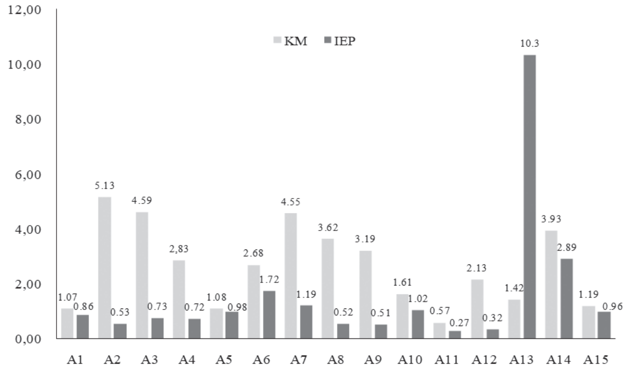


Fig. 5. Coefficient of multiplicativity (KM) and index of ecological plasticity (IEP) in chaenomeles accessions

Kocherina (2007) pointed out that until the establishment of the principle of background traits, the possibility of developing rapid methods of evaluation (without progeny testing) of individual genotypes by their phenotype regarding quantitative traits, was denied categorically by many researchers. However, the author considered that using the orthogonal regression method enables a considerable increase in the efficiency of the breeding process, and could lead to a change in the known breeding models.

It should be noted, however, that the characteristics of one variety, for example, drought tolerance, are determined by the combination in the activity of different genetic and physiological systems, and selection criteria that are appropriate under some conditions, may be inadequate in others. Therefore, in breeding work, studying the genotype-environment interaction, opportunities to reduce the effects of global climate change can and should be sought.

Conclusions

The application of traditional methods in selection-genetic studies is necessary to be combined with the study of the ecological-genetic model of organization of the quantitative trait, revealing new possibilities for estimation.

The results of the ecological-genetic estimation of 15 chaenomeles accessions showed that A14 and A6 possess strong genes of the physiological system of adaptability in terms of productivity and yield. A13, A8, A3, and A11 are characterized by a weak, but positive attractiveness.

Accession A14 was distinguished by negative attractiveness regarding the vegetation period duration, and A6 had positive manifestations of genes for adaptability (good productivity) and attraction (long vegetation period). A7, A10, A5 and A13 were less productive, but can be used in combinative breeding to develop early-ripening forms.

In decorative direction, with positive attraction and adaptability, suitable were A7 and A6 due to the increased number of flowers per bush. Accessions A1 and A2 showed good stability concerning flowers number per bud, and the same can be used as parental components in the decorative direction.

The general adaptation index determined A14, A6 and A7 as highly adaptable genotypes. With high values of the coefficient of multiplicativity were A2, A3, A7 and A8 (5.13–3.62), and with good ecological plasticity – respectively, A13 (IEP = 10.3), A14 (IEP = 2.89), A6 (IEP = 1.72) and A17 (IEP = 1.19).

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Received: **March, 21, 2024**; *Approved*: **April, 27, 2024;** *Published:* **August, 2025**