

Original Article

Genetic variability and selection of natural populations of *Campomanesia adamantium* using REML/BLUP mixed models

Variabilidade genética e seleção de populações naturais de *Campomanesia adamantium* usando modelos mistos REML/BLUP

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Abstract

The Brazilian Cerrado, a biodiversity hotspot, has been significantly impacted by climate change, land use modifications, and unsustainable extractivism, threatening the genetic diversity of many native species. *Campomanesia adamantium* (Cambess.) O. Berg, known as guavira, is a socioeconomically important fruit species in the Central-West region of Brazil. Given the current and potential value of guavira, alongside climate change, agricultural expansion in the Cerrado and inadequate extractivism, studies are necessary to understand and preserve natural populations and select genotypes for guavira breeding programs. The objectives of this study are to evaluate the morphophysiological traits of the fruits, estimate genetic parameters and genotypic values, and identify superior genotypes in natural guavira populations using mixed models (REML/BLUP). We analyzed 360 genotypes from six natural populations in Jardim and Bonito, MS, Brazil. The fruits were assessed for longitudinal and transversal diameters; fruit, pulp, and seed masses; peel thickness and total soluble solids. Significant genetic variability was detected for transverse diameter, fruit mass, and peel thickness, with heritability estimates ranging from low (0.03 for total soluble solids) to moderate (0.57 for peel thickness). Population structure influenced genetic variance, with populations 3 and 5 contributing the highest number of superior individuals. Genotypes 144, 145, 174, and 176 stood out for the largest number of characters shared traits related to the transverse diameter, fruit mass, and peel thickness, by comparing and identifying relationships between sets of genotypes. The study revealed that environmental factors significantly affect genetic variability, highlighting the importance of targeted selection strategies. Our findings provide valuable insights for conservation and genetic improvement programs for *C. adamantium*, ensuring the sustainability and economic potential of this native Cerrado species.

Keywords: guavira, fruit of the Cerrado, phenotypic characteristics, genetic parameters.

Resumo

O Cerrado brasileiro, um hotspot de biodiversidade, tem sido significativamente impactado por mudanças climáticas, modificações no uso da terra e extrativismo insustentável, ameaçando a diversidade genética de muitas espécies nativas. *Campomanesia adamantium* (Cambess.) O. Berg, conhecida como guavira, é uma espécie frutífera socioeconomicamente importante na região Centro-Oeste do Brasil. Dado o valor atual e potencial da guavira, juntamente com as mudanças climáticas, expansão agrícola no Cerrado e extrativismo inadequado, estudos são necessários para entender e preservar populações naturais e selecionar genótipos para programas de melhoramento de guavira. Os objetivos deste estudo são avaliar as características morfofisiológicas dos frutos, estimar parâmetros genéticos e valores genotípicos e identificar genótipos superiores em populações naturais de guavira usando modelos mistos (REML/BLUP). Analisamos 360 genótipos de seis populações naturais em Jardim e Bonito, MS, Brasil. Os frutos foram avaliados quanto aos diâmetros longitudinal e transversal; massas de frutos, polpa e sementes; espessura da casca e sólidos solúveis totais. Foi detectada variabilidade genética significativa para diâmetro transversal, massa do fruto e espessura da casca, com estimativas de herdabilidade variando de baixa (0,03 para sólidos solúveis totais) a moderada (0,57 para espessura da casca). A estrutura populacional influenciou a variância genética, com as populações 3 e 5 contribuindo com o maior número de indivíduos superiores. Os genótipos 144, 145, 174 e 176 se destacaram pelo maior número de caracteres compartilhados relacionados ao diâmetro transversal, massa do fruto e espessura da casca, pela comparação e identificação de relações entre conjuntos de genótipos. O estudo revelou que fatores ambientais afetam significativamente a variabilidade genética, destacando a importância de estratégias de seleção direcionadas. Nossas descobertas fornecem insights valiosos para programas de conservação e melhoramento genético de *C. adamantium*, garantindo a sustentabilidade e o potencial econômico desta espécie nativa do Cerrado.

Palavras-chave: guavira, fruto do Cerrado, características fenotípicas, parâmetros genéticos.

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1. Introduction

Climate change, land use, and soil cover have altered the biodiversity of the Brazilian Cerrado, known for its rich fauna and flora. Changes occur through the expansion of agricultural frontiers, fires, and/or inadequate extractivism, causing losses in native vegetation and natural habitat, compromising the genetic diversity of many species (Françoso et al., 2015; Strassburg et al., 2017; Velazco et al., 2019). Among the compromised plant species is *Campomanesia adamantium* (Cambess.) O. Berg, popularly known as guavira (Crispim et al., 2021). Guavira is distributed in Argentina, Paraguay, and Brazil, where it occurs in the Cerrado biome. The species is socio-economically important for the indigenous and traditional people living in the Central-West Region and was declared a symbolic fruit of the State of Mato Grosso do Sul in 2017 (Zorretto-Pinheiro et al., 2023; Crispim et al., 2021).

Guavira is a perennial shrub measuring 0.50 to 3.0 m in height, with cultural, food, and medicinal importance (Dresch et al., 2015; Crispim et al., 2018; Castro et al., 2023; Santos et al., 2023). Guavira fruits are juicy, acidic, slightly sweet, and have a low caloric value due to their high water content, dietary fiber, and high mineral content (Vallilo et al., 2006, 2008). The peel and pulp are a source of vitamin C and antioxidant compounds (Pereira et al., 2012; Dresch et al., 2015) with medicinal properties (Cardozo et al., 2018; Crispim et al., 2018). The fruits are appreciated and sold by local communities on the shoulders of highways and at regional fairs, which favors inadequate extractivism. They can be consumed fresh and processed to prepare juices, ice creams, jellies, sweets, and drinks (Cardozo et al., 2018; Crispim et al., 2018).

Guavira cultivation has been recommended to recover deforested or degraded areas and agroforestry systems (Zorretto-Pinheiro et al., 2023; Crispim et al., 2021; Santos et al., 2019). The genetic variability of natural populations and the relationships with environmental factors regarding biometric traits and fruit quality need to be known to select superior genotypes considering the potential of the species and the strong pressure from environmental changes (Crispim et al., 2018, 2019). Knowing genetic variability is crucial, as it allows the establishment of conservation strategies, genetic improvement programs, and sustainable management of the species.

Our study focuses on natural populations of perennial plants, which present unbalanced data. Therefore, the use of robust statistical tools such as mixed models is necessary. The appropriate procedure is REML/BLUP, which estimates genetic parameters using the restricted maximum likelihood (REML) method and quantifies genetic gains, in addition to selecting superior plants by predicting genotypic values using the best linear unbiased prediction (BLUP) (Resende, 2016; Yamana et al., 2007). This method is widely used in plant breeding and is efficient in several perennial species, including *Saccharum officinarum* (Carvalho et al., 2020; Moraes et al., 2021; Santos et al., 2023), *Coffea arabica* (Saavedra et al., 2023) and species of the family Myrtaceae, such as *Eucalyptus* spp. (Estopa et al., 2023), *Psidium* spp. (Maitan et al., 2023), and *Campomanesia xanthocarpa* (Homczinski et al., 2022). However, to the best of our knowledge, there are no studies of this nature on *C. adamantium* populations in the literature.

In this context, this study aimed to evaluate the morphophysiological traits of fruits, estimate genetic parameters and genotypic values and identify superior genotypes in natural populations of *C. adamantium* using mixed models.

2. Material and Methods

2.1. Characterization of the study area

The study was conducted in a Cerrado area located in two municipalities: Jardim and Bonito, in the State of Mato Grosso do Sul, Brazil. Three natural populations of guavira were evaluated in each municipality (Figures 1A and 1B).

According to Köppen criteria, the climate of the municipality of Jardim is classified as Aw, that is, a tropical climate with a dry winter. It has a rainy season in the summer, from November to April, and a clear dry season in the winter, from May to October, when mean rainfall totals are less than 50 mm. Rainfall exceeds 750 mm annually, reaching 1800 mm (Amaral et al., 2019). The predominant soils in the municipality of Jardim consist of Argissolo Vermelho-Amarelo (Ultisol), Latossolo Vermelho (Oxisol), and Latossolo Vermelho distroférrico (Oxisol). The original vegetation was mainly composed of Cerrado and Cerrado/sub-deciduous tropical forest transition zones (Mato Grosso do Sul, 2016).

The climate in the municipality of Bonito is Aw, with a mean annual temperature of 23.1 °C and a mean annual precipitation of 1,454 mm. The total rainfall in the driest months, July and August, is very low, reaching 33 and 36 mm, respectively. The highest rainfall is concentrated from October to March (Chagas et al., 2014). The predominant soils in the municipality are Chernossolo Rêndzico (Mollisol), Neossolo Regolítico (Entisol), and Latossolo Vermelho distroférrico (Oxisol). The original vegetation was mainly composed of Cerrado and semideciduous tropical forest (Mato Grosso do Sul, 2016).

The authors followed all Brazilian legal frameworks (Law 13,123/15 and Decree 8,772/16) regarding the Genetic Heritage for scientific research purposes (SISGEN No. A9CDAAE) when accessing plant material in this study. The fruits were harvested in November 2015 from 60 plants of each population, totaling 360 genotypes. Subsequently, they were stored in identified plastic bags, placed in a thermal box with ice, and transported to the Laboratory of Genetics and Plant Breeding at the Federal University of Grande Dourados, Dourados, MS, Brazil, where they were stored for up to five days in a refrigerator at a temperature of 5 °C.

Ten fruits from each plant were selected to evaluate the following traits: i) longitudinal diameter (LD, mm); ii) transverse diameter (TD, mm) – measured with a digital caliper, with a degree of precision of ± 0.01 mm; iii) fruit mass (FM, g) – measured individually on an electronic scale; iv) pulp mass (PM, g) – the epicarp of the fruits was removed using a spatula and the pulp mass with seeds of 10 fruits was estimated; v) seed mass (SM, g) – the seeds were washed in running water for 5 minutes to remove the pulp and weighed individually on an electronic scale; vi) peel thickness (PT, mm) – measured with a digital caliper with an accuracy of ± 0.01 mm; and vii) and total soluble solids (TSS, °Brix) – determined with a digital refractometer.

We identified genetic variability between individuals for all analyzed traits, with the percentages of variances relative to the total variance ranging from 1% (TSS) to 29.77% (PT) (Table 2). The magnitude of the estimated mean heritability ranged from low to moderate (Resende and Duarte, 2007) for the traits of total soluble solids (0.03) and peel thickness (0.57), respectively.

The genetic coefficients of variation (CVg) were high for fruit mass, pulp mass, seed mass, and peel thickness, indicating effective selection for these traits. On the other hand, the relative coefficients of variation (CVr), which represent the ratio between the genetic coefficient of variation and the environmental coefficient of variation, were low, ranging from 0.11 for total soluble

solids to 0.67 for peel thickness. Ideally, these estimates should approach 1.0. However, the interpretation of this parameter must also consider the number of replications, as experimental precision and high accuracy can be obtained even with values below one. Selective accuracy (Ac) was considered moderate to high for most traits, except for the total soluble solids, which was low (0.18).

We applied a selection intensity of 10% aiming to select among the 360 genotypes those with superior performance for the traits evaluated in this study. We performed individual ranking based on the predicted genotypic mean ($\mu + g$) (Table 3). Importantly, we considered the traits that showed significant differences between populations.

Table 1. Deviance analysis for the different traits of the fruits of three natural populations of guavira from Jardim and Bonito, MS, Brazil.

Traits		Effects	
		Genotypes	Population
Longitudinal diameter	Deviance	1626.10	1630.7
	LRT	2.06	8.94**
Transverse diameter	Deviance	1438.40	1449.5
	LRT	6.66**	20.91***
Fruit mass	Deviance	1115.10	1119
	LRT	7.62**	14.00***
Pulp mass	Deviance	2370.20	2376.2
	LRT	2.56	11.15***
Seed mass	Deviance	1346.70	1399.7
	LRT	2.14	60.34***
Peel thickness	Deviance	738.35	713.65
	LRT	30.28***	6.26*
Total soluble solids	Deviance	1788.10	1820.8
	LRT	0.05	37.28***

LTR: Likelihood ratio test; ***, **, *: Significant at the level of 0.1% (10.83), 1% (6.63) and 5% (3.84) and probability, respectively, by the Chi-square test with 1 degree of freedom.

Table 2. Estimates of genetic parameters for the traits longitudinal diameter (LD), transverse diameter (TD), fruit mass (FM), pulp mass (PM), seed mass (SM), peel thickness (PT), and total soluble solids (TSS) in three natural populations of guavira from Jardim and Bonito, MS, Brazil.

Variance components	LD	TD	FM	PM	SM	PT	TSS
Vg	0.41	0.44	0.19	3.61	0.19	0.14	0.09
V _e	4.85	2.66	1.08	37.87	2.17	0.31	8.01
V _p	5.58	3.45	1.37	44.45	3.13	0.47	9.83
h ² mg	0.20	0.33	0.35	0.22	0.20	0.57	0.03
CV _g	3.42	3.67	11.31	11.48	10.53	38.14	2.38
CV _r	0.29	0.40	0.42	0.30	0.29	0.67	0.11
Ac	0.44	0.57	0.59	0.47	0.45	0.75	0.18
Mean	18.71	18.07	3.88	16.56	4.11	0.97	13.74

Vg: genotypic variance; V_e: environmental variance; V_p: individual phenotypic variance; h²mg: mean genotype heritability; CV_g: genotypic coefficient of variation; CV_r: relative coefficient of variation; Ac: selection accuracy.

Table 3. Selection of superior individuals in six natural populations (POP) of guavira for the traits transverse diameter (TD), fruit mass (FM), pulp mass (PM), seed mass (SM), peel thickness (PT), and total soluble solids (TSS), from fruits harvested at two locations, Bonito (L1) and Jardim (L2), MS, Brazil.

Local	Population	TD		Local	Population	FM		Local	População	PM	
		Genotype	u+g			Genotype	u+g			Genotype	u+g
L1	POP3	141	20.12	L1	POP3	142	5.28	L1	POP3	141	20.77
L1	POP3	142	20.07	L1	POP3	144	5.26	L1	POP3	146	20.29
L1	POP3	147	20.00	L1	POP3	147	5.25	L1	POP3	173	20.17
L1	POP3	177	19.91	L1	POP2	82	5.22	L1	POP3	143	19.99
L1	POP3	159	19.91	L1	POP2	84	5.20	L1	POP3	142	19.94
L1	POP3	140	19.89	L1	POP2	87	5.19	L1	POP3	156	19.81
L1	POP3	145	19.85	L1	POP3	159	5.07	L1	POP3	124	19.78
L1	POP3	176	19.78	L1	POP3	177	5.04	L1	POP2	81	19.73
L1	POP3	156	19.73	L1	POP2	99	5.00	L1	POP3	153	19.71
L1	POP3	153	19.68	L1	POP3	141	5.00	L1	POP3	154	19.65
L1	POP3	144	19.67	L1	POP3	176	4.99	L1	POP3	150	19.49
L1	POP3	128	19.62	L1	POP2	117	4.98	L1	POP3	138	19.38
L1	POP3	135	19.57	L1	POP3	124	4.96	L1	POP3	178	19.35
L1	POP3	173	19.54	L1	POP2	81	4.94	L2	POP4	207	19.31
L1	POP3	150	19.54	L1	POP3	156	4.93	L1	POP3	158	19.29
L1	POP3	146	19.53	L1	POP3	174	4.93	L1	POP3	140	19.29
L1	POP2	81	19.51	L1	POP2	116	4.92	L2	POP6	327	19.28
L1	POP3	124	19.50	L1	POP3	145	4.91	L1	POP2	86	19.25
L1	POP3	139	19.48	L1	POP2	64	4.90	L1	POP3	135	19.19
L1	POP3	121	19.46	L1	POP2	96	4.87	L1	POP3	177	19.17
L1	POP3	151	19.45	L1	POP2	114	4.87	L1	POP3	159	19.16
L1	POP2	82	19.45	L1	POP3	140	4.86	L1	POP3	151	19.14
L1	POP3	138	19.44	L1	POP2	85	4.85	L1	POP2	113	19.13
L1	POP3	161	19.44	L1	POP3	150	4.82	L1	POP3	144	19.13
L1	POP3	154	19.43	L1	POP2	80	4.80	L1	POP3	161	19.13
L1	POP3	143	19.43	L1	POP3	173	4.78	L1	POP3	125	19.12
L1	POP3	174	19.41	L1	POP2	90	4.76	L1	POP3	176	19.07
L1	POP3	155	19.40	L1	POP3	154	4.74	L1	POP3	145	19.04
L1	POP2	87	19.38	L1	POP3	153	4.73	L2	POP4	209	19.04
L1	POP3	136	19.37	L1	POP2	113	4.72	L2	POP6	329	19.01
L1	POP3	130	19.35	L1	POP3	130	4.71	L1	POP2	83	18.95
L1	POP3	129	19.34	L1	POP3	128	4.71	L1	POP2	82	18.90
L1	POP3	122	19.33	L1	POP3	155	4.70	L1	POP3	155	18.89
L1	POP3	171	19.32	L1	POP3	151	4.69	L1	POP3	163	18.79
L1	POP2	117	19.30	L1	POP3	146	4.69	L1	POP3	168	18.78
L1	POP3	152	19.30	L1	POP3	135	4.68	L1	POP3	147	18.78

Table 3. Continued...

Local	Population	SM		Local	Population	PT		Local	Population	TSS	
		Genotype	u+g			Genotype	u+g			Genotype	u+g
L1	POP3	142	7.56	L1	POP3	172	0.64	L2	POP5	276	15.08
L1	POP3	178	7.31	L1	POP3	171	0.67	L2	POP5	280	15.08
L1	POP3	124	7.29	L1	POP1	52	0.68	L2	POP5	242	15.04
L1	POP3	154	7.21	L1	POP1	51	0.71	L2	POP5	241	15.04
L1	POP3	179	7.17	L1	POP3	145	0.72	L2	POP5	281	15.02
L1	POP3	173	7.15	L1	POP3	126	0.72	L2	POP5	249	15.02
L1	POP3	177	7.07	L1	POP3	174	0.73	L2	POP5	285	15.02
L1	POP3	180	7.06	L1	POP3	176	0.73	L2	POP5	246	15.02
L1	POP3	128	7.04	L1	POP3	121	0.73	L2	POP5	272	15.01
L1	POP3	123	7.02	L1	POP3	163	0.73	L2	POP5	268	15.00
L1	POP3	150	6.97	L1	POP3	148	0.74	L2	POP5	243	14.99
L1	POP3	125	6.96	L1	POP3	139	0.74	L2	POP5	283	14.99
L1	POP3	140	6.94	L1	POP3	137	0.75	L2	POP5	251	14.97
L1	POP3	155	6.94	L2	POP4	219	0.76	L2	POP5	292	14.97
L1	POP3	165	6.94	L1	POP3	178	0.76	L2	POP5	279	14.96
L1	POP3	143	6.94	L1	POP1	25	0.76	L2	POP5	289	14.96
L1	POP3	144	6.93	L1	POP1	6	0.76	L2	POP5	277	14.96
L1	POP3	139	6.92	L1	POP3	136	0.77	L2	POP5	286	14.96
L1	POP3	138	6.91	L1	POP3	165	0.77	L2	POP5	250	14.96
L1	POP3	171	6.91	L1	POP1	54	0.77	L2	POP5	296	14.96
L1	POP3	121	6.90	L1	POP1	56	0.77	L2	POP5	263	14.94
L1	POP3	163	6.88	L1	POP1	1	0.77	L2	POP5	287	14.94
L1	POP3	136	6.86	L1	POP1	43	0.77	L2	POP5	293	14.94
L1	POP3	159	6.83	L1	POP1	28	0.78	L2	POP5	244	14.94
L1	POP3	160	6.81	L2	POP4	226	0.78	L2	POP5	295	14.94
L1	POP3	168	6.81	L1	POP1	19	0.78	L2	POP5	256	14.94
L1	POP3	134	6.81	L1	POP1	17	0.79	L2	POP5	248	14.93
L1	POP3	146	6.80	L2	POP4	228	0.79	L2	POP5	254	14.93
L1	POP3	176	6.79	L2	POP4	213	0.80	L2	POP5	253	14.93
L1	POP3	137	6.78	L1	POP1	58	0.80	L2	POP5	262	14.93
L1	POP3	147	6.78	L1	POP3	167	0.80	L2	POP5	278	14.93
L1	POP3	156	6.78	L1	POP3	127	0.80	L2	POP5	257	14.92
L1	POP3	122	6.77	L1	POP1	16	0.81	L2	POP5	291	14.92
L1	POP3	152	6.75	L1	POP1	45	0.81	L2	POP5	294	14.92
L1	POP3	170	6.75	L2	POP5	279	0.82	L2	POP5	245	14.92
L1	POP3	164	6.73	L1	POP3	144	0.82	L2	POP5	247	14.92

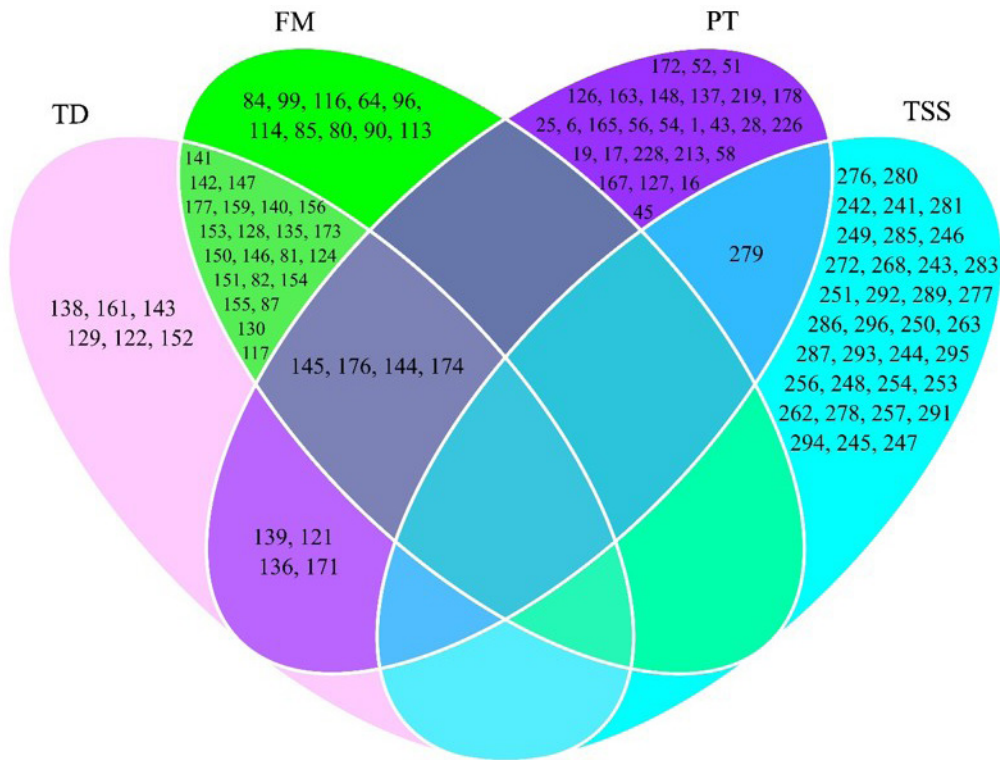


Figure 2. Venn diagram showing the number of overlapping genotypes among the top 10% identified in the natural populations of guavira for the traits transverse diameter (TD), fruit mass (FM), peel thickness (PT), and total soluble solids (TSS).

In this study, we detected genetic variability between different populations for all analyzed traits. Therefore, selection between populations increases the probability of identifying superior individuals, as this approach considers both populations and superior individuals. In general, populations 3 and 5 contributed the majority of genotypes selected for the evaluated traits, suggesting their high potential to originate productive genotypes (Table 3).

Population 3, located in Bonito, presented high percentages of superior individuals in terms of transverse diameter (88.8%), fruit mass (61.1%), pulp mass (75%), and seed mass (100%). All selected individuals for the trait total soluble solids belonged to population 5, located in Jardim.

Quantitative trait breeding rarely manages to bring together several high-performance traits in a single genotype. The Venn diagram is a valuable visual tool for comparing and identifying relationships between sets of genotypes. Genotypes 144, 145, 174, and 176 stood out for the largest number of characters, sharing traits related to the transverse diameter, fruit mass, and peel thickness (Figure 2).

Another relevant intersection occurs between transverse diameter and fruit mass, with a high number of shared genotypes (22). It suggests a possible correlation or association between both traits in the listed genotypes. On the other hand, the intersection between total soluble solids and peel thickness included only one genotype (279).

4. Discussion

The observed significant differences indicate the existence of genetic variability, showing possible genetic gains and higher success in selection between populations to the detriment of individual selection, as they explain part of the total genetic variance (Table 1). We observed no significant differences between genotypes for soluble solids content. However, this trait should be investigated, as it is an indication of the ripening point of fruits for seed harvesting, which must be at least 15.75 °Brix to obtain 95% seed germination (Melchior et al., 2006).

The means of selected individuals in terms of fruit diameter and mass (Table 2) were higher than the values reported by Vieira et al. (2019), who obtained 15.57 ± 0.50 mm and 3.7 ± 0.44 g, respectively, in ten populations collected at Fazenda Santa Madalena ($22^{\circ}08'05''$ S and $55^{\circ}08'17''$ W), in Dourados, MS, Brazil.

The soluble solids content is an important quality factor for several fruits and is related to flavor, as it has a high positive correlation with sugar contents (Vieira et al., 2019). The mean value of the individuals selected in the present study (13.74° Brix) was lower than that found by Vieira et al. (2019), who found around $17.13 \pm 1.45^{\circ}$ Brix. Importantly, the soluble solids content can be influenced by several factors, including ripening, climate and environment, variety, management, and postharvest storage (Campos et al., 2012). Therefore, we can infer that the fruits may have been influenced, as we observed a low

mean value of total soluble solids compared to the mean value reported by Silva et al. (2021) which was 19.24 °Brix. Thus, individuals may not have expressed their potential for this trait, which is a factor that can be evaluated in future studies.

Estimates of genetic parameters allow us to guide selection strategies and obtain gains (Ramalho et al., 2012). Furthermore, they provide valuable insights for implementing effective selection strategies in natural guavira populations. These parameters, related to traits, show the complexity of the genetic and environmental variability present in these populations. Genotypic variance (V_g) shows the presence of genetic diversity in the studied populations, allowing the selection of superior genotypes. However, environmental variance (V_e) exceeds genotypic variance for all traits, indicating that environmental factors play a significant role in the observed variations (Table 2).

The parameter h^2_{mg} is crucial, as it highlights the proportion of genetic variability relative to the total variability. Moderate h^2_{mg} values in traits such as longitudinal diameter, transverse diameter, fruit mass, pulp mass, and peel thickness suggest that selection based on these attributes can be effective, contributing to genetic improvement over generations. On the other hand, the higher proportion of environmental variance affected the heritability estimates for total soluble solids (0.03), considered low (Resende and Duarte, 2007). The higher the heritability estimates, the greater the chances of successful selection. However, the data were collected on fruits from natural guavira populations, which implies higher environmental variance and, consequently, lower heritability than in controlled environments and/or annual species.

The genotypic coefficient of variation (CV_g) provides additional insights into the variability relative to the genotypic mean. Notably, peel thickness has higher CV_g , indicating proportionally greater genotypic variation relative to the genotypic mean. Similarly, this trait may be of particular interest for selection programs, as the expressed genetic variability can be explored in breeding, thus obtaining fruits with smaller or greater peel thicknesses, depending on the objective of the breeding program. We selected individuals with smaller peel thicknesses in this study.

Importantly, estimates of genetic parameters vary depending on the genetic structure of the population and the environmental conditions to which the population was subjected and evaluated (Ramalho et al., 2012). Thus, recognizing that selection must consider environmental variations, as evidenced by V_e and CV_r values, is crucial despite efforts to select based on genetic variability (Table 2). Local adaptability, reflected in the genotypes selected in different locations, highlights the influence of the environment on the expression of traits.

Selection strategies must be complemented by practices that minimize environmental variability, such as controlling growing conditions. In summary, the implementation of selection programs in natural guavira populations must be carefully designed, considering the dynamic interaction between genetic and environmental factors. The search for superior genotypes, supported by an in-depth understanding of heritability and selection

accuracy, can enhance genetic improvement efforts toward the production of more adapted and productive varieties.

Studies using other species have highlighted the variability in the response to selection in natural populations, resulting from the complex interaction between genetic and environmental factors (Silveira et al., 2020; Silva et al., 2021; Gil et al., 2022). Incorporating these experiences can provide valuable information about the potential effectiveness of selection strategies for guavira. Given the significant genetic variability in different populations and locations, the need for genetic improvement strategies that maximize the expression of their genetic potential becomes evident (Table 3). An effective breeding method can be outlined considering the existing genetic variability, prominent traits, and environmental peculiarities.

Initially, direct selection of superior genotypes within populations based on key traits such as transverse diameter, fruit mass, pulp mass, seed mass, peel thickness, and soluble solids proves to be a promising approach. However, this selection must be carefully guided by genetic parameters, especially h^2_{mg} , which indicates the proportion of phenotypic variation explained by genetic variation.

In the context of plant breeding, the graphic representation of the Venn diagram (Figure 2) is useful for analyzing and contrasting different sets of genetic and phenotypic traits or plant populations. It allows us to visualize and understand the intersections and differences between plants with different traits, helping breeders identify traits that are shared or exclusive to certain populations. This intersection is important for plant breeding, as it indicates the presence of individuals that can exhibit desirable characteristics for more than one trait, which can be explored for selection and targeted crossings.

5. Conclusions

There is genetic variability in the morphophysiological traits of fruits in natural populations of *Campomanesia adamantium*, indicating potential for selection and genetic improvement of the species. Heritability estimates ranged from low to moderate, highlighting the influence of the environment on the phenotypic expression of the evaluated traits.

Populations 3 and 5 exhibited a higher number of superior individuals, suggesting that these regions may be strategic for the conservation and sustainable exploitation of the species. The application of the REML/BLUP method enabled the identification of promising genotypes, particularly genotypes 144, 145, 174, and 176, which displayed larger transverse fruit diameters, higher fruit mass, and thinner pericarp thickness.

This study provides valuable insights for conservation and breeding programs of *C. adamantium*, aiming at the preservation of Cerrado biodiversity and the socio-economic valorization of this native species.

Data Availability Statement

Data will be available upon request.

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