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Impact of a New Source of Resistance to Fusarium Wilt in Pigeonpea

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Abstract

Pigeonpea is an important grain legume grown by smallholder farmers in Southern Africa. Fusarium wilt, caused by the fungal pathogen *Fusarium udum* Butler, is the major disease limiting pigeonpea production in the region. This study was designed to evaluate the reaction to fusarium wilt as well as agronomic performance of new elite pigeonpea germplasm in three different countries during the 2001/2002 cropping season using wilt-sick plots. Per cent incidence of fusarium wilt (%FW), grain size and yield, were measured. The genotype ICEAP 00040 consistently showed a high (<20.0%) level of resistance to the disease in all three countries. In contrast, %FW score for the susceptible genotype ICEAP 00068 was 87.5, 92.0 and 90.9% in Kenya, Malawi and Tanzania, respectively. The grain size obtained for ICEAP 00040 at Ngabu (Malawi) was 25.0% larger than that at each of the remaining locations indicating environmental influence on this trait. At all the three locations, ≥ 1.5 ton/Ha of grain yield was obtained for ICEAP 00040 compared with <1.0 ton/Ha for ICEAP 00068. In 2003, this improved resistant genotype (ICEAP 00040) was released for commercial production and will be useful as a good source of resistance in pigeonpea genetic improvement programs in the region.

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is an important grain legume grown in the tropics and subtropics. The crop is grown by smallholder farmers in many countries in Eastern and Southern Africa including Kenya, Malawi, Mozambique and Tanzania where it is intercropped mainly with *Zea mays* (corn), or *Sorghum bicolor* (sorghum) or *Manihot esculenta* (cassava). In these cropping systems farmers grow traditional, long-duration (9–10 months) landraces that yield approximately 0.4 ton/Ha of grain (Mligo and Myaka, 1994).

The nutritious grain of this crop contains approximately 20% crude protein and a wide range of minerals (Amarteifio et al., 2002). It is a valuable complement to cereal-based diets particularly in rural communities that face high risks of malnutrition in parts of Southern Africa.

Fusarium wilt caused by the fungal pathogen *Fusarium udum* Butler, is the most devastating disease of pigeonpea causing an annual loss of >US\$5 million in Kenya, Malawi and Tanzania (Kannaiyan et al., 1984). The pathogen lives in the soil. Between crops it survives in residual plant debris as mycelium and in all its spore forms (Agrios, 1997). The germ tube of the mycelium or spore penetrates seedlings through root tips, wounds or point of formation of lateral roots. The mycelium advances through the xylem causing vascular plugging followed by wilting of stems during flowering and pod-filling stages thus causing yield loss ranging from 30 to 100% (Reddy et al., 1990). Once a field is infested, the pathogen may survive in the soil for several years. Fungal spores can be disseminated to new plants by farm equipment, water, wind or animals, including humans. Use of cultivars resistant to the fungus is the most effective measure for controlling the disease.

Recently, *F. udum* was reported to be spreading in Southern Africa reaching areas in Southern Zambezia (Mozambique) province (Gwata et al., 2005). Spurred by the threat of this disease to the crop in our region, this study was designed to evaluate the (i) reaction to fusarium wilt and (ii) agronomic performance of elite pigeonpea germplasm under high disease pressure in three different countries in Southern Africa. The implications of the disease resistance in the region are discussed.

Materials and Methods

Genetic material

Local and exotic pigeonpea genotypes were used in the study (Table 1). Five genotypes were selected for each

Table 1

The origin of pigeonpea genotypes that were evaluated for reaction to fusarium wilt and agronomic performance at three locations in the 2001/2002 cropping season

Genotype	Country of origin	Evaluation location ^a
ICEAP 00020	Kenya	I, II, III
ICEAP 00040	Kenya	I, II, III
ICEAP 00068 ^b	Kenya	I, II, III
ICEAP 00053	Kenya	I, II
ICPL 87051	India	I
Royes ^c	Malawi	II
ICEAP 00057	Kenya	III
Ex-Lugoba-1 ^d	Tanzania	III

^aResearch stations: I, Kiboko (Kenya); II, Ngabu (Malawi); III, Ilonga (Tanzania).

^bKnown highly susceptible (to fusarium wilt) genotype.

^cCommercial cultivar in Malawi.

^dUnimproved traditional landrace in Tanzania.

location (testing site). The genotypes were selected on the basis of preliminary information obtained from previous large-scale screening of many pigeonpea genotypes in the field, seed availability as well as local farmer-preferences in the area.

Evaluation of reaction to fusarium wilt and agronomic traits

The evaluation of genotypic reaction to fusarium wilt was conducted in wilt-sick plots (Bayaa et al., 1997) at Kiboko (Kenya), Ngabu (Malawi) and Ilonga (Tanzania) research stations where the disease pressure was considered to be high. At the beginning of the cropping season, seed of each genotype was sown in field plots each measuring 5.0 m in length and containing five rows spaced 120 cm apart with 50 cm between plants in the row. Standard agronomic management recommendations for pigeonpea were followed during each season.

At physiological maturity, the per cent incidence of fusarium wilt (%FW) was determined. Initially, individual plants in each plot were scored for wilting (as a symptom of *F. udum*) followed by visual examination of the cross-section of the stem of each candidate plant in order to confirm the presence of a brown ring of discoloured xylem vessels. During harvesting, grain size as measured by 100-grain weight (100-GW) and grain yield were measured.

Each trial was arranged as a completely randomized design with three replications. Statistical analysis of data using statistical analysis system (SAS) procedures (SAS Institute, 1989) was applied. Tukey's method (Ott, 1988) was applied to separate the trait means obtained for each respective set of the five genotypes.

Results

Both the highest (92.0) and lowest (1.7) %FW scores were observed at Ngabu (Malawi) for ICEAP 00068 and ICEAP 00053, respectively (Table 2). The disease incidence in the local cultivar (Royes) was 90.2% compared with <5.0% for ICEAP 00040. The check genotype (ICEAP 00068) showed the highest susceptibility to fusarium wilt at all three locations. In contrast, the

Table 2

The %FW for pigeonpea genotypes scored in wilt-sick plots in three different countries during the 2001/2002 cropping season

Genotype	%FW		
	Kiboko (Kenya)	Ngabu (Malawi)	Ilonga (Tanzania)
ICEAP 00020	16.7 ^a	3.9 ^a	21.2 ^a
ICEAP 00040	13.3 ^a	4.6 ^a	19.2 ^a
ICEAP 00068*	87.5 ^c	92.0 ^b	90.9 ^c
ICEAP 00053	52.7 ^b	1.7 ^a	–
ICPL 87051	24.1 ^b	–	–
Royes	–	90.2 ^b	–
ICEAP 00057	–	–	4.7 ^a
Ex-Lugoba-1	–	–	44.2 ^b

%FW, per cent incidence of fusarium wilt.

Means in the same column followed by the same letter are not significantly different at the 0.05 probability level (Tukey' test).

*Susceptible check genotype at all three locations.

disease incidence in ICEAP 00040 was consistently low (<20.0%) at all three locations. There was a differential host response to the disease by the genotype ICEAP 00053 between the two locations where it was evaluated.

The mean grain size for ICEAP 00040 as gauged by 100-GW (>18.0 g) across the three locations was large (Table 3). However, the grain size obtained for the genotype at both Kiboko (Kenya) and Ilonga (Tanzania) was 25.0% smaller than that observed at Ngabu (Malawi) indicating environmental influence on this trait (Table 3).

Similarly, grain yield was influenced by the location. Nevertheless, at least 1.5 ton/Ha of grain yield was obtained for ICEAP 00040 compared with <1.0 ton/Ha for the susceptible genotype ICEAP 00068 at all the locations. At Ilonga Research Station, the unimproved traditional landrace (Ex-Loguba-1) attained a low grain yield (1.3 ton/Ha) as well as size (100-GW = 10.1 g) but the elite genotypes (ICEAP 00020, ICEAP 00040 and ICEAP 00053) averaged 2.7 ton/Ha (Table 2). Calculation of phenotypic correlation coefficient (*r*) using data from all genotypes in all locations resulted in a linear inverse relationship (*r* = 0.714; Df = 13; P < 0.01) between %FW and grain yield indicating that diminished grain yield could be attributed partly to the disease.

Discussion

The results of this study indicated a high level of wilt resistance in our elite pigeonpea germplasm particularly ICEAP 00040. Classification of ICEAP 00040 as resistant to fusarium wilt was consistent with approaches used in classifying resistance to the disease in other leguminous species. For instance, genotypes showing <10% (Halila and Strange, 1997) and <20% (Bayaa et al., 1997) incidence of fusarium wilt were considered resistant in chickpea (*Cicer aritinum*) and lentil (*Lens culinaris*), respectively. Furthermore, the high disease pressure present in wilt-sick plots under, which these genotypes were evaluated, is not expected

Table 3
The grain size and yield for pigeonpea genotypes evaluated in three different countries during the 2001/2002 cropping season

Genotype	Kiboko (Kenya)		Ngabu (Malawi)		Ilonga (Tanzania)	
	100-GW (g)	GY (ton/Ha)	100-GW (g)	GY (ton/Ha)	100-GW (g)	GY (ton/Ha)
ICEAP 00020	16.4 ^a	1.6 ^b	23.0 ^a	1.7 ^b	19.6 ^b	2.4 ^c
ICEAP 00040	18.3 ^a	2.2 ^c	24.0 ^a	1.9 ^b	18.2 ^b	3.0 ^c
ICEAP 00068*	14.6 ^a	0.6 ^a	18.0 ^a	0.1 ^a	13.5 ^b	0.1 ^a
ICEAP 00053	18.2 ^a	1.3 ^b	22.0 ^a	0.6 ^a	—	—
ICPL 87051	13.9 ^a	0.9 ^a	—	—	—	—
Royes	—	—	16.0 ^a	0.6 ^a	—	—
ICEAP 00057	—	—	—	—	14.2 ^b	2.8 ^c
Ex-Lugoba-1	—	—	—	—	10.1 ^a	1.3 ^b

100-GW = 100-grain weight; GY, grain yield.

Means in the same column followed by the same letter are not significantly different at the 0.05 probability level (Tukey's test).

*Susceptible check genotype at all three locations.

in cropping systems that rotate legumes with other species, thus interrupting the continuous build-up of the inoculum.

Because of its ability to withstand the high disease pressure, wide adaptability and high yield potential, ICEAP 00040 has been attractive to pigeonpea farmers in the region extending from the semi-arid lowlands of eastern Kenya (5°S) to Mozambique (25°S) and was subsequently released in 2003 for commercial production in both Malawi and Tanzania (Silim et al., 2005). The farmers and markets prefer the large, cream grains that are characteristic of the genotype.

The differential host response to *F. udum* observed for genotype ICEAP 00053 was in agreement with the findings reported in a similar study involving an exotic cultivar (ICP 9145) screened for resistance to the disease in Kenya and Malawi (Reddy et al., 1990). This suggested that probably, at least two different pathogenic races of the disease exist in the region. In chickpea, Tekeoglu et al. (2000) reported lines with resistance to one race of fusarium wilt but susceptible to another race, which suggested that different resistance genes confer resistance to different races. Such lines could be useful as race differentials to facilitate identification of races based on host × pathogen interactions. Apart from a study aimed at characterizing *F. udum* isolates from Kenya (Kiprop et al., 2002), there are no reports of attempts to characterize the races of *F. udum* in Southern Africa. In addition, the inheritance of wilt resistance is not fully understood thus limiting breeding programmes aimed at efficiently introgressing the resistance into genotypes with good agronomic traits and adapted to the region. Better understanding of the resistance to the disease could also enhance its manipulation through molecular approaches (Ratnaparkhe et al., 1998; Kumar et al., 2004). Nevertheless, the disease resistance observed in this study could be useful as a good source of resistance in pigeonpea breeding programmes in the region. Likely, the high yielding elite germplasm reported in this study will contribute to food security in Southern Africa.

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