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Original scientific article

GENETIC VARIABILITY IN BULGARIAN MELON COLLECTION - FLOWERING TYPES AND FRUIT QUANTITATIVE TRAITS

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Cucumis melo L. is characterized with a great polymorphism according to many agronomical features. Study the variability of melon flowering and fruit traits is an initial step in the breeding program. The current study aimed to identify the genetic variability in the melon collection according to flowering and fruit traits in order to be used in breeding programs. It was evaluated fifty melon genotypes belong to different groups - *cantalupensis, reticulatus, makuwa, inodorus,* and *agrestis*. The studied collection consists of Bulgarian old cultivars, hybrids, landraces, PI, and introduced lines. Investigated genotypes were characterized by nine quantitative fruit traits - days to flowering, sex expression, days to ripening, fruit length, fruit diameter, flesh thickness, fruit weight, seed cavity diameter, and total soluble solids. It was established great variability in studied characteristics measured by a coefficient of variation from 7.73 to 39.85%. Significant correlations between fruit length, fruit diameter, flesh thickness, cavity diameter, and fruit weight were established. Principal component analysis grouped variables into three components which explain 69.89% of the total variation. Cluster analysis divided genotypes into six groups of similarities. Among the genotypes examined, they have a relatively high level of variability and their polymorphism could be used in a breeding program aimed at combining valuable characters.

Key words: phenotype, Cucumis melo, breeding program, genetic improvement

INTRODUCTION

Melon (*Cucumis melo* L.) is one of the economically important vegetable crops belongs to the *Cucurbitaceae* family. The center of origin is considered tropical Africa. Due to their domestication more than once it is pointed India and China as secondary centers of origin

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(WHITAKER and DAVIS, 1962; PITRAT 2008). Recent investigations pointed to an Asian origin (SCHAEFER *et al*., 2009). PITRAT *et al*. (2000) proposed a classification that divided melons into two groups, sweet and non-sweet. The sweet melons belong to the Cantalupensis (cantaloupe), Reticulatus (muskmelon), Inodorous (honeydew, casaba, crenshaw, canary), and Makuwa (asian melon) groups and the non-sweet belong to the Chate, Flexuosus, and Conomon groups.

In Bulgaria, the most preferred and cultivated melon cultivars belong to Cantalupensis group and Inodorus (honeydew) (VELKOV and PETKOVA, 2014). Cultivars, such as Hybrid 1, Hybrid 15, and Pobeditel are typical representatives of Vidincki koravci type (Cantalupensis group) that are very popular and preferable to Bulgarian consumer. With less importance is characterized cv. Medena rosa belongs to honeydew type (IVANOVA *et al*., 2019).

Generally, the diversity of melon cultivars is as great as the consumer's demand for certain morphological features of the fruit and particular taste qualities. For example, in France are preferred varieties of Charentais type, Piel de Sapo in Spain, Ananas type in the Middle East, Muskmelon in the United States, Asian melon in the Far East, etc. The traits that are desirable in melon can change over time for this reason new requirements for varieties are emerging, which puts the breeder in front of a constant and moving target. In this regard, studying the available genetic resources in melon collections is essential when initiating a breeding program. Variation and selection are the main two processes that are used in each breeding program. Studying variability of traits of interest is an initial step during the development of new cultivars. *C. melo* is distinguished with great polymorphism according to a number of morphological features, particularly fruit traits. Melon fruit weight varies from a few grams to several kilograms (DHILLON *et al*., 2006). The yield is determined by fruit characteristics such as weight, length, and width (ALIAHMADI, 2000). According to NAROUI RAD *et al*., (2010), fruit weight and flesh diameter possess a major effect on the yield variation compared to fruit length and fruit width which traits are of secondary meaning. Other important traits are those related to sex expression and days to ripening. There are several types of flowering as the most important are *monoecious* and *andromonoecious* (PITRAT, 2008). Two genes are involved in the formation of flowers which produced male, female and hermaphrodite (MARTIN *et al*., 2009; DOGIMONT, 2011; BOUALEM *et al*., 2016). Duration to the first harvest of fruits is depending on many factors but the most important are both characteristics - days to flowering and days to ripening. Days to ripening of the fruits are depending on ethylene production which varies between different melon varieties (BURGER *et al*., 2006). The ripening of melon fruits is a process in which are involves a series of changes in color, texture, and flavor. The quality of melon fruit is mostly associated with sugar level and an excellent flavor in mesocarpic tissue. The total soluble solids (TSS) content is a reliable indicator of fruit quality. It is considered that melon fruit flesh must have a TSS of at least 9% to be acceptable. The large genetic variability observed in melon germplasm for TSS and sugar concentration is accounted for mainly by differences in the levels of sucrose (BURGER *et al*., 2000; BURGER *et al*., 2006).

Evaluation of genetic variability in melon fruit traits is of great importance in the initiation of the breeding program directed to increase yield and quality. The current study aimed to identify genetic variability in Bulgarian melon collection as assessed by flowering and fruit traits in order to be used in breeding programs.

MATERIALS AND METHODS

Germplasm

The experiment was carried out in the Maritsa Vegetable Crops Research Institute, Plovdiv, Bulgaria during the period 2017-2018 (42° 9′ N; 24° 45′ E; altitude 160 m). Fifty melon genotypes belong to different groups (*cantalupensis, reticulatus, makuwa, inodorus* and *agrestis*) were evaluated. The studied collection included Bulgarian old varieties, lines, landraces, and introduced materials (Table 1). The landraces were collected in 2014 in the open fields from the region of Plovdiv (South-Central Part of Bulgaria, Figure 1). Introduced materials, old varieties, and lines were used from the Maritsa Institute collection. Melon germplasm was maintained through single plant selections from the S3 generation for the evaluations.

Figure 1. Map of *Cucumis melo* samples collected from the region of Plovdiv.

Experimental conditions

The investigation was conducted in an unheated glasshouse, Venlo type. Terms of the experiment: Sowing 23rd of March in perlite substrate; pricking in 0,5 l pots - 31st; transplanting - 25th of April; harvesting - from 5th of June until 5th of August. Plants were grown according to the technical requirements. A double-row system was used; the scheme of transplanting was 240 cm between the centers of each pair of rows, 80 cm between the two rows within a pair, 45 cm between plants in the rows. Plant density was 1.4 plants per m^2. Plants were grown vertically in the greenhouse until plants reached the support wires (200 cm). Plants were irrigated, fertilized, and protected from pathogens and pests according to standard horticultural practices.

Morphological evaluation

The following characters were measured: days to 50 % flowering, flowering type (at full flowering - 1 *monoecious*, 2 *andromonoecious*, 3 *gynoecious*, 4 *hermaphroditic*), days to ripening (from pollination to mature fruit), fruit length (cm), fruit diameter (cm), flesh thickness (cm), fruit weight (kg), seed cavity diameter (cm) and total soluble solids TSS (°Bx) (measured by using a digital refractometer KERN ORA 32 BA/BB).

Experimental designed

Plots were arranged in a randomized complete block design, with three replications, four plants per plot, and a total of twelve plants per genotype. The trait expression was estimated using all plants per genotype. For analyzing the data Duncan's multiple range test, correlation analysis, principal component analysis (PCA), and cluster analysis, were used. Results were processed by statistical program SPSS 16 (SPSS Inc., USA).

RESULTS

Studied melon collection is presented from genotypes belong to different biological status – landraces (20), varieties (17), lines (12), and one plant introduction (PI) that originated from Bulgaria (29), Turkey (2), Israel (2), France (5), USA (7), China (3) and India (1) (Table 1). The genotypes are classified as a group of Cantalupensis (25), Reticulatus (17), Inodorous (4), Makuwa (3) and Momordica (1). Large genetic variability was observed in melon genotypes according to studied fruit traits (Figure 2).

Figure 2. Variability in fruits of melon genotypes

Table 1. Variability parameters of nine characters in melon genotypes

Genotype	Biological status	Group*	Origin	Flowering type	Days to flowering	Days to ripening		Fruit length (cm)		Fruit diameter (cm)		Flesh thickness (cm)		Seed cavity diameter (cm)		Fruit weight (kg)		TSS %
						Mean	±SE	Mean	±SE	Mean	±SE	Mean	±SE	Mean	±SE	Mean	±SE	
VI-1/6	landrace	Can	Bulgaria	2	63	45,0d-i	6,4	14,9e-m	0,5	14,5a-h	0,5	3,7a-k	0,3	7,0a-g	0,1	1,4c-m	0,2	8,0
I-2 I-4	landrace	Ret	Bulgaria	2	51	35,0m-q	0,6	13,1h-o	0,9	13,5b-k	0,4	3,3a-n	0,2	6,8a-g	0,0	1,1f-q	0,1	10,0
I-2 I-14	landrace	Ret	Bulgaria	2	52	40,0h-n	0,6	11,8j-o	1,2	11,0k-q	0,9	3,0e-o	0,2	4,9g-k	0,5	0,8j-q	0,2	10,0
I-2 I-18	landrace	Ret	Bulgaria	2	55	50,33d	0,3	11,5j-o	0,6	10,3l-q	0,3	2,4mno	0,1	5,5e-k	0,3	0,6m-q	0,1	14,0
5-1-1/1	landrace	Ret	Bulgaria	2	59	65,0b	0,6	11,2k-o	0,7	12,2h-o	0,6	3,3a-o	0,3	5,7d-k	0,1	0,9i-q	0,1	8,0
5-1-1/3	landrace	Ret	Bulgaria	2	59	50,0d-e	0,6	14,3f-n	0,6	15,7ab	0,5	4,2a-d	0,4	7,3a-e	0,2	1,7a-i	0,2	8,0
6/1/1	landrace	Ret	Bulgaria	2	59	44,7e-j	0,3	14,3f-n	0,6	12,6e-l	0,2	3,1d-o	0,1	6,4b-i	0,1	1,1f-q	0,1	11,1
10-10/2	landrace	Can	Bulgaria	1	59	38,0k-p	0,6	16,1d-k	0,5	13,1c-k	0,5	3,4a-n	0,1	6,3b-i	0,2	1,4c-o	0,2	16,1
11-1/5	landrace	Can	Bulgaria	2	59	41,0g-l	0,6	14,3f-n	0,9	11,7j-p	1,0	3,1c-o	0,4	5,4e-k	0,4	1,0g-q	0,2	11,0
12-1/4	landrace	Can	Bulgaria	2	54	35,0m-q	0,6	14,9e-m	1,0	12,4g-n	0,5	3,7a-k	0,5	5,0f-k	0,6	1,19e-q	0,2	12,0
12-1/5	landrace	Can	Bulgaria	1	55	38,3k-o	0,9	9,6no	0,8	9,4pq	0,6	2,7j-o	0,3	4,1k	0,5	0,5q	0,1	7,3
4-8 /1-1	landrace	Can	Bulgaria	2	55	33,3opq	0,9	12,3j-o	0,9	11,8i-p	1,1	3,0e-o	0,4	5,7d-k	0,4	0,9i-q	0,2	7,0
KS 42410	landrace	Ret	Bulgaria	2	52	44,3f-j	1,5	13,4g-o	1,1	9,8opq	0,4	2,7i-o	0,3	4,4ijk	0,3	0,8k-q	0,1	10,0
11/9KS1	landrace	Can	Bulgaria	2	55	32,7pq	1,5	12,1j-o	0,5	9,9n-q	0,1	2,5mno	0,1	5,0g-k	0,1	0,7l-q	0,0	7,3
11/9KS2	landrace	Can	Bulgaria	1	51	35,3l-q	0,3	16,3d-k	0,4	12,7e-l	0,4	3,3a-n	0,2	6,0b-k	0,1	1,2e-q	0,1	7,3
11/9KS3	landrace	Can	Bulgaria	1	51	32,0q	0,6	19,1c-f	0,6	14,9a-f	1,0	3,2b-o	0,7	8,6a	2,5	1,8a-g	0,3	12,3
11/9KS4	landrace	Can	Bulgaria	1	51	47,7d-f	1,5	19,7c-e	1,2	13,5b-k	0,5	3,7a-k	0,4	6,1b-k	0,3	1,7a-i	0,2	6,5
11/9KS5	landrace	Can	Bulgaria	1	51	50,0d-e	0,6	18,8c-f	1,0	14,8a-g	0,7	4,1a-e	0,3	6,6a-i	0,7	1,8a-h	0,1	7,0
A11/9KS6	landrace	Can	Bulgaria	1	53	49,3d-f	1,2	17,7c-i	1,9	15,1a-e	1,1	4,2a-d	0,5	6,6a-h	0,4	1,7a-j	0,6	7,0
Carigradski	variety	Can	Bulgaria	2	59	44,0f-j	0,6	50,3a	0,9	15,0a-e	0,6	3,9a-f	0,1	7,1a-g	0,5	2,1a-d	0,0	10,0
Pobeditel	variety	Can	Bulgaria	1	50	39,0j-o	0,6	18,6c-g	1,1	15,5abc	1,0	3,8a-k	0,3	7,9abc	0,8	2,2abc	0,3	8,0
Hybrid 1	variety	Can	Bulgaria	1	50	39,00j-o	0,6	21,0a-d	0,6	17,3a	0,3	4,33a	0,3	8,7a	0,3	2,8a	0,3	10,0
Medena rosa	variety	Ind	Bulgaria	2	52	53,0d	0,6	18,8c-f	1,0	15,1a-e	1,1	3,26a-n	0,3	8,5a	0,3	1,8a-g	0,2	11,1
Deserten-5	variety	Can	Bulgaria	2	55	50,0d-e	0,6	14,9e-m	1,2	14,2a-j	1,1	3,7a-k	0,4	6,9a-g	0,3	1,5b-e	0,4	13,6
BG14	line	Can	Bulgaria	3	53	40,3h-m	2,9	16,0d-l	1,0	13,5b-k	0,3	3,3a-n	0,2	6,8a-g	0,2	1,4c-p	0,1	10,0
K/15-6	line	Can	Bulgaria	1ms4	52	37,3k-q	1,2	19,6c-e	0,7	14,6a-h	0,9	3,8a-k	0,3	7,1a-g	0,6	1,9a-f	0,2	10,0
BK/1-5-5	line	Can	Bulgaria	1ms4	52	33,3opq	0,3	19,5c-f	0,9	14,4a-h	0,1	3,2a-o	0,2	7,9abc	0,3	1,6a-j	0,1	8,0
11/9C	line	Can	Bulgaria	1ms4	53	34,3n-q	0,3	19,4c-f	1,7	14,5a-h	0,3	4,3ab	0,2	5,9b-k	0,4	1,9a-f	0,2	8,0
L5-1-2	line	Ret	Bulgaria	2	58	46,3d-g	5,8	10,7l-o	0,7	12,9d-l	1,0	3,1c-o	0,5	6,6a-h	0,8	1,0f-q	0,2	8,0
Turcia	landrace	Ind	Turkey	2	48	70,0a	0,6	19,3c-f	1,1	14,4a-i	1,4	3,6a-m	0,2	7,2a-f	1,1	1,8a-f	0,5	8,0
Cesme	variety	Ind	Turkey	2	53	60,0c	0,6	24,8ab	7,2	15,3a-d	0,2	3,9a-g	0,8	7,5a-e	1,5	2,5a	0,7	6,0

Genotype	Biological status	Group*	Origin	Flowering type	Days to flowering	Days to ripening		Fruit length (cm)		Fruit diameter (cm)		Flesh thickness (cm)		Seed cavity diameter (cm)		Fruit weight (kg)		TSS %
						Mean	±SE	Mean	±SE	Mean	±SE	Mean	±SE	Mean	±SE	Mean	±SE	
Ananas	variety	Aim	Israel	1	51	49,0d-f	0,6	16,8c-j	0,4	14,8a-g	1,1	4,5a	0,4	5,8c-k	0,4	1,8a-g	0,3	6,0
AGY/2-2	line	Ret	Israel	3	55	40,7h-m	0,9	15,8d-l	0,2	15,5abc	0,1	3,8a-i	0,1	7,8a-d	0,2	1,74a-i	0,0	11,1
Gynodow	line	Can	France	3	58	40,0h-n	2,6	17,7c-i	0,3	15,3a-d	0,3	3,6a-l	0,4	8,0ab	0,5	2,0a-e	0,1	9,0
Nantais oblong	variety	Can	France	2	50	40,0h-n	2,6	15,9d-l	1,1	14,4a-h	0,9	4,1a-e	0,2	6,3b-j	0,6	1,6b-k	0,3	8,0
Poul	line	Can	France	4	63	40,0h-n	0,6	12,4j-o	0,8	12,4f-n	1,2	2,6k-o	0,1	7,1a-g	1,0	0,9h-q	0,2	6,0
Vedrantais	variety	Can	France	2	57	40,0h-n	0,6	9,5no	0,9	9,9m-q	0,6	2,9f-o	0,2	4,2jk	0,2	0,5pq	0,1	8,0
IRAN-H	line	Can	France	2	52	35,0m-q	0,6	16,2d-k	1,0	11,7j-p	0,3	3,0e-o	0,1	5,7d-k	0,2	1,0f-q	0,1	11,0
WI 998	line	Ret	USA	3	57	42,0g-k	0,6	8,6o	0,1	11,5k-p	0,1	2,5a-l	0,1	6,5a-i	0,1	0,6h-k	0,0	10,0
Georgia 47	variety	Ret	USA	2	51	35,0m-q	0,6	10,2m-o	0,2	11,3kp	0,5	2,7h-o	0,1	5,8c-k	0,3	0,7 k-q	0,1	8,0
HBJ	variety	Ret	USA	2	59	36,3k-q	2,0	16,0d-l	0,6	12,2g-o	0,1	2,8g-o	0,4	6,7a-h	0,7	1,1f-q	0,1	8,0
Edisto-47	variety	Ret	USA	1	55	65,0b	0,6	22,0abc	0,3	12,3g-o	0,3	3,4a-n	0,1	5,6e-k	0,2	1,5b-k	0,0	7,0
WMR-29	line	Ret	USA	2	65	37,7k-p	1,5	12,8i-o	0,2	12,3g-o	0,6	2,9f-o	0,1	6,5a-i	0,7	1,0f-q	0,2	8,0
Seminole	variety	Ret	USA	2	59	36,0l-q	0,6	13,0h-o	1,0	12,5e-m	0,3	3,5a-m	0,2	5,5e-k	0,2	1,0f-q	0,1	10,0
PMR-45	line	Ret	USA	2	52	42,0g-k	0,6	15,2e-m	0,3	13,1c-k	0,7	3,8a-j	0,2	5,5e-k	0,3	1,3c-p	0,2	10,0
K-052/2	variety	Mak	China	2	53	44,7e-j	2,9	12,8i-o	0,6	13,5b-k	0,8	2,8g-o	0,3	7,9abc	0,3	1,3d-q	0,1	13,0
K-053/4	variety	Mak	China	2	53	45,7d-h	2,0	19,6c-f	2,3	11,6j-p	2,1	2,8g-o	0,8	6,1b-k	0,8	1,4c-n	0,5	13,0
K55/4	variety	Mak	China	2	55	44,0f-j	0,6	13,4g-o	1,1	8,83q	0,5	2,1o	0,1	4,6h-k	0,2	0,5opq	0,1	11,0
PI 414723	PI	Mor	India	1	66	37,0k-q	0,6	26,2a	4,8	11,3k-p	1,2	2,3h-o	0,3	6,7a-h	0,6	1,4 c-m	0,6	6,0
Neon	variety	Ind	Unknown	2	62	48,0d-f	0,0	19,5c-f	1,0	14,3a-i	0,3	3,9a-h	0,1	6,6a-h	0,6	2,1abc	0,2	10,0
Average for a trait					54,9	43,0	1,2	16,5	0,9	13,2	0,3	3,4	0,1	6,4	0,2	1,4	0,1	9,3
Range				1-4	48-66	32,0-70,0		8,6-50,3		8,8-17,1		2,1-4,5		4,1-8,7	0,5-2,8	6,0-16,		
CV%					7,73	19,73		37,47		14,69		17,69		17,57		39,85		24,08

a,b,c…p≤0,05 Duncan's multiple range test; CV% - coefficient of variation; nd – not defined; subsp. agrestis Momordica Group (Mor); subsp. melo Cantalupensis Group (Can), Reticulatus Group (Ret), Inodorous (Ind), Makuwa (Mak), Aimeri (Aim); * According to Pitrat et al., 2000; ms-4 – male sterility type 4.

Morphological traits variation

Investigated melon genotypes are characterized with great variability according to evaluated traits which were measured by a coefficient of variation from 7.73 to 39.85% (Table 1). The data shows four types of sex expression. The greatest part of genotypes belongs to *monoecious* and *andromonoecious* flowering types, four to *gynoecioues* (BG14, WI998,

Gynodow, and AGY), and one to *hermaphrodite* (Poul). Three breeding lines are distinguished with male sterility type 4 - K/15-6, BK/1-5-5, and 11/9C.

Days to flowering ranged from 48 (Turcia) to 66 (PI 414723) while days to ripening – from 32 (11/9KS3) to 70 days (Turcia). Significant differences between genotypes were established by fruit metric traits. The highest fruit length was measured in the old variety Carigradski (50.3 cm) and the lowest one in line WI 998 (8.6 cm) as an average for the genotypes is 16.5 cm. Among studied genotypes, Hybrid 1 distinguished with the highest fruit diameter (17.3 cm), and the lowest was recorded in K55/4 (8.8 cm). The range of flesh thickness was from 2.1 cm (K55/4) to 4.5 cm (Ananas) and seed cavity diameter – from 4.1 (12-1/5) to 8.7 cm (Hybrid 1). The fruit weight varied widely between 0.5 kg (12-1/5) and 2.8 kg (Hybrid 1) as average for the trait was 1.4 kg. The content of TSS is a reliable indicator of fruit quality. The results indicated wide differences in TSS content in the investigated melon accessions between 6.0% and 16.1%. The most of the genotypes were characterized with a high value more than 9% TSS. The significant differences among the studied genotypes suggest that variability can be further utilized in a melon breeding program. The estimates of quantitative traits deserve attention in deciding selection criteria for improvement in the concerned characters.

Interactions between nine traits

Correlations between traits played an important part during the selection process. The strongest correlations were found between fruit weight (0.64), fruit diameter (0.90), flesh thickness (0.77), and cavity diameter (0.72) (Table 2).

Table 2. Correlation coefficients between nine traits

	Flowering type	Days to flowering	Days to ripening	Fruit length	Fruit diameter	Flesh thickness	Cavity diameter	Fruit weight	TSS
Flowering type	1.00								
Days to flowering	*0.32	1.00							
Days to ripening	0.02	-0.06	1.00						
Fruit length	-0.25	0.01	0.15	1.00					
Fruit diameter	-0.16	-0.21	0.17	**0.45	1.00				
Flesh thickness	*-0.30	-0.28	0.21	**0.38	**0.83	1.00			
Cavity diameter	0.03	-0.06	0.07	**0.37	**0.82	*0.37	1.00		
Fruit weight	*-0.31	-0.23	0.23	**0.64	**0.90	**0.77	**0.72	1.00	
TSS	0.08	0.04	-0.14	-0.01	-0.10	-0.23	0.08	-0.09	1.00

**. Correlation is significant at the 0.01 level.

*. Correlation is significant at the 0.05 level.

A significant correlation was established between flowering type and days to 50% flowering (0.32). Moreover, significant negative correlations were found between flowering type, flesh thickness (-0.30), and fruit weight (-0.31). Days to ripening and TSS content not correlated between studied traits.

Principal component analysis

Principal components (PC) results showed that the first three components represented 69.47% of the total phenotypic variation of the studied traits (Table 3). The first component which accounted for the highest proportion (38.74%) was mostly correlated with fruit characters such as fruit weight, fruit length, fruit width, flesh thickness, and seed cavity diameter. The second component was dominated by days to 50% flowering and sex expression and explained an additional 16.69% of the phenotypic variation. The third component was associated with the traits of days to ripening and TSS and presented 14.04% of the variation. Additional PCs accounted smaller percentage of total variation were considered not meaningful.

Table 3. Principal component analysis of nine different quantitative traits

Trait	Component		
	1	2	3
Flowering type	-0,115	**0,820**	0,013
Days to flowering	-0,087	**0,746**	-0,018
Days to ripening	0,180	0,130	**0,685**
Fruit length (cm)	**0,646**	-0,089	0,025
Fruit diameter (cm)	**0,948**	-0,129	0,127
Flesh thickness (cm)	**0,709**	-0,366	0,340
Seed cavity diameter (cm)	**0,860**	0,162	-0,138
Fruit weight (kg)	**0,934**	-0,228	0,138
TSS %	0,058	0,137	**0,789**
Eigenvalue	3,76	1,32	1,11
% of variance	38,74	16,69	14,04
Cumulative %	38,74	55,43	69,47

Extraction Method: Principal Component Analysis

Rotation Method: Varimax with Kaiser Normalization

*Bold data are effective in each principal component

Similarities and dissimilarities among melon genotypes

The genotypes were clustered based on the base minimum variance method of WARD (WARD, 1963). Four distinct clusters were identified (Figure 3). The first cluster consisted of 12 genotypes which distinguished with *monoecious* type of flowering, relatively short period of days to 50% flowering and days to ripening, the highest parameters of fruit length, fruit diameter, flesh thickness, seed cavity diameter, and fruit weight. TSS content varied widely. In general, the group is characterized by large fruit and TSS content from low to high level.

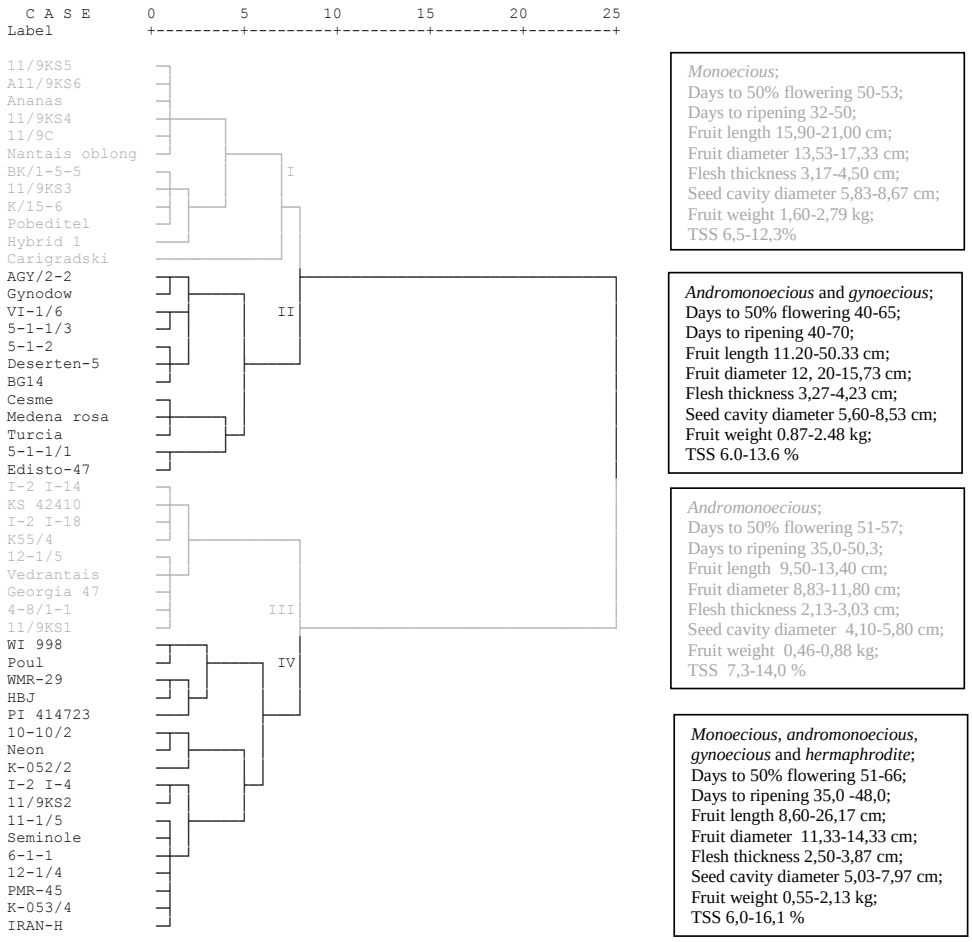

Figure 3. Dendrogram based on nine traits for fifty melon genotypes

The genotypes consisted in the second cluster is characterized with *andromonoecious* and *gynoecious* types of flowering, relatively long flowering period, medium term days to ripening, from medium to large values of fruit length and fruit diameter, flesh thickness is relatively large, as well as seed cavity diameter, fruit weight, and TSS content varies widely. Genotypes grouped in the third cluster are characterized with predominantly *andromonoecious* type of flowering, medium term of flowering period and days to ripening, the lowest value of fruit length, fruit diameter, flesh thickness, seed cavity diameter, fruit weight and content of TSS from low to high. The fourth cluster was presented of 17 genotypes that distinguished with *monoecious*, *andromonoecious*, *gynoecious*, and *hermaphrodite* types of flowering, relatively long term of days to flowering, relatively short period to ripening, fruit length varied in large scale, the

medium value of fruit diameter and flesh thickness, medium to large seed cavity diameter, small to medium fruit weight and TSS varied in great scale.

The obtained results clearly showed the similarity/dissimilarity between studied genotypes. Depending on the breeding purpose it is possible to be combined genotypes from different clusters to obtain new hybrid combinations with desirable characteristics. For example, to combine high fruit weight and short ripening period, genotypes consisted of first and fourth clusters should be crossed.

DISCUSSION

Genetic resources and their evaluation by the means of phenotyping are essential in initiating a new breeding program. One of the tools to improve the quality of the varieties is through the use of natural variability in available melon collections. Both flowering types and fruit traits are of great importance for breeders, seed-producers and growers, especially those traits related to the productivity. In a total of seven flowering types existed in *Cucurbitaceae* family four are established in melon - *monoecious*, *andromonoecious*, *gynoecious,* and *hermaphroditic* (WHITAKER and DAVIS, 1962). In our collection, four types of flowering are available that belong to Canatlupensis and Reticulatus groups (Table 1). Generally, most of the commercial varieties are F_1 hybrids developed on the base of two inbred lines. Usually, female parental line of the hybrid is characterized with *monoecious* type of flowering and male parent component with *andromonoecious* type. In some breeding programs is used male sterility to reduce seed production expenditure. Until now five types of male sterilities are known, established in natural mutants (DOGIMONT, 2011). In our collection, three lines possess type 4 of male sterility discovered by LOZANOV (1983) in Bulgarian old cultivar Vidinski koravci. *Gynoecious* flowering type can also be used as a female parent component but is still not well developed in melon breeding programs compare to cucumber (*Cucumis sativus* L.) where female flowering type is widely used in F_1 hybrids (PITRAT, 2008). The advantages of *gynoecious* lines consists of the easier production of hybrid seeds by using bees to pollinate female flowers.

Days to 50% flowering and days to ripening represent the two components of the vegetation period. The variation of these two traits is great which allows being combined genotypes with a short period of flowering and ripening of fruits. The results indicate that the coefficient of variation of days to ripening is greater (CV%=19.73) compare to days to 50% flowering (CV%=7.73) which means more effectiveness of the first trait during the selection process. Genotypes with different duration of ripening are useful to broaden the period of supply to markets.

Fruit metrical traits are concerning the yield but also are connected to consumer preferences. Some studies agreed with that consideration that genotypes with large fruit size realize more yield (PITRAT, 2008; SZAMOSI *et al*., 2010). On the other hand, consumers prefer a particular fruit size that is conservative behavior. Bulgarian consumers prefer large fruit size approximately between 1.5 and 3.0 kg (MIHOV and LOZANOV, 1983). In our collection, most of Bulgarian landraces and lines are distinguished with this parameter of fruits which is important to a future breeding program.

The quality of fruits is very important character for new varieties in order to be accepted on the market. Many breeders use TSS content as a fast method and relatively accurate for

testing large collections. Generally, melon fruit flesh must have a TSS of at least 9% to be considered acceptable (BURGER, 2006). According to BURGER *et al.* (2010), all accessions showed low TSS contents, thus they could be considered as primitive. In our collection, most Bulgarian landraces, lines and varieties possess a relatively high percentage of TSS which is a suitable genetic source for the breeding purpose (Table 1). The famous Indian snapmelon accession PI 414723 (MCCREIGHT *et al*., 1992) which possesses multiple diseases and pest resistance is available in our collection characterized by low fruit quality (TSS 6.0ºBx).

Knowledge of correlations between yield and its components may support the selection process in case of simultaneous improvement of yield-contributing traits. Significant correlations were found between fruit length, fruit diameter, flesh thickness, cavity diameter, and fruit weight (Table 2). This information may be useful for any future melon-breeding program to obtain more yield and high-quality cultivars. For example, hybridization can be performed between accessions with large fruits. Our results are in agreement with studies that also confirmed that fruit size and weight are strongly correlated with yield (TAHA *et al*., 2003; ZALAPA *et al*., 2008; NAROUI RAD *et al*., 2010; NAROUI RAD *et al*., 2017).

PCA was used to be revealed the most significant trait in the datasets. PCA is a technique that lies within the data framework of multivariate statistical analysis that is employed to identify correlations among traits. The analysis has been allowed to decrease the dimension of the nine quantitative traits to only three components (Table 3). Variation accumulated by the first three PCs was 69.47%, a relatively high percentage of total variation that satisfactorily explained variability among melon genotypes (MARDIA *et al*., 1979). The first component, which accounted for 38.74% of the total variation, was strongly associated with fruit length, fruit diameter, flesh thickness, seed cavity diameter, and fruit weight. NAROUI RAD *et al*. (2017) reported that the first component explains 26.98% of the morphological variation, and fruit weight, length of fruit, cavity diameter, and single plant yield the most important variables composing PC1. These results indicate that traits related to productivity are of significant importance in the assessment of melon genetic collections. This is reasonable because of the natural fruit polymorphism of the species explained in a number of studies (PITRAT *et al*., 2000; DHILLON *et al*., 2006; BURGER *et al*., 2010). The second component, which accounted for 16.69% of the total variation, mainly correlated with the characters of flowering type and days to flowering. The third component, which explained 14.04% of the total variation, was associated with the traits of days to ripening and total soluble solids.

Variables on the same PC and next to each other indicate positive correlations between them, and an increase in one will lead to an increase in the other. Nevertheless, the traits at opposite signs are negatively correlated, and increase in one will decrease in the other and vice versa. Based on the first component, the accessions showing high positive component values exhibited relatively high fruit weight, fruit length, fruit width, and cavity diameter. These results suggested that such traits are suitable both for the estimation of diversity and for the phenotypic characterization of melon in genetic resources.

BIABANI and PAKNIYAT (2008) explain that traits in the same factor component could be influenced by the same gene or close linked genes. The first component consists of elements of productivity that illustrate their strong correlations and linkage. The traits that belong to the second and third components are located at a distance in the genome. It could be expected that

particular parameters of traits that contained in different components such as fruit weight, days to flowering and days to ripening can be combining in one genotype. These data are important for developing a breeding program aimed at combining particular fruit characteristics.

Dendrogram of cluster analysis divided fifty genotypes into four groups of similarities (Figure 3). The first cluster consists almost of the Bulgarian genotypes which distinguished with the largest fruits. The second and third clusters are presented predominantly by Bulgarian genotypes. The fourth cluster is presented mostly by the introduced germplasm. The studied collection is characterized by very distinguished genotypes from different origins which is a good base in the initiation of a new breeding program. It is possible to be combined genotypes with different types of flowering with a relatively high content of TSS, short period to fruit ripening, fruit size and weight with desired parameters.

CONCLUSION

The data presented here can provide a starting point for further characterization of the genetic factors involved in melon fruit quantitative traits. There were established contrasting differences between studied genotypes by fruit traits, supported by multiple range test and data of cluster and factor analysis. Correlations between fruit length, fruit diameter, flesh thickness, cavity diameter, and fruit weight were established. The obtained results are a good base for identifying donors of valuable germplasm and their use in breeding programs in melon for genetic improvement of new varieties.

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GENETIČKA VARIJABILNOST U BUGARSKOJ KOLEKCIJI DINJE – TIPOVI CVETANJA I KVANTITATIVNE OSOBINE VOĆA

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Izvod

Cucumis melo L. se karakteriše velikim polimorfizmom prema mnogim agronomskim karakteristikama. Proučavanje varijabilnosti cvetanja dinje i osobina plodova početni je korak u programu oplemenjivanja. Cilj ove studije je bio da identifikuje genetska varijabilnost u kolekciji dinja prema osobinama cvetanja i plodova kako bi se koristila u programima oplemenjivanja. Procenjeno je da pedeset genotipova dinje pripada različitim grupama - *kantalupensis, retikulatus, makuva, inodorus* i *agrestis*. Kolekcija koja se proučava sastoji se od bugarskih starih sorti, hibrida, populacija, PI i introdukovanih linija. Ispitivani genotipovi okarakterisani su sa devet kvantitativnih osobina ploda – broj dana do cvetanja, polna ekspresija, broj dana do sazrevanja, dužina ploda, prečnik ploda, debljina mesa, težina ploda, prečnik šupljine semena i ukupna rastvorljivost čvrste materije. Utvrđena je velika varijabilnost ispitivanih karakteristika merena koeficijentom varijacije od 7,73 do 39,85%. Utvrđene su značajne korelacije između dužine ploda, prečnika ploda, debljine mesa, prečnika šupljine i težine ploda. Analiza glavnih komponenata grupisala je promenljive u tri komponente koje objašnjavaju 69,89% ukupnih varijacija. Klaster analiza podelila je genotipove u šest grupa sličnosti. Među svim ispitivanim genotipovima, utvrđeno je da imaju relativno visok nivo varijabilnosti i njihov polimorfizam bi mogao da se koristi u programu oplemenjivanja čiji je cilj kombinovanje značajnih osobina.

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