

# An update on the host plant resistance to pigeonpea diseases

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**Abstract:** The production and productivity of pigeonpea is severely constrained by diseases such as Fusarium wilt, sterility mosaic disease and Phytophthora blight. These diseases can be serious alone or as component of complex. Estimates of yield loss as caused by these diseases are not precise. This paper summarises the current knowledge of pigeonpea diseases with special reference to emerging diseases in the light of climate change. Recent developments in host plant resistance including the screening techniques and sources of resistance identified over the last few years have been highlighted in this paper.

**Key words:** emerging diseases, host plant resistance, inheritance, pigeonpea, resistance sources

## Introduction

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is attacked by many soil borne and foliar diseases which results in severe economic losses globally. Among these, fungi and viruses are the largest and most important groups affecting pigeonpea (Table 1). Fusarium wilt (FW), sterility mosaic disease (SMD), and Phytophthora blight (PB) are economically important diseases of pigeonpea. Frequent occurrence of PB has been reported in major pigeonpea growing areas especially under the changed climatic scenario (7). New records of emerging diseases such as Alternaria blight, sudden death and root rots have been reported recently in pigeonpea (12, 14, 15).

Of the available management approaches, host plant resistance is the most reliable, economical and effective method for managing the diseases. In the absence of high yielding and well adopted resistant cultivars, use of certified seeds, sanitation and cropping practices to reduce inoculum, choice of sowing type and time and use of fungicide or bio-control agents would be of help for the management of these diseases. Considerable progress has been made in the past in developing the disease resistance screening techniques, identifying sources of resistance and transferring resistance genes into high yielding, improved and agronomically superior genetic background in pigeonpea. Biotechnological tools such as marker-assisted selection, genetic engineering and wide hybridization to develop crop cultivars with resistance to diseases will play a key role in future disease management programs in pigeonpea (19). In this paper, we have attempted to document the recent progress made towards host plant resistance for economically important diseases of pigeonpea along with future challenges.

## Genetic resistance to pigeonpea diseases







Fusarium wilt (*Fusarium udum* Butler) is the most important disease in Indian subcontinent and Eastern Africa. Occurrence of wilting during flowering to pod filling stage causes yield losses up to 50% - 70%. Another disease severely affecting the pigeonpea yield is sterility mosaic disease (SMD) caused by pigeonpea sterility mosaic virus (PPSMV), a species of the genus *Emaravirus* causing losses up to 95% - 100% with infection occurring early at < 45 days old plants (3). Apart from wilt and mosaic, Phytophthora blight is another important disease that got the status of economic concern (7, 11, 16). The disease is caused by fungus *Phytophthora cajani* K. S. Amin, Baldev & F. J. Williams (16).

FW and SMD incidence differs from place to place due to variability in pathogen. So far 5 variants (I, II, III, IV and V) of *Fusarium udum* have been identified and documented (18) using as many as 15 differentials. We have also observed considerable variability using 73 isolates and 11 differentials collected from seven states in India (Sharma et al unpublished). Three distinct strains (Bangalore, Patancheru and Coimbatore) have been characterized for PPSMV in India (4). So far, no confirmed information regarding pathogen variability is available for *Phytophthora cajani*.

Reliable greenhouse and field screening techniques are available for FW and SMD to identify resistance sources (8). Recent advances in FW and SMD research have facilitated the selection of high-yielding varieties with durable resistance to FW and SMD. Lines derived from crosses with *C. acutifolius* (F. Muell.) Maesen and *C. platycarpus* (Benth.) Maesen have shown resistance to the Patancheru isolate of PPSMV under field conditions (5). Recently new sources of resistance to Fusarium wilt and SMD were identified in a mini-core collection of pigeonpea germplasm at ICRISAT (13). A high level of resistance was found in 24 accessions and combined resistance to FW and SMD was found in five accessions (ICPs 6739, 8860, 11015, 13304, and 14819). Recently, through multi-environment field testing, four genotypes (ICPLs 20094, 20106, 20098 and 20115) have been identified as the most stable and resistant to SMD (17). Three genotypes (ICPLs 20096, 20107, 20110) showed moderately stable performance against SMD. All these lines have medium duration of maturity and could be valuable sources of resistance for a pigeonpea breeding programs to FW and SMD. Four vegetable type genotypes (ICPs 7991, 12059, 13257 and 14291) originated from different countries were found highly resistant with no incidence of FW and SMD (10).

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**Table 1. Distribution and symptoms of important and emerging diseases of pigeonpea**


Diseases	Causal organism	Distribution	Symptoms
Fusarium wilt	<i>Fusarium udum</i> Butler	Bangladesh, Ghana, Grenada, India, Indonesia, Kenya, Malawi, Mauritius, Myanmar, Nepal, Nevis, Tanzania, Thailand, Trinidad and Tobago, Uganda, Venezuela	
Sterility mosaic	Pigeonpea sterility mosaic virus	India, Bangladesh, Nepal, Sri Lanka, Myanmar	
Phytophthora blight	<i>Phytophthora cajani</i> K. S. Amin, Baldev & F. J. Williams	Asia, Africa, Americas, Australia, Dominican Republic, Kenya, Panama, Puerto Rico	
Alternaria blight	<i>Alternaria alternata</i> (Fr.) Keissl. and <i>Alternaria tenuissima</i> (Kunze) Wiltshire	India, Kenya, Puerto Rico	
Sudden death	<i>Fusarium acuminatum</i> Ell. & Ev.	India	
Dry root rot	<i>Macrophomina phaseolina</i> (Tassi) Goid	India, Jamaica, Myanmar, Nepal, Sri Lanka, Trinidad and Tobago	

In previous studies, although several screening techniques and sources of resistance to PB have been reported (7), however, no reliable and repeatable screening technique is available. Recently, Sharma et al (16) first time developed a successful method for obtaining high concentrations of zoospores followed by a reliable screening technique in pigeonpea for PB. Using this new bioassay, over 800 pigeonpea genotypes including released cultivars, earlier reported PB resistant lines, breeding lines and water logging tolerant lines have been screened. Repeated screening of promising genotypes has so far identified four genotypes with a moderate resistance to PB (ICPLs 99004, 99008, 99009 and 99048), which will be used in the further study.

### Inheritance of resistance to pigeonpea diseases

Wilt resistance has been reported to be a monogenic recessive trait (6) and dominant trait (2). Saxena et al (9) have also reported dominant suppressive epistatic effect of a dominant gene over the recessive one for wilt resistance in a cross of a FW susceptible cytoplasmic male-sterility line with four FW resistant fertility restorers. Studies have been done on the inheritance of resistance to SMD and there are major differences in the interpretations made on the nature of resistance. Recently the nature of inheritance of SMD was studied in the segregating population of two crosses, Gullyal white (susceptible) × BSMR 736 (resistant) and BSMR 736 (resistant) × ICP 8863 (susceptible) (1). The above studies showed that the resistant trait was governed by two independent non-allelic genes, designated *SV1* and *SV2*, with inhibitory gene interaction (1). The limited reports available on genetics of PB resistance in pigeonpea suggest that a few major genes may control resistance in the host to PB.

### Future challenges

Considerable progress has been made during the last decade in characterizing the pathogenic variability in *F. udum* and PPSMV, identifying the resistant sources and resistance mechanisms. However, there are still several gaps such as lack of precise knowledge on the existence of pathogen race/strains in *F. udum* and PPSMV, which is essential to develop durable resistant cultivars for different regions. Further, due to the variability in climatic conditions and their unpredictable occurrence, frequent outbreaks of new diseases such as PB, Alternaria blight, sudden death, root rots have become more common in pigeonpea. There is a need to address these diseases, study their biology and epidemiology to develop reliable screening techniques to identify the genetic resistance and resistance mechanism. Marker assisted breeding may be strategically useful to avoid combined effect of environmental interactions and in identification of race-specific resistant genes and their pyramiding. 

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