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Evaluation of Common Bean (Phaseolus vulgaris) Genotypes for Resistance to Root Rot Disease Caused by Pythium aphanidermatum and Pythium splendens under Screen House Conditions

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Abstract
The most important economic species of the genus *Phaseolus* is the common beans (*Phaseolus vulgaris* L.) which is widely cultivated and arguably the most significant leguminous for direct human consumption. It is an important source of dietary protein, calories, dietary fibres and minerals particularly iron and zinc. Root rot disease caused by *Pythium* pathogen is one of the major production constraint in bean growing areas within East Africa. In Tanzania, control measures used by farmers are fungicidal seed treatments which are less effective and not environmentally friendly, soil drainage and crop rotation which are not sustainable in the disease management. This study focused on the evaluation and selection of promising common bean genotypes for resistance to *Pythium* root rot disease from 100 bean genotypes sourced from Tanzania, CIAT and Andean Diversity Panel (ADP). Inoculum of *Pythium aphanidermatum* and *Pythium splendens* were used for challenging the beans genotypes under controlled environment. Experiment was set by randomized completely block design (RCBD) with three replications. Disease severity was assessed based on 1-9 scale; 1 being non-pathogenic and 9 being highly pathogenic. The response of common bean genotypes to *P. aphanidermatum* and *P. splendens* and their interactions were statistically different ($P<0.0001$). Two bean genotypes ADP-014 and ADP-080 showed promising trait of resistance, 38 genotypes showed moderate resistant trait and 57 were susceptible to *Pythium* root rot disease.
Keywords: Inoculum, Leguminous, Pathogenic, Resistant trait, Severity.

1.0 Introduction

Common beans (*Phaseolus vulgaris* L.) is a global significant leguminous crop which is a source of food for human consumption. It is consumed in different forms including the leafy vegetable, pods, green grains and as dry beans (Katungi *et al*., 2009). It is a source of Vitamin – B, calcium, iron, phosphorus and zinc which are essential for human growth, health and development. According to Wortmann (Rusuku *et al.*, 1997), in the developing world, this leguminous crop is produced subsistantly by women farmers' who market approximately 40% of their produce estimated at US $452 million, while the rest of the crop is used for home consumption. In Africa, diseases are estimated to be the second biggest constraint to bean production after low soil fertility (CIAT, 2003). Most destructive diseases are caused by fungal, bacterial and viral causal agents. Different *Pythium* spp. cause seed decay, pre-emergency and post-emergency on beans genotypes, likewise infected common beans seeds or seedlings typically become discolored, chlorotic and soft and decayed even if they germinate and they wilt or even die within 1-3 weeks (Hendrix and Campbell, 1973; Pfender, 1991). Studies conducted by Binagwa (Unpublished) identified eleven species whereby *P. aphanidermatum* and *P. splendens* being the most widely distributed in Mbozi and Lushoto districts in Tanzania and both was pathogenic to several bean genotypes. One of the aggressive and pathogenic species in *Pythium* genus is *P. aphanidermatum* which causes root rot and crown necrosis of mature bean plants, also has a wide host range that cause many economically important root rot disease (Al-Mahmooli *et al.,* 2015; Ben Yephet and Nelson, 1999; Haritha *et al*., 2010). *P. splendens* is known for being pathogenic to young seedlings of several plant species and it causes severe damping-off of seedlings (Linde *et al.,* 1994). Different screening methods found that beans cultivars with colored seeds had higher levels of resistance to this pathogen than white seeded cultivars (Lucas and Griffiths, 2004). It is believed that, one of the most effective, sustainable and environmentally safe methods of control/management of this disease is by the use of resistant beans genotypes (Deng *et al*., 2005).

2.0 Materials and Methods

2.1 Study area, source of genetic materials and Pythium inoculum.

Screen house experiment were conducted at Sokoine University of Agriculture (SUA); Morogoro, Tanzania located at 6°49′S and 37°40′E. A total of 100 common beans genotypes including resistant and susceptible checks were evaluated against *P. aphanidermatum* and *P. splendens*. Thus, 55 genotypes from Centro Internacional de Agricultura Tropical (CIAT) Regional Office Kampala, Uganda, 35 from ADP collections and 10 popular commercial cultivars from Tanzania. *Pythium* inoculum were obtained from SUA Laboratory.

2.2 Preparation of Pythium sp. inoculum and inoculation

Inoculum of *P. aphanidermatum* and *P. splendens* isolates were reactivated by culturing them on fresh Potato Dextrose Agar (PDA) growth media and incubated at 24°C for 10 days. 100g of millet grain was mixed with 70mls of water in 350mls glass vessels and double autoclaved at 121°C for 15 minutes at 2 days intervals and left them to cool. In order to increase inoculum, the prepared substrate (autoclaved grain millet) was mixed with a disc of PDA agar with *Pythium* culture and incubated for 12 days in the darkness at 24°C to allow a uniform growth of mycelia. After every two days the substrate was shaken well to ensure homogenous distribution.

2.3 Screen house experiment.

After the incubation of the inoculum in the dark at 24°C, sterilized soil was mixed with inoculum at a ratio of 1:10v/v. Pots (12cm diameter) were then filled with the mixture. Pots with different *Pythium* isolates were arranged in a randomized complete block design with three replications and assigned bean genotypes randomly. 100 common bean genotypes were evaluated using *P. aphanidermatum* and *P. splendens* making the whole experimental units of 600 pots for first experiment. In each pot with a mixture of sterilized soil and specific inoculum, 4 seeds of each common bean genotypes were planted. After germination, plants were watered every evening to ensure favorable environment for pathogen establishment and development. Three weeks after planting, seedlings were uprooted and washed with tap water to remove soil from the roots. The level of infection on the roots and hypocotyls of seedlings were observed, and disease severity assessed based on 1to 9 scale developed by CIAT with 1 being non-pathogenic and 9 being highly pathogenic (Abawi and Pastor-Corrales, 1990). Generally, common bean genotypes with an average score of 1.0 to 2.9 were considered as resistant while that with 3.0 to 5.9 as moderately resistant and 6.0 to 9.0 as susceptible to *Pythium* root rot disease. Disease scoring was done independently on 4 bean seedlings per each bean genotype. After the first screening experiment, common bean genotypes that showed promising resistant trait and moderately resistant with mean score less than 4.5 were subjected to second screening experiment to ascertain the validity of the initial results.

2.4 Data analysis

Severity score data were subjected to Statistical Analysis Software (SAS) for significant tests of 100 common bean genotypes against the reaction of *P. aphanidermatum* and *P. splendens*, analyzing the interaction of isolates with genotypes and testing mean separation using LSD test at 5% for each isolate. The following; is a linear model for the screen house experiment;

$$\mathbf{Y_{ijk} = \mu + \rho_j + T_i + G_j + T_{i*Gk} + e_{ijk}}$$

Y_{ijk} = Observed from block j of treatment i and bean genotype k
μ= Overall mean for all the observed response
ρ_j= Block effect j the observed response
T_i = Effect of treatment (isolates) for severity of disease
G_j= Responses of bean genotypes to treatment
T_{i*Gk}= Interaction effects of isolates and bean genotypes to disease severity
e_{ijk}= Experimental error

3.0 Results

Poor seedling establishment through "damping-off effect', seed rots, yellowing of leaves, decay and brownish coloration of infected beans root seedlings were observed for several beans genotypes (Figure 1). For known (check) resistant genotypes (RWR-917 and AND-1062) no such symptoms of root rot or hypocotyl infections were observed. Pathogenicity response of *P. aphanidermatum* and *P. splendens* to common beans genotypes were not statically different ($P<0.0641$) with mean scores of 4.98 and 5.05 respectively (Table 1) due to having similar effects in causing root rot disease. Results of the first screening experiment showed two genotypes i.e. ADP-014 and ADP-080 as resistant, 77 genotypes were moderately resistant and 18 genotypes were susceptible to both *P. aphanidermatum* and *P. splendens*. All beans cultivars collected from Tanzania were categorized as moderately resistant having disease scores ranged 4.2 – 5.2. Andean Diversity Panel (ADP) genotypes expressed both resistant and susceptible traits, two genotypes were resistant, one genotype (ADP-620) was susceptible and thirty two genotypes were moderately resistant with overall scores of 3.3 – 5.9. The variations were observed among common

beans genotypes and between the interaction of genotypes and isolates in relation to their ability to cause root rot disease. The response of common bean genotypes to *P. aphanidermatum* and *P. splendens* were highly significant (P<0.0001) for *Pythium* severity indicating that both isolates have positive effects on *Pythium* root rot severity. Also, the interaction of isolates and common bean genotypes showed significant effect (P<0.047) for their effects on disease score indicating that the reaction of common bean genotypes were influenced by different genotype frequencies (Table 2).

From this first evaluation, fifty beans genotypes with scores between 2.6 to 4.5 were selected for the second evaluation in similar screen house. 26 beans genotypes from Andean Diversity Panel, 6 bean genotypes from Tanzania and 18 from CIAT (including checks) were screened against *P. splendens* due to its higher magnitude of mean score values of 5.05. The response of common bean genotypes against *P. splendens* were significantly different (P<0.0001). Similar results were obtained whereby two beans genotypes (ADP-014 and ADP-080) with disease rating scores of 2.17 and 2.42 respectively being resistant as shown in the first experiment (Table 3 and Table 4). Twenty one bean genotypes from the ADP were moderately resistant and three were susceptible with mean score range of 6.08 – 6.17. For the Tanzanian beans genotypes, 5 cultivars were moderately resistant; Njano ndefu (3.0), Jesca (4.3), Soya fupi (5.25), Lyamungo 90 (5.8) Mushindi (4.58) and pesa cultivars were susceptible with 6.17 mean score similar to that of Andean Diversity Panel. Under CIAT sourced cultivars, 12 were moderately resistant and four were susceptible with mean scores greater than 6.17 (Table 3 and Table 4).

4.0 Discussion

The aim of this study was to evaluate and select promising common beans genotypes from a pool of common beans germplasm that might confer resistance to *Pythium* root rot disease in Tanzania. The severity of the root rot disease caused by *P. aphanidermatum* and *P. splendens* in common beans evaluated in this study was slightly different and thus indicates variations in aggressiveness of the species on common bean genotypes. Zhang and Yang, (2000) in their study of pathogenicity of *Pythium* isolates showed differences in aggressiveness among the *Pythium* isolates. The pathogenicity tests caused similar symptoms as that observed by Rusuku (Rusuku *et al.*, 1997). The resistance of beans genotypes to *P. ultimum* is associated with colored seeds, several evaluation of bean germplasm conducted earlier (Dickson and Petzoldt, 19880; Lucas and Griffiths, 2004) found that colored common bean genotypes have higher level of resistance to *Pythium* than white seeded bean genotypes. Also, the most effective long term solution for *Pythium* pathogen control is the use plant host resistance. Previous studies have identified source of resistance to *P. ultimum* from wild accessions of common bean genotypes and progenies obtained by back crossing procedure (Nzungize *et al*., 2011; York *et al.*, 1977)). This study revealed to the works done by Otsyula (1998) which aimed on screening 26 common bean genotypes in which both resistance and susceptible traits were observed.

Screen house experiments showed that pathogenic *P. aphanidermatum* and *P. splendens* cause appreciable damping-off under favorable environment. Establishment and development of disease symptoms were observed after three weeks on several common bean genotypes. Two genotypes (ADP-080 and ADP-014) expressed resistance traits to *P. aphanidermatum* and *P.splendens*. Several other bean genotypes showed a mean score of less than 4.0 when tested with *P. aphanidermatum* and *P. splendens* during both screen house experiments including; ADP-012, ADP-510, ADP-057, ADP-054, ADP-480, ADP-508, ADP-090, BFS-34, ALB-35, ALB-91, KWP-08, KWP-48, and Njano ndefu. This study supports the work of Eastern, Southern and Central Africans' scientists aimed at finding common bean genotypes with root rot host resistant trait through gene introgression techniques and screening of bean accessions against *Pythium* root rot diseases. Once a resistant genotype is identified, it potentially could be grown productively regardless of *Pythium* specie or species combinations that are present, allowing for a wider control of *Pythium* root rot disease through improved host resistance across the major common bean growing regions in Tanzania.

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Table 1: Mean score by magnitude for *Pythium* species

Isolate name	Score mean	t-value	LSD
P. aphanidermatum	4.98	1.97	3.09
P. splendens	5.06	1.98	3.29
+P. splendens	4.53	1.62	2.55

+Isolate used for second screen house experiment LSD: Least Significant Difference

Table 2: Effect of *Pythium* isolates and common beans genotype to root rot severity

Source of variation	DF	MS	F-value	Pr>F	Status
Replication	2	72.319	18.34	<0.0001	***
Pythium isolates	1	0.859	0.22	0.641	NS
Common bean genotypes	99	9.509	2.41	<0.0001	***
Pythium isolates x Common bean genotypes	99	5.092	1.29	0.0466	*
+ P.splendens	49	5.392	2.19	<0.0001	***

*** Highly significant, *Slightly significant (P=0.05), DF= Degree of freedom, MS=Mean Square, NS= Not Significant+ Isolate used for second screen house experiment.

Table 3: General mean score response of common bean germplasm to *P. aphanidermatum* and *P. splendens* 1st screening experiment

Entry	Common bean genotypes	Source of genotype	Mean scores			Status
			P.aphanidermatum	*P.splendens*	Overall Mean	
1	ADP-449	Andean Diversity Panel	5.3d – q	3.8h – p	4.6	MR
2	ADP-019	Andean Diversity Panel	4.3g – r	5.3c – o	4.8	MR
3	ADP-014	Andean Diversity Panel	2.7p – r	2.5m – p	2.6	R
4	ADP-016	Andean Diversity Panel	5.7c – p	4.3e – p	5.0	MR
5	ADP-111	Andean Diversity Panel	4.7e – r	3.7h – p	4.2	MR
6	ADP-027	Andean Diversity Panel	4.0i – r	3.7h – p	3.8	MR
7	ADP-123	Andean Diversity Panel	3.0n – r	6.7a – i	4.8	MR
8	ADP-112	Andean Diversity Panel	2.8o – r	4.2f – p	3.5	MR
9	ADP-651	Andean Diversity Panel	5.8b – o	2.3n – p	4.1	MR
10	ADP-057	Andean Diversity Panel	5.7c – p	2.3n – p	4.0	MR
11	ADP-659	Andean Diversity Panel	4.5f – r	6.0a – k	5.2	MR
12	ADP-080	Andean Diversity Panel	3.3l – r	2.2o – p	2.8	R
13	ADP-054	Andean Diversity Panel	3.2m – r	5.0d – p	4.1	MR
14	ADP-055	Andean Diversity Panel	3.8j – r	7.2a – g	5.5	MR
15	ADP-638	Andean Diversity Panel	2.8o – r	5.0d – p	3.9	MR
16	ADP-480	Andean Diversity Panel	4.5f – r	3.7h – p	4.1	MR
17	ADP-232	Andean Diversity Panel	4.7e – r	3.0kl – p	3.8	MR
18	ADP-447	Andean Diversity Panel	4.0i – r	4.8e – p	4.4	MR
19	ADP-190	Andean Diversity Panel	5.5c – p	5.7b – m	5.6	MR
20	ADP-346	Andean Diversity Panel	5.3d – q	5.5c – n	5.4	MR
21	ADP-508	Andean Diversity Panel	4.7e – r	3.7h – p	4.1	MR
22	ADP-110	Andean Diversity Panel	5.7c – p	3.3j – p	4.5	MR
23	ADP-288	Andean Diversity Panel	4.8e – r	1.8p	3.3	MR
24	ADP-639	Andean Diversity Panel	6.2a – m	5.0d – p	5.6	MR
25	ADP-098	Andean Diversity Panel	3.7k – r	6.0a – k	4.8	MR
26	ADP-031	Andean Diversity Panel	3.2m – r	6.88a – h	5.0	MR
27	ADP-510	Andean Diversity Panel	3.8j – r	3.7h – p	3.8	MR
28	ADP-685	Andean Diversity Panel	7.0a - i	4.0g – p	5.5	MR
29	ADP-090	Andean Diversity Panel	4.3g – r	4.5e – p	4.4	MR
30	ADP113	Andean Diversity Panel	2.7p – r	4.7e – p	3.7	MR
31	ADP-467	Andean Diversity Panel	4.2h – r	4.3e – p	4.2	MR
32	ADP-303	Andean Diversity Panel	4.2h – r	3.7h – p	3.9	MR
33	ADP-620	Andean Diversity Panel	8.0a – d	6.3a – j	7.2	S
34	ADP-001	Andean Diversity Panel	3.7k – r	5.3c – o	4.5	MR
35	ADP-047	Andean Diversity Panel	3.7k – r	5.0d – p	4.3	MR
36	CAL-96	CIAT (Susceptible check)	8.0a – d	8.5a – c	8.2	S
37	AND-1062	CIAT (Resistant check)	2.2r	2.5m – p	2.3	R
38	RWR719	CIAT (Resistant check)	2.3qr	2.7l – p	2.5	R
39	BFS34	CIAT	3.3l – r	5.0d – p	4.2	MR
40	BFS75	CIAT	8.5a – c	5.8a – l	7.2	S
41	BFS412	CIAT	7.3a – g	6.2a – k	6.7	S
42	BFS10	CIAT	5.8b – o	6.8a – h	6.8	S
43	BFS33	CIAT	6.0a – n	3.3j – p	4.7	MR
44	ALB142	CIAT	4.7e – r	6.3a – j	5.5	MR
45	ALB104	CIAT	4.5f – r	4.3e – p	4.4	MR
46	ALB35	CIAT	4.8e – r	4.2f – p	4.5	MR
47	ALB91	CIAT	3.7k – r	4.7e – p	4.2	MR
48	ALB-178	CIAT	5.3d – q	4.3e – p	4.8	MR
49	KFRR-127	CIAT	3.8j – r	4.8e – p	4.3	MR
50	KFRR-225	CIAT	6.0a – n	5.5c – n	5.8	MR
51	KFFR-162	CIAT	4.0i – r	4.7e – p	4.3	MR
52	KFRR-171	CIAT	6.0a – n	4.2f – p	5.1	MR
53	KFRR-237	CIAT	4.e – r	5.7b – m	5.2	MR
54	KFRR-206	CIAT	5.7c – p	4.7e – p	5.2	MR
55	KFRR-282	CIAT	5.3d – q	6.5a – j	5.9	MR
56	KFRR-278	CIAT	4.2h – r	5.8a – l	5.0	MR
57	KFRR-212	CIAT	4.3g – r	6.7a – i	5.5	MR
58	KWP-07	CIAT	6.0a – n	5.3c – o	5.7	MR
59	KWP-08	CIAT	5.0d – r	3.3j – p	4.2	MR

60	KWP-09	CIAT	3.0n – r	4.8e – p	3.9	MR
61	KWP-27	CIAT	3.8j – r	4.5e – p	4.2	MR
62	KWP-28	CIAT	6.2a – m	6.2a – k	6.2	S
63	KWP-29	CIAT	6.3a – l	3.3j – p	4.8	MR
64	KWP-30	CIAT	5.8b – o	6.2a – k	6.0	S
65	KWP-34	CIAT	6.0a – n	3.5i – p	4.8	MR
66	KWP-38	CIAT	3.8j – r	8.2a – d	6.0	S
67	KWP-43	CIAT	5.3d – q	3.5i – p	4.4	MR
68	KWP-48	CIAT	3.8j – r	2.7l – p	3.2	MR
69	KWP-55	CIAT	3.7k – r	5.2d – o	4.4	MR
70	KWP-58	CIAT	5.3d – q	4.5e – p	4.9	MR
71	KWP-97	CIAT	3.0n – r	5.3c – o	4.2	MR
72	KWP-98	CIAT	6.3a – l	4.5e – p	5.4	MR
73	G-18	CIAT	3.5l – r	5.5c – n	4.5	MR
74	G-80	CIAT	7.7a – e	5.7b – m	6.7	S
75	G-37	CIAT	6.2a – m	5.5c – n	5.8	MR
76	G-72	CIAT	8.5a – c	6.3a – j	7.4	S
77	G-49	CIAT	5.8b – o	5.7b – m	5.8	MR
78	KWC-52	CIAT	7.2a – h	7.5a – e	7.3	S
79	KWC-48	CIAT	4.8e – r	6.0a – k	5.4	MR
80	KWC-51	CIAT	6.3a – l	6.8a – h	6.6	S
81	KWC-27	CIAT	4.3g – r	6.7a – i	5.5	MR
82	KWC-32	CIAT	6.2a – m	6.8a – h	6.5	S
83	KWC-22	CIAT	8.0a – d	8.8ab	8.4	S
84	KWC-41	CIAT	5.5c – p	5.5c – n	5.5	MR
85	KWC-18	CIAT	9.0a	9.0a	9.0	S
86	KWC-45	CIAT	6.3a – l	6.8a – h	6.6	S
87	KWC-19	CIAT	8.8ab	6.3a – j	7.6	S
88	KWC-26	CIAT	7.2a – h	6.3a – j	6.8	S
89	KWC-25	CIAT	5.7c – p	6.0a – k	5.8	MR
90	KWC-30	CIAT	7.5a – f	5.8a – i	6.7	S
91	Pesa	Tanzania	4.5f – r	4.2f – p	4.3	MR
92	Mushindi	Tanzania	6.7a – k	2.7l – p	4.7	MR
93	Njano ndefu	Tanzania	3.3l – r	3.7h – p	3.5	MR
94	Njano fupi	Tanzania	3.8j – r	5.7b – m	4.8	MR
95	Jesca	Tanzania	2.2r	5.8a – i	4.0	MR
96	Soya fupi	Tanzania	3.5l – r	4.8e – p	4.2	MR
97	Selian 94	Tanzania	4.0i – r	6.0a – k	5.0	MR
98	Selian 97	Tanzania	6.8a – j	3.7h – p	5.2	MR
99	Lyamungo 90	Tanzania	2.7p – r	5.7b – m	4.2	MR
100	Lyamungo 85	Tanzania	2.8op – r	7.3a – f	5.1	MR

Keys: R= Resistant, MR= Moderate Resistant, S= Susceptible

Means score within column followed by similar letters are not significantly different (P=0.05).

Table 4: General mean score response of common bean germplasm to *P. splendens*

Entry	Common bean genotypes	Source of genotype	Mean score *P. splendens*	Status
1	ADP-449	Andean Diversity Panel	6.17a – e	S
2	ADP-014	Andean Diversity Panel	2.17k	R
3	ADP-111	Andean Diversity Panel	4.00d – k	MR
4	ADP-027	Andean Diversity Panel	5.17b – i	MR
5	ADP-112	Andean Diversity Panel	3.25h – k	MR
6	ADP-651	Andean Diversity Panel	4.58c – k	MR
7	ADP-057	Andean Diversity Panel	3.58f – k	MR
8	ADP-080	Andean Diversity Panel	2.42jk	R
9	ADP-054	Andean Diversity Panel	3.17i – k	MR
10	ADP-638	Andean Diversity Panel	5.83a – g	MR
11	ADP-480	Andean Diversity Panel	3.08i – k	MR
12	ADP-232	Andean Diversity Panel	5.25b – i	MR
13	ADP-447	Andean Diversity Panel	4.17c – k	MR
14	ADP-508	Andean Diversity Panel	3.25h – k	MR
15	ADP-110	Andean Diversity Panel	5.08c – j	MR
16	ADP-288	Andean Diversity Panel	6.08a – f	S
17	ADP-510	Andean Diversity Panel	3.17i – k	MR
18	ADP-090	Andean Diversity Panel	3.50g – k	MR
19	ADP113	Andean Diversity Panel	4.33c – k	MR
20	ADP-467	Andean Diversity Panel	4.42c – k	MR
21	ADP-303	Andean Diversity Panel	4.33c – k	MR
22	ADP-001	Andean Diversity Panel	6.08a – f	S
23	ADP-047	Andean Diversity Panel	4.08c – k	MR
24	ADP-019	Andean Diversity Panel	4.75c – j	MR
25	ADP-123	Andean Diversity Panel	5.00c – j	MR
26	ADP-098	Andean Diversity Panel	5.50b – i	MR
27	CAL-96	CIAT (Susceptible check)	7.67ab	S
28	AND-1062	CIAT (Resistant check)	2.42jk	R
29	BFS34	CIAT	3.33g – k	MR
30	ALB104	CIAT	3.50g – k	MR
31	ALB35	CIAT	5.42b – i	MR
32	ALB91	CIAT	3.42g – k	MR
33	KFRR-127	CIAT	4.42g – k	MR
34	KFFR-162	CIAT	6.58a – c	S
35	KFRR-278	CIAT	5.75a – h	MR
36	KWP-08	CIAT	3.25h – k	MR
37	KWP-09	CIAT	4.83c – j	MR
38	KWP-27	CIAT	4.25e – k	MR
39	KWP-43	CIAT	4.08c – k	MR
40	KWP-48	CIAT	3.50g – k	MR
41	KWP-55	CIAT	6.42a – d	S
42	KWP-97	CIAT	6.08a – f	S
43	Pesa	Tanzania	6.17a – e	S
44	Njano ndefu	Tanzania	3.00i – k	MR
45	Jesca	Tanzania	4.33c – k	MR
46	Soya fupi	Tanzania	5.25b – i	MR
47	Lyamungo 90	Tanzania	4.58c – k	MR
48	Mushindi	Tanzania	4.50c – k	MR
49	G-18	CIAT	4.33c – k	MR
50	BFS33	CIAT	8.25a	S

Keys: R= Resistant, MR= Moderate Resistant, S= Susceptible.
Means score within column followed by similar letters are not significantly different (P=0.05)

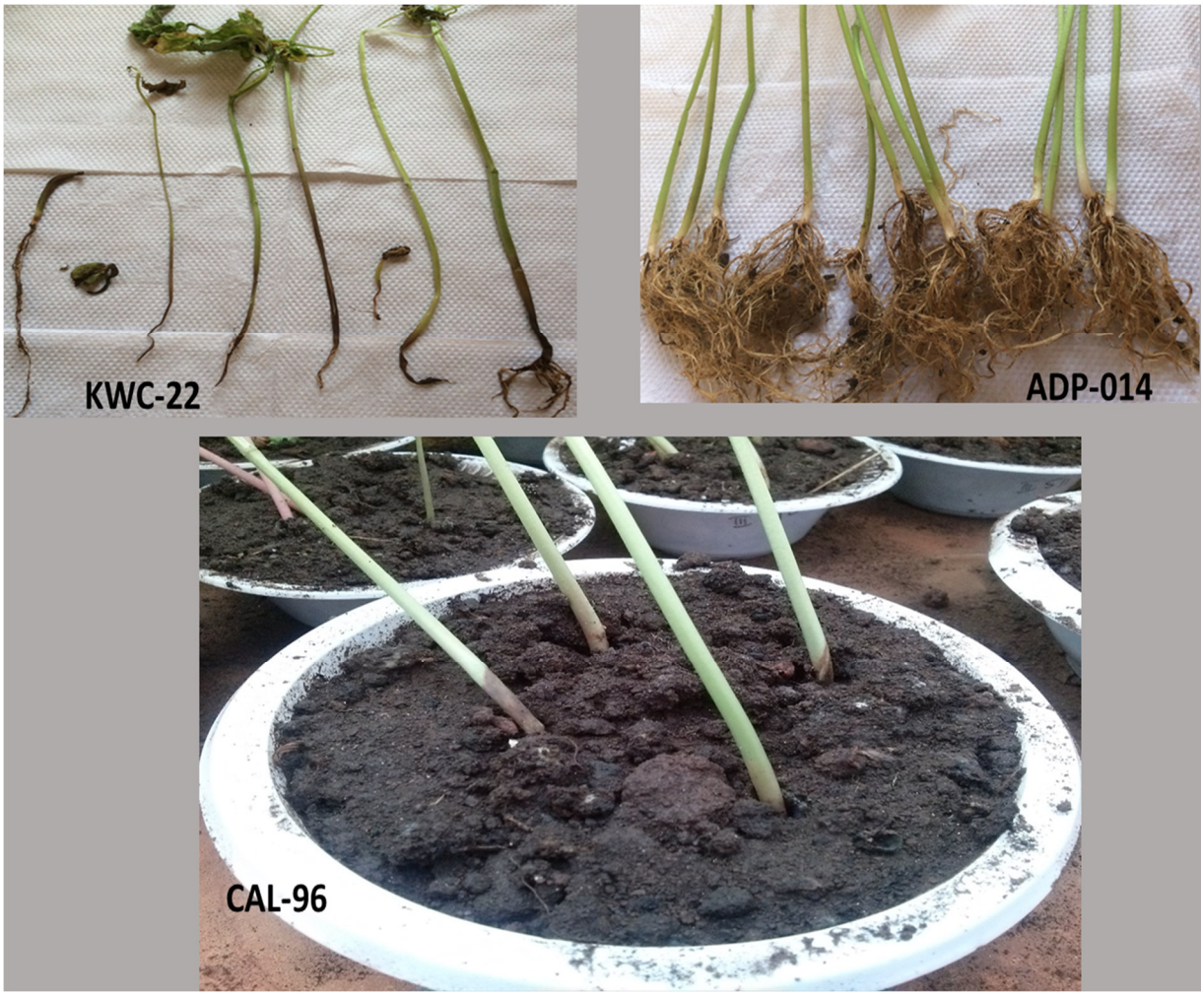

Figure 1: Symptoms observed on common bean genotypes in screen house KWC-22= Susceptible genotype from CIAT germplasm, ADP-014= Resistant genotype from ADP collection, CAL-96= Susceptible check.