Scientific Article

Powdery mildew resistance in pumpkin sub-accessions from the vegetable germplasm bank

Resistência ao oídio em subacessos de abóbora conservado no banco de germoplasma de hortaliças

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ABSTRACT – Powdery mildew is one of the most challenging diseases for pumpkin and squash production, as it can cause significant losses in fruit yield and quality. The objective of this study was to evaluate sub-accessions of *Cucurbita moschata* from the Vegetable Germplasm Bank of the Federal University of Viçosa (BGH-UFV), in Viçosa, Minas Gerais, Brazil, for resistance to powdery mildew (*Podosphaera xanthii*) in young and adult plants. The physiological race of *P. xanthii* used in the experiments was identified using nine differentials. Eighty-seven S_0 sub-accessions were evaluated, along with two commercial cultivars of *C. moschata* as controls. A completely randomized experimental design with three replications was used to evaluate young plants, whereas Federer's augmented block design was used to evaluate adult plants, with seven replications as controls. Inoculation consisted of depositing spores and allowing contact between diseased and healthy plants. Evaluations were based on a subjective rating scale, with estimation of the relative area under the disease progress curve. The *P. xanthii* used in the experiments was identified as race 2US, making this study the first report of this variant in Minas Gerais. A significant difference was found among the *C. moschata* sub-accessions regarding their response to powdery mildew, indicating the existence of genetic variability and allowing for the selection of genotypes. Fifteen sub-accessions of the evaluated germplasm were identified as promising sources for developing lines resistant to powdery mildew.

Keywords: Cucurbit. Pre-breeding. Genetic resources. Plant resistance.

RESUMO – O oídio é uma das doenças que mais causam dificuldades para a produção de abóboras, podendo ocasionar quedas drásticas na produtividade e qualidade dos frutos. O objetivo deste trabalho foi avaliar subacessos de *Cucurbita moschata* conservados no Banco de Germoplasma de Hortaliças da Universidade Federal de Viçosa (BGH-UFV) quanto à resistência ao oídio, em plantas jovens e adultas. A identificação da raça fisiológica do oídio utilizada nos ensaios foi feita por nove diferenciadoras. Foram avaliados 87 subacessos S_0 e dois cultivares comerciais como testemunhas. O delineamento experimental foi inteiramente casualizado para avaliação de plantas jovens, com três repetições, e o delineamento de blocos aumentados de Federer em plantas adultas, com sete repetições para testemunhas. A inoculação foi feita a partir da deposição de esporos e do contato entre plantas doentes e plantas sadias. A avaliação foi feita com base em escala subjetiva de notas, e foi estimada a área abaixo da curva de progresso da doença relativa. A raça fisiológica de *Podosphaera xanthii* utilizada nos ensaios foi identificada como a raça 2US, primeiro relato dessa variante em Minas Gerais e no Brasil. Foi constatada diferença significativa entre os subacessos quanto à reação ao oídio, indicando a existência de variabilidade genética, permitindo a seleção de genótipos. No germoplasma avaliado, foram identificados 15 subacessos como fontes promissoras para o desenvolvimento de linhagens de abóbora resistentes ao oídio.

Palavras-chave: Cucurbita. Pré-melhoramento. Recursos genéticos. Resistência de plantas.

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INTRODUCTION

Powdery mildew is one of the most challenging diseases for the production of squash and pumpkins (HOLDSWORTH et al*.*, 2016), as it has the potential to cause severe losses in fruit yield and quality by reducing photosynthetic capacity, inhibiting plant growth, and inducing early leaf loss. Its causal agents are several fungal species of the family Erysiphaceae; however, *Podosphaera xanthii* is the most significant species in Brazil (McGRATH, 2017). Approximately 50 physiological races of this pathogen have been identified, with races 1 and 2 being the most important in Brazil (RABELO et al., 2017). The genetic variability of *P. xanthii* populations makes physiological race identification valuable information for breeding programs focused on developing powdery mildew-resistant cultivars.

P. xanthii is an obligate parasite whose survival between crop seasons depends on infecting a large number of species from several families; therefore, it has a wide range of hosts (PÉREZ-GARCÍA et al., 2009). Chemical control is the most commonly used method against powdery mildew, consisting of applying contact or systemic fungicides. However, developing powdery mildew-resistant squash and pumpkin cultivars is of great agronomic interest, as disease control

through genetic resistance is one of the most effective and sustainable tools for disease management (HOLDSWORTH et al., 2016).

Identifying resistance sources should be one of the first steps in developing resistant cultivars. The characterization and evaluation of germplasm conserved in banks are essential for identifying genotypes with traits of interest for genetic improvement.

The Vegetable Germplasm Bank of the Federal University of Viçosa (BGH-UFV), Viçosa, Minas Gerais, Brazil, is one of the largest germplasm banks of Cucurbitaceae species in Brazil, housing promising genetic resources for improving economically important traits in squash and pumpkin genotypes. It contains more than 500 accessions, approximately 273 of which belong to to *Cucurbita moschata.* This species is likely the most polymorphic among cucurbits, which has contributed to the identification of several sources of resistance to significant diseases for Cucurbitaceae species (PARIS, 2017).

In this context, the present study aimed to identify the physiological race of the fungal agent causing powdery mildew naturally occurring in Viçosa, specifically in the region known as Zona da Mata of Minas Gerais, and to evaluate sub-accessions of *C. moschata* from BGH-UFV for resistance to powdery mildew in young and adult plants.

MATERIAL AND METHODS

Germplasm

A total of 87 S_0 sub-accessions of *Cucurbita moschata* from the Vegetable Germplasm Bank of the Federal University of Viçosa (BGH-UFV), Viçosa, Minas Gerais, Brazil, were evaluated (Table 1). These sub-accessions originated from several regions of Brazil: three from Bahia (BA), seven from the Federal District (DF), three from Espírito Santo (ES), four from Goiás (GO), 22 from Minas Gerais (MG), two from Paraná (PR), one from Rio de Janeiro (RJ), and 45 from São Paulo (SP).

Table 1. *Cucurbita moschata* sub-accessions (S_0 generation) from the Vegetable Germplasm Bank (BGH) of the Federal University of Viçosa assessed for resistance to powdery mildew, with their respective Brazilian state origins.

S_0 sub-accessions	State origin
BGH-95, BGH-117, BGH-5649	Bahia
BGH-315, BGH-5638, BGH-5639, BGH-5616, BGH-5624A, BGH-5624B, BGH-5630B	Distrito Federal
BGH-1945A, BGH-1945B, BGH-1945C	Espírito Santo
BGH-6593, BGH-6594, BGH-6595, BGH-6587	Goiás
BGH-1004, BGH-5051, BGH-5248, BGH-5694, BGH-6155, BGH-305A, BGH-7907, BGH-7908, BGH-4454, BGH-4590A, BGH-4590B, BGH-4610A, BGH-4681A, BGH-4681B, BGH-4681C, BGH-5224A, BGH-5224B, BGH-5224C, BGH-5659A, BGH-5659B, BGH-6117A, BGH-6117B	Minas Gerais
BGH-7219A, BGH-7219B	Paraná
BGH-291	Rio de Janeiro
BGH-5442, BGH-5451, BGH-5466, BGH-5497, BGH-5528, BGH-5541, BGH-5551, BGH-5552, BGH-5597, BGH-5603, BGH-5453A, BGH-5453B, BGH-5455A, BGH-5456A, BGH-5456B, BGH-5456C, BGH-5472A, BGH-5472C, BGH-5473A, BGH-5473B, BGH-5485A, BGH-5485B, BGH-5493A, BGH-5493B, BGH-5494A, BGH-5494B, BGH-5530A, BGH-5544A, BGH-5544B, BGH-5548A, BGH-5548B, BGH-5554A, BGH-5554B, BGH-5556A, BGH-5560A, BGH-5591A, BGH-5591B, BGH-5591C, BGH-5596A, BGH-5596C, BGH-5598A, BGH-5598B, BGH-5598C, BGH-5606A, BGH-5606B	São Paulo

All evaluated genotypes were obtained through self-fertilizations. This collection contains genotypes with traits of agronomic and nutritional importance, including growth habit, fruit and seed yields, and total pulp carotenoid content (GOMES et al., 2020). Two commercial cultivars were used as controls: Maranhão (Feltrin Sementes) and Tetsukabuto Takayama (Agristar do Brasil).

Experimental site and conditions

Two experiments were conducted at the Horta Velha Education, Research, and Extension Unit (UEPE) of the UFV Department of Agronomy, Viçosa, Minas Gerais (20°45'14"S, 42°52'53"W, and 648.74 m altitude), one with young plants and the other with adult plants.

The experiment with young plants was conducted in a vegetable seed laboratory from August 21, 2020, to October 9, 2020, with a mean temperature of 20±3 °C and relative air humidity ranging from 57% to 94%. Prior to evaluations, seedlings intended for assessment at the juvenile stage were produced in a protected environment in 500-mL polystyrene cups using a commercial substrate (MecPlant – Horta 2 HS) and transferred to the vegetable seed laboratory 30 days after sowing (DAS).

A field experiment with adult plants was conducted in a 0.46-hectare area from August 21, 2020, to December 28, 2020, with a mean temperature of 21±3 °C, relative air humidity ranging from 57% to 95%, and an accumulated rainfall depth of 617.8 mm (Figure 1).

Seedlings intended for field evaluations were produced in 280-mL tube pipes using a commercial substrate (MecPlant – Horta 2 HS) and transplanted to the field at 34 DAS, using a dense spacing of 3 m between plants and 3 m between rows to favor disease dissemination in the field.

Intertwined plants were combed to avoid difficulties in individual evaluation. Plants in the field were irrigated individually ay their base using a hose to avoid wetting their aerial parts and to prevent interference with disease development. No phytosanitary treatment was applied.
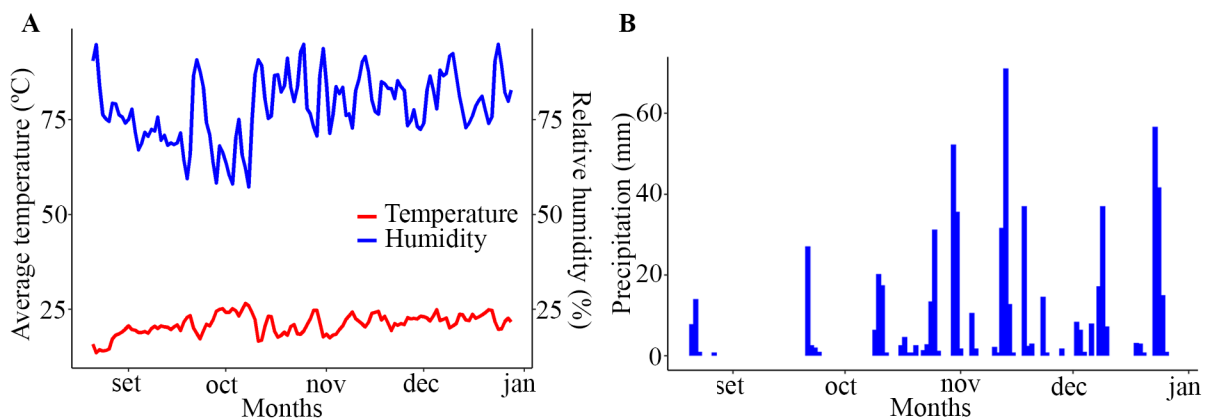
Figure 1. Climate data from August 21 to December 28, 2020, collected by a meteorological station in Viçosa. (A) Mean temperature (°C) and relative air humidity (%). (B) Rainfall depth (mm). Viçosa, MG, Brazil. (INMET, 2020).

Experimental design

A completely randomized design with three replications was used for the experiment with young plants. Each plot consisted of one plant; three fully expanded leaves were evaluated per plant. Eleven of the 87 sub-accessions sown did not have sufficient germination and were used evaluated only in the field.

The field experiment was conducted using Federer's augmented block design, with seven replications for the controls. Controls were randomly distributed in each of the seven blocks, while regular genotypes were divided among all blocks, with 13 regular treatments per block. Each plot contained five plants, but only the three central plants were evaluated.

Obtaining, maintaining, and identifying *Podosphaera xanthii* race

The pathogen was collected from *C. moschata* plants exhibiting symptoms typical of powdery mildew at UEPE. It was confirmed through morphological characterization by observing fibrosin bodies in the conidia, which are characteristic of *P. xanthii*, under an optical microscope.

The pathogen was maintained on seedlings of the cultivar Maranhão, which were kept in a cage at the UEPE warehouse under ambient temperature and humidity conditions (Figure 2). The plants were obtained by sowing in 500-mL disposable polystyrene cups using a commercial substrate (MecPlant; Horta 2 HS). New seedlings that had reached at least the one fully expanded leaf stage were transferred to the breeding cage containing plants colonized by powdery mildew. This process was performed every four to five weeks as the host plants died. Inoculation inside the cage was performed manually by depositing spores from colonized leaves onto healthy seedlings and by allowing contact between leaves and branches. Thus, a constant source of inoculum was maintained to ensure pathogen inoculation for the experiments evaluating plant responses to powdery mildew.

Figure 2. Powdery mildew cultivation for experiments. (A) *Cucurbita moschata* leaf collected in the field exhibiting typical symptoms of powdery mildew. (B) Development of *C. moschata* seedlings for subsequent inoculation. (C) Cage where host plants were maintained. (D) Beginning of colonization on cotyledons. (E) Host plants inside the cage. (F) Detail of a typical symptom on a diseased leaf.

The physiological race of the cultured *P. xanthii* was identified using melon (*Cucumis melo*) cultivars (Edisto47, Hale's Best Jumbo, PMR45, Nantais Oblong, PI124111, PI414723, PMR5, Védrantais, and WMR29), which serves as differentials of powdery mildew races. This set of differential cultivars allows for the discrimination of *P. xanthii* races 1, 2 (with variants 2F and US), 3, 4, 5, and 3.5 (Table 2).

Table 2. Responses of nine differential melon (*Cucumis melo*) cultivars to physiological races of *Podosphaera xanthii*.

Differential	*P. xanthii* races							
	0	1	2F	2US	3	4	5	3.5
Hale's Best Jumbo	S	S	S	S	S	S	S	S
Véndrantais	R	S	S	S	S	S	S	S
Nantais Oblong	R	S	S	S	S	S	S	S
PMR45	R	R	S	S	S	S	S	S
PMR5	R	R	R	R	S	R	R	S
WMR29	R	R	R	H	R	S	S	S
Edisto47	R	R	R	S	R	R	S	S
PI414723	R	R	R	S	R	R	R	R
PI124111	R	R	R	R	R	R	R	S

R = resistant, H = heterogeneous, and S = susceptible. Adapted from Rabelo et al. (2017).

Three plants of each differential cultivar were inoculated at 25 DAS. Evaluations were conducted 15 days after inoculation (DAI) using a subjective 1-to-4 rating scale, following the methodology described by Yuste-Lisbona et al. (2010) for melons: 1 – no sporulation; 2 – low sporulation level; 3 – moderate sporulation level; and 4 - high sporulation level. Based on these scores, the differentials cultivars were classified as resistant (scores 1 and 2) or susceptible (scores 3 and 4).

Inoculation and evaluation of germplasm

Young plants were inoculated at 30 DAS by manually depositing spores with a light sweep using a brush (0.5-inch bristles) and allowing contact between host plants and experimental healthy plants. One symptomatic plant completely colonized (leaves and branches covered by conidia and mycelium), was used as the source of inoculum for every 15 healthy plants.

Young plants with three expanded true leaves were visually evaluated at 4, 7, 9, 11, 13, and 19 DAI. Powdery mildew symptoms in the genotypes were assessed using a subjective 1-to-7 rating scale, characterized by an ascending order of disease severity (Figure 3), following the methodology described by Luitel et al. (2016) for *Cucurbita* spp.
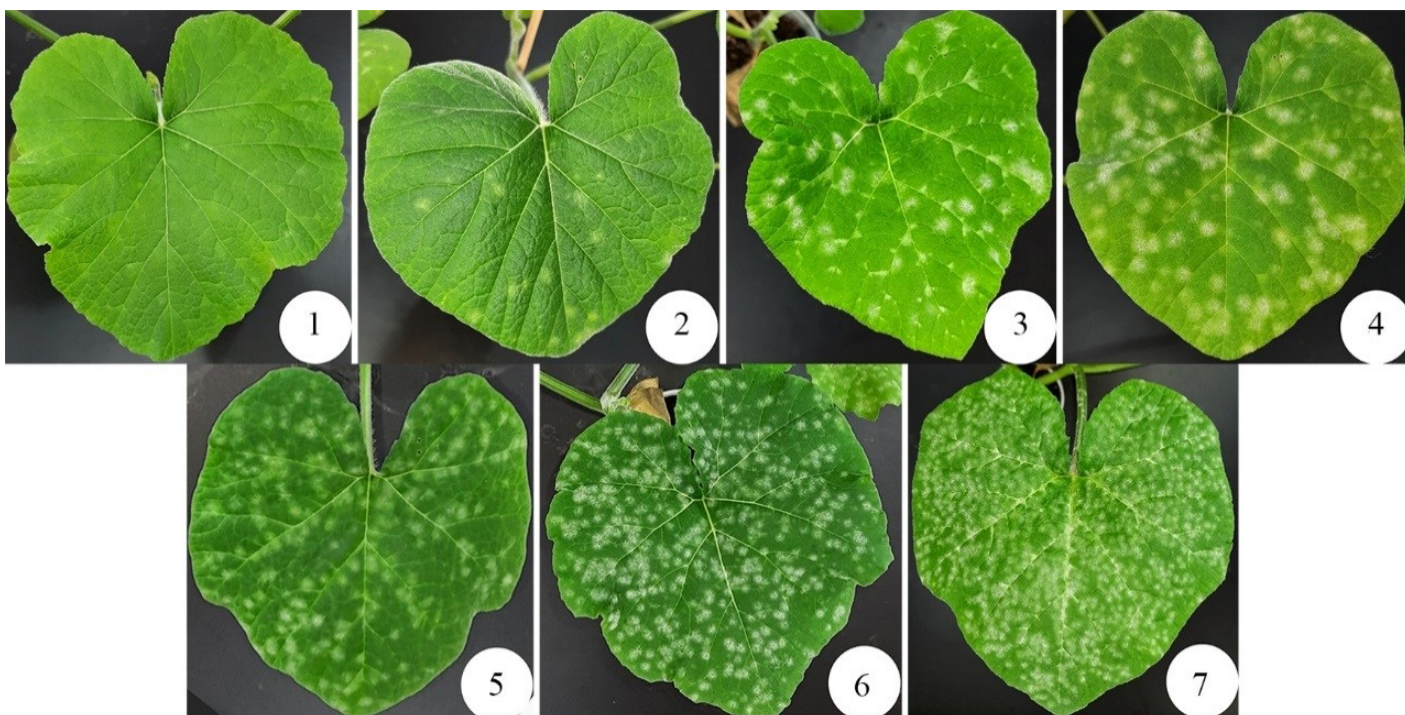
Figure 3. Powdery mildew severity (1-to-7 scale) in leaves of *Cucurbita moschata* sub-accessions: 1 (zero), 2 (≥ 10%), 3 (≥ 20%), 4 (≥ 40%), 5 (≥ 50%), 6 (≥ 70%), and 7 (≥ 90%).

The field experiment (adult plants) was conducted using the same methodology as the young-plant experiment, except for inoculation, which was performed when the plants were already established in the field (30 days after transplanting) and repeated the following week. The entire plant was evaluated at 18, 25, 32, 39, 46, 53, 60, and 67 DAI. Plants were grown until fruits and seeds were obtained through self-fertilization.

The obtained data were used to estimate the area under the disease progress curve (AUDPC) using Equation 1 (LUITEL et al., 2016):

$$\text{AUDPC} = (T_{i+1} - T_i) \times \left(\frac{D_{i+1} + D_i}{2} \right), \tag{1}$$

where T is the time of observation (days) and D is the estimated percentage of area infected by the disease at the ith observation.

The relative AUDPC (rAUDPC) is a summary measure of the accumulated disease evaluation, ranging from zero to one. The rAUDPC was calculated by summing the estimated AUDPC for each interval and dividing by the total number of days multiplied by 100, using Equation 2 (LUITEL et al., 2016):

$$\text{rAUDPC} = \frac{\sum (T_{i+1} - T_i) \times \left(\frac{D_{i+1} + D_i}{2} \right)}{(T_{\text{Total}}) \times 100}, \tag{2}$$

where T is the time (days) at the ith observation, D is the estimated percentage of area infected by the disease at the ith observation, and T_{Total} is the total time of observation (days).

Statistical analyses

The data were subjected to tests for normality and homocedasticity assumptions and then analyzed using analysis of variance (ANOVA) at a 1% significance level to evaluate the effect of genotypes and estimate the coefficients of genetic variation (CVg) and environmental variation (CVe), as well as broad-sense heritability (h^2), using Equations 3, 4, and 5, respectively:

$$\text{CVg}(\%) = \frac{\sqrt{\sigma_g^2}}{X_0} \times 100, \tag{3}$$

$$\text{CVe}(\%) = \frac{\sqrt{\sigma^2}}{X_0} \times 100, \tag{4}$$

$$h^2(\%) = \frac{\sigma_g^2}{\sigma_f^2} \times 100, \tag{5}$$

where σ_g^2 is the genetic variance, σ^2 is the residual variance, σ_f^2 is the phenotypic variance, and X_0 is the overall mean.

Genotypes were classified based on the mean rAUDPC as resistant (mean ≤ 0.20) moderately resistant (0.21 ≤ mean ≤ 0.40), and susceptible (> 0.40) according to the classification proposed by Luitel et al. (2016). Additionally, the responses of young and adult plants were correlated using Spearman's rank correlation.

The disease progress curve was developed for all genotypes, controls, and sub-accessions selected in young plants between 4 and 19 DAI, and in adult plants between 18 and 67 DAI. This provides a comparative perspective of disease evolution over the corresponding time intervals.

All statistical analyses were performed using Genes (CRUZ, 2016) and R software (R CORE TEAM, 2023).

RESULTS AND DISCUSSION

Variability of the pathogen *Podosphaera xanthii*

The physiological race of *Podosphaera xanthii* identified was 2US, based on the responses observed in the differential melon cultivars. The differential cultivar PI414723 was classified as susceptible, which is sufficient to confirm this physiological race. Furthermore, the other differential cultivars showed responses consistent with this finding: Hale's Best Jumbo, Védrantais, Nantais Oblong, Edisto47, and PMR45 were classified as susceptible, while PI124111, PMR5, and WMR29 were classified as resistant. WMR29 could have shown a heterogeneous response to race 2US; however, no susceptibility was observed in this differential cultivar. The susceptibility of PI414723, along with the responses of the other differentials, including the resistance of PMR5 (Figure 4), confirmed the physiological variant US.

Race 2 is among the most frequently reported physiological races of powdery mildew in Brazil. It was first identified in the 2000s in São Paulo (RABELO et al., 2017). Subsequently, it was identified in the Federal District (REIS; BUSO, 2004), followed by the states of Pernambuco and Rio Grande do Norte in 2005 (RABELO et al., 2017) and Paraná, in 2006 (FAZZA, 2006).

Few studies surveying *P. xanthii* races in Minas Gerais are found in the literature. Reis and Buso (2004) reported the occurrence of race 1 in Minas Gerais. Fazza (2006) surveyed races of isolates obtained in Minas Gerais and identified race 2F in pumpkin, which is the only report of this variant for this crop.

Most surveys identifying *P. xanthii* race 2 in Brazil indicate that the variants involved were not previously characterized due to the group of differentials used. Therefore, the present study represents the first report of *Podosphaera xanthii* race 2US in Minas Gerais and Brazil.

Moreover, a comprehensive survey is necessary to identify local physiological races, particularly for decision-making in breeding programs focused on improving disease control efficacy through resistance and to monitor population dynamics of this pathogen.

Figure 4. Response patterns of melon (*Cucumis melo*) differential cultivars to powdery mildew: cultivars PI414723 (susceptibility) and PMR5 (resistance).

Reactions of *Cucurbita moschata* sub-accessions to *Podosphaera xanthii* race 2US

Analysis of variance (ANOVA) indicated a significant effect of genotype on the response to *P. xanthii* in both young and adult *C. moschata* plants (Table 3). This indicates the presence of genetic variance and, therefore, the potential for

selecting agronomically superior genotypes for resistance to powdery mildew. Genetic variability among the available germplasm is fundamental for the genetic improvement of any plant species. Greater variability increases the potential for selecting superior genotypes (CRUZ; REGAZZI; CARNEIRO, 2012).

Table 3. Analysis of variance for relative area under the disease progress curve (AUDPC) in *Cucurbita moschata* sub-accessions (S$_0$ generation) from the Vegetable Germplasm Bank.

Relative AUDPC					
Young plants			Adult Plants		
SV	DF	Mean square	Adjusted SV	DF	Mean square
				6	0.002926**
Genotypes (G)	79	0.009632**	G blocks	88	0.004303**
Residual	160	0.003395	Residual	6	0.000201
σ_g^2	0.002079		σ_g^2	0.002619	
σ^2	0.001132		σ^2	0.000224	
CVg(%)	20.86		CVg(%) (%(earing%)	25.20	
CVe(%)	26.65		CVe(%)	6.20	
CVg/CVe	0.78		CVg/CVe	3.81	
h²(%)	64.75		h²(%)	93.57	
Mean	0.22		Mean	0.23	

SV = source of variation; DF = degrees of freedom; σ_g^2 = genetic variance; σ^2 = residual variance; CVg = coefficient of genetic variation; CVe = coefficient of environmental variation; h^2 = broad-sense heritability. CVg/CVe = CVg-to-CVe ratio. ** 1% significance level.

Few studies have evaluated the responses of sub-accessions from BGH-UFV to various diseases; therefore, the findings of the present study provide valuable information regarding the use of these genotypes in breeding programs as potential sources of resistance. Similarly, Moura et al. (2005) identified *Cucurbita* sp. accessions resistant to Zucchini yellow mosaic virus (ZYMV) while characterizing 37

accessions from BGH-UFV.

The coefficient of genetic variation (Cvg) in the experiment with young plants was 20.86%, lower than that found for adult plants (25.20%) (Table 3). Notably, higher estimated coefficients of genotypic variation indicate greater potential for genetic improvement (CRUZ; REGAZZI; CARNEIRO, 2012). The coefficient of environmental

variation (CVe) was 26.65% for young plants and 6.20% for adult plants, indicating greater environmental influence on young plants. Therefore, increasing the number of replications is recommended in future trials with young plants to mitigate the environmental effect.

Broad-sense heritability (h^2) is an important parameter for plant genetic improvement, as it expresses the relationship between genotypic and phenotypic variance, representing the proportion of phenotypic variation attributable to genetic factors (CRUZ; REGAZZI; CARNEIRO, 2012). Young and adult plants exhibited h^2 values of 64.75% and 93.57%, respectively. Kavya and Shivapriya (2019) studied *Cucumis melo* plants and reported a heritability of 71% for resistance to powdery mildew under field conditions. Shashikumar, Pitchaimuthu, and Rawal (2016) reported heritability ranging from 72% to 97% for *C. melo* plants under protected environmental conditions and from 74% to 93% for field-grown plants. Sharma, Kumar, and Sharma (2017) evaluated the responses of *Cucumis sativus* to powdery mildew and obtained a heritability of 75%. Tetteh, Wehner, and Davi (2013) reported heritability values of 71% for resistance to powdery mildew in leaves and and 79% in branches of *Citrullus lanatus*.

The high heritability values found in the present study, especially for adult plants, suggest that the trait was can be effectively transferred to subsequent generations through selection using less complex breeding methods. Furthermore, the CVg-to-CVe ratio (CVg/CVe) for adult plants was 3.81, higher than 1. Heritability greater than 80%, combined with a CVg/CVe higher than 1, indicates satisfactory selection gains. A CVg/CVe > 1 suggests the predominance of genetic effects over environmental effects, consistent with the hypothesis that superior genotypes with resistance to powdery mildew can be obtained using simpler breeding methods.

The evaluated *C. moschata* genotypes were classified as resistant and moderately resistant, with rAUDPC values ranging from 0.11 to 0.41 in young plants and from 0.10 to 0.38 in adult plants. No genotype was classified as susceptible under the experimental conditions of this study (Table 4). This result may be attributed to less favorable environmental conditions for powdery mildew development, mainly in the field. The mean temperature was low (21 °C) and the mean relative humidity was high (78.36%) during the experimental period, with frequent rainfall beginning in October 2020 (Figure 1).

These environmental conditions ultimately affect disease development and spread, as rainfall washes pathogen structures from the host leaf surface (BEDENDO, 2018). However, the cultivar Tetsukabuto Takayama (control) and sub-accessions such as BGH-305A, BGH-5453A, BGH-5624B, and BGH-5630B exhibited high susceptibility in the field, with rapid disease progression, nearly completely colonization of aerial parts, high spore production, chlorosis, necrosis, and significant leaf loss at 67 DAI. Additionally, the classification proposed by Luitel et al. (2016), although efficiently representing the response of young *C. moschata* plants to powdery mildew, may not have been appropriate for field experiments over extended periods, as in the present study.

Sub-accession BGH-5591C exhibited the lowest rAUDPC value among the genotypes evaluated at the juvenile stage, whereas the control cultivar Tetsukabuto Takayama exhibited the highest value. The highest rAUDPC value for adult plants was also found for the cultivar Tetsukabuto Takayama, whereas accession BGH-5598A exhibited the lowest value (Table 4). Similarly, Ferreira et al. (2016) reported high susceptibility of Tetsukabuto Takayama to diseases such as alternariasis, anthracnose, mildew, and powdery mildew while evaluating 58 *C. moschata* genotypes.

In contrast to the highest rAUDPC values obtained for this control genotype in both experiments, the Spearman correlation coefficient among the other genotypes was 0.12 (Table 4). This low correlation suggests that the response of *C. moschata* young plants to powdery mildew is not necessarily associated to the response of adult plants to powdery mildew.

Forty-four sub-accessions (57%) had consistent classification in both experiments (young and adult plants), with 17 sub-accessions classified as resistant and 27 classified as moderately resistant. Prasanth et al. (2019), studied *Momordica charantia,* another species in the family Cucurbitaceae, and reported that resistance to powdery mildew is genotype-dependent throughout development stages, as also observed in the present study. Different resistance levels to powdery mildew expressed at specific plant development stages have also been reported in *Helianthus tuberosus*, *Triticum aestivum*, and *Oryza sativa* plants (JUNSOPA et al., 2017), with variations according to crop species, pathogens, and environmental conditions during evaluations. Information on the association between resistance in young and adult plants of *C. moschata* may assist plant breeders in accelerating breeding programs, as early selection is more efficient.

BGH-117, BGH-315, BGH-1004, BGH-1945A, BGH-4610A, BGH-5556A, BGH-5596A, BGH-5598B, and BGH-5616C were among the most promising sub-accessions classified as resistant in both experiments, showing a mean rAUDPC of 0.16. BGH-95, BGH-5552, BGH-5649, BGH-5472A, BGH-5472C, and BGH-5596C generated young plants that were classified as moderately resistant (rAUDPC = 0.23); however, their adult plants were classified as resistant (rAUDPC = 0.14), thus identifying them as promising genotypes. Similarly, Gomes et al. (2020) evaluated 91 accessions from BGH-UFV and reported potential for high seed and oil yields in accessions BGH-4610A and BGH-5472A and high carotenoid content in BGH-5598, emphasizing the potential of this germplasm for multiple purposes, including resistance to powdery mildew, as observed in the present study.

Disease progress curves were generated for all evaluated sub-accessions, the controls, and the selected resistant sub-accessions (Figure 5) based on the percentage of diseased leaf area recorded during each evaluation. Disease progress curves differed among these groups over time at both phenological stages. Disease progression was similar for young and adult plants during the initial evaluations; however, it differed in the subsequent evaluations as the disease progressed.

Table 4. Mean values of relative area under the disease progress curve (rAUDPC) and response to powdery mildew in young and adult plants of *Cucurbita moschata* sub-accessions (S_0 generation) from the Vegetable Germplasm Bank (BGH) of the Federal University of Viçosa, and in control plants (commercial cultivars Maranhão and Tetsukabuto Takayama).

Genotypes	Young		Adult		Genotypes	Young		Adult	
Maranhão	0.40	MR	0.25	MR	5455A	0.25	MR	0.31	MR
Tetsukabuto Takayama	0.41	MR	0.38	MR	5456A	0.22	MR	0.29	MR
BGH-95	0.25	MR	0.15	R	5456B	0.14	R	0.23	MR
BGH-117	0.14	R	0.15	R	5456C	0.14	R	0.22	MR
BGH-291	-	-	0.29	MR	5472A	0.23	MR	0.13	R
BGH-315	0.18	R	0.19	R	5472C	0.17	R	0.20	R
BGH-1004	0.14	R	0.16	R	5473A	-	-	0.16	R
BGH-5051	0.17	R	0.28	MR	5473B	0.16	R	0.13	R
BGH-5248	0.16	R	0.22	MR	5485A	0.17	R	0.20	R
BGH-5442	0.23	MR	0.22	MR	5485B	0.25	MR	0.22	MR
BGH-5451	0.30	MR	0.33	MR	5493A	0.20	R	0.20	R
BGH-5466	-	-	0.19	R	5493B	-	-	0.15	R
BGH-5497	0.23	MR	0.19	R	5494A	0.19	R	0.28	MR
BGH-5528	0.23	MR	0.28	MR	5494B	0.26	MR	0.21	MR
BGH-5541	0.18	R	0.24	MR	5530A	0.28	MR	0.25	MR
BGH-5551	0.32	MR	0.24	MR	5544A	0.27	MR	0.31	MR
BGH-5552	0.25	MR	0.15	R	5544B	0.25	MR	0.19	R
BGH-5597	0.20	R	0.17	R	5548A	0.22	MR	0.24	MR
BGH-5603	0.25	MR	0.23	MR	5548B	0.20	R	0.32	MR
BGH-5638	0.26	MR	0.18	R	5554A	0.26	MR	0.19	R
BGH-5639	0.20	R	0.20	R	5554B	0.19	R	0.20	R
BGH-5649	0.26	MR	0.12	R	5556A	0.16	R	0.17	R
BGH-5694	0.19	R	0.20	R	5560A	0.22	MR	-	-
BGH-6155	0.18	R	0.21	MR	5591A	0.18	R	0.20	R
BGH-6593	0.24	MR	0.15	R	5591B	-	-	0.23	MR
BGH-6594	0.32	MR	0.15	R	5591C	0.11	R	0.23	MR
BGH-6595	0.15	R	0.29	MR	5596A	0.22	MR	0.22	MR
BGH-1945A	0.18	R	0.14	R	5596C	0.16	R	0.13	R
BGH-1945B	0.14	R	-	-	5598A	0.22	MR	0.10	R
BGH-1945C	0.27	MR	0.20	R	5598B	0.19	R	0.14	R
BGH-305A	0.21	MR	0.30	MR	5598C	0.23	MR	0.21	MR
BGH-4287A	0.26	MR	0.15	R	5606A	0.22	MR	0.22	MR
BGH-4287B	0.26	MR	0.28	MR	5606B	0.20	R	0.22	MR
BGH-4454A	0.22	MR	0.25	MR	5616C	0.12	R	0.13	R
BGH-4590A	0.16	R	0.21	MR	5624A	0.22	MR	0.16	R
BGH-4590B	-	-	0.19	R	5624B	0.23	MR	0.33	MR
BGH-4610A	0.19	R	0.20	R	5630B	0.23	MR	0.35	MR
BGH-4681A	-	-	0.21	MR	5659A	0.21	MR	0.19	R
BGH-4681B	0.28	MR	0.19	R	5659B	0.32	MR	0.28	MR
BGH-4681C	0.33	MR	0.23	MR	6117A	-	-	0.21	MR
BGH-5224B	-	-	0.24	MR	6117B	-	-	0.18	R
BGH-5224C	0.20	R	0.28	MR	6587A	0.23	MR	0.27	MR
BGH-5453A	0.21	MR	0.32	MR	7219A	0.27	MR	0.16	R
BGH-5453B	0.16	R	0.27	MR	7219B	0.16	R	0.22	MR

Spearman correlation between young and adult plants = 0.12; R = resistant; MR = moderately resistant.
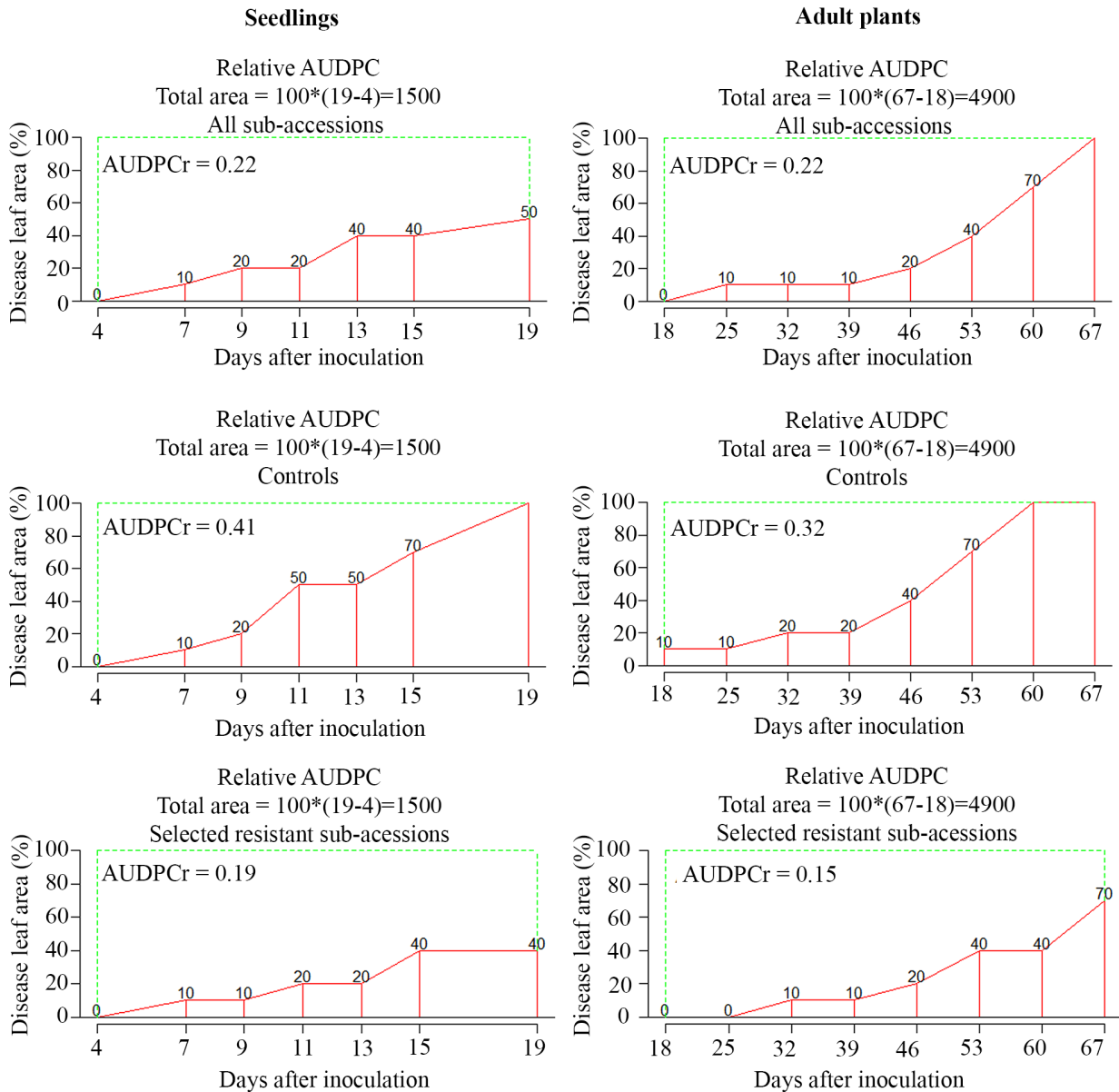
Figure 5. Powdery mildew progress curves (percentage of diseased leaf area) as a function of evaluation times in young and adult plants of *Cucurbita moschata* sub-accessions (S_0 generation) from the Vegetable Germplasm Bank.

Overall, the disease progress curves increased gradually, with the most pronounced increase observed in the controls. The selected resistant sub-accessions exhibited slower curve progression, even remaining steady over certain intervals, suggesting that resistant plants hinder pathogen development. Plants in the field were more resistant to the disease, exhibiting smaller injuries, reduced spore production, and a lower rAUDPC value. This group of traits indicates quantitative or horizontal resistance in the selected sub-accessions, as it affects the disease development rate (CAMARGO, 2018). Quantitative resistance to powdery mildew has been associated with pre-haustorial resistance, which prevents or reduces the formation of haustoria structures responsible for parasitic activity yet is not linked to the necrosis of plant cells in a hypersensitivity reaction

(PÉREZ-GARCÍA et al., 2009). Additionally, quantitative resistance is more uniform against different genotypes of the disease-causing agent (CAMARGO, 2018).

Therefore, the resistance observed in this group of genotypes may also be effective against other physiological races of *P. xanthii*. Zhou et al. (2010) reported that a *C. moschata* line ('Inbred 112-2') was highly resistant to powdery mildew, with a higher stomatal and trichome density, as well as smaller stomata, compared to genotypes susceptible to powdery mildew. These traits are pre-formed structures and, therefore, linked to pre-haustorial resistance, indicating that they are essential for the quantitative resistance of *C. moschata* genotypes to powdery mildew.

The difference in disease progression between the selected resistant sub-accessions and the the other groups

became evident at 9 DAI for young plants and 25 DAI for adult plants (Figure 5). The use of these sub-accessions, combined with minimal fungicide application, especially at the end of the vegetative cycle when disease progresses significantly, can effectively control powdery mildew in *C. moschata* crops. This significant disease progression at the end of the crop cycle may be attributed to the polycyclic nature of powdery mildew and the prolonged presence of the pathogen in the field, which facilitates the production of secondary inoculum, recurrent infections, and secondary dissemination, thus intensifying the advancement of the epidemic in the field (BERGAMIN FILHO et al., 2018).

Luitel et al. (2016) identified 20 promising accessions (*C. moschata*, *C. maxima*, and *Cucurbita* sp.) for resistance to powdery mildew when characterizing 218 *Cucurbita* spp. accessions. Similarly, Kim et al. (2014) reported four resistant accessions (*C. maxima* and *C. moschata*) when characterizing 248 accessions. Almeida et al. (2018) evaluated resistance to powdery mildew using a germplasm collection of *C. moschata* and *C. maxima* from the Active Germoplasm Bank (BAG) of Cucurbitaceae for the Brazilian Northeast region and reported that *C. maxima* accessions were more susceptible than *C. moschata*. No accession was classified as highly resistant to powdery mildew, except for BGC830 (moderate resistance), while all others were classified as highly susceptible or susceptible. In the present study, no genotypes were found to be immune to powdery mildew; however, some genotypes influenced disease development, as demonstrated by a lower disease progression over time in the group of selected resistant sub-accessions (Figure 5).

The 15 selected S_0 sub-accessions (BGH-95, BGH-117, BGH-315, BGH-1004, BGH-5552, BGH-5649, BGH-1945A, BGH-4610A, BGH-5472A, BGH-5472C, BGH-5556A, BGH-5596A, BGH-5596C, BGH-5598B, and BGH-5616C) provided an estimated selection gain of 8.83% for rAUDPC in young plants, and 29.77% in adult plants. The selection of this group of sub-accessions enables significant gains in resistance to powdery mildew.

This study represents one of the first reports characterizing the response of a *C. moschata* germplasm in Brazil to powdery mildew. The results obtained reveal that the *C. moschata* collection of BGH-UFV hold significant genetic sources of resistance to powdery mildew caused by the *Podosphaera xanthii* race 2US, which could subsidize breeding programs.

CONCLUSIONS

Podosphaera xanthii race 2US was identified for the first time in the state of Minas Gerais (MG), Brazil.

Genetic variability for resistance to powdery mildew was observed among the evaluated *Cucurbita moschata* sub-accessions from the Vegetable Germplasm Bank of the Federal University of Viçosa, MG.

Further field evaluations of adult plants are necessary to select *C. moschata* genotypes resistant to powdery mildew.

Sub-accessions BGH-95, BGH-117, BGH-315, BGH-1004, BGH-5552, BGH-5649, BGH-1945A, BGH-4610A, BGH-5472A, BGH-5472C, BGH-5556A, BGH-5596A, BGH-5596C, BGH-5598B, and BGH-5616C are promising sources of resistance to *P. xanthii* race 2US.

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