SCREENING AND MONITORING OF WATERMELON SOURCE MATERIAL BY COMPONENTS OF THE VEGETATION PERIOD IN THE CONDITIONS OF THE FOREST-STEPPE OF UKRAINE

Zahar Linnik[1]

Oksana Sergienko[1] ✉
oksana.sergienko71@ukr.net

Tetiana Harbovska[1]

[1]Department of selection and seed production of vegetable and melon crops
Institute of vegetable and melon growing of National academy of agrarian sciences of Ukraine
1 Institutskaya str., township Selektsiyne, Kharkiv region, Kharkiv district, Ukraine, 62478

✉**Corresponding author**

Abstract

Relevant in the selection of each crop, including watermelon is a comprehensive study of the source material to identify sources of valuable traits and include them in the selection process in order to expand the genetic diversity of the culture. According to the results of research, to create a new source material for heterosis selection of watermelon, screening and monitoring of the vegetation period duration (number of days from germination to ripening) and its components 118 (101 varieties, 17 hybrids) genotypes of watermelon in the forest-steppe of Ukraine have been conducted. Research methods are generally accepted: field experiment, observation, accounting, analysis, statistical. According to the results of determining the duration of the components of the vegetation period, the samples were divided into five groups of ripeness: early (65–80 days) – 80 (68 %), medium-early (81–85 days) – 14 (12 %), medium (86–95 days) – 18 (15 %), medium-late (96–105 days) – 4 (3 %) and late (106 days) – 2 (2 %). Variety-samples, selected by morphological and economically valuable characteristics, belong mainly (80 %) to early and medium-early. Only 6 % of genotypes belong to the medium-late and late-ripening groups. 52 samples with the smallest separate interphase periods were isolated. According to the results of the research, 8 sources with the high early ripeness were identified, the vegetation period of which was 66–70 days: Yellow early 108105 (66 days), Karapuz 108109, Surprise 108121 (67 days), Gift of the sun 108109, Lezheboka honey 108116, Thailand №1 108153 (69 days), Sweet Diamond 107874, Northern Lights 108127 (70 days). Sources are involved in the selection process.

Keywords: watermelon, sample, variety, hybrid, vegetation period, ripeness group, variability, sources.

1. Introduction

Watermelon (*Citrullus lanatus (Thunb.) Matsum. Et Nakai*) is one of the main melon crops, a valuable food product, a source of many vitamins and medicinal components important for health. Watermelon is a dietary product, the value of which is determined by the high content of easily digestible sugars – sucrose, glucose and fructose, as well as salts of iron, folic acid and minerals.

In the conditions of formation of market economy and active processes of integration of Ukraine into the world community the questions of competitiveness of production are the most actual at the present stage. The creation of new varieties and hybrids of watermelon, which will combine in one genotype a set of valuable economic traits (early ripening, cold resistance, high yield, productivity, high taste, resistance to fusarium wilt, etc.) will increase the economic efficiency of growing this crop and meet the population need in melon products [1–3]. In this direction, reliable methods of creating, evaluating and monitoring promising source material according to a set of selection traits should play an increasingly important role.

The consumer needs new genotypes of earlier ripening, cold-resistant with high taste qualities, long storage period and resistance to diseases [2, 4, 5]. It is important to extend the period of consumption, which was ensured by the creation of both early-ripening and late-ripening genotypes by using the sources of these traits, which can serve as valuable samples of the source material of watermelon.

The world gene pool of watermelon is the most valuable source of new high-yielding genotypes that combine resistance to biotic and abiotic environmental factors and other economically valuable traits [6]. As you know, the basis of selection is a valuable source material, concentrated in the collections of genetic banks, institutions and working collections of the breeder.

The annual demand for fruits of melons 20–25 kg per person is not met by production more than twice [7].

The leaders of world watermelon production are China (68 %), Turkey and Iran (3 % each) [7, 8]. According to the results of 2020, Ukraine ranks third in Europe in the production of melons, second only to Russia (740 thousand tons) and Spain (691 thousand tons) with a gross production in 2020 of 687 thousand tons.

In the selection of melons, the Institute of Vegetable and Melon growing of the National Academy of Agrarian Sciences of Ukraine is a recognized leader in the creation of early cold-resistant varieties of watermelon. A number of early-ripening and medium-early varieties were created by synthetic selection: Borchansky, Chornogorets, Garny, Shironinsky [8–10]. New competitive varieties of watermelon Max Plus, Charm have been created [11, 12]. The assortment of watermelon was supplemented by a new exotic variety Sunshine and a new competitive hybrid Fairy Tale F_1 [13, 14].

According to the FAO, more than 130 countries are engaged in the industrial production of watermelon (total area – about 3.5 million hectares, gross harvest – 926 million tons). Crucial importance in the production of watermelon belongs to the varieties and hybrids that determine the consumer qualities of products, demanded by market conditions. The introduction of new heterosis hybrids can increase watermelon yields by at least 15–20 % [2, 7, 15].

As of February 11, 2021, 23 foreign and 6 domestic applicants were entered into the State Register of Plant Varieties Suitable for Distribution in Ukraine. Varietal resources include 88 hybrids and 37 varieties (125 in total), of which 81 hybrids and 9 varieties of foreign selection, Ukrainian – 7 and 28, respectively [16]. The foreign market is represented by watermelon hybrids by 50 %. Breeders from Russia, Hungary, China, Japan, and the United States are working intensively to create heterosis hybrids of watermelon [17–22]. Virtually all foreign companies have switched to hybrids, while they have retained the main popular varieties-brands (AU Producer, Crimson World, Charleston Gray, Shuga Baby, etc.).

An important role in the study of watermelon belongs to the disclosure of its genetic potential. This topical problem can be solved by testing samples of different ecological and geographical groups on a natural background, which will reveal the effectiveness of genetic sources to create new varieties and hybrids [23, 24]. Therefore, a crucial task in the early stages of breeding work is a comprehensive analysis and selection among the source material of forms with a high individual ability to transmit to offspring valuable traits. The involvement of the watermelon diversity of different ecological-geographical and genetic origin, with a set of economically valuable traits, will allow to obtain original self-pollinated lines, which can be promising as both maternal and paternal components of hybrids in heterosis selection [25–28].

The collection of samples is a determining factor in obtaining new hybrids and varieties of melon plants, including watermelon.

The purpose of the study is to assess the collection gene pool of watermelon by the vegetation period duration (number of days from germination to ripening) and its components, selection of sources of early, medium and late-ripening watermelon, establishing features and limits of trait variation by ripeness groups, selection of sources of valuable traits for different directions of varietal and heterosis selection.

2. Research materials and methods

The research was conducted at the Institute of Vegetable and Melon NAAS (Kharkiv region) during 2018–2020 in rain-fed conditions of open ground of selection crop rotation.

The material for the research was the source material, which consisted of 118 samples of the source material (101 varieties and selection samples, 17 hybrids from 13 countries) with different selection characteristics.

The soils of the experimental site are low-humus, medium-loam chernozems with a humus content of 4.0–4.5 %, P_2O_5 – 15 mg/100 g, K_2O – 8–10 mg/100 g. This variety belongs to rather fertile soils, which with favorable water regimes have a significant capacity to supply plants with nutrients. The reaction of the medium in the arable layer is neutral (pH – 7.0–7.5), i.e., favorable for growing watermelon [29].

Meteorological conditions in the years of research (2018–2020) were of a contrasting nature, which allowed to obtain an objective assessment of the samples of the source material in terms of the vegetation period components duration. Climatic conditions during the growth and development met the physiological requirements of watermelon and contributed to the manifestation of all phenotypic traits and the formation of a full-value harvest of watermelon fruits of different ripeness groups.

Research methods. Establishment of experiments and observations and calculations were performed in accordance with generally accepted methods [30, 31]. The standard was placed every 10 samples. The feeding area of one plant is 0.98 m². Number of plants – 20 plants of each sample. The registered area of the plots is 19.6 m². The technology of watermelon cultivation in the experiment complied with DSTU 5045: 2008 [32].

Watermelon genotypes by the vegetation period duration (number of days from germination to ripening) were divided into: early-ripening – 65–80 days, medium-early – 81–85 days, medium-ripening – 86–95 days; medium-late – 96–105 days, late-ripening – 106 days and above [10, 33]. The economic and biological assessment of the genotypes of the source material was carried out in accordance with the "Wide Unified Classification of CMEA of the genus *Citrullus* Schrad" and "Methods of examination of varieties" [34, 35].

In studies to analyze the variability of the duration of interphase periods of genotypes by ripeness groups, the following indicators were used: *Lim* – variation limit ($X_{min}...X_{max}$) and *Am* – variation amplitude ($X_{max}-X_{min}$).

The analysis of experimental data was performed using the ANOVA method. Differences between values in different variants of the experiment were determined using the Tukey test [36], where the differences were considered significant at $P<0.05$ (adjusted for Bonferroni correction) [37].

3. Results and their discussion

In order to evaluate the selection material and identify sources of valuable traits to create a new source material for heterosis selection of watermelon, we screened the gene pool of watermelon.

It was found, that the genotypes, assessed by morphological and economically valuable traits, belong mainly to early and medium-early (68 and 12 %, respectively).

Table 1 shows the characteristics of watermelon genotypes by ripeness group for 2018–2020 studies.

The main number of samples of the watermelon collection studied belonged to the early-ripening and medium-early groups. These two groups included most samples from Ukraine, Japan, China, Korea, as well as samples from the Netherlands and France.

The smallest vegetation period (63–64 days) was inherent to variety-samples: Honeysuckle and Klondike. They can be considered sources of signs of early- ripening – ultra-early. The other 78 genotypes, belonging to the early ripening group, are also sources of early ripeness.

According to the results of phenological observations, the samples were divided into five ripeness groups:

– 1 – early-ripening (65–80 days) – 80 (68 %);
– 2 – medium-early (81–85 days) – 14 (12 %);
– 3 – medium-ripening (86–95 days) – 18 (15 %);
– 4 – medium-late (96–105 days) – 4 (3 %);
– 5 – late-ripening (106 days) – 2 (2 %).
The monitoring of the watermelon gene pool by ripeness groups is shown in Fig. 1.

Table 1
Distribution of watermelon genotypes of different ecological and geographical origin by ripeness groups, 2018–2020

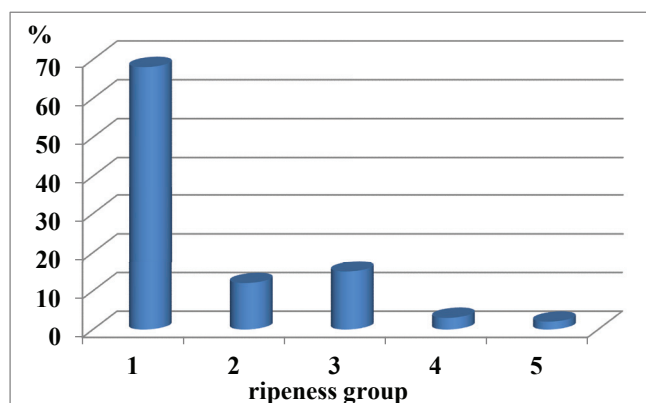| Country of origin	Genotypes number, un	Genotypes number by ripeness group, un				
		Early-ripenng	Medium-early	Medium-ripening	Medium-late	Late-ripening
Ukraine	31	24	5	0	1	1
Russia	27	16	0	8	2	1
Japan	6	6	0	0	0	0
China	13	8	5	0	0	0
Korea	5	5	0	0	0	0
Poland	2	2	0	0	0	0
Czech Republic	5	5	0	0	0	0
Netherlands	5	5	0	0	0	0
France	2	2	0	0	0	0
Moldova	4	4	0	0	0	0
Italy	2	2	0	0	0	0
USA	7	0	2	5	0	0
Thailand	2	0	1	0	1	0
Kazakhstan	3	1	0	2	0	0
Denmark	4	1	1	2	0	0
Totally	118	80	14	18	4	2
%	100	68	12	15	3	2

Fig. 1 Monitoring of the gene pool of watermelon by ripeness groups, 2018–2020: 1 – early-ripening; 2 – medium-early; 3 – medium-ripening; 4 – medium-late; 5 – late-ripening.

According to the results of the research, the variability of 118 genotypes of different ripeness groups according to the vegetation period duration was determined. Taking into account the biology of culture, the most significant in determining the genotype ripeness group is the duration of such phases of development of watermelon plants: "seedlings-flowering of female flowers", "flowering of female flowers-ripening", "seedlings-ripening" **(Tables 2–4).**

21

The data from the studies of genotype variability within the ripeness groups and between the ripeness groups themselves for the component of the vegetation period – the interphase period "seedlings-flowering of female flowers" are shown in **Table 2.**

According to the table, it is seen, that the variation of signs of the vegetation period components duration for the specified interphase period "seedlings-flowering of female flowers" was low $V<10$ % for 1 and 3 ripeness groups and average for 2 and 4 ripeness groups; for the interphase period duration $V>10$ % (respectively 10.04 and 10.77). It should be noted, that the limit of variation of the trait by the ripeness groups was the highest in the group of early-ripening samples and amounted to 17 days, in the group of medium-early samples it was 13 days, in medium-ripening samples – 11, and the lowest in the medium-late group of samples and was 6 days, 1 sample turned out to be late-ripening

Table 2

The variability of the duration of the component indicator of the vegetation period – the interphase period "seedlings-flowering of female flowers" of different ripeness groups of samples of the watermelon gene pool, the average for 2018–2020

No.	Ripeness group (days)	Seedlings-flowering of female flowers				
		Am, days		Lim, days	$X_{av} \pm S_x$	$V \pm S_v$
		min	max			
1	Early-ripening– 65–80	25	42	17	36.21±0.37	9.55±0.72
2	Medium-early – 81–85	28	41	13	36.39±1.05	10.04±2.05
3	Medium-ripening – 86–95	31	42	11	37.21±0.81	8.71±1.54
4	Medium-late – 96–105	32	38	6	35.00±2.67	10.77±5.39
5	Late-ripening – 105	62	62	0	46	–

Note: The numeric data in the table are presented as x±SD (n=20).

The data from the studies of genotype variability within the ripeness groups and between ripeness groups themselves according to the vegetation period component – the interphase period "Flowering of female flowers-ripening" are shown in **Table 3.**

Table 3

The variability of the duration of the component indicator of the vegetation period – the interphase period "flowering of female flowers - ripening" of different ripeness groups of watermelon gene samples, the average for 2018–2020

No.	Ripeness group (days)	Flowering of female flowers - ripening				
		Am, days		Lim, days	$X_{av} \pm S_x$	$V \pm S_v$
		min	max			
1	Early-ripening– 65–80	31	53	22	38.62±0.41	9.85±0.75
2	Medium-early – 81–85	39	56	17	46.33±1.38	10.31±2.10
3	Medium-ripening – 86–95	48	62	14	52.98±1.10	8.32±1.47
4	Medium-late – 96–105	62	70	8	66.00±3.67	7.86±3.93
5	Late-ripening – 105	62	62	0	62	–

Note: The numeric data in the table are presented as x±SD (n=20).

Based on the obtained data, the variation of signs of the vegetation period components duration for the specified interphase period "flowering of female flowers-ripening" was low $V<10$ % for 1, 3 and 4 ripeness groups and average for 2 ripeness group, by the interphase period duration $V>10$ % (10.31). According to the analysis of the data, we noted the same trend, namely the limit of variation of the trait decreased from the early-ripening group of samples to the medium-late. It should be noted, that the limit of variation of the trait by the ripeness groups was the highest in the group of early-ripening samples and amounted to 22 days, in the group of

medium-early samples it was 17 days, in medium-ripening samples – 14, and the lowest in the medium-late group of samples and was 8 days. 1 sample turned out to be late-ripening.

The data from the studies of genotype variability within the ripeness groups and between the ripeness groups themselves by the vegetation period duration are shown in **Table 4.**

Table 4

The variability of the duration of the component indicator of the vegetation period – the interphase period "seedlings-ripening" of different ripeness groups of samples of the gene pool of watermelon, the average for 2018–2020

No.	Ripeness group (days)	Seedlings-ripening				
		Am, days		Lim, days	$X_{av} \pm S_x$	$V \pm S_v$
		min	max			
1	Early-ripening– 65–80	66	80	14	74.84±0.36	4.53±0.34
2	Medium-early – 81–85	81	85	4	82.72±0.54	2.27±0.46
3	Medium-ripening – 86–95	86	95	9	90.19±0.78	3.45±0.61
4	Medium-late – 96–105	100	102	2	101.00±1.00	1.40±0.70
5	Late-ripening – 105	109	109	0	109	–

Note: The numeric data in the table are presented as x±SD (n=20).

The table shows that the variation of signs of the duration of the vegetation period within these ripeness groups was low to V<10 % and amounted to 1.40–4.53. The limit of variation was highest in the group of early-ripening samples due to the wider gradation of days and was 14 days, the medium-early group had the low limit of variation of the sign – 4 days, while in the medium-ripening it was 9 days. The lowest limit of variation of the sign was in the medium-late group, only 2 days.

The gene pool of watermelon was screened according to the components of the vegetation period, based on the results of which genotypes with the shortest duration of separate interphase periods were identified. The following interphase periods and corresponding genotypes are the most informative in terms of early ripeness: "seedlings-fruit formation" (Am=31…58 days) – Yatum Oak (31 days), No. 545 (32 days), Yellow early 108105, Borisfen 108095 (35 days), Klondike 108181 (37 days), Karapuz 108109, Northern Lights 108127 (39 days), Lunar 108093, Honeysuckle 107873 (40 days); "Seedlings-flowering of female flowers" (Am=28…42 days) – Monomakh 108103 (28 days), Yellow early 108105 (29 days), Eastern breeze 108120, Dream 108100 (31 days), Borisfen 108095, Sweet scarlet (32 days)); "Seedlings-stem formation" (Am=16…28 days) – Honeysuckle 107873, Ganusik 108148 (16 days), Wm19, China No. 3 108161, Treasure (17 days), Emperor's hat, Janusik, Sugar kid 108113, Hazel bush, Sweet diamond, Surprise 108121, Volzhanin 108128, Medok 108086, Asar 108087, Photon 108097, Karapuz 108109, Spassky 108143, Minimelonia 108104 (18 days); "Flowering of female flowers – fruit formation" (Am=2…12 days) – Honeysuckle, Sweet Dakota, Hazel bush (2 days), Kherson lights, Whole leaf, Surprise 108121, Costa Rica 108177, Yellow Miracle 108102 and Charleston Gray 1081 3 days).

According to the research results, 8 sources with the high early ripeness were identified, the vegetation period, namely the interphase period "seedlings-fruit ripening" which was 66… 70 days with the amplitude of variation of the gene pool – Am=66… 109 days and Lim=43. These are genotypes: Yellow early 108105 (66 days), Karapuz 108109, Surprise 108121 (67 days), Gift of the sun 108109, Lezheboka honey 108116, Thailand No. 1 108153 (69 days), Sweet diamond 107874 and Northern lights 108127 (70 days).

These variety-samples should be used in the selection process to obtain maternal or paternal lines in the creation of early-ripening heterosis hybrids as sources of a valuable trait – early ripeness. Selection of genotypes with the shortest individual interphase periods allows to model early ripeness, which is useful when creating new competitive hybrids by selecting different parental components. As you know, when selecting parental components of hybrids,

attention is paid to use as a parental form – a form that should be earlier than the mother, which will provide a more complete re-pollination of parental components.

4. Conclusions

According to the results of research, to create a new source material for heterosis selection of watermelon, screening and monitoring of the vegetation period duration (number of days from germination to ripening) and its components 118 (101 varieties, 17 hybrids) genotypes of watermelon in the forest-steppe of Ukraine have been conducted. According to the results of determining the duration of the components of the vegetation period, the samples were divided into five groups of ripeness: early (65–80 days) – 80 (68 %), medium-early (81–85 days) – 14 (12 %), medium (86–95 days) – 18 (15 %), medium-late (96–105 days) – 4 (3 %) and late (106 days) – 2 (2 %). Variety-samples, selected by morphological and economically valuable characteristics, belong mainly (80 %) to early and medium-early. Only 6 % of genotypes belong to the medium-late and late-ripening groups. 52 samples with the smallest separate interphase periods were isolated.

According to the results of the research, 8 sources with the high early ripeness were identified, the vegetation period of which was 66–70 days: Yellow early 108105 (66 days), Karapuz 108109, Surprise 108121 (67 days), Gift of the sun 108109, Lezheboka honey 108116, Thailand No. 1 108153 (69 days), Sweet Diamond 107874, Northern Lights 108127 (70 days). Sources are involved in the selection process.

References

[1] Lymar, A. O. et. al. (2001). Metodyka selektsiinoho protsesu ta provedennia polovykh doslidiv z bashtannymy kulturamy. Kyiv: Ahrarna nauka, 132.

[2] Orliuk, A. P., Didenko, V. P. (2009). Teoretychni i praktychni aspekty selektsii bashtannykh kultur. Kherson: Ailant, 320.

[3] Sokolov, S. D. (2003). Osnovy gibridnogo semenovodstva bakhchevykh kultur. Bakhchevodstvo v Rossii (problemy i puti resheniia). Rossiiskii arbuz. Astrakhan, 20–26.

[4] Lymar, A. O. (Ed.) (2000). Bakhchevye kultury. Kyiv: Agrarna nauka, 330.

[5] Korniienko, S. I., Serhiienko, O. V., Krutko, R. V. (2016). Metodychni pidkhodu doboru ta stvorennia vykhidnoho materialu u heterozysnii selektsii kavuna. Vinnytsia: TOV «Nilan-LTD», 106.

[6] Vavilov, N. I. (1960). Bakhchevye kultury. Izbrannye trudy, 2, 292–329.

[7] FAOSTAT /Food and Agriculture organization of the United Nations. Available at: http://faostat.fao.org/site/567/DesktopDefault.aspx?PageID=567#ancor Last accessed: 03.02.2019

[8] Yarovyi, H. I. et. al. (2006). Sorty kavuna ta ahrotekhnolohiia vyroshchuvannia nasinnia. Kharkiv, 16.

[9] Serhiienko, O. V., Loboda, O. M. (2011). Novyi sortyment kavuna adaptovanyi do pivnichnoi zony bashtannytstva. Aktualni problemy pidvyshchennia efektyvnosti vyrobnytstva ovochevoi produktsii ta nasinnia. Kharkiv, 80–81.

[10] Horova, T. K., Yakovenko, K. I. (Eds.) (2001). Suchasni metody selektsii ovochevykh i bashtannykh kultur. Kharkiv: Osnova, 432.

[11] Serhiienko, O. V., Loboda, O. M. (2010). Novyi kholodostiikyi sort kavuna Maks Plius. Ovochivnytstvo i bashtannytstvo, 56, 306–311.

[12] Serhiienko, O. V. (2010). Novyi rannostyhlyi sort kavuna Sharm. Ovochivnytstvo i bashtannytstvo, 57, 67–71.

[13] Serhiienko, O. V., Loboda, O. M. (2012). Novyi rannostyhlyi sort kavuna Tselebnyi. Visnyk KhNAU. Ser. „Tekhnichni nauky. Silskohospodarski nauky. Ekonomichni nauky", 12, 208–210.

[14] Serhiienko, O. V. (2016). Novyi heterozysnyi hibryd kavuna Kazka F1. Ovochivnytstvo i bashtannytstvo, 62, 281–287.

[15] Serhiienko, O. V., Mohylna, O. M., Linnik, Z. P., Lukianchykova, O. A. (2020). Metodychni pidkhody z vykorystannia identyfikovanoho za morfolohichnymy henamy liniinoho materialu u heterozysnii selektsii kavuna. Kharkiv, 100.

[16] Derzhavnyi reiestr sortiv roslyn, prydatnykh do poshyrennia v Ukraini (vytiah) (2021). Derzhavna sluzhba z okhorony prav na sorty roslyn Ukrainy. Kyiv, 348–352.

[17] Lymar, V. A., Shashkova, N. I., Shablia, O. S., Kholodniak, O. H. (2020). Ways of innovative development of the melon growing industryin the South Ukraine. Scientific Bulletin of Kherson State University. Series Economic Sciences, 38, 18–24. doi: http://doi.org/10.32999/ksu2307-8030/2020-38-3

[18] Shablia, O. S. (2012). Metodychni pidkhody shchodo vyznachennia konkurentospromozhnosti vitchyznianykh sortiv bashtannykh kultur. Tavriiskyi naukovyi visnyk, 80, 156–161.

[19] Elatskov, Iu. A. (2012). Rasshirenie geneticheskogo raznoobraziia kollektsii arbuza dlia razlichnykh napravlenii selektsii. Trudy po prikladnoi. botanike, genetike i selektsii, 170, 236–240.

[20] Brytik, O. A. (2015). Rezultaty hibrydnoi selektsii kavuna stolovoho. Tavriiskyi naukovyi visnyk, 91, 21–24.

[21] Nunhems Ukraina. Available at: http://www.nunhems.ua/www/nunhemsinternet.nsf/id/UA_UK_Watermelon-WMW Last accessed: 04.02.2019

[22] Svitovyi rynok kavuna ta dyni (2019). Available at: https://www.profihort.com/2019/06/svitovij-rinok-kavuna-ta-dini-2/ Last accessed: 04.03.2019

[23] Sergienko, O. V. (2020). Izmenchivost i uroven proiavleniia selektsionnykh priznakov sortov i gibridov F1 arbuza. Sovremennoe sostoianie i perspektivy razvitiia otraslei plodovodstva i ovoshchevodstva. Almalibak, 381–385.

[24] Sergienko, O. V., Linnik, Z. P., Lukianchikova, O. A. (2021). Novii gibrid arbuza Met F1. Strategiia i prioritety razvitiia zemledeliia i selektsii v Belarusi. Dostizheniia nauki – proizvodstvu. Minsk, 100.

[25] Sergienko, O. V. (2006). Kollektsionnye obraztsy arbuza kak istochniki khoziaistvenno-tsennykh priznakov i svoistv. Innovatsionnye tekhnologi v selektsii i semenovodstve selskokhoziaistvennykh kultur. Moscow: VNIISSOK, 2, 256–258.

[26] Tekhanovich, G. A., Elatskova, A. G., Elatskova, Y. A. (2019). Genetic sources for breeding bushy and short-vine watermelon cultivars. Proceedings on Applied Botany, Genetics and Breeding, 180 (2), 89–94. doi: http://doi.org/10.30901/2227-8834-2019-2-89-94

[27] Varivoda, E. A., Koleboshina, T. G., Kornilova, M. S. (2020). Collection accessions and source material as a determining factor for producing new melon cultivars. Proceedings on Applied Botany, Genetics and Breeding, 181 (2), 23–27. doi: http://doi.org/10.30901/2227-8834-2020-2-23-27

[28] Didenko, V. P., Brytik, O. A. (2002). Stvorennia heterozysnykh hibrydnykh populiatsii F1 kavuna z vykorystanniam materynskykh linii monotsiinoho typu. Kherson, 11.

[29] Kuzmychov, V. P. (1965). Grunty Kharkivshchyny i pidvyshchennia yikh rodiuchosti. Kharkiv: Prapor, 100.

[30] Dospekhov, B. A. (1985). Metodika polevogo opyta. Moscow: Kolos, 351.

[31] Bondarenko, H. L., Yakovenko, K. I. (Eds.) (2001). Metodyka doslidnoi spravy v ovochivnytstvi i bashtannytstvi. Kharkiv: Osnova, 369.

[32] DSTU 5045:2008. Kavun, dynia, harbuz. Tekhnolohiia vyroshchuvannia. Zahalni vymohy. [Chynnyi vid 2009-07-01] (2009). Kyiv: Derzhspozhyvstandart Ukrainy, 11.

[33] Fursa, T. B., Malinina, M. I., Artiugina, Z. D. et. al. (1985). Rukovodstvo po aprobatsii bakhchevykh kultur. Moscow: Agropromizdat, 181.

[34] Fursa, T. B., Korneichuk, V. A., Rakochi, L. (1989). Shirokii unifitsirovannii klassifikator SEV roda Sitrullus Schrad. Leningrad, 29.

[35] Metodyka provedennia ekspertyzy sortiv kavuna zvychainoho (Citrullus lanatus (Thunb) Matsum. et Nakai) na vidminnist, odnoridnist i stabilnist (2015). Kyiv, 27.

[36] Armstrong, R. A. (2014). When to use the Bonferroni correction. Ophthalmic and Physiological Optics, 34 (5), 502–508. doi: http://doi.org/10.1111/opo.12131

[37] Tukey, J. W. (1949). Comparing Individual Means in the Analysis of Variance. Biometrics, 5 (2), 99–114. doi: http://doi.org/10.2307/3001913