



# Agromorphological characterization and molecular evaluation of a marker associated with *Zym-1* allele resistance of local zucchini genotypes

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Received: 10 January 2025 / Accepted: 24 April 2025 / Published online: 13 May 2025  
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**Abstract** Zucchini (*Cucurbita pepo* L.) is a widely cultivated vegetable with high economic value and important nutritional value. *Zucchini yellow mosaic virus* (ZYMV) is the most common virus diseases that causes loss of productivity in Zucchini cultivation. This study was conducted to determine of 250 Zucchini in the S3 stage genotypes, in terms of agromorphological characteristics such as plant morphology, fruit characteristics and yield and to determine the resistance levels of the genotypes to ZYMV. As a result of molecular analysis, 43 genotype were found to be homozygous dominant (RR) and 10 genotype as heterozygous (Rr).resistant to *Zym-1* allele. According to the results of factor analysis, 12 significant factors were identified. As a result, factor analysis, used in plant morphological characterisation studies, allows a systematic examination of a large number of variables that affect the morphological characteristics

of plants, and this method is considered a critical tool for understanding the relationships of plants with environmental and genetic factors. At the end of the study, morphological variability was found high among the Zucchini genotypes. This evaluation of plant trait variability can assist geneticists and breeders to identify populations with desirable characteristics for inclusion in zucchini breeding programs. In addition, the levels of resistance to these disease are crucial for breeding programs aimed at developing cultivars resistant to disease.

**Keywords** Cluster analysis · Correlation · *Cucurbita pepo* · Factor analysis · Molecular marker · *Zym-1*

## Introduction

The introduction of zucchini (*C. pepo* L.) genotypes for agro-morphological characterization is essential for understanding the diversity and adaptability of this economically significant crop. Zucchini, a member of the *Cucurbitaceae* family, is cultivated globally for its edible fruits and is recognized for its nutritional value, including high levels of vitamins and minerals (Blanca et al. 2011). The morphological traits of zucchini, such as fruit size, shape, and color, exhibit considerable variation, which is crucial for breeding programs aimed at improving yield and disease resistance (Öztürk et al. 2022). This variability is

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influenced by both genetic factors and environmental conditions, which can affect growth patterns and productivity (Lúcio et al. 2021).

Plant morphology can be observed in several main parts: leaves, stems, roots, flowers and fruit. These parts provide in-depth studies of the plant's overall structure, since plant morphology includes fundamental studies of specific groups for identifying plants. The morphology of a plant type is one of the characteristics that is easily observed (Şavkan and Türkmen 2023; Şavkan et al. 2024, 2025a). The agromorphological characterization of zucchini genotypes involves assessing various traits, including plant height, leaf morphology, flowering time, and fruit characteristics. Such evaluations are vital for identifying genotypes that are well-suited to specific growing conditions and for enhancing breeding strategies (Montero-Pau et al. 2017).

Genetic variation in vegetable breeding is significant and is considered the basis for cultivar breeding. Population richness of local species is preserved in regions where genetic diversity is cultivated (Priori et al. 2018). Part of this diversity has been collected by researchers and stored in active germplasm banks of various institutions (Silva et al. 2024). In addition, correct identification and classification of species is crucial for managing germplasm collections. In addition, many researchers have stressed the importance of characterising morphology as a fundamental step towards resolving taxonomic conflicts (Olatunji and Afolayan 2018; Öztürk et al. 2022; Şavkan and Türkmen 2023; Şavkan et al. 2025b). Understanding zucchini genotypes is vital for conservation of genetic resources. In the face of changing agricultural practices, maintaining diverse genotypes is crucial for food security and disease prevention (Xanthopoulos et al. 2019). Researchers can identify those with desirable characteristics for cultivation and conservation by evaluating the agro-morphological traits of various zucchini genotypes. Moreover, the genetic diversity within *C. pepo* L. is significant, with various landraces and cultivars displaying unique traits (Ntuli et al. 2016). This diversity is a valuable resource for breeders seeking to develop new varieties that can withstand biotic stresses, such as viral infections, including ZYMV (Beloti et al. 2021).

The evaluation of zucchini (*C. pepo* L.) genotypes for resistance to ZYMV is a critical area of research, particularly given the significant impact of this virus

on zucchini production worldwide. ZYMV, a member of the *Potyvirus* genus, is notorious for causing severe symptoms such as leaf distortion, yellow mosaic patterns, and stunted growth, which can lead to considerable economic losses in cucurbit crops (Beloti et al. 2021; Chinnaraja et al. 2021; Eyong et al. 2021). The virus is transmitted by aphids. Therefore, resistant genotypes need to be developed as a sustainable management strategy (Tohamy et al. 2018; Beloti et al. 2021).

The socioeconomic importance of zucchini in tropical regions, particularly in countries like Colombia and Brazil, underscores the urgency of breeding efforts aimed at enhancing resistance to ZYMV (Beloti et al. 2021; Pereira et al. 2021). The development of resistant genotypes can reduce the spread of the virus and reliance on chemical measures, which can harm the environment and health. The search and selection of these resistant genotypes can boost resilience and sustainability in agriculture (Tohamy et al. 2018; Kondratenko et al. 2021). Breeding programmes using marker-assisted selection (MAS) have shown promise in producing pumpkin varieties with improved resistance to ZYMV. Genetic diversity in the genus *Cucurbita* is key to overcoming this limitation. Studies show that combining ZYMV-resistant genotypes with strategic breeding using markers can result in robust crop varieties that can thrive in the presence of this virus (Pachner et al. 2015; Kondratenko et al. 2021). However, the challenge remains that many existing zucchini genotypes exhibit limited resistance, necessitating the exploration of genetic diversity within the species and related *Cucurbita* species for potential sources of tolerance (Pachner et al. 2015; Amoroso et al. 2022).

Recent advancements in molecular techniques have facilitated the identification of specific genetic markers associated with ZYMV resistance, enabling marker-assisted selection in breeding programs (Pachner et al. 2015; Sawazaki et al. 2018). For instance, studies have identified several dominant resistance genes, such as *Zym-0*, *Zym-1*, and *Zym-2*, which can be pyramided to enhance resistance durability (Pachner et al. 2015; Sawazaki et al. 2018). Capuozzo et al. (2017) reported that the major gene *Zym-1* is required for a high degree of resistance expression to ZYMV. This was analysed both phenotypically and genotypically. *Zym-1*'s main role in ZYMV resistance was confirmed by the high percentage of co-segregation

between SNP1 and resistant phenotypes in analysed populations. Pachner et al. (2015) stated that the combined distribution of seven ZYMV-resistance genes identified in *C. pepo* L. is essential for maximum resistance expression and durability. Various combinations of these will result in a phenotypic spectrum of resistance expression, and *Zym-1* is essential. In this study, these *Zym-1* gene was used for molecular genetic selections. Accordingly, the *Zym-1* gene was used for molecular genetic selection in this study.

In conclusion, both screening the *Zym-1* gene conferring ZYMV resistance with the *Zymv*-SNP1 marker and determining agro-morphological traits of zucchini (*C. pepo* L.) genotypes represents a multifaceted approach that integrates traditional breeding practices with modern genetic techniques. As global demand for zucchini continues to grow, this comprehensive research not only aims to improve the productivity and resistance of zucchini crops in the face of viral threats, but also contributes significantly to the broader goals of sustainable agriculture and biodiversity conservation.

## Material ve method

### Plant material

The material of our study consisted of 250 pumpkin genotypes consisting of local populations, standard and hybrid varieties in Turkey at S3 level selected from previous breeding studies. Seeds were planted in vials filled with a peat-perlite (2:1) mixture, with 5 plants from each genotype. After preparing the soil in the greenhouse, the seedlings were grown in the vials until they were ready for transplanting. Transplanting was done when the seedlings reached the appropriate size. The seedlings were planted next to the drippers above rows. Regular irrigation and maintenance procedures were carried out.

### Agro-morphological characters

Morphological parameters of each plant were examined, and selfing was performed to ensure the progress of the breeding stage in the existing genotypes for Zucchini selection breeding. The morphological characteristics of the lines were determined by taking measurements and observations throughout the

vegetation. The study used the UPOV descriptor list. Qualitative data were observed, and quantitative data were measured on 5 marketable Zucchini fruits from each genotype. The measurements and observations made are as follows (UPOV 2006). Quantitative data collected from observation includes the following characteristics of the plant: growth habit (bush, semi-trailing, trailing), branching (absent, present), degree of branching (weak, medium, strong), attitude of petiole (excluding lower external leaves) (erect, semi-erect, horizontal), green color on the stem (only light, only dark, partly light and partly dark), tendrils on the stem (absent to rudimentary, well-developed), leaf blade size (small, medium, large), incisions on the leaf blade (light, medium, strong), leaf blade marbling (absent, present), green color of upper surface of leaf (light, medium, dark), leaf blade surface area (very small, small, medium, large, very large), petiole length (short, medium, long), petiole thickness (small, medium, large), petiole cross-sectional shape (round, triangular), the number of the prickles of petiole (few, medium, many) and the silvering of leaf blade (absent, present).

The observations regarding fruits are related to presence of neck in immature fruit (absent, present), the curving of the neck in unripe fruit (absent, present), length in unripe fruit (short, medium, long), major colors in unripe fruit (white, cream, yellow, orange, green, partly white and partly yellow, partly green and partly yellow), the intensity of major colors in unripe fruit (light, medium, dark), shape of the cross-section in unripe fruit (round, grooved, angular, lobed), presence of wart in unripe fruit, gloss in unripe fruit (light, medium, strong), and a comparison of vein color with the color of the other part of the unripe fruit (same, different), color of linear bands on the vein in immature fruit (whitish, yellow, orange, green), resence of mottling in immature fruit (present, absent), type of mottling in immature fruit (scattered, scattered and fragmented, scattered and banded, scattered, fragmented and banded), color of mottling in immature fruit (whitish, yellow, orange, green), conspicuousness of the spots on the skin of the immature fruit (weak, medium, strong), size of the blossom mark on the immature fruit (small, medium, large), protrusion of the blossom mark on the immature fruit (present, absent), general shape of the fruit (transverse elliptical, globular, top-shaped, broadly elliptical, ovate, elliptical, cylindrical, tapered cylindrical,

pear-shaped, bottle-shaped, club-shaped). Quantitative data measured includes fruit diameter (mm), fruit length (cm), and fruit weight (g).

### Molecular marker analyses

DNA extraction was performed according to a modified CTAB procedure (Doyle and Doyle 1987) in young leaves. The DNA amount was quantified spectrophotometrically by a NanoDrop ND-1000 Spectrophotometer (NanoDrop Technologies), and the quality was checked electrophoretically with a 1.5% agarose gel.

Zymv-SNP1 primer (Capuozzo et al. 2017) was used in the molecular study steps that were followed to measure the degree of resistance to *Zym-1* allele in the selected zucchini genotypes, and the information of the primer used is given in the Table 1. In the PCR procedures, it was decided to add RNase enzyme due to the lack of clear images and dimer formation as a result of electrophoresis of PCR products in 1.5% agarose gel. CAPS analysis consisted of a PCR reaction followed by digestion with Bgl II restriction enzyme. Polymorphism was detected by separating the total volume of treated DNA on a 2% agarose gel (1 × Tris–acetate–EDTA) containing SYBR® Safe DNA Gel Stain (Takara) and visualized under a UV transilluminator. Evaluation was based on the allele length values obtained by electrophoretic restriction of the marker used for each line with the Bgl II enzyme for the Zymv SNP1 allele.

### Statistic analyses

All characters were measured in the greenhouse and at normal harvest time. Characters were analyzed according to the identification form developed by UPOV for *Cucurbita* species with reference TG/76/8 (UPOV 2006). Fruit character analyses were performed on five fruits of each plant. These characters were described according to Kaiser–Meyer–Olkin (KMO) Test ve Bartlett'in Küresellik Test, so that the feasibility of the analysis could be determined.

Using the multivariate procedure applied in JMP (18.00) (2018) statistical software, the factor analysis based on 35 agro-morphological features were performed by scoring the data obtained from the materials selected after selection according to the UPOV scale values, to identify the variation models within the zucchini accession groups.

## Results and discussion

Agro-morphological studies were carried out with 35 measurements and observations on 250 genotypes at S3 level. At the end of the study, the distribution rates of the criteria of the morphological characteristics were given in all the genotypes.

### Morphological traits

In the vegetative observations analysed in the research, 2 of the genotypes were observed as bushy, semi-trailing (246 plants) and 2 genotypes were observed as trailing. While all of the genotypes showed a branching tendency, the degree of branching was found to be low (6 plants), moderate (140 plants) and strong in 104 plants. Shoot development in the stem was absent or poorly developed in 134 plants and 116 plants had well developed shoots, while stem green colour was observed as light only in 123 genotypes, dark only in 68 genotypes and finally light and dark in 59 genotypes. These parameters provide important information about plant morphology and growth habits. The growth patterns of plants shed light on genetic diversity and adaptation to the environment and these findings are supported by previous studies on zucchini (Kebrom 2017; Perez-Moro et al. 2024; Şavkan et al. 2025a).

When the observations on the leaves were analysed; the posture of the petiole was found to be erect in 3 plants, semi-erect in 245 plants and lying down in 2 plants. In petiole length, short (31), long (79) and mostly medium (140) petioles were found. In petiole thickness; thin (65 pieces), thick (15 pieces) and

**Table 1** Zymv-SNP1 primerinin sekansı

Marker	Primer sequence (5' → 3')	Enzyme	Reference
Zymv-SNP1-F	CAGAATCAGACCGCCATTGATA	Bgl II	Capuozzo et al. (2017)
Zymv-SNP1-R	ACTTCTGGCTCCTCGCAAATAC		

mostly medium (170 pieces). Regarding the prickliness of the petiole; 8 lines were very prickly, 96 plants were medium prickly, 146 plants were few prickly, and the cross-sectional shape of the petiole was found to be round in all plants. When the observations on the leaf blade were analysed; leaf blade swelling was present in 32 lines, while no swelling was detected in 218 lines. Leaf blade lobing was observed as slight (19 lines), moderate (120 lines) and strong in 111 genotypes. Leaf blade size was recorded as small in 2 genotypes, medium (107) and large in 141 genotypes. In the leaf blade area; small (2 plants), medium (104 plants), large (138 plants) and very large in 7 plants. The presence of silvering on the leaves was absent in 224 lines, while silvering was observed in 26 lines. Finally, the green colour of the upper surface of the leaf blade was only light (17 plants), medium (155 plants) and dark (78 plants). It can be seen that there is a considerable variation in the observations made on leaf structure and characteristics in the study. In this regard, the data obtained in the studies conducted by many researchers support our findings (Şavkan and Türkmen 2023; Perez-Moro et al. 2024; Şavkan et al. 2025a).

When analysing the structural characteristics of the immature fruit, 196 genotypes were found to have no neck and 54 genotypes were found to have a neck. The curvature of the fruit neck was scored as absent (235 genotypes) and present (15 genotypes). With regard to the cross-sectional shape of the fruit, 86 genotypes were round and 164 genotypes were angular. With regard to the presence of nodules on the fruit, these were classified as absent (238 genotypes) and present (12 genotypes). In addition, the size of the flower mark on the fruit was determined as small (201), medium (44) and large (5); in terms of flower mark protrusion, it was determined that 210 genotypes were absent and 40 genotypes were present. Finally, when analysing the general shape of the fruit, 1 genotype was oval, 8 genotypes were oval, 36 genotypes were brain-shaped, 124 genotypes were cylindrical, 75 genotypes were golf club-shaped and 3 genotypes were armoudi-shaped.

Regarding the colour parameters of the immature fruit, in terms of the number of main colours in the fruit, whitish (40), green (203), whitish and yellow (5) and green-yellow (6) were determined; in terms of the intensity of the main colour, 136 genotypes were determined as light, 80 genotypes as medium

and 34 genotypes as dark. With regard to the glossiness of the fruit, 71 genotypes were light, 33 genotypes were strong and most of them (146 genotypes) were medium. When the vein colour was compared with the main colour, it was determined that it was the same in 240 genotypes and different in 10 genotypes. In terms of the colour of the bands on the vein, whitish (36) and green (214) were observed. Spotting on the fruit was not observed in only 1 genotype. In terms of the type of mottling, 247 genotypes were scattered and 2 genotypes were scattered and fragmented; the colour of the spots was whitish in 213 genotypes, yellow in 4 genotypes and green in 32 genotypes; the conspicuousness of the spots on the peel was weak (120), medium (121) and strong (9).

The study of the structural and colour characteristics of immature fruit is an important area of research for plant breeding and agricultural productivity. These data show that fruit morphology varies according to geographical differences, environmental conditions and genetic structure. Monforte et al. (2013) reported that fruit morphology is associated with genetic diversity and this should be taken into account in plant breeding studies. In the literature on this topic, many studies reporting high diversity in terms of morphological traits in the various plants support our findings (Hegde et al. 2014; Li et al. 2019; Berame et al. 2020; Şavkan and Türkmen 2023). Understanding these traits is very important for breeding programmes aimed at increasing yield and fruit quality. This is because these findings highlight the importance of considering different parameters to optimise breeding and selection of summer squash cultivars according to market demand.

In this study, three agronomic characters such as fruit weight, fruit diameter and fruit length of squash plants (*Cucurbita pepo* L.) were analysed. In the study on 250 genotypes, the minimum fruit diameter was 18.5 mm (genotype BTA 269) and the maximum was 66.13 mm (genotype BTA 271). In terms of fruit length, the lowest value was 12 cm (genotype BTA 37) and the highest value was 51 cm (genotype BTA 242). In terms of fruit weight, the lightest fruit was 0.095 g (genotype BTA 167) and the heaviest fruit was 0.533 g (genotype BTA 268) (Table 2). In a study conducted by Kurtar et al. (2020), differences were found at 5% significance level between varieties in terms of fruit diameter and fruit length, but no difference was observed in terms of fruit weight. Similarly,

**Table 2** Some statistical values of immature fruits

	Fruit width (mm)	Fruit length (cm)	Fruit weight (g)
Mean	46.89	17.03	251.05
Std Dev	7.72	4.29	88.30
Std Err Mean	0.489	0.272	5.596
Variance	59.62	18.46	7797.34
CV	16.47	25.22	35.17
Minimum	18.5	12	95
Maximum	66.13	51	533
Median	46.9	16	232

in a study conducted by Şavkan et al. (2025a), significant differences were found in fruit diameter, fruit length and fruit weight in summer squash. In a study conducted by Nacar et al. (2011), fruit related characters were analysed and it was determined that 22.04% were short, 37.28% were medium and 40.68% were long in terms of maximum length. In addition, in terms of maximum diameter, 8.47% were small, 86.45% were medium and 5.08% were large. This situation is largely consistent with the data in our present study and the differences are thought to be caused by the differences in the starting material, regional differences and the effect of environmental conditions. This allows to obtain more information about the genetic diversity of the study materials and their sensitivity to environmental influences. The quantitative characters analysed provide important findings in terms of efficiency in plant breeding and constitute an important basis for the determination and development of targeted traits (Table 2).

### Factor analysis

Factor analysis in morphological characterisation studies allows the morphological characteristics of plants to be examined systematically. Particularly in cases where there are many interrelated variables affecting the morphological characteristics of plants, it summarises the relevant characteristics into fewer factors by revealing the relationships between these variables. Thus, it provides researchers with more understandable, manageable and easily interpretable data sets (Karaköy et al. 2017; Yilmaz and Kökten 2019). To assess whether a dataset is suitable for factor analysis, preliminary tests such as the Kaiser–Meyer–Olkin (KMO) test and Bartlett’s sphericity test are performed. The results of the KMO and

**Table 3** KMO and Bartlett’s Test

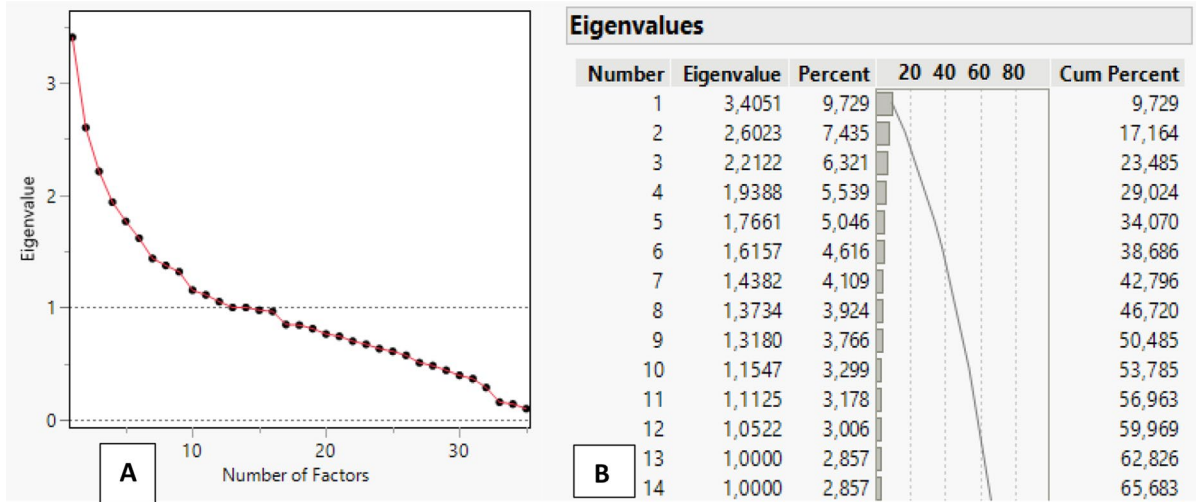
Kaiser–Meyer–Olkin Test	Measure of sampling adequacy	557
Bartlett’s test of Sphericity	ChiSquare	2129.311
	DF	595
	Sig	< 0.0001*

Bartlett’s tests shown in Table 3 indicate that there is sufficient correlation between our morphological observations and that factor analysis is appropriate for this data set. Therefore, factor analysis is considered a logical and appropriate method to reveal the hidden factors in our morphological observations.

Each eigenvalue obtained from the factor analysis shows the total (cumulative) variance explained by a factor. Table 4A shows the scree plot graph of the eigenvalues. As a result of the analysis, 14 factors were identified according to this graph. The eigenvalues of the identified factors are shown in Table 4B.

The Varimax method, which is the most commonly used orthogonal rotation method, was used in the rotation process to determine the number of important factors in the analysis, the number of variables in each factor, and the distribution of the variables according to the factors. The aim of factor rotation is to obtain namable and interpretable factors. Factor loadings express the weight of the variables in each factor. These values indicate the degree of relationship between the variables and the selected factors. If a variable has the strongest correlation with a factor, it is the element of that factor (Nakip 2003). As a result of the analysis, 12 important factors were identified using the varimax method. The variance values and rotations of the resulting factors are shown in Table 5.

**Table 4** Loading graph of eigenvalues obtained from factor analysis (4 A) and variance values (4B)



**Table 5** Matrix of factor variance values and factor loadings determined as a result of factor rotation analysis

Variance Explained by Each Factor				Rotated Factor Loading											
Factor	Variance	Percent	Cum Percent	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5	Factor 6	Factor 7	Factor 8	Factor 9	Factor 10	Factor 11	Factor 12
G	0.850394	-0.068739	0.024421	0.019748	0.127046	-0.033777	-0.009600	0.071022	0.037208	0.004808	0.019117	0.032773			
K	0.841474	-0.081758	0.003655	-0.001281	0.135764	-0.044873	0.013380	0.030956	-0.026378	0.049912	-0.034425	0.001073			
M	0.486869	-0.016992	-0.028085	-0.109536	-0.076377	0.026221	0.072810	-0.020693	-0.037751	-0.024035	-0.004590	0.070902			
B	-0.000000	-0.000000	0.000000	-0.000000	-0.000000	-0.000000	0.000000	-0.000000	0.000000	0.000000	0.000000	0.000000			
S	-0.045738	0.857345	0.013358	0.112668	-0.000680	0.052988	0.056147	-0.147667	-0.009905	-0.027277	-0.123226	-0.064318			
V	-0.020400	0.850965	-0.001336	0.164428	-0.066357	0.002547	-0.053222	-0.107284	-0.023747	-0.070303	-0.096046	0.091947			
W	-0.095406	0.288103	-0.151205	0.277387	0.041911	0.050382	-0.137899	-0.036022	-0.008384	-0.227854	-0.019261	0.203559			
AC	-0.156446	0.266293	0.010074	0.163114	-0.006279	0.049358	-0.113203	0.222638	-0.072495	-0.120496	0.029121	0.117048			
AG	-0.070671	-0.019943	0.831946	0.011298	0.083840	-0.138413	-0.309169	-0.045412	-0.071470	0.027595	-0.054867	-0.048346			
AI	0.032595	0.068775	0.792076	0.041009	0.122973	0.108422	0.363480	-0.052714	-0.044433	0.031471	-0.092112	0.003800			
T	-0.068414	0.172049	0.002255	0.712120	-0.076730	0.068411	0.053992	-0.006882	-0.001085	-0.115451	0.090984	0.063174			
E	-0.076538	0.062190	0.015819	0.554585	-0.128106	0.037736	0.067362	0.037707	-0.077861	-0.015971	-0.046018	0.017341			
AB	0.031810	0.123605	-0.045833	0.508811	-0.023920	0.209560	-0.040834	0.012936	0.108630	0.109518	0.003716	-0.135913			
V	0.068739	-0.131436	0.196068	0.283254	-0.083243	-0.054159	0.039454	-0.069824	-0.001080	0.061926	0.178804	0.138757			
N	-0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.000000	-0.000000			
C	0.008405	-0.007515	0.050848	-0.015713	0.658039	0.025322	0.071966	0.071189	-0.103826	0.070954	0.014256	0.017652			
F	0.341816	-0.025079	-0.029124	-0.124785	0.580668	-0.009852	-0.008678	0.116071	-0.017664	-0.065133	0.002117	0.041832			
O	-0.013835	-0.000717	0.112951	-0.183742	0.350129	-0.104754	0.036289	-0.091412	0.110215	0.091480	0.012427	0.077833			
L	0.297354	-0.046815	0.082431	0.062027	0.314745	-0.033611	0.038586	0.059537	-0.228439	-0.288208	-0.117485	-0.149546			
R	-0.080280	0.047406	-0.017383	0.149012	-0.043299	0.674346	0.016072	-0.042762	-0.056936	-0.068604	-0.004533	-0.168880			
Q	0.036349	-0.008098	0.028950	0.043211	0.040516	0.611029	0.096301	-0.122408	0.065587	0.015096	-0.002307	0.123447			
AF	0.025167	0.072457	-0.200200	0.092734	-0.160188	0.272777	0.151884	0.035451	-0.080135	0.018615	0.055935	0.074456			
AH	0.076756	-0.041405	0.014607	0.058062	0.118382	0.202773	0.808199	-0.093402	-0.021651	-0.015621	0.020980	-0.003314			
AD	0.090669	-0.117591	0.063478	-0.046749	0.052699	-0.064161	-0.062709	0.492317	0.028127	0.001822	-0.044737	-0.076716			
U	-0.061211	0.027183	-0.106368	0.020808	0.063217	-0.096628	0.004379	-0.029786	0.456234	-0.026257	-0.000006	0.230043			
AE	0.019508	-0.313941	-0.179785	-0.018428	-0.075859	-0.022543	0.040431	0.435837	0.039053	0.042443	0.112034	-0.151896			
A	0.013590	0.011798	0.019401	0.013108	-0.080985	-0.065124	-0.005521	0.029786	0.029786	0.046906	0.046906	0.008549			
D	-0.074862	-0.038936	0.082346	0.066987	0.045222	0.050018	0.027147	0.010439	0.477715	-0.076632	0.094071	0.067226			
H	-0.044958	0.030585	0.162541	0.110665	-0.024505	-0.024366	0.067796	0.087439	-0.315586	0.050911	0.117529	0.117617			
I	0.208009	-0.091181	-0.067848	-0.037579	0.125799	-0.013605	0.035035	0.103560	-0.077554	0.451054	-0.183723	0.067100			
P	-0.271034	-0.068334	0.067813	0.023082	-0.013559	-0.086021	0.055109	0.004510	-0.011414	0.353113	0.159389	0.031734			
X	-0.010105	0.027350	0.181095	-0.057856	-0.016452	0.043184	-0.189637	-0.082716	-0.014884	0.280964	0.043150	-0.182581			
Z	-0.036426	-0.053673	-0.025331	-0.014876	-0.011956	0.045427	-0.036561	0.062803	-0.018733	-0.019443	0.414845	0.019516			
AA	0.033679	-0.139837	-0.078462	0.094373	0.050054	-0.072686	0.192236	0.037476	0.011790	0.073388	0.322707	-0.134684			
J	0.273054	0.113836	-0.024441	0.004852	0.107301	0.012289	0.002158	-0.055069	0.037960	0.053056	-0.020658	0.371830			

A, Plant Growth; B, Plant branching; C, Degree of branching; D, Posture of the petiole in the plant; E, Green colour of the stem; F, Stem bolts; G, Leaf blade size; H, Leaf blade lobes; I, Green colour of the upper surface of the leaf blade; J, Leaf blade swelling; K, Leaf blade area; L, Petiole length; M, Petiole thickness; N, Cross-sectional shape of petiole; O, Number of prickles on petiole; P, Silvering; Q, Neck of immature fruit; R, Curvature of neck of immature fruit; S, Main colour of immature fruit; T, Intensity of main colour in unripe fruit; U, Shape of cross section in unripe fruit; V, Wilting in unripe fruit; W, Brightness in unripe fruit; X, Unripe fruit, Comparison of the colour of the vein with the colour of the other part of the fruit; Y, Colour of the bands on the vein in unripe fruit; Z, Spotting in unripe fruit; AA, Type of spots in unripe fruit; AB, Spot colour in unripe fruit; AC, Conspicuousness of spots on the peel of immature fruit; AD, Size of blossom mark on immature fruit; AE, Protrusion of blossom mark on immature fruit; AF, General shape of fruit; AG, Diameter of fruit; AH, Length of fruit; AI, Weight of fruit

The factor loadings matrix shows how much each variable is related to each factor. When naming the factors, factor loadings of 0.4 and above are generally

considered important and comments are made on the factors with high factor loadings. Thus, Factor 5 (C, F, O, L) and Factor 9 (A, D, H) are related to plant

and leaf structure, whereas Factor 1 (G, K, M and P), Factor 10 (I, P) and Factor 12 (J) are related to leaf characteristics. Factor 4 (T, E, -AB,) is related to stem and fruit colour characteristics, while Factor 8 (U, AD, AE), Factor 11 (X, AA) and Factor 2 (S, Y, AE) are related to fruit structural characteristics. Factor 6 (R, Q) is related to fruit neck structure, while factor 3 (AI, -AG) and factor 7 (AH, AG, AI) are thought to be related to fruit yield characteristics. According to the results of the factor analysis, when making a selection, we can evaluate whether the desired traits are suitable for the desired agricultural objectives by selecting the factors that are suitable for the selection objective. For example, if leaf characteristics are important in my selection criteria, Factor 1, Factor 10 and Factor 12 should be considered, if fruit yield is important, Factor 3 and Factor 7 should be emphasised. In many studies, such analyses are important for the conservation and development of plant diversity (Karaköy et al. 2017; Haspolat 2024). In conclusion, factor analysis in plant morphological characterisation studies allows the systematic examination of a large number of variables that affect plant morphological traits, and this method is considered an important tool for understanding the relationships of plants with environmental and genetic factors. Indeed, the important contributions of such analyses in areas such as plant breeding, conservation and diversification have been reported by many researchers (Bağcı

and Mutlu 2014; Okçu 2016; Emirzeoğlu and Başak 2020; Şahin 2023).

#### Screening for disease resistance

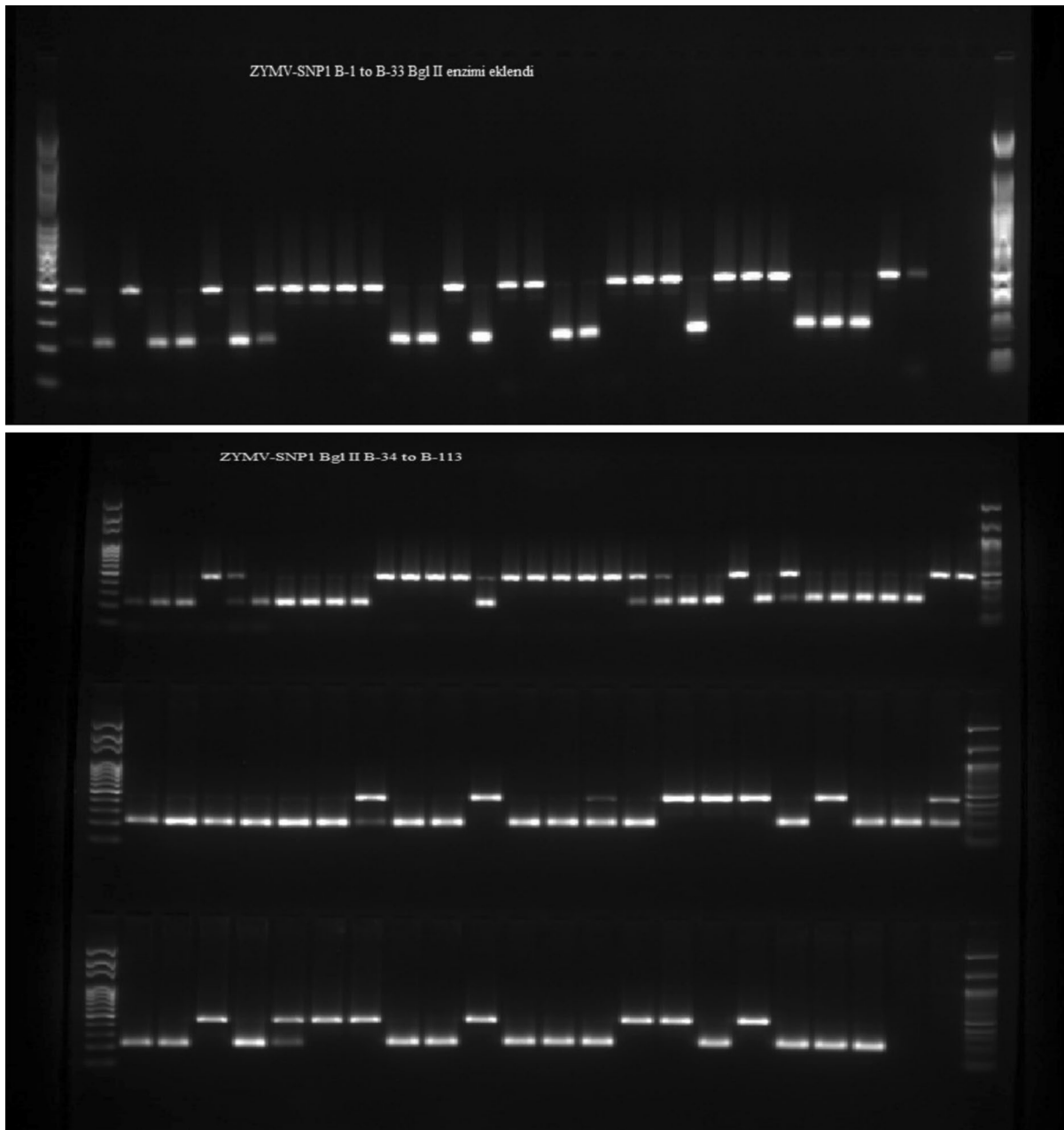
Molecular studies were carried out at the Biotechnology Laboratory of Beta Ziraat ve Tic. A.Ş. and ZymvSNP-1 CAPS marker (Capuozzo et al. 2017) was used in this study to determine the zucchini genotypes resistant to ZYMV. As a result of the study, 53 of them were found to be resistant to *Zym-1* allele. Of these resistant genotypes, 43 were classified as homozygous dominant (RR) and 10 as heterozygous (Rr). The remaining 55 genotypes were homozygous recessive (rr) (Table 6). These results provide important data for the genetic analysis of resistance to *Zym-1* allele. The band images are shown in Fig. 1.

The development of genetic resistance for effective control of ZYMV is an important part of plant breeding efforts. In particular, the identification of genetic markers that enhance resistance to ZYMV is considered a critical step for future breeding programmes (Capuozzo et al. 2017; Niraula and Fondong 2021). The Zymv-SNP1 primer used in the study was a critical tool for determining resistance to ZYMV. This primer has been reported to be effective in identifying genetic markers associated with ZYMV resistance (Capuozzo et al. 2017). In addition, the use of this primer increases the accuracy of

**Table 6** Resistance levels of the zucchini genotypes in the study against Zymv-1 allele

Genotype No.	Resistance	Genotype No.	Resistance	Genotype No.	Resistance	Genotype No.	Resistance
BTA 1	RR	BTA 26	RR	BTA 52	RR	BTA 85	RR
BTA 3	RR	BTA 27	RR	BTA 53	RR	BTA 87	RR
BTA 6	RR	BTA 28	RR	BTA 54	RR	BTA 91	Rr
BTA 8	Rr	BTA 32	RR	BTA 55	Rr	BTA 94	RR
BTA 9	RR	BTA 33	RR	BTA 56	Rr	BTA 96	Rr
BTA 10	RR	BTA 37	RR	BTA 59	RR	BTA 97	RR
BTA 11	RR	BTA 38	Rr	BTA 61	Rr	BTA 98	RR
BTA 12	RR	BTA 45	RR	BTA 67	RR	BTA 101	RR
BTA 15	RR	BTA 46	RR	BTA 68	RR	BTA 106	RR
BTA 17	RR	BTA 47	RR	BTA 75	Rr	BTA 107	RR
BTA 18	RR	BTA 48	RR	BTA 78	RR	BTA-110	RR
BTA 22	RR	BTA 49	Rr	BTA 81	Rr		
BTA 23	RR	BTA 50	RR	BTA 83	RR		
BTA 24	RR	BTA 51	RR	BTA 84	RR		

RR, Resistant; Rr, Heterozygous; rr, All other genotypes are resistant



**Fig. 1** Gel image of PCR products after treatment with Bgl II cutting enzyme. 4a contains genotypes between B-1 and B-33. 4b contains the image of genotypes between B-34 and B-113. B is used to indicate that the genotypes have been bulked

genetic analyses and provides a sensitive method for identifying resistance genes (Capuozzo et al. 2017; Beloti et al. 2021). The use of such molecular markers allows faster development of new resistant varieties in plant breeding and more effective strategies to control this virus (Guner et al. 2019; Niraula and

Fondong 2021; Shrestha et al. 2023). In addition, the development of genetic resistance and crop protection products to prevent the spread of ZYMV is critical for sustainable agricultural practices (Moya-Ruiz et al. 2023; Rahman 2024).

In conclusion, this molecular study was an important step in the identification of *Zym-1* allele resistant genotypes in zucchini. The identification of 53 resistant genotypes provides a basis for the identification of genetic resources to be used in future plant breeding studies and allows the development of genetic resistance strategies to control ZYMV. This will be an important contribution to the development of strategies to reduce the negative impact of ZYMV on agricultural production and increase the productivity of zucchini crops (Radouane et al. 2021; Ghanem 2023). Such studies are also needed to ensure the sustainability of agriculture and to develop effective strategies to control plant diseases (Amoroso et al. 2022; Derbalah et al. 2022). In addition, the marker we used in our study to determine genotypes resistant to ZYMV virus has been successfully used in many virus disease resistance studies (Beloti et al. 2021; Çetin et al. 2021; Shrestha et al. 2023). This marker worked successfully in our study and was effective in determining tolerant genotypes in agreement with the previous studies mentioned above.

## Conclusion

The zucchini (*Cucurbita pepo* L.) is a widely cultivated vegetable with high economic and nutritional value. This study investigated the morphology of the plant, fruit characteristics and yield, and resistance levels of genotypes against *Zym-1* allele by molecular marker. Agro-morphological characterisation refers to the evaluation of plant characteristics, growth behaviour and adaptation to environmental conditions. Determining traits like fruit characteristics and yield is crucial for increasing agricultural productivity and developing varieties resistant to stresses such as climate change. According to the results of the factor analyses carried out in the study, 12 factors were identified. In this context, when selecting according to the factors identified, we can assess whether the desired traits are suitable for the desired agricultural objectives by selecting the factors that are suitable for the selection objective. For example, if leaf characteristics are important in my selection criteria, factor 1 and 10 should be taken into account, if general fruit shape and yield are important, factors 2, 3 and 7 should be used. As a result of molecular analysis, 43 genotype were found to be homozygous dominant

(RR) and 10 genotype as heterozygous (Rr).resistant to *Zym-1* allele. The study also identified 113 promising genotypes at the S4 level for future agricultural research and breeding programmes. This valuable information provides important insights to increase the efficiency of targeted selection and improve disease management in zucchini production.

**Acknowledgements** The data collected in this study were taken from the master thesis of Abdurrahman YAŞAR (Thesis no: 796794). We thank all staff members of the R&D greenhouse of Beta Tohumculuk A.Ş. for the technical support and for supplying all facilities during the experiments.

**Author contributions** The contributions of all authors are defined as follows: study concept and design: Ö. T. and A.Y.; Analysis and interpretation of results: A.N. Ş.; preparing a draft text: A.N. Ş. and Ö. T. All authors reviewed the results and approved the final version of the article.

**Funding** Open access funding provided by the Scientific and Technological Research Council of Türkiye (TÜBİTAK).

**Data availability** No datasets were generated or analysed during the current study.

## Declarations

**Conflict of interest** The authors declare no competing interests.

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## References

- Amoroso C, Andolfo G, Capuozzo C, Donato A, Martínez C, Tomassoli L et al (2022) Transcriptomic and genomic analysis provides new insights in molecular and genetic processes involved in zucchini zymv tolerance. BMC Genomics. <https://doi.org/10.1186/s12864-022-08596-4>
- Bağcı M, Mutlu H (2014) Üç macar fiği (*Vicia pannonica* crantz.) çeşidinde farklı dozlarda gama ışını

- uygulanmasının m1 generasyonunda bazı bitkisel özellikleri üzerine etkileri. Tarla Bitkileri Merkez Araştırma Enstitüsü Dergisi. <https://doi.org/10.21566/tbmaed.10598>
- Beloti I, Maciel G, Alves I, Pereira L, Lemes E (2021) Zucchini lineages with levels of resistance to zymv and sqmv viruses. *Rev Colomb Cienc Hortíc.* <https://doi.org/10.17584/rcch.2021v15i1.10693>
- Berame J, Lawsın N, Miguel F, Chavez J (2020) Morphological variations of mangosteen fruits from luzon and mindanao islands, the Philippines. *Biodivers J Biol Divers.* <https://doi.org/10.13057/biodiv/d210729>
- Blanca J, Cañizares J, Roig C, Ziarolo P, Nuez F, Picó B (2011) Transcriptome characterization and high throughput srs and snps discovery in *Cucurbita pepo* (*Cucurbitaceae*). *BMC Genomics.* <https://doi.org/10.1186/1471-2164-12-104>
- Capuozzo C, Formisano G, Iovieno P, Andolfo G, Tomassoli L, Barbella M et al (2017) Inheritance analysis and identification of snp markers associated with zymv resistance in *Cucurbita pepo*. *Mol Breed.* <https://doi.org/10.1007/s11032-017-0698-5>
- Çetin AN, Uncu AT, Şen F, Erdeğer ŞN, Türkmen Ö (2021) Determination of resistance levels to *Fusarium oxysporum* f. sp. melonis and ZYMV and homogeneity in some melon genotypes. *Alinteri J Agric Sci* 36(1):01–06. <https://doi.org/10.47059/alinteri/V36i1/AJAS21001>
- Chinnaraja C, Kollam M, Ramsabhag A, Jayaraman J (2021) Genome characterization of *Zucchini yellow mosaic virus* infecting cucurbits reveals the presence of a new genotype in trinidad and tobago in the caribbean region. *Adv Virol* 166(6):1661–1669. <https://doi.org/10.1007/s00705-021-05048-4>
- Derbalah A, Abdelsalam I, Behiry S, Abdelkhalek A, Abdelfatah M, Ismail S et al (2022) Copper oxide nanostructures as a potential method for control of *Zucchini yellow mosaic virus* in squash. *Pest Manag Sci* 78(8):3587–3595. <https://doi.org/10.1002/ps.7001>
- Doyle JJ, Doyle JL (1987) A rapid DNA isolation procedure from small quantities of fresh leaf tissues. *Phytochemical-Bull* 19:11–15
- Emirzeoğlu C, Başak H (2020) Orta anadolu biber genotiplerinin farklı tuz konsantrasyonlarına tolerans düzeylerinin belirlenmesi. *Uluslar Tarım Yaban Hayatı Bilimleri Dergisi* 6(2):129–140. <https://doi.org/10.24180/ijaws.689347>
- Eyong O, Ekpiken E, Iso O (2021) Occurrence, distribution and identification of viruses infecting some cucurbits across major cucurbit-growing areas in cross river state, Nigeria. *Annu Res Rev Biol* 36(6):46–54. <https://doi.org/10.9734/arrb/2021/v36i630389>
- Ghanem G (2023) Antiviral activities of three *Streptomyces* spp. against *Zucchini yellow mosaic virus* (zymv) infecting squash (*Cucurbita pepo* L.) plants. *Egypt J Biol Pest Control.* <https://doi.org/10.1186/s41938-023-00750-8>
- Guner N, Pesic-VanEsbroeck Z, Rivera-Burgos L, Wehner T (2019) Screening for resistance to *Zucchini yellow mosaic virus* in the watermelon germplasm. *HortScience* 54(2):206–211. <https://doi.org/10.21273/hortsci13325-18>
- Haspolat G (2024) Farklı karanfil (*Dianthus* spp.) türlerinde morfolojik karakterizasyon. *Anadolu Ege Tarımsal Araştırma Enstitüsü Dergisi* 34:160–167. <https://doi.org/10.18615/anadolu.1465646>
- Hegde S, Hegde G, Mulgund G, Upadhy V (2014) Pharmacognostic evaluation of leaf and fruit of *Capsicum frutescens* (*Solanaceae*). *Pharmacogn J* 6(3):14–22. <https://doi.org/10.5530/pj.2014.3.3>
- JMP-18 (2018) JMP statistics software (17.00) for cluster and principal component analysis (PCA). Available at: [https://www.jmp.com/en\\_us/home.html](https://www.jmp.com/en_us/home.html). Accessed Date: 15 Sep 2024
- Karaköy T, Demirbaş A, Toklu F, Karagöl E, Uncuer D, Özkan H (2017) Ülkemizin farklı bölgelerinden toplanan bakla (*Vicia faba* L.) yerel populasyonlarının agronomik ve morfolojik karakterizasyonu. *Kahramanmaraş Sütçü İmam Üniv Tarım ve Doğa Dergisi*, 20:356–361. <https://doi.org/10.18016/ksudobil.349299>
- Kebrom TH (2017) A growing stem inhibits bud outgrowth—the overlooked theory of apical dominance. *Front Plant Sci* 8:309506. <https://doi.org/10.3389/fpls.2017.01874>
- Kondratenko S, Sergienko O, Lancaster Y (2021) Comprehensive study of selection-value lines of zucchini on the level of damage by the *Zucchini yellow mosaic virus* (ZYMV) and manifestation of other diseases. *Eureka Life Sci* 6:8–16. <https://doi.org/10.21303/2504-5695.2021.002186>
- Kurtar ES, Seymen M, Türkmen Ö, Çetin AN (2020) Işınlanmış Polen tekniği ile elde edilmiş dihaploid yazlık kabak (*Cucurbita Pepo* L.) saf hatlarının meyve ve tohum özellikleri. *Bahçe* 49(1):7–11
- Li J, Song C, He C (2019) Chinese lantern in physalis is an advantageous morphological novelty and improves plant fitness. *Sci Rep.* <https://doi.org/10.1038/s41598-018-36436-7>
- Lúcio A, Diel M, Tartaglia F, Melo P, Tischler A, Lambrecht D et al (2021) Production cycle and characterization of italian zucchini genotypes by the logistic model. *Hortic Bras* 39(3):264–271. <https://doi.org/10.1590/s0102-0536-20210304>
- Monforte A, Díaz A, Caño-Delgado A, Knaap E (2013) The genetic basis of fruit morphology in horticultural crops: lessons from tomato and melon. *J Exp Bot* 65(16):4625–4637. <https://doi.org/10.1093/jxb/eru017>
- Montero-Pau J, Blanca J, Esteras C, Martínez-Pérez E, Gómez P, Monforte A et al (2017) An SNP-based saturated genetic map and QTL analysis of fruit-related traits in zucchini using genotyping-by-sequencing. *BMC Genomics.* <https://doi.org/10.1186/s12864-016-3439-y>
- Moya-Ruiz C, Gómez P, Juárez M (2023) Occurrence, distribution, and management of aphid-transmitted viruses in cucurbits in Spain. *Pathogens* 12(3):422. <https://doi.org/10.3390/pathogens12030422>
- Nacar Ç, Aras V, Denli N, Keleş D (2011) Morphological characterization and determination of relationship among squash (*Cucurbita pepo* L.) lines. *Alatarm* 10(1):13–18
- Nakip M (2003) Pazarlama araştırmaları teknikler ve (SPSS destekli) uygulamalar, Seçkin Yayıncılık, 1. Baskı, Ankara.
- Niraula P, Fondong V (2021) Development and adoption of genetically engineered plants for virus resistance: advances, opportunities and challenges. *Plants* 10(11):2339. <https://doi.org/10.3390/plants10112339>
- Ntuli N, Madakadze R, Zobolo A (2016) Ethno-botanical knowledge on diversity of *Cucurbita* landraces grown in northern Kwazulu-Natal, South Africa. *Univers J Plant*

- Sci 4(3):35–41. <https://doi.org/10.13189/ujps.2016.040302>
- Okçu M (2016) Gümüşhane ve çevresinde bazı önemli tıbbi ve aromatik bitkilerin özelliklerinin belirlenmesi. Gümüşhane Üniv Fen Bilimleri Enstitüsü Dergisi. <https://doi.org/10.17714/gufbed.2016.06.001>
- Olatunji TL, Afolayan AJ (2018) Contributions to the classification of *Capsicum annum* L. and *Capsicum frutescens* L. in West Africa using morphological traits. Not Bot Horti Agrobo Cluj-Napoca 47(1):135–142. <https://doi.org/10.15835/nbha47111204>
- Öztürk H, Dönderalp V, Bulut H, Korkut R (2022) Morphological and molecular characterization of some pumpkin (*Cucurbita pepo* L.) genotypes collected from Erzincan province of Turkey. Sci Rep. <https://doi.org/10.1038/s41598-022-11005-1>
- Pachner M, Paris H, Winkler J, Lelley T (2015) Phenotypic and marker-assisted pyramiding of genes for resistance to *Zucchini yellow mosaic virus* in oilseed pumpkin (*Cucurbita pepo*). Plant Breed 134(1):121–128. <https://doi.org/10.1111/pbr.12219>
- Pereira M, Alexandre M, Chaves A, Souza A, Bernacci L, Nagai A et al (2021) Endemic atlantic forest species of Caryophyllales as inhibitors of viral infection in zucchini. Hortic Bras 39(2):146–154. <https://doi.org/10.1590/s0102-0536-20210204>
- Perez-Moro C, D'Esposito D, Pérez-de-Castro A, Ercolano M, Capuozzo C, Guadagno A (2024) Comparative analysis of *Cucurbita pepo* genomes shed light in agronomic traits variation. <https://doi.org/10.21203/rs.3.rs-4162066/v1>
- Priori D, Barbieri RL, Mistura CC, Villela JCB (2018) Caracterização morfológica de variedades crioulas de abóboras (*Cucurbita maxima*) do sul do Brasil. Rev Ceres 65:337–345. <https://doi.org/10.1590/0034-737X201865040006>
- Radouane N, Ezrari S, Belabess Z, Tahiri A, Tahzima R, Massart S et al (2021) Viruses of cucurbit crops: current status in the mediterranean region. Phytopathol Mediterr 60(3):493–519. <https://doi.org/10.36253/phyto-12340>
- Rahman A (2024) When an intruder comes home: gm and ge strategies to combat virus infection in plants. Agriculture 14(2):282. <https://doi.org/10.3390/agriculture14020282>
- Şahin Ö (2023) Evaluation of studies conducted to investigate the effectiveness of plant material in noise control. Düzce Üniv Orman Fakültesi Ormançılık Dergisi 19(1):1–20. <https://doi.org/10.58816/duzceod.1245307>
- Şavkan AN, Türkmen Ö (2023) Morphological characterization and selection in some summer squash (*Cucurbita pepo* L.) genotypes. Yuzuncu Yıl Univ J Agric Sci 33(4):665–674. <https://doi.org/10.29133/yyutbd.1332485>
- Şavkan AN, Başak H, Türkmen Ö (2024) Morphological characterization of some capia pepper (*Capsicum annum* L.) genotypes. Kahramanmaraş Sütçü İmam Üniv Tarım Ve Doğa Dergisi 27(6):1332–1342. <https://doi.org/10.18016/ksutarimdog.a.vi.1440798>
- Şavkan AN, Dal Canbar Y, Türkmen Ö (2025a) Identification and selection of genetic diversity of some selected summer squash (*Cucurbita pepo* L.). Yuzuncu Yıl Univ J Agric Sci 35(1):121–134. <https://doi.org/10.29133/yyutbd.1567738>
- Şavkan AN, Başak H, Uncu AT, Türkmen Ö (2025b) Morphological characterization and molecular marker-assisted selection for resistance to *Tobacco mosaic virus* (TMV) and *Tomato spotted wilt virus* (TSWV) in S2 population of capia pepper (*Capsicum annum* L.). Genet Resour Crop Evol 72:767–782. <https://doi.org/10.1007/s10722-024-02013-3>
- Sawazaki H, Yuki V, Ortiz M, Banja W, Marubayashi J, Fonseca K et al (2018) Markers for rapid evaluation of virus resistance for tyldv in tomato, zymv and prsv-w in zucchini and lmv in lettuce and hybrid seeds in pumpkin. Am J Plant Sci 9(11):2205–2216. <https://doi.org/10.4236/ajps.2018.911159>
- Shrestha S, Tobias C, Bhandari H, Bragg J, Nayak S, Goddard K et al (2023) Mapping quantitative trait loci for biomass yield and yield-related traits in lowland switchgrass (*Panicum virgatum* L.) multiple populations. G3 Genes Genome Genet. <https://doi.org/10.1093/g3journal/jkad061>
- Silva NCD, Queiróz MAD, Barbosa BL (2024) Evaluation and morpho-agronomic characterization of pumpkin accessions from the semiarid region of the northeast of Brazil. Rev Caatinga 37:e11614
- Tohamy M, Kheder A, Sulaiman T (2018) Biological, serological and molecular characterization of egyptian *Zucchini yellow mosaic virus* isolate infecting squash plants in fayoum governorate. Zagazig J Agric Res 45(6):2377–2388. <https://doi.org/10.21608/zjar.2018.47880>
- Upov (2006). *Cucurbita pepo* L. International union for the protection of new varieties of plants. Available at: <https://www.upov.int/portal/index.html.en>. Erişim Tarihi: 15 May 2024
- Xanthopoulou A, Montero-Pau J, Kissoudis C, Blanca J, Picó B, Tsaballa A et al (2019) Whole-genome resequencing of *Cucurbita pepo* morphotypes to discover genomic variants associated with morphology and horticulturally valuable traits. Hortic Res. <https://doi.org/10.1038/s41438-019-0176-9>
- Yılmaz H, Kökten K (2019) Kadmiyum (cd) uygulamasının tane sorgumda (*Sorghum bicolor* L.) bazı morfolojik özellikler üzerine etkisinin belirlenmesi. Türk Tarım Doğa Bilimleri Dergisi 6(3):447–456. <https://doi.org/10.30910/turkjans.595347>

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