

Wilt Disease of Pigeon Pea [*Cajanus cajan* (L.) Millsp.] Caused by *Fusarium Oxysporum* F. Sp. *Udum*

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Abstract

Pigeonpea (*Cajanus cajan*) cultivation is adversely affected by *Fusarium* wilt, caused by the pathovar of *F. udum*. In the absence of related studies, this paper re-analyzed and described some published works. These included a survey of 25 locations and 7 genotypes described by Biswas and his colleagues (2020), and a study conducted by Ravikumara and his colleagues (2022), in which they reported results of 11 host differentials, and mean wilt scores against 60 *F. udum* isolates from 5 state locations. The highest wilt incidence across locations in the published studies were from Anjad (26%) and Sanawad (23.8%). More elevated un-weighted mean wilt scores were reported from West Bengal (14.57% from 3 locations) and Madhya Pradesh (14.42% from 10 locations) locations. Among the host differentials evaluated in 2022, ICP 9173 showed the lowest (4.48%) wilt incidence. In 2022 greenhouse trials, ICP 8863 showed 3.33% wilt, and the remaining check lines, Parwati and ICP 2376, showed 90% wilt incidence. Based on the studies, researchers should employ an integrated pest management approach alongside pathogen-isolate validation.

Keywords: *Cajanus cajan*; *Fusarium udum*; *Fusarium oxysporum*; vascular wilt; pigeonpea genotypes; field incidence; host differentials; resistance screening.

1. Introduction

1.1 Background of pigeon pea and importance of wilt disease

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is a legume of agricultural importance in dry and humid regions. It provides food, fodder and fuel as well as improving soil fertility through biological nitrogen fixation. However, Grain legumes are often neglected in comparison to food and fodder crops. But increased emphasis has been placed on the development of pigeonpea in view of the scarcity of grain legumes in dryland agriculture and its relatively higher adaptation to normal and deficit irrigation and marginal fertilizers. Furthermore, pigeonpea has good potential for genetic improvement and has the potential to be transformed into an ideal grain legume crop.

Fusarium wilt is reported to occur in virtually all pigeonpea growing areas of the world. The pathogen is soilborne and survives in the field for long periods. Often the first sign of the disease is the wilting of the plant. Later on the plant shows yellowing of the leaves and the stem turns brown. Dead and healthy plants may be seen in the same pigeonpea stand. Under field conditions the disease may go unnoticed because the presence of a single wilted plant does not indicate that the field is infested.

A taxonomic distinction is necessary. Based on the research collected, *Fusarium udum* Butler is the pathogen accepting for pigeonpea wilt. *Fusarium oxysporum* is a related species complex and a well-studied cause of vascular wilt of other hosts. It provides information on colonial growth and specialization to other hosts. It is inappropriate to interpret tests done against *F. udum* to be infection by *F. oxysporum*. The scope of this research is restricted to *F. udum*. Other literature on *Fusarium* is cited to illustrate approaches and/or management strategies for vascular wilt of other systems (Di Pietro et al., 2003; Gordon, 2017; Srivastava et al., 2023).

Image 1: Typical external wilt symptom appearance in a pigeonpea-like field condition



Explanation: The field view illustration shows a drying plant among other plants. This illustration is to help you identify a symptom of FND, and is not for assessment.

Image 2: Cajanus cajan botanical morphology for crop identification



Explanation: This plate illustrates various stages of the pigeonpea plant. Blanco (1843)

Image source: https://commons.wikimedia.org/wiki/File:Cajanus_cajan_Blanco1.167-cropped.jpg

1.2 Problem statement and research gap

Observers have a tough time linking wilt symptoms to management practices for several reasons. Most importantly, the pressure from the pathogens that cause wilt varies. Some areas have numerous, well-defined, wilted fields; other areas have random, scattered, wilted fields. A genotype that is rated as wilt-resistant in one greenhouse study may not be if it is challenged by a different isolate or is grown in a different environment. Genotype X has been grown in several different wilt-susceptible fields in the same state. Even if the soil, climate and other conditions are similar from field to field, the prior history of how a field has been grown and the amount of living inoculum that is still in the soil can vary from field to field. Because of all these variables, the term “wilt-prone area” is vague and unhelpful. A more accurate approach is to define the locations of the fields, describe the symptoms, and name the genotypes that were tested (Sharma et al., 2016; Ravikumara et al., 2022).

It is necessary to screen a broader range of *F. udum* isolates because different pathogenic variants can exist and may result in varying degrees of symptoms on a standard host panel. Support for this hypothesis is provided by molecular studies on *F. udum* as well as studies on pigeonpea defense response mechanisms (Biswas et al., 2020; Srivastava et al., 2023). However, these studies do not fully validate the hypothesis.

This study integrates four levels of observation; variation at each level is analyzed and reported. This includes variation among field collections, laboratory replications, and state averages as well as differentials in host responses. Studies report high levels of variability among field collections and laboratory replications. Based on studies integrated in this report, relatively little wilting has been observed in host entries. This study outlines the scope of integration possible when studies are conducted in a complementary manner, but stopping short of stating definite

conclusions. The focus of this work is interdisciplinary integration of published studies and an evaluation of host entries that have been reported to wilt the least.

2. Review of Literature

2.1 Pathogen biology, disease cycle and symptom expression

Soil-borne pathogens thrive on vascular plants and are known to cause diseases including wilt. Several *Fusarium* species are known to cause diseases in different plants, and survive in a variety of plant and soil debris. Susceptible host plants provide entry into the vascular system of the plant. Xylem, the vascular system of the plant, plays a pivotal role in the transport of water and other nutrients to different parts of the plant. If any pathogen clogs the xylem, it creates an obstruction in the water transport system of the plant and causes the plant to wilt. Chlorosis is the discoloration of the plant due to lack of pigments. Disease mechanisms of *Fusarium* species remain the same and are broadly similar to pigeonpea wilt. *Fusarium* wilt of pigeonpea is caused by *Fusarium udum*. *Fusarium* wilts are classified based on the host plant and therefore mechanisms of one species cannot be extrapolated to another. These wilts fall under the major plant pathogenic fungi. Host colonization by pathogenic fungi is attributed to a variety of factors including secreted proteins and other toxins.

In case of pigeonpea, *Fusarium* wilt, symptoms take a long time to develop and do not become evident until the later stages of plant growth and development. Initial symptoms include partial, or complete yellowing and collapse of leaves. Sometimes, dried up and withered plants are seen growing among the normal plants. These symptoms occur due to blockage of the vascular system of the plant by *Fusarium*. Internal symptoms are diagnosis and more reliable than external symptoms. *Fusarium* wilts are some of the most common soil-borne pathogens of plants. These pathogens remain problematic due to the lack of an adequate cure and control strategies. A variety of advanced molecular diagnostic tools and old methodologies help in the identification of *Fusarium* wilts.

Studies on *Fusarium oxysporum* species complex have shown that there are lineages that can colonize multiple host plants. One of the pathogenic traits is carried on mobile chromosomes. Studies on different plant diseases have shown that some *Fusarium oxysporum* can colonize a single host plant. However, the presence of *Fusarium oxysporum* that can colonize pigeonpea does not necessarily imply that *Fusarium oxysporum* that affects pigeonpea carries that pathogenic trait. Similarly, the presence of *Fusarium oxysporum* that can colonize other plants does not necessarily mean that *Fusarium oxysporum* that can colonize a particular plant belongs to the same species. There are multiple examples that show that it is important to determine the true identity of a pathogen, and a genus name alone should not be used to determine a pathogen's host range.

With regard to pigeonpea, there is evidence that *Fusarium udum* can colonize pigeonpea, and sequencing has shown that *Fusarium udum* has genes, enzymes, and other factors that can help it colonize pigeonpea. However, not all cases of *Fusarium udum*-infected pigeonpea have been proven. Field epidemiology and other environmental variables should be considered. In general, when looking at pigeonpea, it should be determined what factors help *Fusarium* colonize pigeonpea (Srivastava et al., 2023; Ravikumara et al., 2022).

2.2 Host resistance, genotype variability and genomic resources

According to Varshney et al. (2020), wilt resistance should be managed sustainably, and one way of achieving this is to reduce reliance on treating wilt-infested soils. Wilt resistance is not a constant; it varies with place and time (Sharma et al., 2016). In multiple-location screening, Sharma and colleagues observed important contributions of genotype and environment as well as genotype by environment interaction. Thus, performance of a genotype in one screening location cannot project its performance in another location. Genotypes evaluated in screening locations are always compared to a set of standard check genotypes.

The development of genome sequences and resequencing of accessions has enabled identification of genetic variations and developed markers for improvement of wilt resistance in pigeonpea. While accessions may be sequenced, this does not necessarily mean they carry durable wilt resistance. This can only be ascertained by genetic marker assessment in the context of target pathogen populations (Varshney et al., 2012, 2017; Singh et al., 2012).

Published genotype screening helps connect the genetics of agricultural crops to field performance. Biswas et al. (2020) screened local landraces Richa, Desi Nimar and Desi Tur, Parwati and WB-20/105 against ICP 8863 and ICP

2376. Richa and ICP 8863 showed less wilt, while Parwati and ICP 2376 showed more wilt. Land races are locally cultivated crop varieties. Screening land races for diseases can help identify (un)known plant resistances. Screening land races does not guarantee that all crop plants with a land race name respond similarly to different pathotypes of the same disease.

Host differentials panels test crop plants against several pathotypes. Eleven crop plants in Ravikumara et al. (2022) were challenged against 60 pathotypes of *Fusarium oxysporum* f. sp. *cubense*. Some crop plants were challenged with several *F. oxysporum* pathotypes and showed resistance against pathotypes. However, further research cannot validate that crop plants resistant to several pathotypes act as ‘resistance’ against pathotypes in other cropping systems. To determine crop plants resistant to *F. oxysporum* in a particular cropping system, integration of pathotypes with genomic and field research is essential (Biswas et al. 2020, Srivastava et al. 2023).

2.3 Management approaches and biological control

Integrated management approaches take account of the fact that complete elimination of soil-borne wilt pathogens is not likely. Resistance in crop varieties is the most critical element of defense. Pathogens can be managed to some degree using cultural practices such as crop rotation with non-hosts, removal of infected crop residues, and sanitation. Integrated soil management is focused on maintaining and improving the health of crop species. This is achieved primarily by manipulating soil conditions and soil organisms to favor the crops grown, and can be integrated into farm management systems to support a variety of crops. Long-term recommendations for soil management must be modified based on the specific regional cropping systems and the most likely soil-borne pathogens. While integration is supported in most situations, Edel-Hermann & Lecomte (2019) and Gordon (2017) show that persistence and host specificity of *Fusarium* pathogens vary between different pathosystems.

There is potential for integration of biological control methods. As described by Dave and Ingle (2021), *Streptomyces* sp. S-9, when applied on pigeonpea, shows potential to prevent and/or suppress *Fusarium* wilt and promote plant growth. Furthermore, Reddy et al. (2024) identified some potential biological control agents for *F. udum*. However, these studies evaluated specific organisms and situations, and hence we cannot assume that an unrelated microbial formulation would assist in controlling *Fusarium* wilt on farmers’ fields. It is essential to examine the soil ecology and evaluate the consistency of results across crop growing seasons.

The most adequate management strategy for *Fusarium* wilt is to integrate the knowledge on diagnosis of the pathogen, use of resistant varieties, and agricultural practices to reduce the favorable conditions for the pathogen. While the integration of agricultural practices to reduce the pathogen favorable conditions is encouraged, similarly, the integration of other strategies such as laboratory and field research to improve the resistance of the variety is encouraged. From a scientific standpoint, the integration of various approaches should be encouraged to manage *Fusarium* wilt (Sharma et al., 2016; Dave & Ingle, 2021; Reddy et al., 2024).

Table 1: Literature themes and their relevance to pigeonpea wilt

Theme	Established evidence	Relevance to this analysis	Principal sources
Pathogen biology	Root infection and vascular colonisation; pathogen diversity	Interpret field and causal symptoms distinguish species	Di Pietro et al. (2003); Srivastava et al. (2023)
Host resistance	Contrasting genotype response and environment-dependent stability	Interpret greenhouse and multi-isolate rankings	Sharma et al. (2016); Biswas et al. (2020)
Management	Resistance together with sanitation, rotation and microbial tools	Translate descriptive patterns into testable interventions	Dave & Ingle (2021); Reddy et al. (2024)

Explanation: The three elements of literature connect the disease process, the response of the plant, and the management of the situation without treating *Fusarium* wilt, for which direct evidence is available for pigeonpea.

3. Materials and Methods

3.1 Sources of observations and variables

We analyzed the published results of Biswas et al. (2020) and Ravikumara et al. (2022). The first source documented village-level cases of wilt and greenhouse observations for five local landraces and two control genotypes. The authorship team conducted the surveys between October 2014 and January 2015. Biswas et al. (2020) published the results. Therefore, “2020” indicates the result’s publishing year and does not represent a field season. Ravikumara et al. (2022) cited mean wilt responses of eleven pigeonpea genotypes to 60 isolates of *Fusarium udum* and the average wilt incidence at the state level in India where these trials were conducted.

Variables were recorded at the field level for state, district, village or tehsil; percentage and grade of disease incidence; and screening. Screening records showed genotype, source of infection, number of plants assessed per replicate, number of plants that wilted, and the observer’s reaction. Fifteen means of the five reported states and eleven responses of hosts were treated as different entities because of differences in the location covered, pathogen samples, and studies. The report gives means for several cultivars. Numbers in the report are means for each cultivar, not values for a single sample. The report also did not give new data to identify wilt pathogens of pigeonpea. Pathogen identification is based on data from earlier studies.

Table 2: Published observation groups and variables considered

Observation group	Records	Recorded variables	Analysis
Village incidence (2020 publication)	25 locations	State; district; village; wilt (%); grade	Unweighted site means; range; category frequency
Genotype screening (2020 publication)	7 genotypes × 5 replicates	Six plants per replicate; wilt count; reaction	Count-based incidence; comparative host graph
State incidence (2022 publication)	5 reported state means	State; reported mean (%)	Descriptive profile; no pooled trend
Host differentials (2022 publication)	11 cultivars; 60 isolates	Cultivar; mean wilt (%); band	Sorted published mean and reaction

Explanation: Four groups of evidence are presented below. Evidence from the same individuals were not combined to create artificial single samples for experimentation.

3.2 Disease incidence and reaction classification

When the number of affected plants and number evaluated were reported, wilt incidence was calculated as the ratio of wilted plants to the total number evaluated, multiplied by 100. This ratio represents the proportion of assessed plants that were wilted. This does not reflect the severity of the symptoms on the affected plants. In the greenhouse study, 30 assessments (five replicates of six plants each) were made for each genotype. Incidence was calculated using the combined total of affected plants and reported without rounding. Published values were also reported to acknowledge minor differences in the values reported (Biswas et al., 2020).

Qualitative field incidence was identified as VLI (very low incidence), LI (low incidence), MI (moderate incidence), HI (high incidence) and VHI (very high incidence). No threshold values were assigned to the incidence categories where symptoms were rounded. Genotype categories of resistance and susceptibility were also reported. In the host-differential study, if the mean symptoms of the plants were less than the level of the MR (moderately resistant) class, the plants were considered to be resistant. In this study, the levels of susceptibility were indicated by the presence of a necrotic spot or lesion on the leaves (Biswas et al., 2020; Ravikumara et al., 2022).

Table 3: Incidence and resistance indicators used in the results

Indicator	Measurement or retained label	Interpretation
Site incidence	Recorded percentage at each village/tehsil	Range and within-state variation
Field grade	VLI / LI / MI / HI / VHI	Frequency among 25 locations
Genotype response	Wilted / 30×100 and published class	Relative response in the specified greenhouse test
Host differential	Published mean across 60 isolates; R / MR / S	Cross-isolate host response, not a site estimate

Explanation: Different reaction systems are invented to solve various problems. They should not be replaced by one another unless a unified classification is provided.

3.3 Statistical and graphical analysis approach

The analysis reports counts, averages, minima, maxima, and rank-ordered data. The state means are based on the 25 previous locations. The state means were calculated by averaging the site percentages within a state, and therefore, represent the sampled locations within the state and should not be interpreted as an estimation of abundance of farms or greenhouses within the state. Grade means and proportions are based on 25 observations and therefore, do not represent an estimation of abundance. Genotype values are based on plant counts, and host differential and 2022 state means were reported as published values and therefore represent the average of the published samples.

Five figures were produced using Python and Matplotlib: Included are state-wise bar charts showing earlier sites, a pie chart showing five field grades, a chart showing genotype and incidence, a chart showing a host differential, and an integrated description of later state averages. The last figure shows state means using a line solely forational ease in understanding, and does not imply continuity or a series in time. Since the original studies did not use common sampling, this paper does not compute pooled estimates of treatment effects, does not perform tests of significance, and does not compute national estimates or ranges. It discusses results only when specifically attributed to their original studies.

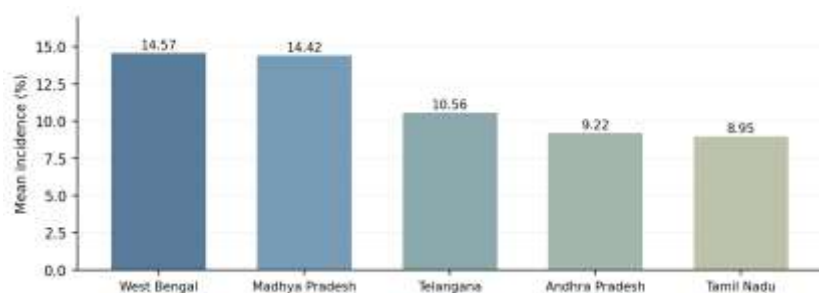
4. Results

4.1 Village-level wilt incidence pattern in observations reported in 2020

The previous 25 samples comprised of villages and tehsils reported incident of wilt in the range of 4.50% to 26.00% with an average of 12.04%. It was reported that the wilt mean was 14.57% in West Bengal and 14.42% in Madhya Pradesh. There was very little difference between the means of the two states, and considering the sampling differences and the number of sampling units, it is not appropriate to rank the state level impact of the disease. The mean values of other states reported in the study were 10.56% for Telangana, 9.22% for Andhra Pradesh and 8.95% for Tamil Nadu. The values referred to in the study represent the wilt infection in the sampled units of the states and do not represent wilt infection in all pigeonpea growing units of the states (Biswas et al., 2020).

An incidence of 26.0% was reported from Madhya Pradesh at Anjad in Barwani district. The second highest incidence of 23.80% was reported from Sanawad, Khargone district, Madhya Pradesh. Bhikangaon in Madhya Pradesh and Julwania in Chhattisgarh, which are part of the same sampling unit, reported wilt incidence of 5.00% and 8.50% respectively. The lowest incidence of 4.5% was reported from Perayambetti Gate, Tamil Nadu and Shakapur, Madhya Pradesh (4.66%). The West Bengal unit reported wilt incidence of 10.00% and 15.60% and 18.10% respectively. Based on such isolation units, it can be understood that the wilt situation in the state is complex and though state mean wilt incidence may be relatively low, localized pockets may indicate a high wilt situation.

Graph 1: Mean Fusarium wilt incidence by state among field locations reported in 2020



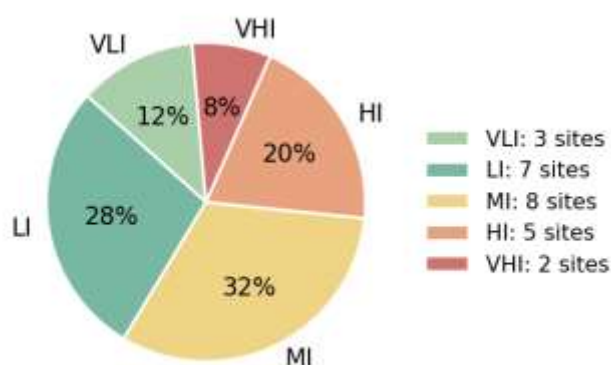
Explanation: Each bar shows the average of the site (web page) percentages for that particular state/region. West Bengal and Madhya Pradesh show similar averages for this series. However, the greatest site prevalence (within the state/region) is found in Madhya Pradesh.

4.2 Distribution of field severity grades

The 25 sites cover the complete range of field categories, including three of the four very-low-incidence sites, seven of the eight low-incidence sites, eight of the nine moderate-incidence sites, five of the seven high-incidence sites, and both of the very-high-incidence sites. Moderate- and low-incidence sites together account for 15 of the 25 sites, or 60%. High- and very-high-incidence sites account for the remaining 25% and 7%, respectively. The very-low-incidence sites account for the remaining 12% of the cases. An arithmetic mean of the sites would mask the true variability. The source reports both moderate and low-level sites as well as very-high level “wilt hot spots.”

Because frequencies of categories reflect the distribution of elevated disease, a category frequency distribution of sites would be useful in plant disease surveillance to determine the approximate number of sites with elevated levels of disease in a region. The overall frequency of sites in the low- and moderate-incidence categories does not preclude the need to examine the consistent and persistent wilt oncidium of sanawad and anjad. The sites represent ordinal assessment of field conditions, and the frequencies do not represent evaluations of acreage in the field or a severity index of wilt.

Graph 2: Distribution of recorded field wilt incidence grades



Explanation: Eighth site was moderate and seven sites were low. The remaining seven sites were high or very high. The pie chart represents no information besides location. This includes no data for plants, farms, hectares or states.

4.3 Genotype-wise wilt incidence and reaction

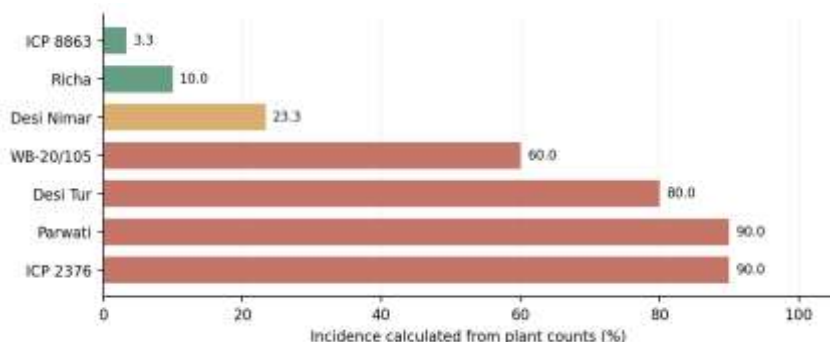
The 30 assessed plants of each of the seven greenhouse entries were evaluated for Basmati plant wilt. According to the 2020 report, one wilted plant of the 30 assessed in ICP 8863 (3.33%) and three wilted plants of landrace Richa (10%) were considered resistant. The remaining 27 assessed plants of ICP 8863 and all the 30 assessed plants of Richa were wilted. Desi Nimar was also retained in the susceptible category as 23.33% of the assessed plants were wilted. About 60% of the assessed plants of WB-20/105 and Desi Tur (80%) and 90% of Parwati and ICP 2376 plants were wilted. The 2020 report stated that these four entries were highly susceptible.

Of the entries evaluated, the difference in wilt percentage between ICP 8863 and 90% entry was 86.67%. Landrace Richa of the sampling population showed the next lowest wilt percentage and is deserving of further evaluation. The wilt percentage reported for the entry in the greenhouse does not necessarily indicate the wilt percentage in the field.

The field site of Parwati reported a wilt percentage of 8.60, but the greenhouse evaluation report was 90%. Field reports and laboratory evaluations should be considered jointly.

The 2020 report also documented evaluation of molecular response of Basmati accessions. Some of the Basmati accessions reported herein were a part of that study. The expression values of the genes reported in that study were not repeated here. The counts of the wilted plants reported herein were done to evaluate the responses of the accessions to Basmati wilt under different degrees of challenge. The reports do not evaluate the potential of the accessions for commercial cultivation (Biswas et al., 2020; Varshney et al., 2017).

Graph 3: Count-based wilt incidence among seven pigeonpea genotypes



Explanation: The green bars show the two resistant entries in the greenhouse test. The values are calculated from the totals of 30 assessed plants. The colors of the bars show the classification of the source reaction.

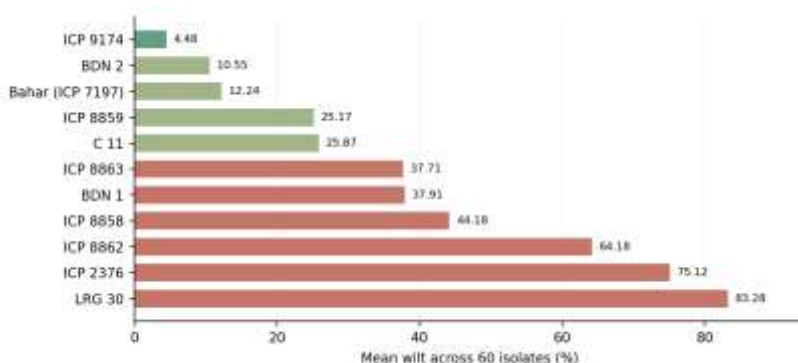
4.4 Host differential response across 60 *Fusarium udum* isolates

The cultivars in the study had a range of average wilting. ICP 9174 showed the least wilting (4.48%). Other cultivars wilted between 10% to 25% including BDN 2 (10.55%), Bahar (ICP 7197; 12.24%), C 11 (25.87%), and ICP 8859 (25.17%). ICP 8863 (37.71%), BDN 1 (37.91%), ICP 8858 (44.18%), ICP 8862 (64.18%), ICP 2376 (75.12%), and LRG 30 (83.28%) wilted more than 35%. The difference between the least wilting and most wilting cultivars was 78.80 percentage points (Ravikumara et al., 2022).

An instructive comparison is ICP 8863: The 2020 Greenhouse count reported 3.33% wilting. The 2022 report published a mean of 37.71% wilting of a larger, separate, isolate panel. Any differences in wilting in Greenhouse studies does not necessarily indicate the presence or increase of a pathogen. It may indicate a lack of sufficient resistance in the plants studied for the particular pathogen under investigation. ICP 2376 demonstrated wilting in both studies, and while the percentages reflect other tests, wilting was overall higher in ICP 2376.

The 2022 article identified nine pathogenic variants in the *F. udum* population. These results showed that a single diagnostic challenge is not sufficient. Ravikumara et al. (2022) included a representation of cultivar means and speculated reaction bands, which are depicted in the figure. Unfortunately, the figure does not represent a matrix of all the *Fusarium* isolates in relation to the cultivars. Therefore, it cannot be determined by the figure which *Fusarium* isolate overcame the resistance of a particular cultivar.

Graph 4: Host-differential response across 60 *Fusarium udum* isolates



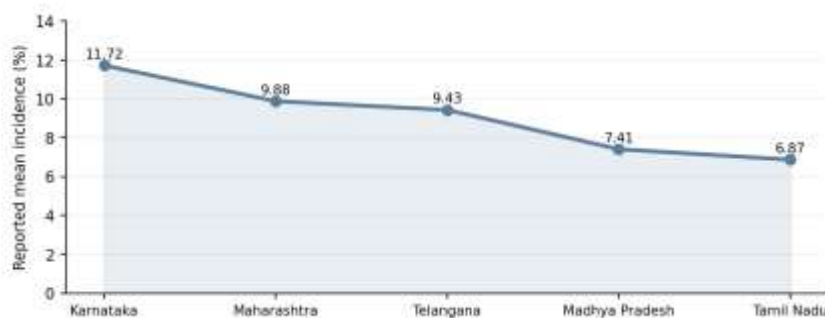
Explanation: Of the published cultivar means, ICP 9174 has the smallest mean and LRG 30 has the largest mean. For this separate, isolate-panel study, the means R, MR, and S follow the grouping based on the means of the cultivars.

4.5 State-level mean incidence in the 2022 publication

Surveys conducted by various state governments reported that 11.72% of farmers in Karnataka, 9.88% of farmers in Maharashtra, 9.43% of farmers in Telangana, 7.41% of farmers in Madhya Pradesh and 6.87% of farmers in Tamil Nadu reported wilt incidences in their fields. The highest to lowest difference in means reported by various state governments is 4.85% difference. Estimates reported in the article are aggregate values. The authors did not report sample values, and/or variance values reported by individual state governments (Ravikumara et al., 2022).

Madhya pradesh and tamil nadu are in different positions than what was reported in earlier studies. this does not indicate improvement or regression between 2020 and 2022. two years separate the publication of the article and the sampling of the fields. in addition, two different sets of farmers and a different set of sampled fields indicate that there is variability based on where and when studies were conducted. The later source describes wilt incidences greater than means reported in the article.

Graph 5: State-level mean incidence reported in the 2022 study



Explanation: The connected points represent five state categories in the publications and are not to be interpreted as representing time. The values have been kept separate from the means of the earlier 25 sites.

5. Discussion

5.1 Interpretation of spatial and genotype variation

The results show three kinds of variation. First, sites in the same state (Madhya Pradesh) record significant variation in field incidence, e.g. 5.00–26.00%. Second, in some instances, the same greenhouse conditioning protocol resulted in varying proportions of wilted plants, e.g. among host entries challenged in the greenhouse. Finally, variation is shown in standard host differentials when challenged with different *Fusarium udum* isolates. Again, all results indicate variation (Biswas et al., 2020; Ravikumara et al., 2022).

What caused the variations observed in the study? There are several. The density of soil-borne pathogens, previous cultivation of susceptible crops, the weather and soil moisture conditions, and the age of the crop, among others, could explain the variations. In the case of this study, there was no uniform documentation of the variables stated above across all the worksheets. Therefore, it would not be justified to say that one location had a higher level of wilt due to a particular rotation or rainfall condition. It is likely that other factors influenced wilt levels in the study location. Establishing the influences would require further study (Gordon, 2017; Srivastava et al., 2023).

The field and screening series demonstrate that genotype and locality can not always be considered as equivalent. In a low-incidence village there may be susceptible materials in the presence of low level of inoculum. An accession that shows resistance against the isolate used in the screening may show susceptibility against a more aggressive isolate. Local variability in responses to ICP 8863 is relevant here. Responses of the seven entry source gave an average infection of 3.33%, while the multi-isolate panel gave an average infection of 37.71%. The sourced responses are to be taken relative to the contexts in which they were obtained, and the multi-environment screening studies demonstrate significant genetic x environment interactions. Therefore, to support a claim of resistance, the context in which the screening was done should also be provided.

From a practical point of view, the authors consider that low levels of resistance in a population should be taken as indicative of reduced incidence of high level of visible wilt in the population. Further evaluation to test the limits of the resistance may be justified based on the results of this study. Broad level resistance to a pathotype of the target

disease needs to be assessed in multiple locations, growing seasons and against various pathogenic variability. Descriptive data may justify further evaluation without establishing a cause.

5.2 Implications for breeding and integrated disease management

There are several implications for breeding programs. For the short-term, we can protect and assess host material that has not been widely used. Richa is a local landrace, which was previously evaluated as a favorable source, whereas ICP 9174 was evaluated as a low mean source in a later evaluation. For the long-term, they should be considered as different sources of resistance. Their differences stem from various evaluation methods. Both should be assessed against a collection of confirmed *F. udum* sources, using standardized evaluation methods, along with suitable susceptible and resistant checks (Biswas et al., 2020; Ravikumara et al., 2022).

Work on the development of molecular markers coupled with the defense-related pathways of pigeonpea may provide markers that are stably inherited and play a role in reducing wilting.

Some published pigeonpea sequences and accession resequencing have improved the potential to use these resources. The recently released *F. udum* genome sequence provides clues to effector and pathogen repertoire. A marker should be formally evaluated against field observed plant phenotype and pathway before being used for selection (Singh et al., 2012; Varshney et al., 2017; Srivastava et al., 2023).

The most practical development pathway is iterative: Consider agriculture response values and diversity indices, assess agronomic performance and only then combine varieties using agriculture practices that are affordable to the farmer. These practices help identify high yielding crops without being dependent on crop varieties ranked high from on-farm trial results or from a single location. Farmers are cautioned against adopting and relying on results obtained from inadequate inoculation environments.

5.3 Limitations of the evidence and interpretation

This study uses previously published data, limiting its scope and potentially its accuracy. The author completed 25 field observations, which, similar to the published data, do not purport to be a statistically significant sample of all pigeonpea-producing regions in the states reported. State averages derived from the field observations are interpreted to provide an estimate of the prevalence of the pathogen in a state. The field observations used to develop the state averages do not purport to provide an estimate of the absolute prevalence of the pathogen state-wide. It should be noted that the categories of field observation used to describe the health status of the pigeonpea plants are qualitative and should not be misconstrued to be based on a plant count.

The authors report the results of a greenhouse assessment to screen pigeonpea genotypes against five race-TALI pathogen isolates. The screen recorded 30 plants to a genotype and reported means, which, according to the authors, should be interpreted in the context of management and other environmental and pathogen variability. The means reported should not be generalized to state-wide prevalence of the pathogens assessed. The authors reported the 2022 host assessment means to provide an estimate of the effect of pathogen isolates on specific pigeonpea cultivars, which, according to the authors, would require additional assessments to ascertain.

there are also limitations due to the timing of when data could be reported. Data from 2020 are from field observations collected from 2014 to 2015. More recent work was published in 2022. Treating the time of publication as the time of data collection would create a false impression that the work is time sequential. There are also differences in the districts studied, the persons who hosted the parasite, the means of parasite exposure, and the scorekeepers, which also prevent pooling the results. Results obtained from studies of *F. udum* cannot be assigned or generalized to studies of *F. oxysporum*. The main value of this synthesis is to illustrate the body of work conducted to date and to identify naming inconsistencies in working the adversaries.

6. Conclusion and Future Scope

Variation in the expression of symptoms of pigeonpea wilt occurs at different levels. These levels include differences among fields, genotypes of pigeonpeas and pathotypes of the wilt causing fungus. Field incidences of the disease reported by Biswas et al. (2020) ranged from 4.50 to 26.00%. Anjad and Sanawad in Madhya Pradesh recorded the highest incidences. Pigeonpea wilt is widely distributed and occurs throughout most of the growing areas of pigeonpeas. Although, for this study, data from West Bengal and Madhya Pradesh were used, it was observed that

means computed from site counts from both the states were closely related, thus underscoring the need to analyze site counts from various localized areas rather than interpreting data from states in general. In the greenhouse studies conducted by the author, wilt symptoms were least observed in plants of ICP 8863 and Richa. In the later study, symptoms in plants of ICP 9174 were less in the presence of a 60 isolate panel of the wilt fungus (Ravikumara et al. 2022).

The two investigations identify the importance of the test context for resistance evaluation. ICP 8863 differed from the counted greenhouse data and thus extrapolations based on limited testing data are inadequate. Subsequent studies must incorporate coreartum checks and representatives of *F. udum*, clear delineation of reactions, and collaborative field and laboratory studies. Rational integration of pathogen management with pathogen diagnostic tools and disease risk assessment in the field may facilitate determination of resistant plant populations and better interpretation of resistance in the field (Sharma et al., 2016; Srivastava et al., 2023).

In the meantime, improvement in resistant plant populations may be possible through integration of several complementary interventions. The desired effect, i.e. long term integration of stable host resistance with other management practices, may be attainable. Heterogeneity may exist across *Fusarium* wilt pathosystems, and, thus, it may not be valid to assume that integrating management practices across various *Fusarium* wilt pathosystems will not be effective (Dave and Ingle, 2021).

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