SEMINA
Ciências Agrárias

DOI: 10.5433/1679-0359.2026v47n2p611

Resistance levels to coffee leaf rust in Brazilian Arabica cultivars under field conditions

Níveis de resistência à ferrugem alaranjada em cultivares brasileiras de café arábica em condições de campo

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Highlights

IPR 105, Sabiá-Una, IPR 107, IAC 125 RN, and IPR 104 are highly resistant cultivars.
Cultivars derived from Híbrido de Timor and Icatu showed different resistance levels.
Some reportedly resistant cultivars did not exhibit the expected resistance levels.
Disease severity and resistant-plant percentage aid resistance characterization.

Abstract

Over the decades, germplasms derived from Híbrido de Timor (HdT) and Icatu have been recognized as important sources of resistance to coffee leaf rust (CLR), caused by *Hemileia vastatrix*, in *Coffea arabica*. However, multiple reports of resistance breakdown underscore the need for continuous cultivar evaluation. This study characterized the current resistance levels of Arabica coffee cultivars to CLR in northern Paraná state, Brazil. The study was conducted in an experimental field in Londrina, Paraná, using 23 *C. arabica* cultivars. CLR severity was assessed in 2022, 2023, and 2024, with scores ranging from 1.0 to 5.5. Resistance characterization was further supported by the percentage of highly resistant (HR) plants per cultivar. Several cultivars derived from HdT, Icatu, or both exhibited only intermediate resistance and lacked HR plants. Low resistance levels were observed in cultivars generally classified as HR in Brazil, such as 'IAC Obatã 4739', 'Sarchimor MG8840', and 'Arara'. Only 'IPR 104', 'IAC 125 RN', 'Sabiá-Una', 'IPR 107', and 'IPR 105' were identified as HR cultivars, all of which exhibited 100% HR plants and were therefore considered likely to be homozygous. The presence of HR and non-HR plants within 'IPR 102' and 'Asabranca' suggests a possible heterozygosity and indicates the need for within-cultivar

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Received: Jun. 10, 2025 Approved: Out. 07, 2026

selection to develop new resistant lines. These findings indicate that, while some major resistance genes remain effective, most cultivars display varying levels of quantitative resistance. Furthermore, because the percentage of HR plants reflects the degree of homozygosity, the classification of CLR resistance can be enhanced by incorporating this parameter.
Key words: *Coffea arabica. Hemileia vastatrix.* Quantitative resistance. Qualitative resistance. *SH genes.*

Resumo

Ao longo das décadas, os germoplasmas de Híbrido de Timor (HdT) e Icatu têm sido reconhecidos como importantes fontes de resistência à ferrugem alaranjada (CLR), causada por *Hemileia vastatrix,* em *Coffea arabica.* No entanto, devido a múltiplos relatos de quebra de resistência, a contínua avaliação de cultivares é essencial. Assim, este estudo teve como objetivo caracterizar os níveis atuais de resistência de cultivares de café arábica à CLR no norte do Paraná. O estudo foi conduzido em um campo experimental em Londrina, Paraná, Brasil, com a utilização de 23 cultivares de *C. arabica.* A severidade da CLR foi avaliada em 2022, 2023 e 2024, por meio de escala de notas variando de 1,0 a 5,5. Além da severidade média da CLR, a caracterização da resistência foi determinada pela porcentagem de plantas altamente resistentes (HR) em cada cultivar avaliada. Várias cultivares derivadas de HdT, de Icatu ou de ambas exibiram apenas resistência intermediária e não apresentaram plantas HR. Baixos níveis de resistência foram observados em cultivares geralmente classificadas como HR no Brasil, como 'IAC Obatã 4739', 'Sarchimor MG8840' e 'Arara'. Somente 'IPR 104', 'IAC 125 RN', 'Sabiá-Una', 'IPR 107' e 'IPR 105' foram identificadas como HR, as quais apresentaram 100% de plantas HR e, portanto, em estado de homozigose. A porcentagem de plantas segregantes para HR observada em 'IPR 102' e 'Asabranca' indicou uma possível heterozigosidade e a necessidade de seleção dentro dessas cultivares para o desenvolvimento de novas linhagens resistentes. Esses resultados sugerem que, embora alguns genes *SH* permaneçam eficazes contra *H. vastatrix,* a maioria das cultivares apresenta níveis variados de resistência quantitativa. Além disso, por refletir o grau de homozigose, a classificação de resistência a CLR pode ser aprimorada pela incorporação da porcentagem de plantas HR.
Palavras-chave: *Coffea arabica. Hemileia vastatrix.* Resistência quantitativa. Resistência qualitativa. Genes *SH.*

Introduction

Coffee is one of the most important commodities in global trade and a major export product for tropical and subtropical developing countries (International Coffee Organization [ICO], 2025). Biotic factors nevertheless cause substantial yield losses in coffee crops, primarily through fungal pathogens affecting *Coffea arabica.* Coffee leaf rust (CLR), caused by *Hemileia vastatrix* Berk. & Br., has historically been and remains the most significant disease of Arabica coffee (Zambolim, 2016; Zambolim & Caixeta, 2021). Developing CLR-resistant genotypes has therefore been a central objective of coffee breeding programs for more than a century (Talhinhas et al., 2017).

Breeding efforts for CLR resistance advanced substantially following the initiation of studies on Híbrido de Timor (HdT)

by the Centro de Investigação de Ferrugens do Cafeeiro (CIFC), in the mid-20th century (Silva et al., 2018; Zambolim et al., 2024). The discovery of resistance in HdT also prompted research at other institutions on artificial hybridization between *C. arabica* and *C. canephora* (Talhinhas et al., 2017; Zambolim & Caixeta, 2021). In Brazil, the Instituto Agronômico (IAC) crossed *C. arabica* cv. Bourbon Vermelho with tetraploid *C. canephora* genotypes to develop rust-resistant genotypes. The resulting hybrids underwent multiple backcrosses with Arabica coffee cultivars, including those from the Mundo Novo and Catuaí groups, giving rise to the Icatu population (Eskes & Costa, 1983). Since then, germplasm derived from HdT and Icatu has been extensively used by Brazilian coffee breeders (Sera et al., 2022; Zambolim et al., 2024).

Most Arabica coffee germplasm carrying introgressed genes from *C. canephora* is considered an essential source of CLR resistance in Latin America (Zambolim, 2016; Zambolim & Caixeta, 2021). Of the 131 *Coffea arabica* cultivars currently registered with the Brazilian Ministério da Agricultura, Pecuária e Abastecimento [MAPA] (2026), 84 carry introgressed genes from *C. canephora* (Carvalho et al., 2022). According to Sera et al. (2022), thirty-three cultivars are classified as highly resistant (HR), only three of which are not derived from HdT or Icatu germplasm. An additional 38 cultivars are classified as having intermediate resistance to CLR, and all of these are derived from HdT and/or Icatu germplasm (Sera et al., 2022).

Maintaining durable genetic resistance remains a major challenge for breeders due to the variability of pathogen populations (Zambolim & Caixeta, 2021). The pathogen's high evolutionary potential has contributed to the emergence of complex races through consecutive mutations in virulence genes and possible introgression or recombination events across different coffee-growing regions (Cabral et al., 2016; Silva et al., 2018; Zambolim & Caixeta, 2021). Although 16 races of *Hemileia vastatrix* have been identified in Brazil, many additional races may yet exist (Zambolim et al., 2024). Because the current number of differential clones is insufficient to identify potentially emerging races, race characterization may be incomplete, and some races may remain unidentified (Zambolim & Caixeta, 2021). Zambolim and Caixeta (2021) therefore proposed designating unidentified races occurring in local pathogen populations as pathotypes.

Resistance in cultivars derived from Icatu and HdT has gradually been overcome since the early 21st century in several Latin American countries (Cabral et al., 2016; Zambolim & Caixeta, 2021). Some cultivars previously classified as HR may now exhibit moderate or low resistance, depending on the H. vastatrix race or pathotype population present (Sera et al., 2022). The breakdown of qualitative (vertical) resistance has also highlighted additional resistance mechanisms. This resistance is attributed to genes with secondary or polygenic effects, and even when major-gene resistance is overcome, some cultivars may still exhibit higher resistance levels than fully susceptible ones (Eskes & Costa, 1983; Sera et al., 2022; Lima et al., 2025). Quantitative or non-specific resistance is common in germplasm carrying introgressed *C. canephora* genes, including cultivars derived from HdT and Icatu (Sera et al., 2022; Zambolim et al., 2024).

CLR resistance classifications have been frequently revised for several cultivars, often differing from their original characterization (Del Grossi et al., 2013; Sera et al., 2022; Zambolim et al., 2024; Lima et al., 2025). Even cultivars classified as HR may still contain segregating plants that develop the disease (Del Grossi et al., 2013; Matiello et al., 2024). The proportion of HR plants can help determine whether major resistance genes are present in a homozygous or heterozygous state and whether further within-cultivar selection is warranted. Assessing current resistance levels is particularly relevant in Brazilian cultivars. This study characterized the resistance of Brazilian *C. arabica* cultivars to CLR in northern Paraná.

The experiment was conducted at the experimental field area of the Instituto de Desenvolvimento Rural do Paraná – IAPAR-EMATER (IDR-Paraná), in Londrina, Paraná, Brazil (23°21′37″S, 51°09′50″W; altitude of 586 m). The soil at the site is classified as Dystrophic Red Latosol, and the climate is Cfa (humid subtropical, with dry winters and hot summers), according to the Köppen-Geiger classification (Aparecido et al., 2016).

A total of 23 *C. arabica* cultivars, planted in 2017 at a spacing of 3.00 × 0.60 m, were evaluated in a randomized complete block design with four replications and ten plants per plot. Six cultivars were developed by IDR-Paraná, five by the Instituto Agronômico (IAC), three by the Empresa de Pesquisa Agropecuária de Minas Gerais (EPAMIG), and nine by Fundação Procafé, according to MAPA (2026). Table 1 lists the germplasm origins, reported resistance levels to CLR, and the institutions responsible for cultivar development and registration.

Table 1
Description of the 23 *Coffea arabica* cultivars included in this study, including their germplasm origins, reported resistance levels to coffee leaf rust (RL), and maintainer institutions

Cultivars	Germplasm origins[1]	RL[1]	Maintainer institution[2]
IPR 102	Catuaí Vermelho IAC 99 × Dwarf Icatu[3]	IR	IDR-Paraná
IPR 103	Catuaí Vermelho IAC 99 × Dwarf Icatu[3]	IR	
IPR 104	Villa Sarchi CIFC 971/10 × Híbrido de Timor 832/2	HR	
IPR 105	Catuaí Vermelho IAC 81 × (Catuaí Vermelho IAC 81 × IAC 1110-8[4])	HR	
IPR 107	Iapar 59[5] × Mundo Novo IAC 376-4	HR	
IPR 108	Iapar 59[5] × (Catuaí Vermelho IAC 99 × Dwarf Icatu[3])	IR	
Tupi IAC 1669-33	Villa Sarchi CIFC 971/10 × Híbrido de Timor 832/2	HR	IAC
IAC 125 RN	Villa Sarchi CIFC 971/10 × Híbrido de Timor 832/2	HR	
Obatã IAC 1669-20	Catuaí Vermelho × (Villa Sarchi CIFC 971/10 × Híbrido de Timor 832/2)	HR	
IAC Obatã 4739	Obatã IAC 1669-20 × Catuaí Amarelo	HR	
Catuaí Vermelho IAC 99	Caturra Amarelo IAC 476 × Mundo Novo IAC 374-19	S	

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MGS Aranãs	Catimor UFV 1603-215 × Icatu IAC H3851-2	IR	EPAMIG
MGS Paraíso 2	Catuaí Amarelo IAC 30 × Híbrido de Timor UFV 445-46(6)	IR	
Sarchimor MG8840	Villa Sarchi CIFC 971/10 × Híbrido de Timor 832/2	HR	
Arara	Catuaí Vermelho × (Villa Sarchi CIFC 971/10 × Híbrido de Timor 832/2)	HR	Fundação Procafé
Sabiá-Una	Catucaí Amarelo × (Catimor UFV 386 × Acaiá)	IR	
Acauãnovo	Mundo Novo IAC 388-17 × Sarchimor IAC 1668	HR	
Asabranca	Mundo Novo IAC 388-17 × Sarchimor IAC 1668	HR	
Guará	Icatu Vermelho × Catuaí	IR	
Catucaiam 24137	Icatu Vermelho × Catuaí	IR	
Japy	Icatu Vermelho × Catuaí	IR	
Azulão	Icatu Vermelho × Catuaí	IR	
Rouxinol	Icatu Vermelho × Catuaí	IR	

[(1)]HR = highly resistant, IR = intermediate resistance, and S = susceptible, according to Carvalho et al. (2022) and Sera et al. (2022); [(2)]According to MAPA (2026); [(3)]Dwarf Icatu = *C. arabica var.* Catuaí Amarelo × [*C. arabica* var. Mundo Novo × (*C. canephora* var. Robusta × *C. arabica* var. Bourbon Vermelho)] (Carvalho et al., 2022); [(4)]IAC 1110-8 = BA-10 accession derived from Balehonnur Arabica germplasm (BA Series) (Sera et al., 2022); [(5)]Iapar 59 = Villa Sarchi CIFC 971/10 × Híbrido de Timor 832/2; [(6)]HdT UFV 445-46 = genotype derived from the Híbrido de Timor CIFC 2570.

Phenotypic evaluations of coffee leaf rust severity (CLRS) were conducted using a rating scale ranging from 1.0 to 5.5, where: 1.0 = plants without leaf lesions; 1.5 = lesions ranging from "flecks" to chlorosis, without sporulation; 2.0 = chlorotic lesions with sporulation in the lower third, with slight severity (0.1 - 5.0%); 2.5 = chlorotic lesions with sporulation in the lower third, with slight severity (5.01 - 10%); 3.0 = chlorotic lesions with sporulation in the lower and middle thirds, with slight to moderate severity (10.01 - 20%); 3.5 = chlorotic lesions with sporulation in the lower and middle thirds, with moderate to slight (20.01 - 30%) and slight severity; 4.0 = chlorotic lesions with sporulation in the lower, middle, and upper thirds, with moderate to high severity (30.01 - 40% of leaves); 4.5 = chlorotic lesions with sporulation in the lower, middle, and upper thirds, with high severity (40.01 - 60%); 5.0 = chlorotic lesions with sporulation in the lower, middle, and upper thirds, with very high severity (> 60%); 5.5 = chlorotic lesions with sporulation in the lower, middle, and upper thirds, with very high to high severity.

Field evaluations were conducted in July 2022, June 2023, and June 2024 under high natural infection pressure, as indicated by severe disease symptoms in the susceptible cultivar 'Catuaí Vermelho IAC 99'. Although race II is predominant among the 16 *H. vastatrix* races identified in Brazil (Sera et al., 2022; Zambolim et al., 2024), no studies have characterized the physiological races specific to Northern Paraná. In addition, Zambolim and Caixeta (2021) reported the frequent presence of complex, unidentified

pathotypes in field trials and HdT-derived germplasm. The local *H. vastatrix* population was therefore considered a naturally occurring mixture of pathotypes or a complex of unidentified physiological races.

No fungicides were applied during the study period to avoid interference with the expression of genetic resistance to *H. vastatrix.* Soil fertilization was based on soil analysis recommendations for Paraná state. Weed management, as well as insecticide and acaricide applications, followed standard practices for coffee crops (Matiello et al., 2024).

To reduce potential environmental effects and variation associated with biennial reproductive cycles and plant vegetative status, mean CLRS was calculated from the annual assessment data collected over the three-year evaluation period. The assumptions of normality and homogeneity of variances were assessed using the Shapiro–Wilk and Bartlett's tests, respectively, before analysis of variance (ANOVA) was performed. Means were then compared using the Scott–Knott test at the 1% significance level in R software, version 4.3.1 (R Core Team, 2025) with the AgroR package (Shimizu et al., 2023).

The segregation rate among plants of each cultivar was evaluated based on the percentage of highly resistant plants (*%HR*). Plants that consistently received scores of 1.0 or 1.5 in all three years were classified as highly resistant (HR). Plants with scores ≥ 2.0 were not classified as HR because they exhibited varying levels of rust sporulation. For each i cultivar, *%HR* was calculated as the ratio of the number of HR plants (nHR_i) to the total number of evaluated plants (n_i), expressed as: $\%HR = (nHR_i / n_i) \times 100$.

ANOVA showed a significant difference in mean CLRS among cultivars over the three-year evaluation period, with the Scott-Knott test identifying seven distinct groups (Table 2). Because this classification produced a relatively large number of groups, we used a different system from the conventional categories of highly resistant, moderately resistant, slightly resistant, moderately susceptible, and susceptible (Sera et al., 2022; Lima et al., 2025) or susceptible, partially resistant, and resistant (Carvalho et al., 2022). The cultivars were instead assigned to six resistance levels: extremely low, very low, low, moderate-low, moderate, and highly resistant.

Table 2
Mean values from field evaluations of Arabica coffee cultivars for three-year mean coffee leaf rust severity (CLRS) and the percentage of highly resistant plants (%HR), based on the local population of Hemileia vastatrix in the experimental area in Londrina, Paraná, Brazil

Cultivars	CLRS[(2)]	%HR[(3)]
Catuaí Vermelho IAC 99	4.53 [a]	0
Catucaiam 24137	4.31 [a]	0
Guará	4.05 b	0
IAC Obatã 4739	3.93 b	0
IPR 103	3.92 b	0
Japy	3.87 b	0
Sarchimor MG 8840	3.86 b	0
Azulão	3.59 c	0
MGS Paraiso 2	3.47 c	0
Rouxinol	3.45 c	0
Arara	3.26 c	0
Obatã IAC 1669-20	3.10 d	0
IPR 108	2.99 d	0
MGS Aranãs	2.95 d	2.50
Tupi IAC 1669-33	2.61 e	4.55
Acauãnovo	2.43 e	2.78
IPR 102	1.85 f	46.43
Asabranca	1.70 f	64.94
IPR 104	1.49 g	100.00
IAC 125 RN	1.38 g	100.00
Sabiá-Una	1.33 g	100.00
IPR 107	1.32 g	100.00
IPR 105	1.22 g	100.00
General mean	**2.90**	**-**
C.V.	**8.34%**	**-**

[(1)] Cultivars were ranked in descending order of CLRS values; [(2)] CLRS is the mean of the data collected in 2022, 2023, and 2024, based on scores ranging from 1.0 to 5.5, with lower values indicating higher resistance and higher values indicating greater disease severity. Means followed by the same letter do differ significantly according to the Scott-Knott test at 1% probability; [(3)] %HR was calculated as the ratio of the number of HR plants consistently scored as 1.0 or 1.5 across all three years of evaluation (nHR_i) to the total number of plants evaluated (n_i), expressed as: $\%HR = (nHR_i / n_i) \times 100$.

'Catuaí Vermelho IAC 99' and 'Catucaiam 24137' were the most susceptible cultivars to coffee leaf rust (CLR) over the three-year evaluation period and differed significantly from the other cultivars. Except for 'IAC Catuaí SH3', cultivars in the "Catuaí" group originate from the cross between 'Caturra Amarelo IAC 476-11' and 'Mundo Novo IAC 374-19' and are susceptible to CLR (Carvalho et al., 2022; Sera et al., 2022). The susceptibility of 'Catucaiam 24137', along with 'Catuaí Vermelho IAC 144', was also reported by Del Grossi et al. (2013) in a field study conducted under natural conditions in Londrina. Sera et al. (2022) reported that even susceptible genotypes, such as those in the Catuaí group, may possess minor genes that confer quantitative resistance, making them less susceptible than cultivars in the Bourbon group. We therefore classified 'Catuaí Vermelho IAC 99' and 'Catucaiam 24137' as having extremely low resistance, corresponding to the susceptible category commonly used by other authors (Del Grossi et al., 2013; Carvalho et al., 2022; Sera et al., 2022; Lima et al., 2025).

'Guará', 'IAC Obatã 4739', 'IPR 103', 'Japy', and 'Sarchimor MG8840' differed from 'Catuaí Vermelho IAC 99' and 'Catucaiam 24137' but exhibited higher CLRS values than the other 16 cultivars, placing them in the very low resistance category. 'Azulão', 'MGS Paraíso 2', 'Rouxinol', and 'Arara' were classified as having a low resistance level because, although their mean CLRS values were lower and statistically different from those of the seven most susceptible cultivars, they also differed from the 12 more resistant cultivars.

The classification of 'Guará', 'IPR 103', 'Japy', 'Azulão', 'MGS Paraíso 2', and 'Rouxinol' is consistent with Carvalho et al. (2022), who described these cultivars as having intermediate or partial resistance. This type of resistance is influenced by minor-effect genes, resulting in slight resistance and often being described as "moderate susceptibility" (Sera et al., 2022). 'Azulão' is considered partially resistant to CLR (Sera et al., 2022) or even slightly susceptible (Lima et al., 2025). By contrast, Lima et al. (2025) classified 'IPR 103', 'Japy', and 'MGS Paraíso 2' as HR. Our results are consistent with those of Sera et al. (2022), who report that some cultivars may exhibit low levels of resistance depending on pathogen variability.

Lima et al. (2025) also reported a high level of resistance to CLR in seedlings of 'Acauãnovo', 'Arara', 'Asabranca', 'IAC 125 RN', 'IPR 105', 'IPR 107', 'MGS Aranãs', and 'Obatã IAC 4749'. Their study used inoculum derived from a local pathogen population collected in southern Minas Gerais state, meaning that differences in pathogen populations may account for variation in the resistance response of some cultivars. In our field study conducted under natural conditions, only 'IPR 105', 'Sabiá-Una', 'IPR 107', 'IAC 125 RN', and 'IPR 104' were among the most resistant cultivars, differing significantly from the other 18 cultivars. These five cultivars were classified as HR and presented 100% HR plants, indicating that their resistance is likely inherited in a homozygous state.

'IPR 105', 'IPR 107', 'IAC 125 RN', and 'IPR 104' are commonly classified as HR to CLR (Carvalho et al., 2022; Sera et al., 2022; Lima et al., 2025). However, no prior studies have reported the resistance level of 'Sabiá-Una'. According to Matiello et al. (2024), 'Sabiá-Una' originated from a spontaneous hybridization between 'Sabiá Tardio' (Catimor

UFV 386 × Acaiá) and 'Catucaí Amarelo', both of which have been classified as partially resistant to CLR (Sera et al., 2022). 'Sabiá-Una' therefore carries *C. canephora* introgressions from both HdT and Icatu germplasm. Despite also being derived from Icatu and HdT germplasms, 'MGS Aranãs' and 'IPR 108' exhibited lower CLR resistance. 'MGS Aranãs', 'IPR 108', and 'Obatã IAC 1669-20' were classified as moderately low in resistance because they were more resistant than the other 11 cultivars.

No HR plants were identified among the cultivars classified as having extremely low, very low, or low resistance. Among the cultivars deemed moderately low in resistance, 'Obatã IAC 1669-20' and 'IPR 108' had no HR plants, whereas 2.5% of the plants of 'MGS Aranãs' were classified as HR. Intermediate resistance is frequently reported for 'Obatã IAC 1669-20', while most studies classify 'IPR 108' as intermediate, partial or moderately resistant (Carvalho et al., 2022; Sera et al., 2022; Zambolim et al., 2024), consistent with the present results. By contrast, 'MGS Aranãs' has been classified as HR (Zambolim et al., 2024; Lima et al., 2025), but also as intermediate or partially resistant (Carvalho et al., 2022; Sera et al., 2022).

'Tupi IAC 1669-33', 'Acauãnovo', 'IPR 102', and 'Asabranca' exhibited lower mean CLRS values and differed statistically from the 14 more susceptible cultivars described above. Among these four cultivars, 'IPR 102' and 'Asabranca' had lower mean CLRS values than 'Tupi IAC 1669-33' and 'Acauãnovo'. However, %HR plants in 'Tupi IAC 1669-33', 'Acauãnovo', 'IPR 102' and 'Asabranca' were 4.55%, 2.78%, 46.43%, and 64.94%, respectively. When only HR plants were considered, the mean CLRS values were 1.47 for 'IPR 102' and 1.49 for 'Asabranca'. Conversely, the means for the non-HR plants were 2.50 for 'IPR 102' and 2.14 for 'Asabranca', values similar to the overall CLRS means of 'Tupi IAC 1669-33' and 'Acauãnovo'. Based on these results, 'Tupi IAC 1669-33', 'Acauãnovo', 'IPR 102', and 'Asabranca' were classified as having moderate resistance in the present study.

Escape from CLR infection may explain the low percentages of HR plants found in 'Tupi IAC 1669-33', 'Acauãnovo', and 'MGS Aranãs'. By contrast, the higher percentages recorded in 'IPR 102' and 'Asabranca' may be attributable to heterozygosity for major *SH* resistance genes. Previous studies have reported that certain plants from Icatu germplasm carry *SH6-SH9* genes, but with some degree of heterogeneity (Eskes & Costa, 1983). However, HR plants are rarely found in Icatu-derived cultivars, while intermediate levels of resistance, including moderate resistance and moderate susceptibility, are more common (Sera et al., 2022). Lima et al. (2025) also reported fewer resistant cultivars derived from Icatu than from HdT and BA Series germplasms.

Icatu derivatives are commonly classified as intermediate or partially resistant (Carvalho et al., 2022; Sera et al., 2022). The mean CLRS of the non-HR plants of 'IPR 102' indicates a higher level of resistance among plants derived from Icatu germplasm. Given the similar origin of 'IPR 102' and 'IPR 103', the greater resistance of non-HR plants of 'IPR 102' is likely due to a larger number of quantitative trait loci inherited from Icatu. We hypothesize that 'IPR 102' and 'Asabranca' may carry *SH* genes in a heterozygous state that have not yet been overcome by CLR, inherited from their respective parental

lines (Dwarf Icatu and Sarchimor IAC 1668). This hypothesis could be tested through a progeny trial by advancing generations of self-fertilization from multiple HR individuals of these two cultivars. Identification of one or more progenies with 100% HR plants in the next self-fertilized generation would provide strong support for this hypothesis and open the possibility of releasing new cultivars derived from these homozygous progenies.

Resistance to CLR is typically assessed using symptom severity scores, particularly for quantitative (horizontal) resistance under controlled or field conditions (Del Grossi et al., 2013; Lima et al., 2025). However, most studies overlook the percentage of HR plants within a population. In our study, the numerical differences between the mean severity scores of cultivars classified as moderately resistant were substantially larger than those observed among HR cultivars. Although a moderate-high resistance category is plausible, no Arabica coffee cultivars in this study fell into this group. 'Asabranca' and 'IPR 102' occupied an intermediate position between the moderately resistant and HR groups, but both were classified as moderately resistant because they contained non-HR plants.

'Asabranca' is frequently cited as HR to CLR, while 'IPR 102' is often reported as intermediate or moderately resistant (Carvalho et al., 2022; Sera et al., 2022; Zambolim et al., 2024; Lima et al., 2025). However, these authors did not account for the percentage of HR plants, potentially leading to inaccurate resistance classifications. Had classification relied solely on statistical differences in mean CLRS, 'IPR 102' and 'Asabranca' might have been misclassified as having higher resistance levels. Incorporating the percentage of HR plants may therefore be important for accurate resistance classification. Even in the absence of any hypothetical *SH* genes that have not been overcome by the pathogen, 'IPR 102' and 'Asabranca' exhibited a high level of resistance. This suggests that advanced progenies from subsequent generations could achieve resistance levels comparable to the five most resistant cultivars identified in this study.

For many years, 'IAC Obatã 4739', 'Sarchimor MG8840', 'Arara', 'Obatã IAC 1669-20', 'Tupi IAC 1669-33', 'Acauãnovo', 'IPR 102', and 'Asabranca' have been considered HR in Brazil (Carvalho et al., 2022; Zambolim et al., 2024; Lima et al., 2025). However, Sera et al. (2022) reported that some of these cultivars may exhibit either HR or partial resistance to CLR depending on the races or pathotypes present in a given location. Such variability may be associated with differences in the aggressiveness of *H. vastatrix* populations across geographic regions. Our results suggest that the resistance of these eight cultivars was overcome by the fungal populations present in Londrina.

The results for 'Tupi IAC 1669-33' were consistent with those of Silva et al. (2018), who reported that its CLR resistance was overcome in a study involving different *H. vastatrix* races. Similarly, Del Grossi et al. (2013) found that 'IPR 104' was significantly more resistant than 'Tupi IAC 1669-33'. Despite sharing the same genetic origin, the significant differences among 'Sarchimor MG8840', 'Tupi IAC 1669-33', 'IPR 104', and 'IAC 125 RN' suggest differences in the number of resistance genes, consistent with the findings of Silva et al. (2018). According to these authors, some genotypes derived from

HdT may possess fewer resistance genes than others. This variation in resistance gene composition may account for the different resistance levels among genotypes (Sera et al., 2022; Zambolim & Caixeta, 2021) and may reflect reductions in the number of resistance factors, as observed in Indian genotypes derived from HdT (Zambolim & Caixeta, 2021).

These reductions in the spectrum of resistance may have occurred due to selection over successive generations. This hypothesis aligns with Sera et al. (2022), who found that some 'Tupi IAC 1669-33' plants carried fewer resistance genes. A similar loss of resistance factors during selection may have affected 'Obatã IAC 1669-20', 'IAC Obatã 4739', and 'Arara', as indicated by the significant differences observed among the other Sarchimor-derivatives. The lower resistance levels may also be attributed to subsequent hybridizations with Catuaí cultivars. One such case is 'MGS Paraíso 2', which originated from 'Catuaí Amarelo IAC 10' and HdT CIFC 2570. Crosses between HdT derivatives and susceptible *C. arabica* plants tend to reduce the number of resistance factors, as evidenced by the differentials CIFC H420/2 and CIFC H420/10, which originated from the hybridization of 'Catimor CIFC HW26/14' and 'Mundo Novo 1535/33' (Zambolim & Caixeta, 2021). Notably, a single cross with the Mundo Novo cultivar was sufficient to reduce the number of resistance factors: CIFC H420/10 retains *SH5, SH6, SH7,* and *SH9,* whereas CIFC H420/2 possesses only *SH5* and *SH8.*

The results of this study suggest that 'IPR 105', 'Sabiá-Una', 'IPR 107', 'IAC 125 RN', and 'IPR 104' exhibit high resistance to CLR and 100% HR plants, consistent with a homozygous state. In contrast, some segregating plants of 'IPR 102' and 'Asabranca' exhibited strong resistance, indicating the need for further within-cultivar selection to develop new resistant lines in a homozygous state. Notably, 'IPR 105' is the only HR cultivar in this study that is not derived from HdT or Icatu; rather, it originates from the BA-10 accession (Carvalho et al., 2022). Genotypes from the BA Series are known to carry the SH3 gene from *C. liberica,* which is among the few resistance genes not yet overcome by races or pathotypes of *H. vastatrix* in Latin American countries (Zambolim, 2016; Sera et al., 2022). The comparable resistance observed in 'Sabiá-Una', 'IPR 107', 'IAC 125 RN', and 'IPR 104' may indicate that certain HdT-derived resistance genes also continue to provide durable rust resistance.

However, the reliance of the remaining cultivars on HdT germplasm raises concerns regarding potential resistance breakdown, which could cause significant losses for growers cultivating these specific materials. The resistance of 'IAC Obatã 4739', 'Sarchimor MG8840', 'Arara', 'Obatã IAC 1669-20', 'Tupi IAC 1669-33', 'Acauãnovo', 'IPR 102', and 'Asabranca' was overcome in Londrina, where these cultivars exhibited varying degrees of intermediate resistance. The breakdown of resistance in HdT and Icatu-derived cultivars is likely driven by the high degree of variation among *H. vastatrix* subpopulations across different Brazilian regions, as suggested by Cabral et al. (2016). This vulnerability is particularly evident in certain Sarchimor-derived germplasm, such as 'Obatã IAC 1669-20', 'Arara', 'Sarchimor MG8840', and 'IAC Obatã 4739', which failed to express high levels of resistance. Moreover, 'Sarchimor MG8840' and 'IAC Obatã 4739' displayed

greater symptom severity, suggesting that resistance conferred by quantitative trait loci may be less effective than that observed in other cultivars.

Evaluating cultivar reactions to pathotypes from local pathogen populations provides valuable insight into region-specific resistance levels. Previous studies have demonstrated that a single cultivar can exhibit variable resistance depending on the growing region (Del Grossi et al., 2013; Sera et al., 2022; Lima et al., 2025). This variation may result from the local predominance of specific strains and complex interactions among the environment, pathogen, and host (Lima et al., 2025). Furthermore, the selection pressure exerted on HdT-derived resistance tends to favor the emergence of complex races in regions where these cultivars are grown (Talhinhas et al., 2017; Zambolim & Caixeta, 2021).

According to Lima et al. (2025), field studies provide a broader and more challenging perspective for assessing resistance to CLR in Arabica coffee cultivars, reflecting the complexity of the underlying host-pathogen interactions. Beyond generating valuable insights for coffee breeding programs, these findings may also inform decisions regarding the selection of cultivars for specific coffee-growing regions. Future studies on Brazilian cultivars derived from HdT germplasm (e.g., Catimor, Sarchimor, and Catuaí × HdT) should incorporate artificial inoculations with physiological pathotypes of *H. vastatrix* carrying known virulence genes.

Acknowledgments

The authors gratefully acknowledge the financial support of the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES), the Instituto Nacional de Ciência e Tecnologia do Café (INCT Café), and the Consórcio Brasileiro de Pesquisa e Desenvolvimento do Café (Consórcio Pesquisa Café).

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