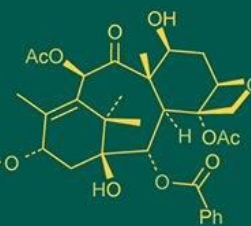
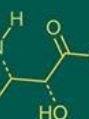
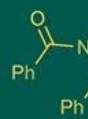


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Screening of pigeonpea cultivars/genotypes against stem canker caused by *Macrophomina phaseolina* (Tassi) Goid

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Abstract

Pigeonpea (*Cajanus cajan* L. Millspaugh) is a vital legume in semi-arid regions, providing protein to millions in developing countries. Its yield is significantly affected by biotic stresses, particularly stem canker caused by *Macrophomina phaseolina*, a soil-and seed-borne pathogen. Breeding resistant varieties offers an economical and sustainable disease management strategy. The study was conducted to assess the reaction of different pigeonpea cultivars/genotypes to stem canker under controlled conditions using the sick pot method. The experiment took place at the College Farm, N. M. College of Agriculture, Navsari, during the *kharif* seasons of 2021-22 and 2022-23. Ten cultivars/genotypes were evaluated and disease incidence was recorded from flowering to pod formation. Significant variation was observed in their response to *Macrophomina phaseolina*. In 2021-22, only GJP-1 was resistant, six were moderately resistant and three were moderately susceptible. In 2022-23, GJP-1 and GT-1 were resistant, five were moderately resistant and three were moderately susceptible. Over both years, GJP-1 consistently showed the lowest disease incidence, confirming its resistance. The study highlights the presence of useful genetic resistance against *M. phaseolina* in pigeonpea germplasm. Resistant and moderately resistant cultivars identified in this study can serve as valuable sources for resistance breeding programmes. Further multi-location and large-scale evaluations are suggested to confirm stability of resistance and to support sustainable management of stem canker in pigeonpea.

Keywords: *Macrophomina phaseolina*, pigeonpea, stem canker, resistant, incidence

Introduction

Pigeonpea (*Cajanus cajan* L. Millspaugh) is an important legume crop of rainfed agriculture in the semi-arid tropics. It is also known as arhar, tur dal, red gram, congopea. Pigeonpea is popular food in developing tropical countries. The Indian subcontinent, Eastern Africa and Central America are the world's three main pigeonpea producing regions. Pigeonpea are cultivated in more than 25 tropical and subtropical countries, either as a sole crop or intermixed with cereals, such as sorghum (*Sorghum bicolor* L.), pearl millet (*Pennisetum glaucum* L.) and maize (*Zea mays* L.) or with other legumes, such as peanuts (*Arachis hypogaea* L.) (Zore, 2018) [1]. The total world acreage under pulses cultivation area was recorded during 2022 is about 959.68 lakh ha with production of 973.92 lakh tones and productivity was 1015 kg/ha. It revealed that the India ranked first in area and production with 38 percent and 28 percent respectively of world area and production. In India area, production and productivity of pigeonpea were 40.68 lakh ha, 33.12 lakh ton and 814 kg/ha respectively (FAOSTAT, 2022) [2]. Pigeonpea is poor man's source of protein; it contains high levels of protein and the important amino acids methionine, lysine and tryptophan. Plants produce forage quickly and can be used as a perennial forage crop or used for green manure, often grown as a shade crop for tree crops or vanilla, a cover crop, or occasionally as a wind break hedge.

Macrophomina phaseolina is primarily a soil and seed-borne fungal pathogen that incites the disease by producing microsclerotia/pycnidia (Farr *et al.*, 1995; Pun *et al.*, 1998) [3,4]. It has a wide host range of more than 500 species from 75 families with heterogeneous host specificity *i.e.*, the ability to infect monocots as well as dicots and can exhibit non-uniform distribution in the soil (Mayek-Perez *et al.*, 2001; Su *et al.*, 2001) [5,6].

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The first record of pathogen of dry root rot seems to be from India as *M. cajani* (Syndow and Butler, 1916) [7]. It is synonym of *M. phaseoli*. The disease is also reported from Australia, Myanmar, Sri Lanka, Vietnam and Zambia (Nene and Sheila, 1990) [8]. In India, the first report of stem canker of pigeonpea occurrence was reported by Kannaiyan *et al.* (1979) [9] in part of Eastern Uttar Pradesh (Varanasi and Mirzapur districts). Recently, the stem canker incited by *M. phaseolina* has emerged as one of the important pathogens of different agricultural crops, including pigeonpea (Kaur *et al.*, 2012a) [10]. Stem Canker disease, caused by *M. phaseolina* is potentially a serious disease in pigeonpea that occurs from flowers to physiological maturity stage. The incidence of stem canker has increased gradually in recent years to reach an alarming proportion. The disease also occurs in states of Bihar, Madhya Pradesh, Maharashtra, Orissa, Uttar Pradesh, Andhra Pradesh, Tamil Nadu, Rajasthan and Gujarat (Kannaiyan *et al.*, 1979) [9]. Considering the above facts, incidence of stem canker caused by *M. phaseolina* identify in different pigeonpea cultivars/genotypes under pot study.

Materials and Methods

The experiment on screening of pigeonpea cultivar/genotypes against pigeonpea stem canker was conducted at College Farm, N. M. College of Agriculture, Navsari Agricultural University, Navsari for two consecutive years *kharif* 2021-22 and 2022-23. Different ten pigeonpea cultivars/genotypes (Table 1) were collected from Pulse Research Station, NAU, Navsari. Ten cultivar/genotypes were screened against stem canker by using sick pot technique

For the sowing purpose Pigeonpea seeds were surface sterilized with HgCl₂ (0.1%) for a minute and washed repeatedly thrice in sterile water to remove the traces of HgCl₂. Eight seeds were sown in each pot (60 cm diameter

capacity) containing sterilized black soil and FYM incorporated with culture of the test pathogen *M. phaseolina* multiplied (@ 25 g/kg) on sorghum grain. Each cultivar/genotype was replicated thrice. The moisture content of the soil reduced after flowering to create the soil condition favourable for infection.

Observations were recorded for stem canker incidence from flowering to pod formation stages by counting healthy plants (without stem canker symptoms) and stem canker diseased plants. The disease incidence was computed by taking into consideration of number of plants infected and number of plants survived for all the cultivars/genotypes. The percent incidence was calculated by using following formula.

$$\text{Percent disease incidence (\%)} = \frac{\text{Number of infected plant}}{\text{Total number of plant examined}} \times 100$$

The mean percent disease incidence of all the cultivars/genotypes were calculated by taking the average of incidence in both the year and categorized into different categories (as per scale Modified from Agarwal, 2003) [11] given in Table 2.

Table 1: List of pigeonpea cultivars/genotypes used for the screening against the *M. phaseolina*

Sr. No	Cultivars/Genotypes
1.	GT-105
2.	GT-104
3.	AVPP-1
4.	ICPL-87119
5.	GNP-2
6.	GJP-1
7.	GT-1
8.	UPAS-120
9.	BDN-2
10.	ICPL-87

Table 2: Disease rating scale for Macrophomina stem canker disease of pigeonpea

Grade	Incidence	Disease Reaction
1	1-10 % incidence	Resistant
2	11-25 % incidence	Moderately Resistant
3	26-50 % incidence	Moderately Susceptible
4	51-75 % incidence	Susceptible
5	>75 % incidence	Highly Susceptible

Results and Discussion

Use of resistant varieties is an ideal, the simplest practical and the cheapest method for the control of plant diseases. Moreover, it does not disturb natural eco-system and avoids hazards use of fungicides and insecticides hence reduce environmental pollution as well as it stabilizes the yield. The identification of the source of resistance is a basic need in breeding for disease resistance. Considering these facts, during *kharif* 2021-22 and 2022-23 pigeonpea cultivars/genotypes were sown in the pot condition for screening against pigeonpea stem canker disease under artificial inoculation condition. The screening was carried out as per standard method given in materials and methods.

The mean percent disease incidence of stem canker in all the cultivars/genotypes was calculated in both the season *kharif* 2021-22 and *kharif* 2022-23 and categorized into different categories (as per scale Modified from Agarwal, 2003) [11] and which were described in Table 3-4, Figure 1, 2 and 3.

The data of *kharif* 2021-22 revealed that out of ten pigeonpea cultivars/genotypes evaluated for stem canker incidence, only one cultivar, GJP-1, was found resistant (R), recording the lowest disease incidence of 8.33 percent. Six cultivars/genotypes, namely GT-1, GNP-2, GT-105, GT-104, BDN-2 and ICPL-87, were categorized as moderately resistant (MR) with disease incidence of 12.50, 12.50, 16.67, 20.83, 20.83 and 25.00 percent, respectively. The remaining three cultivars/genotypes, UPAS-120, AVPP-1 and ICPL-87119, exhibited higher disease incidence of 33.33, 37.50 and 45.83 percent, respectively and were therefore classified as moderately susceptible (MS) to stem canker (Table 3; Figure 2).

During *kharif* 2022-23, evaluation of the same ten pigeonpea cultivars/genotypes indicated that two cultivars, GJP-1 and GT-1, were categorized as resistant (R) with 4.17 and 8.33 percent disease incidence, respectively. Five cultivars/genotypes, namely GT-105, GNP-2, GT-104, BDN-2 and ICPL-87, were recorded as moderately resistant

(MR), registering 12.50, 12.50, 16.67, 16.67 and 20.83 percent disease incidence, respectively. The remaining cultivars/genotypes, UPAS-120, AVPP-1 and ICPL-87119, showed relatively higher disease incidence of 29.17, 33.33

and 41.67 percent, respectively and were thus categorized as moderately susceptible (MS) to stem canker (Table 3; Figure 3).

Table 3: Screening of pigeonpea cultivars/genotypes against stem canker caused by *M. phaseolina* in pot

Sr. No.	Cultivars/genotypes	Kharif 2021-22		Kharif 2022-23		Mean	Final disease reaction
		Percent disease incidence (PDI)*	Disease reaction	Percent disease incidence (PDI)*	Disease reaction		
1	GT-105	16.67	MR	12.50	MR	14.58	MR
2	GT-104	20.83	MR	16.67	MR	18.75	MR
3	AVPP-1	37.50	MS	33.33	MS	35.42	MS
4	ICPL-87119	45.83	MS	41.67	MS	43.75	MS
5	GNP-2	12.50	MR	12.50	MR	12.50	MR
6	GJP-1	8.33	R	4.17	R	6.25	R
7	GT-1	12.50	MR	8.33	R	10.42	MR
8	UPAS-120	33.33	MS	29.17	MS	31.25	MS
9	BDN-2	20.83	MR	16.67	MR	18.75	MR
10	ICPL-87	25.00	MR	20.83	MR	22.92	MR

*Mean of three replications PDI-Percent disease incidence

Table 4: Reaction of pigeonpea cultivars/genotypes against stem canker caused by *M. phaseolina* in pot conditions during kharif 2021-22 and 2022-23

Disease reaction	Disease incidence	PDI (%)	No of cultivars/genotypes	Name of cultivars/genotypes
Resistant (R)	1-10 %	6.25	1	GJP-1
Moderately Resistant (MR)	11-25%	10.42, 12.50, 14.58, 18.75, 18.75, 22.92	6	GT-1, GNP-2, GT-105, GT-104, BDN-2, ICPL-87
Moderately Susceptible (MS)	26-50 %	31.25, 35.42, 43.75	3	UPAS-120, AVPP-1, ICPL-87119
Susceptible (S)	51-75 %	-	-	-
Highly Susceptible (HS)	>75 %	-	-	-

Note: R = Resistant, MR = Moderately Resistant, MS = Moderately Susceptible, S = Susceptible, HS = Highly Susceptible

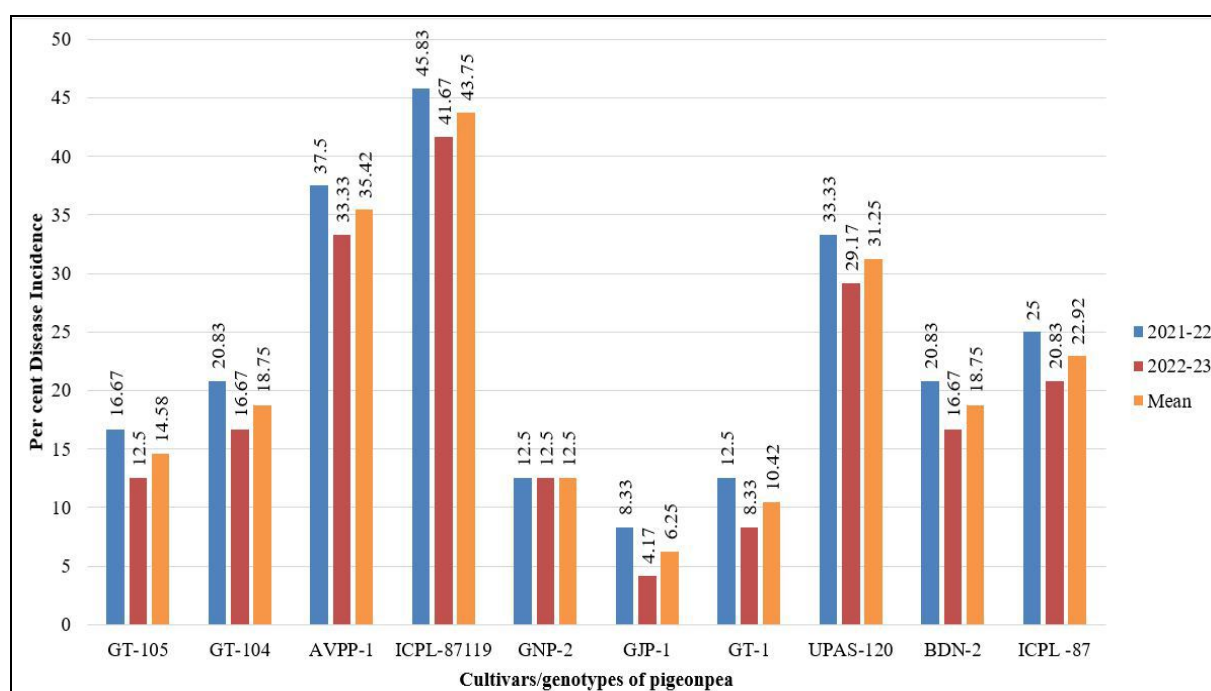


Fig 1: Screening of pigeonpea cultivars/genotypes against *Macrophomina phaseolina* caused stem canker in pot during kharif 2021-22 and 2022-23

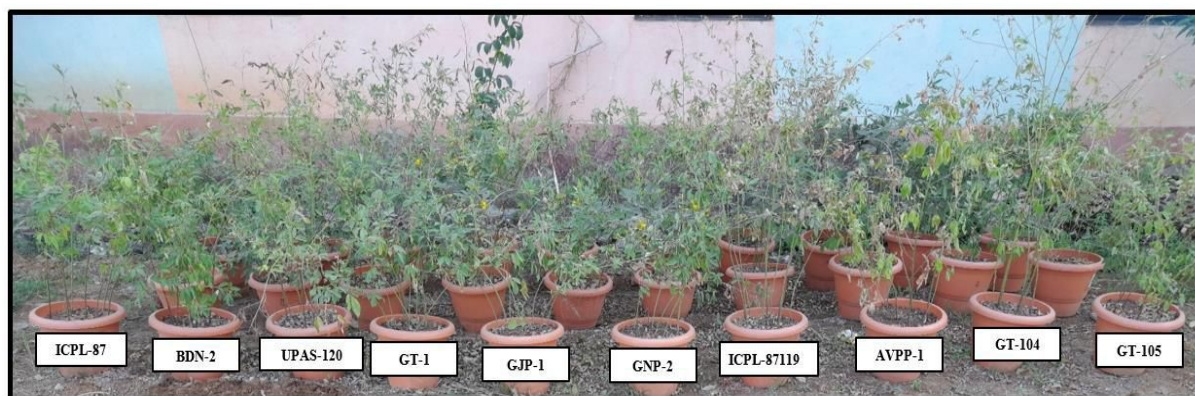


Fig 2: Screening of pigeonpea cultivars/genotypes against *Macrophomina phaseolina* in pot during kharif 2021-22

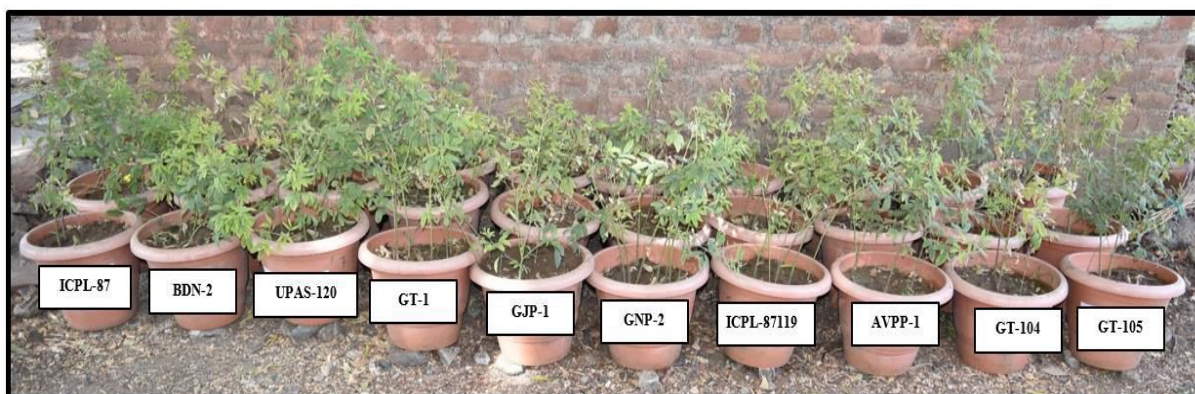


Fig 3: Screening of pigeonpea cultivars/genotypes against *Macrophomina phaseolina* in pot during kharif 2022-23

The data presented in Table 4 revealed that the mean percent disease incidence of stem canker in all the cultivars/genotypes indicates that out of ten cultivars/genotypes only one variety GJP-1 was found resistant (R) against stem canker during both year with 6.25 percent incidence and hence categorized as resistant against stem canker. Six cultivars/genotypes viz., GT-1, GNP-2, GT-105, GT-104, BDN-2 and ICPL-87 were categorized as moderately resistant (MR) with 10.42, 12.50, 14.58, 18.75, 18.75 and 22.92 percent disease incidence, respectively. While remaining three cultivars/genotypes viz., UPAS-120, AVPP-1 and ICPL-87119 were recorded with 31.25, 35.42 and 43.75 percent disease incidence and categorized as moderately susceptible against stem canker during both the year.

Previously screening of varieties/genotypes of pigeonpea against *M. phaseolina* was carried out by different scientists Lokesh and Benagi (2005) [12] found two genotypes PT-221 and ICPL-90097 had resistant reaction and DEPS-9, Gullalli local, GS-1, ICPL-89049, Phy-K-2, TAT-9621 and V-50 recorded moderately resistant reaction against *M. phaseolina* in pigeonpea. Chaudhari (2013) [13] recorded minimum percent number of infected plant was in BDN-2 which was followed by SKNP-1034, GT-1, Vaishali and ICPL-87119 hence regarded as moderately resistant towards *M. phaseolina* of pigeonpea. Swamy (2014) [14] found four genotypes viz., GRG-2010, BSMR-736, ICP-8863 (Maruti) and ICP-87119 (Asha) showed moderately resistant reaction against *M. phaseolina* in pigeonpea. Zore (2018) [1] found three varieties viz., BDN-711, BDN-708 and BDN-716 were found resistant and two varieties Vipula and Nirmal showed maximum disease incidence and categorized as susceptible against *M. phaseolina* of pigeonpea.

Conclusion

Productivity of pigeonpea is seriously affected by several biotic stresses, among which stem canker caused by *Macrophomina phaseolina* has emerged as an important and increasingly destructive disease. The present investigation clearly demonstrated the existence of considerable variability in resistance among pigeonpea cultivars/genotypes against stem canker under artificial inoculation conditions. During both seasons, none of the cultivars/genotypes were found completely free from stem canker incidence and all the cultivars/genotypes were more or less infected by the *M. phaseolina*. The cultivars/genotypes found resistant against *M. phaseolina* can be manipulated for breeding programme to evolve resistant varieties for further evaluation. Future studies should emphasize large-scale and multi-location evaluation of pigeonpea genotypes to confirm stability of resistance against stem canker. Integration of host plant resistance with suitable agronomic and disease management practices may further enhance sustainable control of the disease.

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