

**Cite this article:** Vasylenko A.O., Vus N.O., Bezuhlyi I.N., Bezuhla O.N., Shevchenko L.N., Kucherenko Ye.Yu., Hliantsev A.V. Donors of valuable breeding traits of pea (*Pisum sativum* L.). The Journal of V. N. Karazin Kharkiv National University, Series "Biology", 2021, 36, 74–82.

## ••• ФІЗИОЛОГІЯ РОСЛИН ••• PLANT PHYSIOLOGY •••

UDC: 635.656: 631.527: 575

### Donors of valuable breeding traits of pea (*Pisum sativum* L.) A.O. Vasylenko, N.O. Vus, I.N. Bezuhlyi, O.N. Bezuhla, L.N. Shevchenko, Ye.Yu. Kucherenko, A.V. Hliantsev

Analysis of the existing basic collections and identification of the core collections with clearly defined properties are important stages of the plant genetic banks activities. The NCPGRU pea collection has not been studied through this lens. The article presents results of the study of pea (*Pisum sativum* L. subsp. *sativum*) accessions as donors of valuable breeding traits for its multipurpose use in agriculture and processing industries. We examined 307 accessions representing the breeding material from the working pea collection of the Laboratory of Grain Legume Breeding of the Plant Production Institute named after V.Ya. Yuriev and the collection accessions of various eco-geographical origins of the National Center for Plant Genetic Resources of Ukraine (NCPGRU). Eleven donors were selected by one or more important agronomic traits in combination with valuable economic characteristics (yield, performance, protein content in seeds, disease resistance (Fusarium wilt and Ascochyta blight)). The cultivars Modus, Efektnyi (multi-flowering (*fn fn*)), leafless (tendrill) (*af*), Tsarevych (seed shedding resistance (*def*)), leafless (*af*), and SL DTR 94-120 (multi-flowering (*fn fn*)), luhansk type of determinancy (*d*)) were chosen as donors for the grain pea breeding. Orpella (anthocyanin pigmentation of the corolla (*A*)) and Rezonator (stem length (*Le*)) were used for the grain/fodder pea breeding; Kharkivskiy Yantarnyi and Banan (seed culinary qualities) – for the groats pea breeding; Stambovyi (parchmentless pods (*pv*)), fascicle stems (*fa fas*) and Asgrow seed (wrinkled seeds (*r*)), leafless (*af*), multi-flowering (*fn fn*)) – for the garden pea breeding; Violena (the *rb* gene carrier – amylose-free starch) – for the technical pea breeding. All the accessions proved their donor capacities. A qualitatively new input material for practical selection has been derived by means of hybridization with some cultivars (Kharkivskiy Yantarnyi, Banan, Tsarevych, Violena, Asgrow seed). Further study of the NCHRRU pea collection aimed at identification of valuable accessions and creation a core collection is essential.

**Key words:** pea, collection, donors, genetic trait control, breeding, breeding value.

#### About the authors:

A.A. Vasylenko – Plant Production Institute named after V.Ya. Yuriev of the NAAS of Ukraine, Moskovskiy Ave., 142, Kharkiv, Ukraine, 61060, avase2015@gmail.com, <https://orcid.org/0000-0003-0081-5894>  
 N.O. Vus – V.N. Karazin Kharkiv National University, Svobody Sq., 4, Kharkiv, Ukraine, 61022; LLC "Nertus Agro", Netchenskaya Str., 25, Kharkov, Ukraine, 61010, vus.nadezhda@gmail.com, <https://orcid.org/0000-0001-7098-9158>  
 I.M. Bezuglyi – Plant Production Institute named after V.Ya. Yuriev of the NAAS of Ukraine, Moskovskiy Ave., 142, Kharkiv, Ukraine, 61060, bigora3@gmail.com, <https://orcid.org/0000-0003-3578-2092>  
 O.M. Bezugla – Plant Production Institute named after V.Ya. Yuriev of the NAAS of Ukraine, Moskovskiy Ave., 142, Kharkiv, Ukraine, 61060, olgabezuglaya61@gmail.com, <https://orcid.org/0000-0002-1458-1630>  
 L.M. Shevchenko – Plant Production Institute named after V.Ya. Yuriev of the NAAS of Ukraine, Moskovskiy Ave., 142, Kharkiv, Ukraine, 61060, lara.xiaomi2016@gmail.com, <https://orcid.org/0000-0003-1410-9456>  
 E.Yu. Kucherenko – Plant Production Institute named after V.Ya. Yuriev of the NAAS of Ukraine, Moskovskiy Ave., 142, Kharkiv, Ukraine, 61060, Egorkucherenko91@gmail.com, <https://orcid.org/0000-0002-9313-7385>  
 A.V. Glyantsev – Plant Production Institute named after V.Ya. Yuriev of the NAAS of Ukraine, Moskovskiy Ave., 142, Kharkiv, Ukraine, 61060, avglyancev@gmail.com, <https://orcid.org/0000-0002-5848-4533>

#### Introduction

Pea is one of the most important legume crops. In terms of world production, it ranks second after the bean (FAOSTAT, 2021). Being the basic object of genetic research since G. Mendel and Ch. Darwin, it has not lost its importance in genetics and breeding yet. Ukraine is among the top 10 pea producing countries; the collection of the National Center for Plant Genetic Resources of Ukraine (NCPGRU) is among the 10 largest world collections.

Since the beginning of the 21<sup>st</sup> century, the scientific and international community attitude to genetic resources has changed fundamentally (Zhuchenko Jr., 2014). The modern breeding process

requires extended studies and analyses of the plant pool available, in particular, its genetic characteristics. Attention to genetic resources has rose due to the narrowing genetic base of the breeding cultivars and reduction in their genetic variability (heterogeneity, heterozygosity), which increase epiphytotic risk.

The objectives and prospects of breeding and seed production cannot be achieved without mobilizing the world's plant resources. Here, national breeding centers have the real advantages, as they possess unique genetic donors for the most important species that are resistant to the most harmful abiotic and biotic stressors and have a high nutritional value (Zhuchenko, 2012). Thus, in Belarus, new cultivars and hybrids based on collections of genetic resources were introduced in agriculture and forestry with an economic effect of \$ 116.9 million and \$ 5.7 million, respectively (Privalov et al., 2016).

M.A. Vishnyakova demonstrated the possibilities and necessity of more efficient use of the legumes' gene pool in new directions of breeding: symbiotic, ecological, ecotypic, phytocenotic, and bioenergetic (Vishnyakova, 2012). The pea collection of the All-Russian Research Institute of Plant Industry comprises 8,057 accessions (as at 01/01/2014); of these, the 685 are from the Mediterranean pool (center of the crop origin). Commercial cultivars and landraces account for 46.0 % and 38.0 %, respectively, while wild forms and accessions with unknown status comprise 1.5 % and 13.0 %. A long-term analysis allowed identifying individual accessions that are sources of alleles determining valuable traits (Vishnyakova et al., 2016). Having studied retrotransposons in 3,020 accessions of the pea collection of the John Innes Center (Great Britain), which is one of the most diverse and representative collections of the world gene pool of the genus *Pisum* L., the researchers found that the greatest genetic diversity is represented not by breeding cultivars, but by their wild congeners. At the same time, "wild" alleles are rarely present in cultivars, and the genome of pea cultivars is rather poor. As a result, the knowledge about the pea gene pool has been expanded, which contributes to its more efficient application in the breeding practice (Jing et al., 2010).

The pea collection of Ukraine (NCPGRU) contains 2,683 specimens (as at 01/01/2018); 49 % of them are breeding cultivars created in Ukraine and/or other countries (Kobyzeva et al., 2018). The gene pool is evaluated in terms of a wide range of morphological and agronomic characteristics. The studied accessions are being used to form collections for different purposes. Unfortunately, the National Center for Plant Genetic Resources of Ukraine has no accessible genotypic and/or phenotypic database of available accessions (Smykal et al., 2012).

In India, where the chickpea is the legume crop number one, a similar work has already been done. In the Indian National Genebank (New Delhi), the available gene pool of the basic collection had been fully assessed; the especially valuable accessions were selected, which provided basis for a core collection. To increase selection efficiency, the basic chickpea collection (14,651 accessions) was evaluated by eight quantitative and 12 qualitative agronomic and morphological traits. The database is now publicly accessible (Singh et al., 2012; Archak et al., 2016).

A.A. Churakov and L.I. Valiulina emphasize that assessment of genetic resources in a particular region can increase selection efficiency. For example, in the Krasnoyarsk Krai, the growing period of pea plants (80–90 days) is a limiting trait when assessing the resource material. Therefore, the material involved in crossing has to combine this growing period and a set of economically useful traits (Churakov et al., 2021).

In China, the pea basic collection contains almost 5,000 specimens from 70 countries. To assess the accessions' genetic diversity, a core collection of 731 specimens from 67 countries was analyzed with the use of 21 SSR primers. This study showed the greatest genetic heterogeneity of the Asian accessions. The European accessions ranked the second place, while the accessions from the other countries were less heterogenic. It turned out that 48 accessions (6.57 % of the collection) cover 84.4 % of all allelic variations (Zong et al., 2008).

An investigation of genetic resource collections by modern methods of genome analysis can evaluate not only genetic diversity of the modern gene pool, but also evolutionary relationships and development paths of agricultural crops (Jing et al., 2010).

An amount of the studied collection material can be quite extensive while the number of accessions chosen for the further research can be very small. Nevertheless, this is the promising material that determines selection effectiveness. When assessing a garden pea collection, consisted of 277 specimens of different eco-geographical origins, I.M. Kaigorodova et al. (2013) chose only six accessions with several valuable agronomic traits. Based on the traits relevant for the crop breeding, O.V. Alikina and

A.G. Besedin (2016) selected only 25 out of 522 accessions from the garden pea collection of the All-Russian Research Institute of Plant Industry.

Given the available diversity of initial material, a chose of the most promising parents for crossing remains a challenging task of selection. Comprehensive studies of genetic resource collections are a way to solve this problem (Merezhko, 2005). At the same time, it is obvious that the current prevailing trends in the choice of parental pairs for crossing (the best commercial cultivars) inevitably lead to an increase in genetic vulnerability of closely related cultivars. Only few of numerous cultivars involved in hybridization are proved to be outstanding donors of economically valuable traits and corresponding blocks of co-adapted genes (resistance, performance, quality, etc.) (Zhuchenko Jr., 2014).

Based on the above, our **purpose** was to reveal and identify accessions with a pool of valuable economic characteristics that can be donors for one or more agronomic traits.

### Study objects and methods

The research objects were 307 accessions (*Pisum sativum* L. subsp. Sativum) representing the pea breeding material from a working collection of the Laboratory of Grain Legume Breeding of the Plant Production Institute named after V.Ya. Yuriev as well as the collection accessions of different eco-geographical origin deposited in the National Center for Plant Genetic Resources of Ukraine (NCPGRU) and defined as a source of valuable traits. The field experiments were carried out in the scientific crop rotation of the Plant Production Institute named after V.Ya. Yuriev (Kharkiv, Ukraine) in 2016–2020 in accordance with the methods of field experimentation (Dospekhov, 1985).

The pea collection accessions were studied according to "Guidelines on studying genetic resources of grain legumes" (Kobyzeva et al., 2016). Morphological description of the accessions, their classification by economic and biological features, identification of the genes of the above-mentioned traits were performed by morphological and phenological methods specified in the Classifier of the genus *Pisum* (CMEA's international classifier..., 1990; Makasheva, 1979; Genetics of domestic plants..., 1990).

Carriers of the *r* and *rb* mutations were identified by the starch granule morphology and the amylose content in starch (Wang et al., 1998; Hedley et al., 1996). Starch granule morphology was analyzed in light microscopy (Large workshop on plant physiology, 1978) after 48-hour fixation of seeds in a mixture of 96 % ethanol, glycerin and water (in a ratio of 1 : 1 : 1) and 0.01 M sodium azide as a bacteriostatic preservative. After fixation, the seeds were grounded in a porcelain mortar. Granules were photographed with a DMC-FZ300 digital camera and microscopically analyzed in a Biolam-15 microscope with the lens  $\times 40$ .

### Results and discussion

The NCPGRU's pea collection has no complete genetic database. A pea genetic collection formed in 2014 was the first step in resolving this problem (Bezuhla et al., 2014). Donor identification is the next important stage in the gene pool classification and systematization. The field and laboratory investigations conducted in the Laboratory of Grain Legume Breeding and the Laboratory of Genetic Resources of Grain Legumes and Groats Crops resulted in identification the donors of valuable agronomic traits.

The modern trend in the pea breeding is creating vegetable cultivars, which, in addition to high yields and protein content in seeds, have good culinary properties (cooked seed weight/dry seed weight ratio, cooking time, palatability). The cultivars Kharkivskiy Yantarnyi (UD0101296), UKR and Banan (UD0101543), UKR, have confirmed their donor capacities for the "seed culinary quality" trait. They have good cooking properties: seed cooking coefficient 2.26; cooking time 80–90 min. (rating "good"), excellent palatability (7+). Kharkivskiy Yantarnyi and Banan are leafy, mid-tall (the stem length is 105–110 cm and 80–110 cm, respectively), highly productive (their yields amount to 5.5 t/ha), high-protein (the protein content in seeds is 23–26 % and 24–28 %, respectively) cultivars. Kharkivskiy Yantarnyi has bright orange cotyledons. These cultivars have moderate resistance to *Fusarium* wild (5 points) and *Ascochyta* blight (7 points). When these cultivars were used as female components in regular crosses, the obtained hybrids got higher protein content in seeds (by 6–12 %) and better culinary quality than their parents (Bezuhlyi et al., 2018; Vasylenko et al., 2018).

In peas, like in many other legumes, flowers develop in racemes on the specialized lateral flower-bearing stems (I2), while the main stem (I1) grows indefinitely. Usually, the pea racemes have two flowers. In addition to fundamental interest, data on the regulation of inflorescence development and

formation of multi-flowered inflorescences are of particular practical value for the breeding of new high-performance pea cultivars (Sinjushin, Liberzon, 2016).

We distinguished the cultivars Modus (UD0101938) and Efektnyi (UD0102018) as donors of a "multi-flowering" trait controlled by the *fn fn* genes. Being leafless, these cultivars form three fully developed pods in the first and/or second productive node. Resistance to Fusarium wilt: Modus – 3 points, Efektnyi – 5 points; to Ascochyta blight: Modus and Efektnyi – 5 points each. The cultivars' potential capacity amounts to 6.0 t/ha; both of them are lodging resistant and suitable for direct combining.

The "leafless" trait is attributed to the *af* gene, which is phenotypically manifested as the formation of tendrils instead of normal leaves that increases lodging resistance. Leafless pea cultivars are considered to give some 10 % lower yields (Pesic et al., 2013). When lodging, yield losses in leafy pea cultivars reach 32–43 % compared to the tendril (leafless) cultivars (Bugrej, Avdeenko, 2012). Seed shedding is prevented by the *def* gene expression, causing hypertrophy of the seed pedicel tissue. After seed ripen, seed pedicels do not come off and remain attached to the central raphes of the beans (Makasheva, 1979; Genetics of domestic plants..., 1990; Ayeh et al., 2011). This mutation can slightly decrease the yield due to a lower seed number per pod. Nevertheless, in a zone with unstable precipitation, the losses caused by an overmature stand can be outstanding, and the cultivation of non-shedding pea cultivars is economically profitable (Zelenov, 2013). Seed non-shedding makes it possible to reduce losses during harvest by 10–20 % (Zubov, Katyuk, 2007). A combination of these features was discovered in Tsarevych (UD0102105) that gives the reason to recommend it as a donor of both "leafless" and "shedding resistance" traits. The cultivar yield amounts to 6.0 t/ha (Bezuhlyi et al., 2016); it is highly resistant to lodging (8–9 points), suitable for direct combining, shows weak resistance to Fusarium wilt (3 points) and high resistance to Ascochyta blight (7 points).

Determinant forms are of particular value in breeding, since their seeds ripen from lower to upper productive nodes processes more evenly than that in the indeterminate forms. On the other hand, they have a number of disadvantages: poor performance (only 3–4 pods on the main stem), late fruiting and a tendency to generate lateral shoots (Alikina, Besedin, 2016). The breeding line SL DTR 94-120 was distinguished as a donor of the "determinancy" and the "multi-flowering". The determinancy is caused by the *r* genes, manifested phenotypically as the presence of 1–2 productive nodes only; two carpophores emerge from the last node. A determinant type of the stem growth ensures shorter anthesis and a good yield due to the total apical meristem transformation into the apical inflorescence (Kotlyar et al., 2019). Such cultivars can be used for post-harvest crops in areas with sufficient precipitation or with irrigation. In the breeding line DTR 94-120, the reduced number of productive nodes, characteristic of determinant cultivars, is compensated by the "multi-flowering" *fn fn* gene that makes it possible to form a sufficient performance. The line is leafy; its performance is 7.2 g of seeds per plant; the stem length is 55–65 cm; the protein content in seeds is 21–23 %; the resistance is moderate, to Fusarium wild – 5 points, and to Ascochyta blight – 7 points.

The listed traits ("multi-flowering" (*fn fn*), "leafless" (*af*), "shedding resistance" (*def*), and "determinancy" (*r*)) are monogenic, recessive and clearly diagnosed by phenotype (Ellis et al., 2010) (Fig. 1). Therefore, when such donors are involved in both simple combination and backcrossing, the trait appearance in a hybrid confirms its monogenicity.

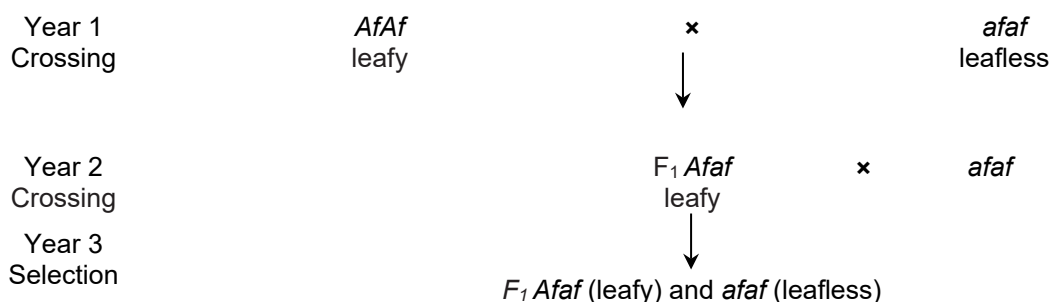


Fig. 1. An example of a complex pea hybridization scheme

Grain/fodder cultivars can be sown as a monocrop for commercial grain and as a mixed crop with cereals for green fodder, hay and silage. In the grain/fodder pea breeding, both anthocyanin-free cultivars and cultivars with anthocyanin pigmentation of the corolla (field pea) are used in crossing as initial forms (Kosterin, 2015). We chose the leafy cultivar Orpella (UD0100520), a carrier of the "anthocyanin pigmentation of the corolla" trait controlled by the *A* gene. This cultivar shows good performance (an average seed weight per plant is 10.4 g; an average number of beans per pod is 4.7); it is resistant to Fusarium wilt (5 points) and Ascochyta blight (5 points).

Grain/fodder cultivars are to have long stems and many leaves. The pea stem length (up to 150 cm) is controlled by the *Le* gene, which is responsible for the gibberellin synthesis. It also can stimulate internode growing in the pea plants (Martin et al., 1997). The cultivar Rezonator (UD0100668) is a donor of the "long stem" trait; it is a leafy cultivar with a maximum of seed performance of 5.0 t/ha and green mass productivity of 30.0–35.0 t/ha. In the phase of the bean complete filling, the percentage of green beans is 32–34 % of the total number of seeds; the protein content in seeds is 22–24 %; the resistance to Fusarium wilt and Ascochyta blight is 3 and 5 points, respectively.

The "anthocyanin pigmentation of the corolla" and the "stem length" traits are monogenic and dominant. Selection is conducted in  $F_2$  hybrids with the trait control in subsequent generations.

Vegetable cultivars can be grouped into two categories with a purpose of green seed and green pod production. Green seeds are used as raw material for canning and processing industries. When breeding these cultivars, it is necessary to pay attention at the green seeds' yield, seed yield per plant, contents of dry matter and carbohydrates in seeds, seed color and size, etc. Mature seeds are wrinkled, which is a characteristic feature of these cultivars. This trait is controlled by the *r* gene (linkage group (LG) 7 (Genetics of domestic plants..., 1990)) responsible for the higher concentration of sucrose in developing corcules of pea plants that, in turn, increases water absorption, cell size, and fresh seed weight. During maturation, such seeds experience significant water loss, which makes the seed surface wrinkled. In addition to this morphological variation, the mutation also causes changes in the amount of lipids and storage proteins (legumins) (Bhattacharyya et al., 1993).

Since Asgrow seed (UD0101648, USA) is a donor of a bulk of important traits: "wrinkled seeds" (*r* gene) (Tymchuk et al., 2017), "leafless (tendrill)" (*af* gene), "multi-flowering" (*fnfna* gene), it was proposed for creating new vegetable (garden) cultivars. The protein content in dry seeds is 22.0–27.8 %; the starch content is 26.85 %; the sugar content in seeds in the phase of technical ripeness (green peas) is 3.92–5.32 %. The cultivar is highly resistant to Fusarium wilt (7 points) and Ascochyta blight (5 points).

Garden cultivars, used to obtain green pods in the "unripe, flat and long pod" phase, have very wide parchmentless pods. Two non-complementary recessive genes – *p* and *v*, determine a parchmentless or «sugar» pod; each of them reduces the parchment layer in great extent, and, acting together, they eliminate it completely. These genes determine thick shells of pea pods that makes the whole pod (with shell) edible (McGee, Baggett, 1992). Shtambovyi Sakharnyi (UD0101816, Russia) is a donor of the "parchmentless (sugar) pods" (*pv*) and "fascicle stems" (*fa fas*) traits. The fascicle stem is attributed to two independent genes, *fa* in LG 4 and *fas* in LG 3. This trait changes both the stem architecture and the physiology of plant blossoming and ripening. Its characteristic feature is a pod grouping at the top of the stem; consequently, the pea plants lodge and become vulnerable to drought during the short periods of their anthesis and pod formation (Gawłowska, Święcicki, 2016; Siniushin, Gostimskii, 2008). Shtambovyi Sakharnyi is highly resistant to Fusarium wilt (7 points) and Ascochyta blight (7 points).

In the modern processing industry, pea is considered a source of high-quality starch. Therefore, creation of cultivars with a high starch content in seeds and a high amylose/amylopectin ratio is another direction of breeding. Carriers of the *rb* mutation in pea (LG 3 (Genetics of domestic plants..., 1990)) are richer in the oil content in seeds than the carriers of smooth-seed and *r* mutation (Wang et al., 1990). An influence of the *rb* locus on the starch content in pea seeds is mediated by changes in the ADP-glucose pyrophosphorylase activity in developing corcules (Smith et al., 1989). The *RRrbrb* genotype is characterized by a higher content of amylopectin in the seed starch (Bhattacharyya et al., 1993). Phenotypically, the *RRrbrb* genotype manifests itself as wrinkled cotyledons and simple starch granules.

In the pea collection studied, we distinguished only one carrier of the *rb* gene, the cultivar Violena (UD010077). The amylose rate in seed starch of Violena is only 28.2 %, compared with 63.9 % of amylose in the carriers of the *r* gene (Asgrow seed). Analyzing crosses and light microscopy of the seed samples have also confirmed the presence of the *rb* gene (Tymchuk et al., 2017; Vasylenko et al., 2017).

In *Violena*, the starch content in seeds is 26.85 %; the protein content is 21–23 %. It has an average resistance to *Fusarium* wilt (3 points) and high resistance to *Ascochyta* blight (7 points).

### Conclusions

Since the National Center for Plant Genetic Resources of Ukraine has no publicly accessible genotypic and phenotypic databases of available pea specimens, our work on identification of the donors of valuable agronomic traits can provide the beginning of a creation of pea core collection in the NCPGRU.

In practical terms, the use of presented donors with a set of economic performance in specialized breeding programs can increase their efficiency. Eleven donors were selected for various directions of pea breeding: *Modus* and *Efeknyi* (multi-flowering, leafless (tendrils)), *Tsarevych* (seed shedding resistant, leafless), *SL DTR 94-120* (multi-flowering, determinancy), *Orpella* (anthocyanin pigmentation of the corolla), *Rezonator* (stem length), *Kharkivskiy Yantarnyi* and *Banan* (culinary qualities of seeds), *Stambovyi* (parchmentless pods, fascicle stems), *Asgrow sead* (wrinkled seeds, leafless, multi-flowering), and *Violena* (amilose-free starch).

In the future, the need in more profound studies of genetic resources by both the classical methods and the molecular genetic technologies will be growing.

### References

- Alikina O.V., Besedin A.G. (2016). Starting material to create garden pea cultivars in the Kuban. *Vegetable Crops of Russia*, 1(30), 14–17. (in Russian)
- Archak S., Tyagi R.K., Harer P.N. et al. (2016). Characterization of chickpea germplasm conserved in the Indian National Genebank and development of a core set using qualitative and quantitative trait data. *The Crop Journal*, 4, 417–424. <https://dx.doi.org/10.1016/j.cj.2016.06.013>
- Ayeh K.O., Lee Y., Ambrose M.J. et al. (2011). Growth, seed development and genetic analysis in wild type and *Def* mutant of *Pisum sativum* L. *BMC Res*, 4, 489. <https://doi.org/10.1186/1756-0500-4-489>
- Bezuhla O.M., Vasylenko A.O., Kobyzeva L.N., Bezuglyi I.M. (2014). Genetic collection of pea (*Pisum sativum* L.). *Selection and Seed Industry*, 105, 104–121. (in Ukrainian)
- Bezuhlyi I.M., Vasylenko A.O., Potiomkina L.M. et al. (2018). Palatability of pea cultivars bred by the Plant Production Institute named after V.Ya. Yuriev. *Bulletin of the Center for Science Provision of Agribusiness in the Kharkiv region*, 24, 136–144. (in Ukrainian)
- Bezuhlyi I.M., Vasylenko A.O., Hliantsev A.V., Shevchenko L.M. (2016). Innovations in pea breeding at the Plant Production Institute named after V.Ya. Yuriev. *Bulletin of the Center for Science Provision of Agribusiness in the Kharkiv region*, 20, 99–106. (in Ukrainian)
- Bhattacharyya M., Martin C., Smith A. (1993). The importance of starch biosynthesis in the wrinkled seed shape character of peas studied by Mendel. *Plant Mol Biol.*, 22(3), 525–531. <https://doi.org/10.1007/BF00015981>
- Bugrej I.V., Avdeenko A.P. (2012). Efficiency and the reasons of drowning of grades of peas with different morphotypes of sheet. *Modern Problems of Science and Education*, 1, 287. URL: <http://www.science-education.ru/ru/article/view?id=5608> (in Russian)
- Churakov A.A., Valiulina L.I. (2021). Genetic resources of garden pea – a source of efficient breeding at Krasnoyarsk Scientific and Research Institute of Agriculture. URL: [http://www.kgau.ru/new/all/uni/01/konferenc/2\\_3.pdf](http://www.kgau.ru/new/all/uni/01/konferenc/2_3.pdf) (in Russian)
- CMEA's international classifier of the genus *Pisum* L. (1990). Leningrad. 51 p. (in Russian)
- Dospekhov B.A. (1985). *Methods of field experiment*. Moscow: Agropromizdat. 351 p. (in Russian)
- Ellis T.H.N., Hofer J.M.I., Timmerman-Vaughan G.M. et al. (2010). Mendel, 150 years on. *Trends Plant Sci.*, 16, 590–596. <https://doi.org/10.1016/j.tplants.2011.06.006>
- FAOSTAT. (2021). URL: <http://www.fao.org/faostat/en/#data/QC>
- Gawłowska M., Świącicki W. (2016). The *fa2* gene and molecular markers mapping in the *gp* segment of the *Pisum* linkage group V. *Journal of Applied Genetics*, 57(3), 317–322. <https://doi.org/10.1007/s13353-015-0335-0>
- Genetics of domestic plants: grain legumes, vegetables, gourds. (1990). Leningrad: Agropromizdat. 287 p. (in Russian)

- Hedley C.L., Bogracheva T.Ya., Lloyd J.R., Wang T.L. (1996). Manipulation of starch composition and quality in pea seeds. *Agri-food quality: an intrerdisciplinary approach*. Eds. G.R. Fenwick, C.L. Hedley, R.C. Richards, S. Khorkar. Cambridge: RoyalSoc. Chem. P. 138–148.
- Jing R., Vershinin A., Grzebyta J. et al. (2010). The genetic diversity and evolution of field pea (*Pisum*) studied by high throughput retrotransposon based insertion polymorphism (RBIP) marker analysis. *BMC Evol. Biol.*, 10, 44. <https://doi.org/10.1186/1471-2148-10-44>
- Kaigorodova I.M., Pronina E.P., Pishnaya O.N. (2013). Study of perspective models of pea as genetic sources in breeding for quality and productivity. *Vegetable Crops of Russia*, 1, 30–34. <https://doi.org/10.18619/2072-9146-2013-1-30-34> (in Russian)
- Kobyzeva L.N., Bezugla O.M., Silenko S.I. et al. (2016). Guidelines on studying genetic resources of grain legumes. Kharkiv: Publishing House "Stil". 84 p. (in Ukrainian)
- Kobyzeva L.N., Bezuhla O.M., Biriukova O.V. (2018). History and present of the Laboratory of Genetic Resources of Grain Legumes and Groats Crops and the NCPGRU's research results. *Theoretical Studies and Practical Achievements of the Plant Production Institute named after V.Ya. Yuriev of NAAS: history and present (1908–2018)*. Kharkiv. P. 54–71. (in Ukrainian)
- Kosterin O.E. (2015). Prospects of the use of wild relatives for pea (*Pisum sativum* L.) breeding. *Vavilov Journal of Genetics and Breeding*, 19(2), 154–164. (in Russian)
- Kotlyar I.P., Ushakov V.A., Pronina E.P., Kaygorodova I.M. (2019). Nature of the inheritance of number of fertile nodes in determinant forms of vegetable pea. *Rossiiskaia selskokhoziaistvennaia nauka*, 6, 11–14. <https://doi.org/10.31857/S2500-26272019611-14> (in Russian)
- Large workshop on plant physiology. Mineral nutrition. Physiology of the cell. Growth and development. (1978). Ed. B.A. Rubin. Moscow: Vysshaya Shkola. 408 p. (in Russian)
- Makasheva R.Kh. (1979). *Pea. Grain legumes*. Leningrad: «Kolos». IV(1). 322 p. (in Russian)
- Martin D.N., Proebsting W.M., Hedden P. (1997). Mendel's dwarfing gene: cDNAs from the *Le* alleles and function of the expressed proteins. *Proc. Natl. Acad. Sci. USA*, 94(16), 8907–8911. <https://doi.org/10.1073/pnas.94.16.8907>.
- McGee R.J., Baggett J.R. (1992). Inheritance of stringless pod in *Pisum sativum* L. *Journal of the American Society for Horticultural Science (USA)*, 117(4), 628–632.
- Merezhko A.F. (2005). Principles of search for and creation of donors of valuable traits in plant breeding. *Identified Gene Pool of Plants and Breeding*. St Petersburg. P. 189–205. (in Russian)
- Pesic V., Djordjevic R., Kadhum E. et al. (2013). Influence of the *afila* gene on grain yield in pea (*Pisum sativum* L.). *Bulgarian Journal of Agricultural Science*, 19(2), 186–193.
- Privalov F., Kilchevskiy A., Grib S. et al. (2016). Bank of plant genetic resources. *Science and Innovations*, 10(164), 24–27. (in Russian)
- Singh M., Bhardwaj C., Singh S. et al. (2016). Chickpea genetic resources and its utilization in India: Current status and future prospects. *Indian J. Genet.*, 76(4), 515–529. <https://doi.org/10.5958/0975-6906.2016.00070.5>
- Siniushin A.A., Gostimskii S.A. (2008). Genetic control of fasciation in pea (*Pisum sativum* L.). *Genetika*, 44(6), 807–814.
- Sinjushin A., Liberzon A. (2016). Contribution to genetic control of flower number in pea (*Pisum sativum* L.) *Ratarstvo i povrtarstvo*, 53(3), 116–119. <https://doi.org/10.5937/ratpov53-11949>.
- Smith A.M., Bettley M., Bedford I.D. (1989). Evidence that the *rb* locus alters the starch content of developing pea embryos through an effect on ADP glucose pyrophosphorylase. *Plantphysiology*, 89(4), 1279–1284. <https://doi.org/10.1104/pp.89.4.1279>
- Smykal P., Aubert G., Burstin J. et al. (2012). Pea (*Pisum sativum* L.) in the genomic era. *Agronomy*, 2, 74–115. <https://doi.org/10.3390/agronomy2020074>
- Tymchuk S.M., Vasylenko A.O., Pozdnyukov V.V. et al. (2017). Evaluation of garden pea (*Pisum sativum* L.) collection accessions for carriers of the *r* and *rb* mutations. *The Bulletin of Ukrainian Society of Geneticists and Breeders*, 15(1), 14–19. (in Russian)
- Vasylenko A.O., Bezuhlyi I.M., Shevchenko L.M. et al. (2018). Creation of pea breeding material with improved quality of seeds. *Selection and Seed Industry*, 114, 18–25. (in Ukrainian)
- Vasylenko A.O., Tymchuk S.M., Suprun O.G. et al. (2017). Content and fatty acid composition of oil in seeds of pea mutants with modified starch. *Legumes and Groat Crops*, 3(23), 33–39. (in Russian)
- Vishniykova M.A. (2012). Prospects of using genetic resources of grain legumes in the modern system of agricultural nature management. *Legumes and Groat Crops*, 3, 25–29. (in Russian)

- Vishnyakova M.A., Aleksandrova T.G., Bulynstev C.V. et al. (2016). The genetic resources of grain legumes from the Mediterranean region in the collection of the All-Union Research Institute of Plant Breeding: diversity and use. *Agricultural Biology*, 51(1), 31–45. (in Russian)
- Wang T.L., Bogracheva T.Y., Hedley C.L. (1998). Starch: as simple as A, B, C? *J. Exp. Bot.*, 49, 481–502.
- Wang T.L., Hadavizideh A., Harwood A. et al. (1990). An analysis of seed development in *Pisum sativum*. XIII. The chemical induction of storage product mutants. *Plant Breeding*, 105, 311–320. <https://doi.org/10.1111/j.1439-0523.1990.tb01290.x>
- Zelenov A.N. (2013). On the non-shedding trait in pea. *Legumes and Groat Crops*, 2(6), 79–85. (in Russian)
- Zhuchenko A.A. Jr. (2014). Ecological and genetic principles of mobilization of the world genetic resources of higher plants. *Education, Science and Production*, 2, 9–17. (in Russian)
- Zhuchenko A.A. (2012). The present and future of the adaptive system of plant breeding and seed production based on the identification and systematization of their genetic resources. *Agricultural Biology*, 5, 3–19. (in Russian)
- Zong X.-X., Guan J.-P., Wang Sh.-M. et al. (2008). Genetic diversity and core collection of alien *Pisum sativum* L. germplasm. *Acta Agronomica Sinica*, 34(9), 1518–1528. [https://doi.org/10.1016/S1875-2780\(09\)60003-1](https://doi.org/10.1016/S1875-2780(09)60003-1)
- Zubov A.Ye., Katyuk A.I. (2007). Breeding of high-yielding, top-quality and easily producible pea cultivars. *Achievements of Science and Technology of AIC*, 8. URL: <https://cyberleninka.ru/article/n/selektsiya-urozhaynyh-vysokokachestvennyh-i-tehnologichnyh-sortov-goroha> (in Russian)

### Донори цінних селекційних ознак гороху посівного (*Pisum sativum* L.)

А.О. Василенко, Н.О. Вус, І.М. Безуглий, О.М. Безугла, Л.М. Шевченко,  
Є.Ю. Кучеренко, А.В. Глянцев

Важливий етап роботи генетичних банків рослин – аналіз існуючої базової колекції і виділення серцевинних колекцій з чітко визначеними властивостями. Для колекції гороху НЦГРРУ така робота раніше не проводилася. У статті представлені результати роботи з ідентифікації донорів цінних селекційних ознак гороху посівного (*Pisum sativum* L. subsp. *sativum*), з урахуванням багатопільового використання культури у сільському господарстві і переробній промисловості. Об'єктами вивчення були 307 зразків з робочої колекції селекційного матеріалу гороху, який був створений у лабораторії селекції зернобобових культур Інституту рослинництва імені В.Я. Юр'єва, і колекції Національного центру генетичних ресурсів рослин України (НЦГРРУ) різного еколого-географічного походження. Виділено 11 зразків донорів за однією чи декількома важливими агрономічними ознаками з комплексом цінних господарських характеристик (урожайність, продуктивність, вміст білка у насінні, стійкість до хвороб (фузаріоз та аскохітоз)). В якості донорів для використання за напрямками селекції виділено: для зернового напрямку використання – сорти Модус, Ефектний (багатоквітковість (*fn fna*), вусатий тип листа (*af*)), Царевич (стійкість до осипання насіння (*def*), вусатий тип листа (*af*)), СЛ ДТР 94-120 (багатоквітковість (*fn fna*), луганський тип детермінантності (*dtr*)); для зерноукісного напрямку використання – Орпелла (антоціанове забарвлення вінчика (*A*)), Резонатор (довжина стебла (*Le*)); для харчового напрямку використання – Харківський янтарний, Банан (кулінарна якість насіння); для овочового напрямку використання – Штамбовий (безпергаментний тип боба (*pv*), фасційований тип стебла (*fa fas*), Asgrow seed (зморшкуватий тип насіння (*r*), вусатий тип листа (*af*), багатоквітковість (*fn fna*)); для технічного напрямку використання – Віолена (носії гену *rb* – амілопектиновий тип крохмалю). Всі зразки підтвердили донорські властивості. Шляхом гібридизації з використанням деяких сортів (Харківський янтарний, Банан, Царевич, Віолена, Asgrow seed) отримано якісно новий вихідний матеріал для практичної селекційної роботи. Зроблено висновки про необхідність подальшого вивчення колекції гороху НЦГРРУ з метою ідентифікації цінних зразків та створення серцевинної колекції.

**Ключові слова:** горох, колекція, донори, генетичний контроль ознаки, селекція, селекційна цінність.

#### Про авторів:

А.О. Василенко – Інститут рослинництва імені В.Я. Юр'єва НААН України, Московський пр., 142, Харків, Україна, 61060, [avase2015@gmail.com](mailto:avase2015@gmail.com), <https://orcid.org/0000-0003-0081-5894>

Н.О. Вус – Харківський національний університет імені В.Н. Каразіна, майдан Свободи, 4, Харків, Україна, 61022; ТОВ «Нертус Агро», вул. Нетеченська, 25, Харків, Україна, 61010, [vus.nadezhda@gmail.com](mailto:vus.nadezhda@gmail.com), <https://orcid.org/0000-0001-7098-9158>

І.М. Безуглий – Інститут рослинництва імені В.Я. Юр'єва НААН України, Московський пр., 142, Харків, Україна, 61060, [bigora3@gmail.com](mailto:bigora3@gmail.com), <https://orcid.org/0000-0003-3578-2092>

О.М. Безугла – Інститут рослинництва імені В.Я. Юр'єва НААН України, Московський пр., 142, Харків, Україна, 61060, [olgabezuglaya61@gmail.com](mailto:olgabezuglaya61@gmail.com), <https://orcid.org/0000-0002-1458-1630>



Л.М. Шевченко – Інститут рослинництва імені В.Я. Юр'єва НААН України, Московський пр., 142, Харків, Україна, 61060, lara.xiaomi2016@gmail.com, <https://orcid.org/0000-0003-1410-9456>

Є.Ю. Кучеренко – Інститут рослинництва імені В.Я. Юр'єва НААН України, Московський пр., 142, Харків, Україна, 61060, Egorkucherenko91@gmail.com, <https://orcid.org/0000-0002-9313-7385>

А.В. Глянцев – Інститут рослинництва імені В.Я. Юр'єва НААН України, Московський пр., 142, Харків, Україна, 61060, avglyancev@gmail.com, <https://orcid.org/0000-0002-5848-4533>

**Доноры ценных селекционных признаков гороха посевного (*Pisum sativum* L.)**  
**А.А. Василенко, Н.А. Вус, И.Н. Безуглый, О.Н. Безуглая, Л.Н. Шевченко, Е.Ю. Кучеренко,**  
**А.В. Глянецв**

Важный этап работы генетических банков растений – анализ существующей базовой коллекции и выделение сердцевинных коллекций с четко определенными свойствами. Для коллекции гороха НЦГРРУ такая работа ранее не проводилась. В статье представлены результаты работы по идентификации доноров ценных селекционных признаков гороха посевного (*Pisum sativum* L. subsp. *sativum*) с учетом многоцелевого использования культуры в сельском хозяйстве и перерабатывающей промышленности. За годы исследования было изучено 307 образцов (*Pisum sativum* L. subsp. *sativum*), представляющих селекционный материал из рабочей коллекции гороха, созданной в лаборатории селекции зернобобовых культур Института растениеводства имени В.Я. Юрьева, и коллекцию Национального центра генетических ресурсов растений Украины (НЦГРРУ) различного эколого-географического происхождения. Выделено 11 образцов доноров по одному или нескольким важным агрономическими признакам с комплексом ценных хозяйственных характеристик (урожайность, продуктивность, содержание белка в семенах, устойчивость к болезням (фузариоз и аскохитоз)). В качестве доноров для использования по направлениям селекции выделены: для зернового направления использования – сорта Модус, Эффектный (многоцветковость (*fn fn*), усатый тип листа (*af*)), Царевич (устойчивость к осыпанию семян (*def*), усатый тип листа (*af*)) и СЛ ДТР 94-120 (многоцветковость (*fn fn*), луганский тип детерминантности (*dtr*)); для зерноукосного направления использования – Орпелла (антоциановая окраска венчика (*A*)), Резонатор (длина стебля (*Le*)); для пищевого направления использования – Харьковский янтарный, Банан (кулинарное качество семян); для овощного направления использования – Штамбовый (беспергаментный тип боба (*pv*), фасцированный тип стебля (*fa fas*)), Aсgrow sead (морщинистый тип семян (*r*), усатый тип листа (*af*), многоцветковость (*fn fn*)); для технического направления использования – Виолена (носитель гена *rb* – амилопектиновый тип крахмала). Путем гибридизации с использованием некоторых сортов (Харьковский янтарный, Банан, Царевич, Виолена, Aсgrow seed) получен качественно новый исходный материал для практической селекционной работы. Сделаны выводы о необходимости дальнейшего изучения коллекции гороха НЦГРРУ с целью идентификации ценных образцов и создания сердцевинной коллекции.

**Ключевые слова:** горох, коллекция, доноры, генетический контроль признака, селекция, селекционная ценность.

**Об авторах:**

А.А. Василенко – Інститут рослинництва імені В.Я. Юрьєва НААН України, Московський проспект, 142, Харків, Україна, 61060, avase2015@gmail.com, <https://orcid.org/0000-0003-0081-5894>

Н.А. Вус – Харьковский национальный университет имени В.Н. Каразина, пл. Свободы, 4, Харьков, Украина, 61022; ТОВ «Нертус Агро», ул. Нетеченская, 25, Харьков, Украина, 61010, vus.nadezhda@gmail.com, <https://orcid.org/0000-0001-7098-9158>

И.Н. Безуглый – Інститут рослинництва імені В.Я. Юрьєва НААН України, Московський проспект, 142, Харків, Україна, 61060, bigora3@gmail.com, <https://orcid.org/0000-0003-3578-2092>

О.Н. Безуглая – Інститут рослинництва імені В.Я. Юрьєва НААН України, Московський проспект, 142, Харків, Україна, 61060, olgabezuglaya61@gmail.com, <https://orcid.org/0000-0002-1458-1630>

Л.Н. Шевченко – Інститут рослинництва імені В.Я. Юрьєва НААН України, Московський проспект, 142, Харків, Україна, 61060, lara.xiaomi2016@gmail.com, <https://orcid.org/0000-0003-1410-9456>

Е.Ю. Кучеренко – Інститут рослинництва імені В.Я. Юрьєва НААН України, Московський проспект, 142, Харків, Україна, 61060, Egorkucherenko91@gmail.com, <https://orcid.org/0000-0002-9313-7385>

А.В. Глянецв – Інститут рослинництва імені В.Я. Юрьєва НААН України, Московський проспект, 142, Харків, Україна, 61060, avglyancev@gmail.com, <https://orcid.org/0000-0002-5848-4533>

Подано до редакції / Received: 22.03.2021

Прорецензовано / Revised: 07.04.2021

Прийнято до друку / Accepted: 11.05.2021