

COMPREHENSIVE STUDY OF SELECTION-VALUE LINES OF ZUCCHINI ON THE LEVEL OF DAMAGE BY THE YELLOW MOSAIC VIRUS (ZYMV) AND MANIFESTATION OF OTHER DISEASES

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Abstract

The work is aimed at the selection of linear samples of zucchini (*Cucurbita pepo* L. var. *Giromontia* Duch.) with increased complex resistance to abiotic factors of cultivation – zucchini yellow mosaic virus (ZYMV), powdery mildew, bacteriosis and other viral pathogens. Selection studies on choosing virus-resistant zucchini lines from the United Kingdom, Italy, the United States and Spain have identified a number of important correlations levels of resistance to ZYMV and to harmful microorganisms and viruses, belonging to other genera. The assessment of the resistance of the selected zucchini lines to the complex of studied diseases was performed on a 9-point scale of the classifier of the Council for Mutual Economic Assistance (CMEA). In total, during 2017–2019, 20 lines of zucchini were studied in the field. According to the complex resistance to all pathogens (zucchini yellow mosaic virus, green speckled mosaic, white mosaic and cucumber mosaic, bacteriosis and fusarium wilt), four lines have been identified – LZ 17-11, RVL-19, LZ 17-45 and LZ 17-49, which were resistant at the level of points 7 and 9 on the scale of CMEA. The possibility of selecting potentially resistant linear zucchini genotypes for ZYMV based on correlations with the manifestation of other diseases that occurred in the field has been confirmed. The highest level of correlation $0.59 < r_p < 1.0$ is observed when comparing the degree of powdery mildew development and symptoms of ZYMV (17 statistically confirmed values of the pairwise correlation coefficient or 80.95 %). A similar indicator for the pair “bacteriosis/ZYMV” is 14 statistically confirmed values of the pairwise correlation coefficient or 66.67 % ($-1.0 < r_p < 0.99$), and for the pair “field viruses of other origin/ZYMV” – 11 values, which is 52.38 % ($-1.0 < r_p < 0.93$). Zucchini samples were identified, in which statistically significant correlations were observed for all pairs of comparative traits. Among them, the variety-standard Chaklun and 4 more lines – LZ 17-1, LZ 17-8, LZ 17-50 and LZ 17-44 ($-1.0 < r_p < 0.92$). The analysis of correlations shows a complex genetic organization of signs of resistance in zucchini lines to the studied pathogens and a high dependence of the manifestation of these signs on the response of the genotype of the line. One of the proofs of this experimental fact is that in all comparative pairs of indicators of the degree of development of certain diseases there are linear genotypes with both positive and negative values of Pearson correlation coefficients (r_p). The high level of statistically significant correlations revealed gives grounds for wide use of correlation analysis in selection work for choosing lines potentially resistant to the complex of the most common diseases in vegetable agrocenoses.

Keywords: zucchini yellow mosaic virus (ZYMV), zucchini line, correlation analysis, field and laboratory resistance.

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1. Introduction

Zucchini (*Cucurbita pepo* L. var. *Giromontia Duch.*) is a vegetable pumpkin plant, the fruits of which begin to be harvested for consumption in the phase of technical ripeness. As a vegetable crop, it is characterized by precocity, cold resistance, high genetic yield potential. Among other advantages of zucchini – high nutritional, dietary and therapeutic properties due to the successful ratio of mineral salts, low fiber and low calorie [1, 2].

In the agricultural market of Ukraine the most popular are varieties and hybrids of F_1 zucchini with a compact habit of the bush and a yield of not less than 40 t/ha. Zucchini forms are valued during the growing season, in which the phase of technical ripeness of the fruit occurs at 40–42 days, and the fruiting period lasts as long as possible [3–5]. Growing zucchini is economically profitable, as it is accompanied by low labor and energy costs. Among consumers of vegetable products, white fruit varieties and hybrids F_1 of Ukrainian selection are in the greatest demand: Chaklun, Akrobat, Aspirant, Hrybovsky 37, Haydamaka, Svitozar, Tsukeshka, Zebra, Atilla F_1 , Otaman F_1 , Sadko F_1 , Dinar F_1 . All the above Ukrainian varieties and hybrids of F_1 , as breeding innovations, are characterized by certain economically valuable properties, which are mainly manifested in the agro-climatic conditions, in which they were created.

Recently, certain changes in environmental stressors have taken place in vegetable agrocenoses, which are mainly related to global climate change. These stressors do not allow to fully realize the genetic potential of varieties and hybrids of F_1 zucchini, the selection of which was carried out under other conditions of a more temperate climate [6, 7].

This is especially true of resistance to biotic factors both under conditions of growing zucchini in irrigated and rainy conditions. The main limiting factor is the defeat of phyto virus infections, which lead to significant yield losses [8–10]. Of all the known phyto viruses that infect zucchini plants, the most economically dangerous is the zucchini mosaic virus (ZYMV). Therefore, in modern virology and molecular genetics, much attention is paid to the study of its biological and serological features and molecular structure [11, 12]. ZYMV, distributed on all continents, belongs to the genus *Potyvirus* of the family *Potyviridae*. In members of the *Cucurbitaceae* family, this virus causes quite severe symptoms of defeat, which lead to losses of 25 to 50 % of the yield, depending on the strain pathogenicity [13].

To counteract the spread of this virus, methods of selection of highly adaptive sources of resistance are introduced in genetic selection work, on the basis of which resistant varieties and hybrids of F_1 zucchini are created [14]. The optimization of breeding programs to create virus-resistant forms of zucchini is carried out by developing methods of marker-associative selection, which are based on the presence of linkage or association between the DNA marker and the target gene for resistance to ZYMV [15]. To date, the genetics of resistance to ZYMV directly in zucchini is still at an early stage of study.

Partial resistance to the virus has been shown to be controlled by eight genes. These genes were identified as a result of studying the F_2 population, obtained after hybridization of a wild pumpkin *Nigerial Local* with a cultivar of zucchini [16, 17]. In such phylogenetically close to zucchini varieties as watermelon, melon and cucumber, the expression of genes for resistance to ZYMV was also detected [18].

Thus, the above issues indicate the high relevance of immunological experiments to search for genotypes of zucchini with increased resistance to ZYMV and other dangerous pathogens. To successfully solve the problem of creating highly resistant varieties and hybrids of F_1 , further improvement of existing breeding and genetic methods of source material, enrichment of existing breeding methodology with new methods of molecular genetics and immunology are required.

The aim of the study is to select linear samples of zucchini (*Cucurbita pepo* L. var. *Giromontia Duch.*) with increased complex resistance to abiotic factors of cultivation – zucchini yellow mosaic virus (ZYMV), powdery mildew, bacteriosis and other pathogens of viral diseases.

2. Materials and Methods

The work to study the response of zucchini lines to artificial infection with yellow mosaic virus in the laboratory and field assessment of resistance to other viruses and pathogens was conducted during 2017–2019. Field tests of the lines were carried out on the experimental basis of the Institute of Vegetable and Melon Growing of the National Academy of Agrarian Sciences of Ukraine (Selektsiyne village, Kharkiv region, Ukraine). Laboratory tests – on the experimental basis of LLC “Agrogen Novo” (Kharkov, Ukraine). A working collection of zucchini lines, originating from Great Britain, the USA, Italy and Spain with a total of 20 samples, was used as an object of research (**Table 1**). The standard was a variety of Ukrainian selection Chaklun, which is included in the State Register of Plant Varieties of Ukraine. At the start of the study in 2017, all linear samples had the F_6I_6 generation. In subsequent years of research, the lines were propagated by multiple self-pollination.

Methodological aspects and results of the research on artificial contamination of zucchini lines in the laboratory are described in detail in [19]. To evaluate the source material of zucchini for resistance to ZYMV in the laboratory, the classical protocol of the method of mechanical grafting of ZYMV vectors was used. This grafting involves rubbing infectious plasmid DNA according to the method of Gibbs and Harrison, described in [20]. After receiving infected plants, infected leaf juice was used to further infect healthy zucchini plants [19]. The evaluation of the resistance of experimental samples of zucchini to the virus of yellow mosaic zucchini was carried out on the basis of “Methods of phytopathological studies for artificial infection” [21].

In accordance with this technique, for the analysis of experimental samples of zucchini plants used a 9-point scale to assess the degree of their resistance to ZYMV. The maximum level of stability corresponds to 9 points, the minimum – 1 point.

The development of the disease was determined by a 9-point scale of resistance. According to this gradation, 9 points correspond to highly resistant samples, in which a lesion of the plant surface is either absent or occurs from 0.1 to 10 %. Resistant samples correspond to 7 points with a lesion of the plant surface from 11 to 25 %. Moderately resistant samples correspond to 5 points with a lesion of the plant surface from 26 to 50 %. Non-resistant or susceptible samples correspond to 3 points with a lesion to the plant surface from 51 to 75 %. Extremely non-resistant samples correspond to 1 point with a lesion of the plant surface of more than 75 % [21].

The presence of ZYMV in linear samples was analyzed by enzyme-linked immunosorbent assay (Bioreba DAS-ELISA kit was used) [22].

The field research on zucchini was conducted in the field during 2017–2019, their agronomic support was generally accepted for vegetable plant varieties for the agro-climatic zone of the Eastern Forest-Steppe of Ukraine [24]. In the open ground, zucchini is particularly demanding of its fertility and its mechanical composition. The predecessor in the experiments was barley, after which the soil was peeled to a depth of 8–10 cm, and plowed to a depth of 25–27 cm in the first half of October. After early spring harrowing, cultivation was carried out to a depth of 10–12 cm, immediately before sowing – pre-sowing cultivation to a depth of 5–6 cm. Then the field was marked in two directions with a row spacing of 70 cm. Sowing of experiments was carried out in 2017 – on May 17, in 2018 and 2019 – on May 11. Sowing was carried out manually according to the scheme 70×70 cm with a sowing rate of 3–4 kg/ha and with a depth of seed wrapping of 5 cm. When the seedlings appeared, the first inter-row tillage and manual weeding were carried out. After breaking through, 4 plants were left in the nest, providing 75–80 thousand plants per hectare. During the growing season, two inter-row tillages were carried out.

The development of diseases in the field was determined on a 9-point scale of CMEA lesions at the end of the growing season of plants of the studied lines of zucchini. The following gradation was used – no lesions on the surface of the plant or individual organ (highly resistant sample, point 9 of the CMEA scale). The degree of disease is from 0.1 to 10 % of the leaf ap-

paratus of plants (resistant sample, point 7 of the CMEA scale). The degree of disease is from 10.1 to 25 % of the plant surface (moderately resistant sample, point 5 of the CMEA scale). The degree of lesion is from 26.1 to 50 % of the plant surface (susceptible sample, point 3 of the CMEA scale). The degree of lesion is more than 50.1 % (highly susceptible sample, point 1 of the CMEA scale) [25].

Table 1

Collection samples of zucchini lines that were artificially infected with yellow mosaic virus in the laboratory and analyzed for the manifestation of other diseases in the field

No.	Sample name	Catalogue No.	Origin
1	Chaklun variety, st	Z-1768	Ukraine
2	LZ 17-1	Z-1891	Great Britain
3	LZ 17-2	Z-1901	Great Britain
4	LZ 17-4	Z-1907	Great Britain
5	LZ 17-5	Z-1918	Great Britain
6	LZ 17-7	Z-1928	Great Britain
7	LZ 17-8	Z-1939	Great Britain
8	LZ 17-10	Z-1953	Great Britain
9	LZ 17-11	Z-1963	Great Britain
10	LZ 17-42	Z-2112	Great Britain
11	LZ 17-44	Z-2019	Italy
12	LZ 17-45	Z-2043	Italy
13	LZ 17-47	Z-2037	USA
14	LZ 17-48	Z-2038	Italy
15	LZ 17-49	Z-2113	Italy
16	LZ 17-50	Z-1964	Great Britain
17	RVL-19	Z-1972	Great Britain
18	VL-90	Z-1986	Spain
19	VL-91	Z-1994	Spain
20	VL-92	Z-2005	Spain
21	Vedi	Z-2024	Italy

Note: previously the list of linear samples was presented by the authors of the article in the paper [23]

3. Results

Summary data from years of research on the level of resistance of linear material to the studied pathogens in the field are summarized in **Table 2**. Most lines, a total of 19 samples, had a high resistance to field viral diseases at 9 points. The exception is one line LZ 17-5, which had a similar figure at 7 points. In terms of resistance to bacteriosis, the vast majority of lines also had high resistance (9 points). Exception is 4 lines – LZ 17-4, LZ 17-50, VL-90 and LZ-91, in which this indicator was at the level of resistant genotypes (7 points of the CMEA scale). In terms of resistance to powdery mildew, the studied linear samples showed a more contrasting reaction from the presence of medium-resistant genotypes to absolutely resistant (**Table 2**). Only 1 line – LZ 17-11 – was noted for high stability at the level of 9 points. The group of resistant genotypes (7 points) included the largest number of lines, a total of 16 samples. Another 4 lines showed a moderate response to the defeat of the pathogen “powdery mildew” (5 points). Among them are LZ 17-2, LZ 17-4, LZ 17-5 and LZ 17-42. According to the studied resistance points, the standard variety Chaklun had a high resistance to viral diseases and bacteriosis (9 points) and a stable reaction to the pathogen “powdery mildew” (7 points).

For the period of 2017–2019, 1 linear sample – LZ 17-11 should be distinguished for complex resistance to all pathogens. There were 10 lines, in which resistance to viral diseases, bacteriosis was at the level of 9 points, and the manifestation of powdery mildew, these lines had a stable reaction at the level of 7 points similar to the standard variety. In particular, these are the following samples – LZ 17-2, LZ 17-4, LZ 17-5, VL-92, LZ 17-44, LZ 17-45, Vedi, LZ 17-47, LZ 17-48, LZ 17-49.

Table 2

The level of field resistance of zucchini lines to the main pathogens, according to the average data of 2017–2019

No.	Sample	Disease development degree, %			Resistance point 9 (by the CMEA scale)		
		powdery mildew	Viruses	Bacteriosis	powdery mildew	Viruses	Bacteriosis
1	Chaklun, st	21.38	1.67	4.58	7	9	9
2	LZ 17-1	36.25	2.50	5.0	5	9	9
3	LZ 17-2	33.75	1.67	7.50	5	9	9
4	LZ 17-4	28.75	10.0	12.50	5	9	7
5	LZ 17-5	20.0	11.67	9.17	7	7	9
6	LZ 17-7	20.0	9.17	6.67	7	9	9
7	LZ 17-8	21.25	2.50	5.0	7	9	9
8	LZ 17-10	17.50	0.83	11.67	7	9	7
9	LZ 17-11	2.50	0.83	2.50	9	9	9
10	LZ 17-50	18.75	8.33	10.83	7	9	7
11	RVL-19	13.75	7.50	7.50	7	9	9
12	VL-90	17.50	5.0	10.83	7	9	7
13	VL-91	15.0	1.67	11.67	7	9	7
14	VL-92	18.75	2.50	5.83	7	9	9
15	LZ 17-42	26.25	0.83	6.67	5	9	9
16	LZ 17-44	17.50	9.17	6.67	7	9	9
17	LZ 17-45	13.75	5.83	9.17	7	9	9
18	Vedi	18.75	3.33	9.17	7	9	9
19	LZ 17-47	16.25	5.0	7.50	7	9	9
20	LZ 17-48	18.75	0.0	9.17	7	9	9
21	LZ 17-49	23.75	0.83	5.0	7	9	9
	HIP _{0.05}	3.27	3.65	3.22	–	–	–

An important element of selection work is to establish a link between the response of plants of selected linear genotypes both to the damage of the ZYMV virus in the laboratory and to the damage of harmful microorganisms of different biological nature in the field. Therefore, for a more comprehensive assessment of the degree of resistance of linear samples of zucchini to pathogens of different biological nature, a pairwise correlation analysis was performed. At the same time, we compared pairs of quantitative indicators “Degree of disease development”, which relate to ZYMV and powdery mildew, bacteriosis, and other viral infections that occurred in the field (Table 2). According to field observations, symptoms of viral diseases, such as green speckled mosaic, white mosaic and cucumber mosaic were observed.

Data on the correlation analysis are summarized in **Table 3**.

The analysis of the level of resistance to ZVMV in the laboratory is presented in [19]. As a result of artificial infection, it was found, that the highest level of resistance (9 points) was marked by 3 lines (LZ 17-7, VL-90, VL-91). There were three more lines (LZ 17-11, LZ-17-42, VL-92), which were resistant to the virus at the level of point 7 and a relatively resistant degree of disease development after their artificial infection (the variability of the correlation coefficient was $V=20, 7-23.1\%$). The average resistance to the virus (5 points) was the standard Chaklun variety [19]. The analysis of the degree of disease of the linear material, under the conditions of their ZYMV damage, allowed them to differentiate according to the level of stability of this indicator over the years of research. The lowest level of coefficient of variation ($V<5\%$) belonged to a single sample LZ 17-44, which belongs to the group of moderately resistant genotypes. A group of linear samples, LZ 17-11, LZ 17-47, LZ 17-50, in which the variation of this indicator was moderate ($V=6-16\%$), was distinguished. The medium-resistant variety Chaklun had the following indicators of the degree of disease development – $27.8\pm 3.54\%$ ($V=22.0\%$) [19].

Of the 63 correlation pairs, 20 were found to be statistically insignificant. There were 15 statistically significant, moderate and very strong correlations ($-0.5 < r_p < 0.99$) among the ZYMV and powdery mildew “disease development degree” pairs. Another 2 cases showed the existence of a

functional relationship between the manifestation of the studied features ($r_p=1.0$). The largest number of samples was registered with positive correlations ($r_p=0.57-1.0$). This group includes the standard variety Chaklun (K-1768) and 11 other lines: LZ 17-5, LZ 17-7, LZ 17-11, LZ 17-50, RVL-19, VL-90, LZ 17-42, LZ 17-44, Vedi, LZ 17-48, LZ 17-49. Negative, statistically significant correlations ($r_p=(-0.88)-(-0.59)$) were inherent to 5 lines: LZ 17-1, LZ 17-2, LZ 17-8, LZ 17-10, VL-92.

Table 3

Correlation relationships in linear samples of zucchini between the degree of disease development in the field and the results of the laboratory test for resistance to yellow mosaic zucchini virus (according to generalized data 2017–2019)

No.	Sample	Correlation coefficient (r_p) between pairs of indicators of the development degree of the studied diseases		
		powdery mildew/yellow mosaic virus	Bacteriosis/yellow mosaic virus	Field viruses/yellow mosaic virus
1	Chaklun variety, st	0.92	-0.87	-0.61
2	LZ 17-1 (Z-1891)	-0.82	-1.0	-0.57
3	LZ 17-2 (Z-1901)	-0.68	-0.41	0.73
4	LZ 17-4 (Z-1907)	-0.12	-0.80	-0.12
5	LZ 17-5 (Z-1918)	0.57	-0.28	0.02
6	LZ 17-7 (Z-1928)	1.0	-0.12	0.29
7	LZ 17-8 (Z-1939)	-0.72	-0.96	0.72
8	LZ 17-10 (Z-1953)	-0.88	0.64	-0.48
9	LZ 17-11 (Z-1963)	0.79	0.99	0.14
10	LZ 17-50 (Z-1964)	0.92	-0.71	0.74
11	RVL-19 (Z-1972)	0.91	-1.0	-0.42
12	VL-90 (Z-1986)	1.0	-1.0	0.47
13	VL-91 (Z-1994)	0.04	-0.78	-1.0
14	VL-92 (Z-2005)	-0.59	-0.13	-0.81
15	LZ 17-42 (Z-2112)	0.97	-1.0	0.25
16	LZ 17-44 (Z-2019)	0.90	-0.96	-0.95
17	LZ 17-45 (Z-2043)	0.05	0.54	0.66
18	Vedi (Z-2024)	0.85	-0.06	0.52
19	LZ 17-47 (Z-2037)	0.20	0.13	0.32
20	LZ 17-48 (Z-2038)	0.63	0.09	0.93
21	LZ 17-49 (Z-2113)	0.91	-0.57	0.42

Note: in the table, statistically significant values of the Pearson pair correlation coefficient (r_p) at the significance level are highlighted in bold $p<0.05$

It has been established, that there were 10 statistically significant moderate, strong and very strong correlations ($-0.5<r_p<0.99$) between the pairs of quantitative indicators “Disease development degree”, which belong to the yellow mosaic virus and the pathogen “Bacteriosis”. Another 4 cases showed the existence of a negative functional relationship between the manifestation of these features ($r_p=-1.0$). Unlike the previous correlation pair, this one had mostly negative connections, which indicates the existence of a certain pattern (Table 3). In particular, negative correlation pairs ($-1.0<r_p<0.57$) were marked by the standard Chaklun variety (K-1768) and 11 other lines: LZ 17-1, LZ 17-4, LZ 17-8, LZ 17-50, RVL-19, VL-90, VL-91, LZ 17-42, LZ 17-44, LZ 17-49. Positive correlation coefficients ($0.54<r_p<0.99$) for this pair of features were inherent to 3 lines – LZ 17-10, LZ 17-11 and LZ 17-45 (Table 3).

The correlation between the development of diseases in the laboratory and field conditions initiated by viruses had the most ambiguous assessment and the least number of statistically significant values of pairwise correlation coefficients in linear samples of zucchini. As shown in Table 3, of the 20 lines, only 11 had statistically significant confirmations of the correlation coefficient. At the same time, five lines had negative values ($-1.0<r_p<-0.57$), and six had positive values ($0.66<r_p<0.3$). In this case, the sample VL-91 had a negative functional relationship ($r_p=-1.0$). The

group of samples with negative values of the correlation coefficient included the standard variety Sorcerer and the following lines – LZ 17-1, VL-91, VL-92, LZ 17-44. To the group with positive values – LZ 17-2, LZ 17-8, LZ 17-50, LZ 17-50, Vedi, LZ 17-48.

The correlation between the development of diseases in the laboratory and field conditions, initiated by viruses, had the most ambiguous assessment and the least number of statistically significant values of pairwise correlation coefficients in linear samples of zucchini. As shown in **Table 3**, of the 20 lines, only 11 had statistically significant confirmations of the correlation coefficient values. At the same time, five lines had negative values ($-1.0 < r_p < -0.57$), and six had positive values ($0.66 < r_p < 0.3$). In this case, the sample VL-91 had a negative functional relationship ($r_p = -1.0$). The group of samples with negative values of the correlation coefficient included the standard Chaklun variety and the following lines – LZ 17-1, VL-91, VL-92, LZ 17-44. To the group with positive values – LZ 17-2, LZ 17-8, LZ 17-50, LZ 17-50, Vedi, LZ 17-48.

Thus, the possibility of choosing genotypes of zucchini potentially resistant to the yellow mosaic virus for the selection process by correlations with respect to the manifestation of other diseases that occurred in the field was confirmed. The highest level of correlation is observed when comparing the degree of powdery mildew development and symptoms of yellow mosaic virus (17 statistically confirmed values of the pairwise correlation coefficient or 80.95 %). A similar indicator for the pair “bacteriosis/ZYMV” is 14 statistically confirmed values of the pair correlation coefficient or 66.67 %, and for the pair “field viruses ZYMV” – 11 values, which is 52.38 % (**Table 3**). There were five experimental samples of zucchini, in which statistically significant correlations were observed for all pairs of traits. Among them, the standard variety Chaklun (K-1768) and 4 more lines – LZ 17-1, LZ 17-8, LZ 17-50 and LZ 17-44.

The analysis of correlations shows the complex genetic organization of signs of resistance in zucchini lines to the studied pathogens and the high dependence of the manifestation of these signs on the response of the genotype of the line. One of the proofs of this experimental fact is that in all comparative pairs of indicators of the degree of development of certain diseases there are linear genotypes with both positive and negative values of linear Pearson pair correlation coefficients (r_p). The high level of detected, statistically significant, correlations gives grounds for the widespread use of correlation analysis in selection work to select potentially resistant lines to the complex of the most common diseases in vegetable agrocenoses. This is especially true of the relationship between ZYMV resistance and resistance to powdery mildew. The lowest dependence is observed when comparing levels of resistance to viral pathogens. The obtained experimental data have a high practical value, as they allow in a relatively short time to select highly resistant lines of zucchini to the complex of diseases for their further involvement in breeding research programs for further selection of a set of other economically valuable traits. In the further research program, the authors of the article plan to investigate the patterns of manifestation of signs of stability of selection-valuable lines of zucchini with the involvement of other genetic and statistical methods – factor analysis and construction of nonlinear correlation and regression models to predict the level of these traits.

4. Conclusions

During the research period of 2017–2019, 4 lines were identified (LZ 17-11, RVL-19, LZ 17-45 and LZ 17-49), which had a complex resistance to pathogens of all diseases at the level of points 7 and 9 on the CME scale. Under the conditions of the experiment in the laboratory, the resistance to the zucchini mosaic virus was studied. In the field, the zucchini lines, studied for resistance to ZYMV, had symptoms of the following other diseases – powdery mildew, fusarium wilt and green speckled, white and cucumber mosaic. Relevant indicators for the Chaklun standard variety – resistance to the pathogen “powdery mildew” – 5 points, viruses – 7 points, bacteriosis – 7 points.

The possibility of choosing genotypes of zucchini potentially resistant to the yellow mosaic virus for the selection process by correlations with respect to the manifestation of other diseases that have occurred in the field has been confirmed. The highest level of correlation ($-0.59 < r_p < 1.0$) is observed when comparing the degree of powdery mildew development and symptoms of yellow mosaic virus (17 statistically confirmed values of the pairwise correlation coefficient or 80.95 %). A similar indicator for the pair “bacteriosis/ZYMV” is 14 statistically confirmed values of the pair-

wise correlation coefficient or 66.67 % ($-1.0 < r_p < 0.99$), and for the pair “field viruses/ZYMV” – 11 values, which is 52.38 % ($-1.0 < r_p < 0.93$). Zucchini samples were identified, in which statistically significant correlations were observed for all pairs of traits. Among them, the Chaklun standard variety and 4 more lines – LZ 17-1, LZ 17-8, LZ 17-50 and LZ 17-44 ($-1.0 < r_p < 0.92$).

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