

FIELD SURVEILLANCE OF PAPAYA LEAF CURL VIRUS AND BEMISIA TABACI IN PUNJAB, PAKISTAN AND IMPACT OF PaLCuV DISEASE ON FRUIT QUALITY OF FOUR COMMERCIAL PAPAYA HYBRIDS

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Abstract

This study assessed the prevalence of papaya leaf curl virus (PaLCuV) disease and its whitefly vector (*Bemisia tabaci*) infestation on four commercial papaya hybrids i.e., Gold F1 [GF1], Red King [RK], Red Lady [RL], and Yellow King [YK] across ten major papaya-growing districts of Punjab province, of Pakistan i.e., Bahawalpur [BHP], Multan [MLT], Sahiwal [SHW], Toba Tek Singh [TTS], Faisalabad [FSD], Sargodha [SGD], Jhelum [JHL], Gujranwala [GJW], Sialkot [SLK], and Narowal [NWL] during 2022-2023 and 2023-2024. Field surveys were conducted annually in three orchards per district, with each orchard serving as a replication within a randomized complete block design (RCBD). Data on percent disease prevalence (PDP) and whitefly infestation levels were collected from first-year cultivated plants. Statistical analysis employed General Analysis of Variance (ANOVA) in GenStat 10th edition, pooling residuals across both years while accounting for year effects. Results revealed significantly higher PDP and whitefly infestation across all four hybrids and all ten districts during 2023-2024 compared to 2022-2023. Hybrid susceptibility varied significantly and Gold F1 consistently exhibited the highest vulnerability, recording average maximum PDP (71.5%) and average maximum whitefly infestation (172.17 whiteflies /plant) in Bahawalpur district. Conversely, Yellow King showed the greatest resistance, with average minimum PDP (10.5%) and average minimum whitefly infestation (29.67 whiteflies /plant) observed in Jhelum district. These findings highlight critical spatial, temporal, and genotypic variations in PaLCuV and whitefly pressure for papaya cultivation in Punjab of Pakistan. The color of healthy and papaya leaf curl virus infected fruits of four papaya hybrids (Yellow King, Red Lady, Gold F1, and Red King) was evaluated through Chroma meter and significant results were recorded among the color values of healthy and PaLCuV infected fruits. The PaLCuV infection ruin the papaya fruits commercially and nutritionally.

INTRODUCTION

Papaya (*Carica papaya* L.) belongs to family Caricaceae, (Bajwa et al., 2018; Udavatha et al., 2022), and it is a widely grown tropical fruit, ranking as the fourth most-produced worldly, after pineapples, bananas, and mangoes (Alam et al., 2024). It also gaining significant importance in Pakistan, particularly in the Punjab province due to its high nutritional value and economic benefits (Yasmeen et al., 2025). In 2022-23, global papaya production was approximately 14.23 million tons, with India leading the output, followed by the Dominican Republic, Mexico, and Brazil (FAOSTAT, 2023). In Pakistan, papaya is cultivated on an area of 1.67 thousand hectares and gaining average papaya fruit yield 0.012 million tons (FAOSTAT, 2023). However, the cultivation of papaya in the country is threatened by various biotic and abiotic stresses, including viral diseases and insect pests (Udavatha et al., 2022). Among the major viral diseases affecting papaya, Papaya leaf curl virus (PaLCuV) is a significant concern. This disease, transmitted by the whitefly (*Bemisia tabaci*), causes severe leaf curling, stunting, and reduced fruit yield (Raj et al., 2008; Naveed et al., 2023). Whitefly itself is a polyphagous pest that can transmit various plant viruses and cause direct damage to crops through sap-sucking (Naveed et al., 2023; Aqsa Abbas, 2025). While foliar symptoms are well-documented, quantitative data on its impact on critical fruit quality parameters the coloration, flavor, and morphology of fruits remain sparse. In recent years, there has been an increasing prevalence of PaLCuV disease and whitefly infestation in papaya orchards of Punjab province of Pakistan. The disease and pest outbreaks have led to significant economic losses for farmers (Biratu, 2022). To address this issue, it is crucial to monitor the disease and pest prevalence, identify the factors influencing their spread, and develop effective management strategies. By understanding the spatial and temporal patterns of disease and pest outbreaks, targeted control measures to could be adopted to minimize crop losses and ensure sustainable papaya production in Punjab province of Pakistan. Therefore, main four objectives of this study were:

To assess the prevalence of PaLCuV disease and whitefly infestation in ten districts of Punjab.

To compare the disease prevalence and infestation levels among four popular papaya hybrids.

To identify the factors influencing the severity of PaLCuV disease and whitefly infestation.

To evaluate the color analysis of healthy and diseased papaya fruits from four commercially significant papaya hybrids.

MATERIALS AND METHODS

Selection of papaya growing districts:

The papaya growing districts were Bahawalpur (BHP), Multan (MLT), Sahiwal (SHW), Toba Tek Singh (TTS), Faisalabad (FSD), Sargodha (SGD), Jhelum (JHL), Gujranwala (GJW), Sialkot (SLK), and Narowal (NWL).

Selection of papaya hybrids:

The studies were planned to assess the percent disease prevalence (PDP) of papaya leaf curl virus (PaLCuV) and whitefly infestation on four papaya hybrids named Gold F1 (GF1), Red King (RK), Red Lady (RL), and Yellow King (YK).

Experimental design:

The PaLCuV disease prevalence and whitefly infestation were recorded from three papaya orchards in each district and each papaya orchard considered as one replication for each papaya hybrid in each year under the randomized complete block design (RCBD) (Montgomery, 2005). The hundred papaya plants for each papaya hybrid were randomly selected in each papaya orchard considered as one replication.

Evaluation of fruit quality parameter

The quality parameter color was measured to assess the effect of PaLCuV infection on papaya fruit quality at Food Technology Section, Post-Harvest Research Center, Ayub Agricultural Research Institute, Faisalabad.

Data collection:

Twelve orchards were visited in each district for the collection of PaLCuV disease prevalence and whitefly infestation data on four hybrids in each year. The data was collected during the two years (2022-2024) of study, on the 1st year cultivated papaya plants. For the sake to assess the effect of PaLCuV on papaya fruit

quality, from one replication, 3 healthy as control and 3 infected plants (on the basis of typical symptoms) were randomly selected and tagged and three representative fruits were sampled from each healthy and infected plant. Fruits were harvested at the commercial standard stage for papaya that is the "color break" stage, where the base skin color begins to change from green to yellow/orange. The fruit peel and pulp color were measured using a Chroma meter, recording CIE L* (lightness), a* (red-green), and b* (yellow-blue) values.

Statistical analysis of data:

PaLCuV disease prevalence and whitefly infestation data was analyzed by general analysis of variance to pool residual of both years using computer software GenStat 10th edition (Steel and Torrie, 1986; George and Mallery, 2019; George and Mallery, 2024). One district is considered as one location during the analysis of variance. The **average main** and interactive means of percent disease prevalence and whitefly infestation were used to determine the significant differences among the treatment by Fisher's protected LSD test at a 5% significance level after analysis of variance (Anova). The data of quality parameter was also subjected to analysis of variance (ANOVA) using statistical software. Treatment means (Healthy vs. Infected) for each hybrid were separated using Fisher's protected LSD test at a 5% significance level after analysis of variance (Anova). Data are presented as mean $\pm$ standard deviation.

RESULTS AND DISCUSSION

This integrated study provides a complete pathway from field-level susceptibility to post-harvest quality collapse, establishing a direct chain: Genetic Susceptibility $\rightarrow$ Enhanced Vector Colonization $\rightarrow$ Increased Disease Prevalence $\rightarrow$ Catastrophic Fruit Quality Loss. The epidemiological data confirmed that Papaya hybrid is the primary factor governing disease prevalence (PDP) and whitefly infestation, exceeding even location and year effects. ANOVA tables 1 and 2 depicted that level of resistance/susceptibility of papaya hybrids has more significant effects on the percent disease prevalence and whitefly infestation than locations. Different hybrids or varieties of different crops is the primary source of variation in the development of infections

also documented in other studies. In similar studies, the level of resistance/susceptibility of commercial rice varieties surpassing the other effect of sowing or planting dates, against the infection of *Bipolaris oryzae* Miyak causing narrow brown leaf spot disease in rice (Mani et al., 2017; Iqbal et al., 2022). Another study is evident many Ty genes in wild and/or cultivated tomato varieties/hybrids, confirmed the various levels of resistance to tomato leaf curl virus (ToLCV) transmitted by *Bemisia tabaci* and causes tomato (yellow) leaf curl disease (TYLCD/ToLCD) ToLCV (Prabhandakavi et al., 2021). The year (2023-24) was a more significant factor than locations aligned with emerging entomological models of *Bemisia tabaci* population dynamics under climate variability. After various level of genetic resistance/susceptibility of papaya hybrids, the effect of years was the second most important source of variation on the PDP and whitefly infestations. In the two year study on narrow brown leaf spot disease of rice, it was revealed that the higher primary inoculum from year one leads to higher disease development in next year, which is compounded by potential climate factors favoring the disease epidemic (Iqbal et al., 2022). Therefore, PDP and whitefly infestation was significantly observed more prominent during the years 2023-24 rather than 2022-23. The effects of years were assessed during the statistical analysis. Other study on the PaLCuV depicted that disease was successfully transmitted by *Bemisia tabaci* (whitefly) from naturally infected papaya to healthy seedlings of papaya, tobacco, tomato and chilli and all the inoculated test species displayed typical leaf curl symptoms indicating the association of a whitefly transmissible infectious agent, a begomovirus, with the leaf curl disease of papaya (Raj et al., 2008). The tables 3 and 4 depicted that main and interactive means (PH $\times$ Yr, L $\times$ Yr, and L $\times$ PH $\times$ Yr) of years on the PDP and whitefly infestations were found to be highly significant. The main and interactive means of percent disease prevalence (PDP) of papaya leaf curl virus (PaLCuV) disease and whitefly infestation were found highly significant i.e., papaya hybrids, locations, years, papaya hybrids $\times$ locations, papaya hybrids $\times$ years, locations $\times$ years, papaya hybrids $\times$ locations $\times$ years. The significant papaya hybrid $\times$ year interaction exhibited that environmental stressors unmask genetic vulnerabilities, making already susceptible hybrids like

Gold F1 disproportionately worse in high-pressure years. Maximum PDP was recorded on papaya hybrid Gold F1 (71.5%) in district Bahawalpur and minimum on papaya hybrid Yellow King (10.5%) in district Jhelum. The significant Location $\times$ Papaya Hybrid interaction, with maximum severity in Bahawalpur, is not only climatic. It is documented that it is a major cotton-growing region. *Bemisia tabaci* is a polyphagous pest that migrates from cotton to alternative hosts like papaya, creating a regional inoculum bridge (Jones, 2003; Gaffke et al., 2024; Aqsa Abbas, 2025). So, maximum whitefly infestation was recorded on same papaya hybrid Gold F1 (172.17%) in district Bahawalpur and minimum on papaya hybrid Yellow King (29.67%) in district Jhelum. Maximum average main PDP (51.33%) and average main whitefly infestation (126.75%) on all papaya hybrids were recorded in district BHP and minimum average main PDP (21.17%) and whitefly infestation (53.25%) in district JHL. Maximum average main PDP (45.93%) and whitefly infestation (105.72%) were recorded on papaya hybrid Gold F1. The high susceptibility of Gold F1 mirrors the "plant vigor" hypothesis, where lush, soft growth often selected for in high-yielding F1 hybrids can inadvertently increase attractiveness to phloem-feeding insects (Gaffke et al., 2024). The minimum average main PDP (10.50%) and whitefly infestation (56.05%) were recorded on papaya hybrid Yellow King in all districts. The results strongly corroborate the hierarchy of resistance reported in other begomovirus-vegetable pathosystems. The consistent performance of papaya hybrid Yellow King as the least susceptible hybrid, showing the lowest PDP (10.5%) and whitefly infestation (29.67%), parallels results in tomato, where certain genotypes exhibit both antibiosis (reduced vector survival) and antixenosis (non-preference) against *B. tabaci* (Prabhandakavi et al., 2021). The main average PDP of PaLCuV disease was statistically at par in districts MLT and FSD, GJW and SLK, SGD and NWL. While main average whitefly infestations were statistically at par in districts TTS and SHW, and SGD and NWL. The interactive average PDP of **Interactive average** means of whitefly infestation were statistically at par in another two districts FSD (103.83%) and TTS (102.50%) on papaya hybrid RL. The interactive average means of whitefly infestation

PaLCuV disease was statically at par in three districts MLT, TTS and BHP. Among them, average interactive PDP in two districts MLT (57.00%) and TTS (55.50%) recorded on papaya hybrid Gold F1 and in BHP (54.67%) on papaya hybrid Red Lady respectively as depicted in Table. The interactive average PDP of PaLCuV disease was statically at par in three districts MLT (46.00%), FSD (47.50%) and TTS (44.17%) on papaya hybrid Red Lady. The interactive average PDP of PaLCuV disease was statically at par in three districts TTS (35.00%), SHW (36.33%) and SGD (34.50%) on papaya hybrids Red King and Gold F1 respectively. The interactive average PDP of PaLCuV disease was statically at par in two districts SLK (31.50%) and NWL (30.67%) on papaya hybrids Red King and Gold F1 respectively. The interactive average PDP of PaLCuV disease was statically at par in five districts. Among them, in district MLT (25.83%) on papaya hybrid YK and in three districts GJW (25.50%), SGD (26.67%) and JHL (24.50%) on papaya hybrid RL and on papaya hybrid RK in districts SGD (26.83) and NWL (26.67%) respectively. The interactive average PDP of PaLCuV disease was statically at par in four districts. Among them, in three districts FSD (20.67%), TTS (20.83%) and SHW (19.33%) on papaya hybrid YK, and in district JHL (20.83%) on papaya hybrid RK. The interactive average PDP of PaLCuV disease was statically at par in three districts SLK (15.33%), GJW (14.33%), and NWL (13.50%) on papaya hybrid YK.

The interactive average means of whitefly infestation were statistically at par in two districts MLT and BHP, in district MLT (132.00%) on papaya hybrid GF1 and in district BHP (131.33%) on papaya hybrid RL. Similarly, the interactive average means of whitefly infestation were statistically at par in other two districts TTS and BHP, in district TTS (123.17%) on papaya hybrid GF1 and in district BHP (120.83%) on papaya hybrid RK. The interactive average means of whitefly infestation were statistically at par in another two districts MLT and SHW, in district MLT (113.00%) on papaya hybrid RK and in district SHW (110.50%) on papaya hybrid GF1. The

were statistically at par in three districts GJW, SHW and TTS, in district GJW (94.50%) on papaya hybrid GF1 and in other two districts SHW (93.00%) and TTS (91.00%) on papaya hybrid RK. The interactive

average means of whitefly infestation were statistically at par in three districts BHP, GJW and SLK. In district BHP (82.67%) on papaya hybrid YK, in district GJW (82.00%) on papaya hybrid RK and in district SLK (81.67%) on papaya hybrid GF1. The interactive average means of whitefly infestation were statistically at par in three districts NWL, SGD and JHL. In district NWL (64.00%) on papaya hybrid RK and in other two districts SGD (62.67%) and SLK (61.67%) on papaya hybrid RL. The interactive average means of whitefly infestation were statistically at par in three districts JHL, GJW and SLK. In district JHL (54.67%) on papaya hybrid RK and in other two districts GJW (49.50%) and SLK (48.00%) on papaya hybrid YK. The interactive average means of whitefly infestation were statistically at par in three districts NWL (36.00%), SGD (33.33%) and JHL (29.67%) on the same papaya hybrid YK. Once an infection begins, the interactions among pathogens, crops, and environmental conditions design the pattern of the disease development, influencing both its spread and severity depending on the virulence of pathogen, plant host susceptibility and favorable environmental conditions (Ilan R. Crute, 1996; Iqbal et al., 2022).

and flesh of healthy and PaLCuV-infected papaya fruits at the commercial "color break" stage. The letter L indicated the lightness (0 = black to 100 = white) of color of peel and flesh of healthy and PaLCuV infected fruits of four papaya hybrids. The L values indicated disease caused a significant increase in lightness, indicating paler, and washed-out appearance. The letter a^* indicated the variation from red to green (*positive values = redness, and negative values = greenness). Diseased flesh shows drastic reduction in positive a^* , indicating loss of red pigments (lycopene/beta-carotene). The a^* values redness parameters showed the most dramatic disease effect in red-fleshed varieties. The letter b^* indicated the color variation yellowish to blue (positive values = yellowness). The b^* values yellowness decreased significantly across all tissues specially in papaya hybrids Yellow King and Gold F1. Diseased tissues show reduced b^* , indicating loss of yellow carotenoids. The data depicted a consistent and clear pattern of color degradation in PaLCuV-infected fruits, which directly correlates with a extreme loss of marketability and consumer attraction. The severe drop in positive a^* and b^* values in the flesh indicated

The papaya hybrid Gold F1 identified as highly susceptible to the begommo viruses through field observations also exhibited the most significant decline in quality during subsequent laboratory analysis, specifically using colorimetric analysis. This depicted how genetic resistance/susceptibility directly impacts the physiological and biochemical responses to an infection, which are quantifiable through techniques like colorimetric. The color degradation in infected fruits provides quantitative evidence of metabolic disruption caused by PaLCuV infection (Rahoutei et al., 2001). The less negative a^* value in diseased peel (indicating retained greenness) is a direct visual marker of the virus interrupting the normal ripening-related senescence pathways. Table 5 presented the colorimetric data (L , a^* , b^*) for the peel and flesh of healthy and PaLCuV-diseased fruits for the four papaya hybrids, and depicted the prominent color reduction. All three main effects (papaya hybrids, infection status, and tissue type) showed highly significant effects ($p < 0.001$) on all three color parameters CIE L^* , a^* or b^* . There is significant difference in color values CIE L^* , a^* or b^* for the peel a systemic failure in synthesizing and accumulating key carotenoids: lycopene (red) and beta carotene (yellow-orange). The color loss is not cosmetic; it highlighted a significant decrease in provitamin A and antioxidant levels. The papaya fruits from PaLCuV-infected plants are undesirable for commercial fresh market and food processing industry (e.g., baby food, purees). Red-fleshed papaya hybrids (red king and red lady) depicted significant loss in a^* values. Papaya hybrid Gold F1 showed the highest rise in L^* value for flesh indicating significant texture degradation. The flesh tissue showed larger absolute changes in a^* values for papaya hybrids Red King and Red Lady. The peel tissue had greater percentage changes in b^* values across all hybrids. The significant Papaya Hybrids $\times$ Infection Status $\times$ Tissue Type interaction revealed that PaLCuV disease affected the peel and flesh of different papaya hybrids according to their genetics. Another study on the identification of novel begomo viruses linked with leaf curl disease of papaya (*Carica papaya* L.) in India also revealed that PaLCuV infected fruits remained under developed and never reached to full maturity (Udavatha et al., 2022) which corroborated the results of present study.

Table1: General analysis of variance of PDP on four papaya hybrid (PH) in the ten districts (D) for the years 2022-23 and 2023-24

S.O.V.	D.F.	S.S.	M.S.	V.R.	F. Pr.
R stratum	2	1835.108	917.554	166.34	
PH ^a	3	24117.83	8039.278	1457.4	<.001
L [†]	9	22540.98	2504.554	454.04	<.001
Yr [◇]	1	7593.75	7593.75	1376.63	<.001
PH×L	27	2989.917	110.738	20.08	<.001
PH×Yr	3	156.55	52.183	9.46	<.001
L×Yr	9	995.5	110.611	20.05	<.001
PH×L×Yr	27	869.533	32.205	5.84	<.001
Residual	158	871.558	5.516		
Total	239	61970.73			

**Highly significant F. Pr.≤0.01

[†]Locations,^aPapaya Hybrids,[◇]Years

CV (R Stratum)

10%

CV (R. Units Stratum) 07%

Table 2: General analysis of variance of whitefly infestations on four papaya hybrid (PH) in the ten districts (D) for the years 2022-23 and 2023-24

S.O.V.	D.F.	S.S.	M.S.	V.R.	F. Pr.
R stratum	2	6076.22	3038.11	52	
PH ^a	3	78321.03	26107.01	446.85	<.001
L [†]	9	129193.2	14354.8	245.7	<.001
Yr [◇]	1	36113.07	36113.07	618.11	<.001
PH×L	27	10109.47	374.42	6.41	<.001
PH×Yr	3	1254.03	418.01	7.15	<.001
L×Yr	9	7562.43	840.27	14.38	<.001
PH×L×Yr	27	2477.8	91.77	1.57	0.047
Residual	158	9231.11	58.42		
Total	239	280338.4			

**Highly significant F. Pr.≤0.01

[†]Locations,^aPapaya Hybrids,[◇]Years

CV (R Stratum) 7.3%

CV (R. Units Stratum) 09%

Table 3: Comparative main and interactive (L×PH) means of PDP on four papaya hybrids (PH) at ten locations (L) for the years (Yr) 2022-23 and 2023-24

Papaya Hybrids						
Locations		GF1	RL	RK	YK	Main Means
	BHP	71.50 ^a	54.67 ^c	50.33 ^d	28.83 ^{ij}	51.33 A
	MLT	57.00 ^c	46.00 ^e	45.83 ^{ef}	25.83 ^j	43.67 B
	FSD	62.17 ^b	47.50 ^e	43.00 ^f	20.67 ^k	43.33 B
	TTS	55.50 ^c	44.17 ^e	35.00 ^h	20.83 ^k	38.88 C
	SHW	48.17 ^{de}	39.83 ^g	36.33 ^h	19.33 ^k	35.92 D
	GJW	39.17 ^g	25.50 ^j	28.33 ^{ij}	14.33 ^l	26.83 E
	SLK	31.83 ^{hi}	31.50 ⁱ	28.17 ^{ij}	15.33 ^l	26.71 E
	SGD	34.50 ^h	26.67 ^j	26.83 ^j	12.33 ^{lm}	25.08 F
	NWL	30.67 ⁱ	28.83 ^{ij}	26.67 ^j	13.50 ^l	24.92 F
	JHL	28.83 ^{ij}	24.50 ^j	20.83 ^k	10.50 ^m	21.17 G
Main Means		45.93 ^A	36.92 ^B	34.13 ^C	18.15 ^D	GM 33.78

Means having the same letters did not differ significantly at 5% level of significance by Fisher's Protected LSD test

Table 4: Comparative main and interactive (L×PH) means of whitefly infestation on four papaya hybrids (PH) at ten locations (L) for the years (Yr) 2022-23 and 2023-24

Whitefly infestations on Papaya Hybrids						
Locations		GF1	RL	RK	YK	Main Means
	BHP	172.17 ^a	131.33 ^b	120.83 ^c	82.67 ^g	126.75 A
	MLT	132.00 ^b	125.00 ^{bc}	113.00 ^d	72.83 ^h	110.71 B
	FSD	127.00 ^{bc}	103.83 ^e	99.83 ^{ef}	67.67 ^{hi}	99.58 C
	TTS	123.17 ^c	102.50 ^e	91.00 ^f	71.00 ^{hi}	96.92 D
	SHW	110.50 ^d	98.17 ^{ef}	93.00 ^f	69.83 ^{hi}	92.87 D
	GJW	94.50 ^f	81.50 ^{gh}	82.00 ^g	49.50 ^j	76.87 E
	SLK	81.67 ^g	79.00 ^{gh}	74.17 ^{gh}	48.00 ^j	70.71 F
	SGD	79.50 ^{gh}	62.67 ⁱ	66.50 ^{hi}	33.33 ^k	60.5 G
	NWL	69.67 ^{hi}	65.67 ^{hi}	64.00 ⁱ	36.00 ^k	58.83 G
	JHL	67.00 ^{hi}	61.67 ⁱ	54.67 ^j	29.67 ^k	53.25 H
Main Means		105.72 ^A	91.13 ^B	85.9 ^C	56.05 ^D	GM 84.70

Means having the same letters did not differ significantly at 5% level of significance by Fisher's Protected LSD test

Table 5: Tissue color analysis of healthy and papaya leaf curl virus infected papaya fruits of four papaya hybrids

Papaya Hybrid	Tissue	<i>L* Value</i>	<i>a* Value</i>	<i>b* Value</i>
Yellow King	Peel (Healthy)	66.2 ± 2.1 ^a	-11.5 ± 1.5 ^a	58.7 ± 3.0 ^a
	Peel (Diseased)	71.5 ± 3.5 ^b	-8.4 ± 2.8 ^b	37.0 ± 4.5 ^b
	Flesh (Healthy)	68.7 ± 1.7 ^c	5.8 ± 0.9 ^c	63.2 ± 2.5 ^c
	Flesh (Diseased)	75.6 ± 2.3 ^d	2.2 ± 1.3 ^d	44.7 ± 3.8 ^d
Red Lady	Peel (Healthy)	63.1 ± 1.6 ^e	18.7 ± 2.1 ^e	52.6 ± 2.8 ^e
	Peel (Diseased)	70.4 ± 4.2 ^f	8.7 ± 3.4 ^f	40.7 ± 5.1 ^f
	Flesh (Healthy)	55.5 ± 1.3 ^g	32.4 ± 2.4 ^g	38.3 ± 2.0 ^g
	Flesh (Diseased)	65.7 ± 3.3 ^h	15.4 ± 3.3 ^h	42.4 ± 4.2 ^h
Gold F1	Peel (Healthy)	66.9 ± 2.1 ⁱ	-10.5 ± 1.3 ⁱ	60.2 ± 2.5 ⁱ
	Peel (Diseased)	74.5 ± 3.5 ^j	-6.7 ± 2.8 ^j	36.0 ± 4.8 ^j
	Flesh (Healthy)	70.4 ± 1.3 ^k	8.7 ± 0.7 ^k	65.4 ± 2.2 ^k
	Flesh (Diseased)	78.7 ± 2.7 ^l	3.6 ± 1.4 ^l	48.6 ± 4.0 ^l
Red King	Peel (Healthy)	60.6 ± 1.6 ^m	20.5 ± 1.7 ^m	48.4 ± 2.3 ^m
	Peel (Diseased)	68.7 ± 4.6 ⁿ	9.8 ± 3.0 ⁿ	38.6 ± 5.5 ⁿ
	Flesh (Healthy)	52.8 ± 1.2 ^o	35.9 ± 1.7 ^o	32.7 ± 1.8 ^o
	Flesh (Diseased)	63.4 ± 3.3 ^p	12.7 ± 4.5 ^p	40.3 ± 4.5 ^p

Means within each color parameter (L, a*, or b*) having the same superscript letter are not significantly different (p>0.05). Different superscript letters indicate statistically significant differences (p<0.05) according to Fisher's Protected LSD test. L (Lightness): * LSD_{0.05} = 2.14

a (Red-Green): * LSD_{0.05} = 1.79

b (Yellow-Blue): * LSD_{0.05} = 2.66

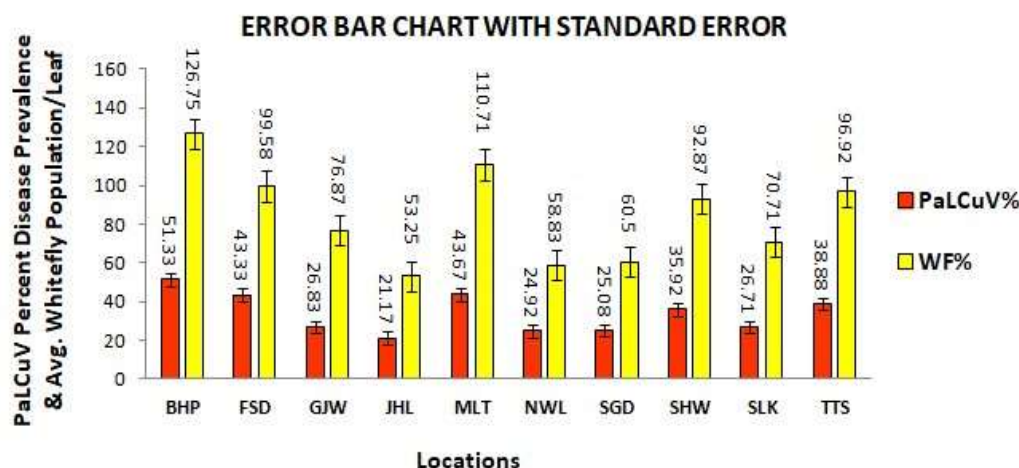


Figure 1: Error bar chart with standard errors depicting the estimated errors of means of PDP on the samples of four papaya hybrids taken from their respective populations of papaya orchards. The four papaya hybrids in the ten districts have shown significant variation in their genetic resistance/susceptibility to the PDP of PaLCuV.

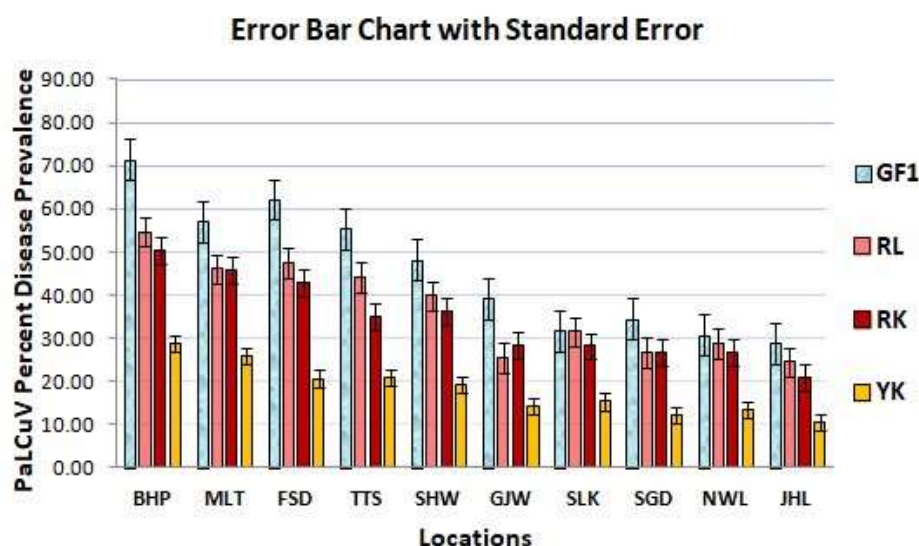


Figure 2: Error bar chart with standard errors depicting the estimated errors of means of PDP on the samples of four papaya hybrids taken from their respective populations of papaya orchards during the both years 2022-23 and 2023-24. The four papaya hybrids have shown significant variation in their genetic resistance/susceptibility to the PDP of PaLCuV disease during the both years.

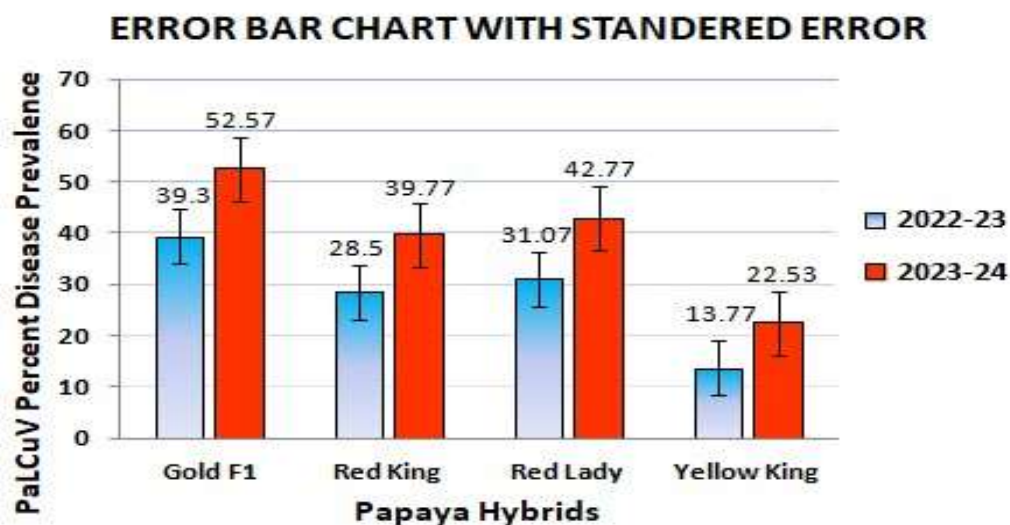


Figure 3: Error bar chart with standard errors depicting the estimated errors of means of PDP and whitefly infestations on the samples of four papaya hybrids taken from their respective populations of papaya orchards of ten districts.

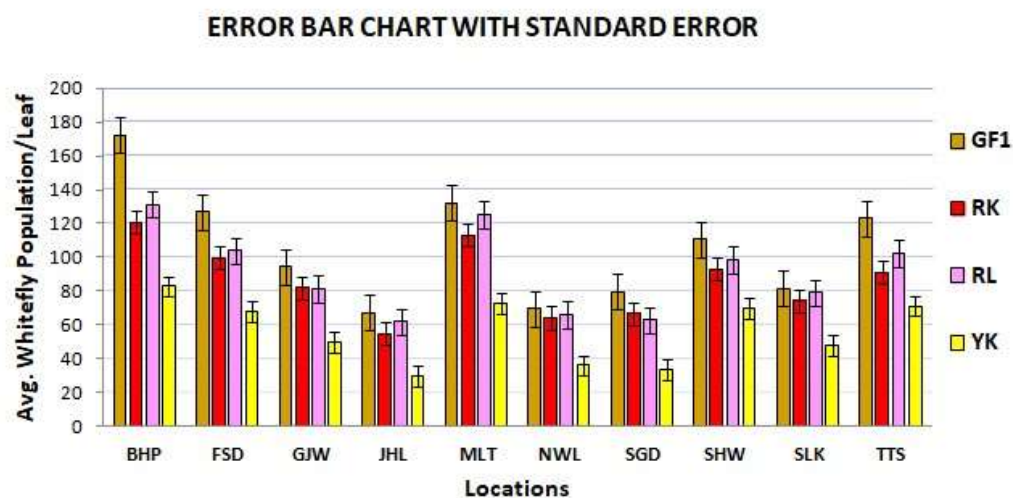


Figure 4: Error bar chart with standard errors depicting the estimated errors of means of whitefly infestations on the samples of four papaya hybrids taken from their respective populations of papaya orchards of ten districts during the both years of study.

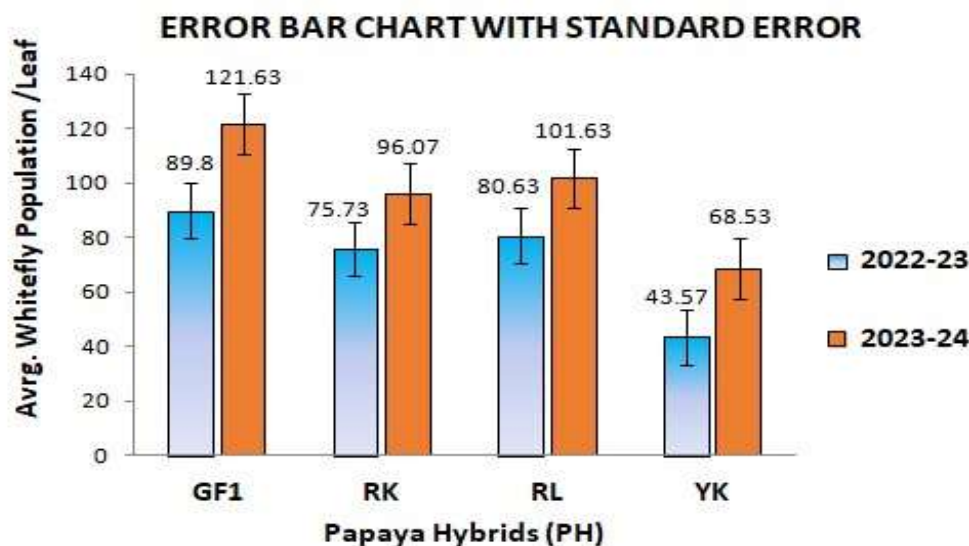


Figure 5: Error bar chart with standard errors depicting the estimated errors of means of whitefly infestations on the samples of four papaya hybrids during the both years of study.

There are positive and critical implications of correlation between field susceptibility (high PDP) of papaya hybrids and their post-harvest quality loss (severe color/flavor degradation). It means that on the basis of visual symptoms of PaLCuV infection on papaya fruits and plants it can be predicted that entire papaya orchard blocks that will produce unmarketable fruit. This can inform harvest logistics and market planning. Breeding programs must therefore incorporate post-infection quality metrics as basic selection criteria. Further it is concluded that papaya hybrids Yellow King and Red Lady depicted performed better than Red King or Gold F1. In cotton growing districts, the management of whitefly is most important to manage the PaLCuV disease. Papaya orchards should be distanced from cotton as precautionary measure. Pack-houses should implement simple, low-cost Chroma meters. Whitefly pest scouting should be in routine practice. It is concluded that this research bridges the gap between disease epidemiology of papaya plants and food science of papaya fruits. The genetic susceptibility of a papaya hybrid to PaLCuV is the dominant factor not only in disease spread but also in determining the final economic value of the papaya fruit harvest through its definitive impact on color, taste, and shape. In the metabolic system of papaya fruits and plants main disrupter is virus infection. Future work

must focus on molecular basis identification of the resistance genes in papaya hybrids against both the virus and its vector.

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