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Research Article

Prevalence and Host Resistance to Common Bean Rust Disease in Western and Central Kenya

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Rust, caused by *Uromyces appendiculatus* (Pers.) Unger, is among the most devastating diseases of the common bean (*Phaseolus vulgaris* L.) worldwide. The pathogen is highly genetically variable, causing severe epidemics under favourable weather conditions. The objectives of this study were to determine the distribution of bean rust in major production areas in Kenya and identify potential sources of resistance for breeding. A field survey was conducted in five counties targeting smallholder common bean farmers in western and central Kenya, where data on the incidence and severity of bean rust and crop management practices by farmers were recorded. Additionally, seeds of the evaluated genotypes were collected from farms visited for further testing. A total of 77 common bean genotypes were subjected to natural infection under field conditions and inoculated with races 29–1, 29–3, 61–1, and 63–1 of rust under greenhouse conditions at the University of Embu. The gene pool affiliation of the genotypes was determined through the phaseolin protein marker analysis. Rust incidence and severity data were subjected to an analysis of variance using GenStat statistical software. The results showed that bean rust occurred in all counties although there were significant differences ($P < 0.001$) in incidence and severity among the surveyed localities. Based on a 1–9 severity rating scale, Bungoma County recorded the highest mean severity of 3.99 and an incidence of 71%. Cultivar grown, use of fungicides, management of residues, and crop spacing had a significant effect on bean rust severity. Under field and greenhouse conditions, the genotypes revealed high variations in response to rust, with 71% of the genotypes being susceptible under greenhouse inoculations. Enclave, MU#13, UN2-Darkgreen, UN6-Nakholo, Kat X56, and KMR-11 genotypes were identified as resistant and can be used as prospective parents in common bean improvement programs in Kenya. This study revealed high occurrence and distribution of common bean rust and thus provides critical baseline information for common bean rust management in Kenya.

1. Introduction

The common bean (*Phaseolus vulgaris* L.) is an important and versatile component of food, nutrition, and economic systems for rural and urban populations around the world [1]. Beans are rich in proteins, vitamins A, B_6, C, K, folic acid, and essential minerals such as calcium, potassium, iron, manganese, copper, and phosphorus [2]. Such nutrients are useful in complementing carbohydrate-rich foods such as cereals, tubers, and root crops. According to FAOSTAT [3], the global production of dry and green beans in 2019 was 28.9 million tons and 26.9 million tons, respectively. The per capita consumption of common beans in Kenya is relatively high, at approximately 14 kg–66 kg per year [4, 5]. Despite the importance of common beans as a pulse and vegetable crop, relatively low yields have been reported across years, and this can be explained by abiotic and biotic stresses, e.g., pests and disease [6].

Rust, caused by *Uromyces appendiculatus*, is among the major diseases decimating common bean fields wherever it occurs [7, 8]. The pathogen has high virulence variability and is distributed throughout the globe, constraining common bean production in humid subtropical and tropical regions and creating intermittent severe epidemics in moist temperate areas [8]. The occurrence of common bean rust is influenced by factors such as altitude, agronomic practices, temperature, relative humidity, leaf surface moisture, and host factors [9–12]. Bean rust disease first appears on the

upper and lower leaf surfaces as circular chlorotic or white spots that form reddish-brown pustules and yellow tissue surrounding single large or small groups of uredia [13]. Under these favourable conditions, the pathogen causes premature leaf yellowing, senescence, and total leaf fall resulting in 65– 100% yield losses in common beans [14, 15]. Most farmers mainly rely on the use of chemical and cultural methods, which are expensive for many small-holder farmers [16, 17]. Host plant resistance is, therefore, considered a sustainable method of managing the disease.

Incorporation of rust disease resistance genes into common bean cultivars grown in Kenya was achieved more than two decades ago and resulted in the release of resistant cultivars under the Grain Legume Project (GLP). However, due to the broad pathogenic variability of the rust fungus [18] and lack of focus on the pathogen in current breeding programs, informal reports have shown that the disease is slowly re-emerging resulting in losses among small-holder farmers in Kenya. A study by Odogwu et al. [19] reported high rust incidence and severity in the neighbouring country, Uganda. Therefore, there is a need for monitoring the changing virulence patterns in Kenya to prevent potential epidemics in the future and for the deployment of durable bean rust resistance genes. In addition, periodic collection and characterization of bean rust is essential, as it informs on virulence diversity, the dynamics of epidemics, and the development of common bean cultivars.

Resistance against bean rust disease is mainly conditioned by 14 major dominant genes, which are derived from the two common bean gene pools (Andean and Mesoamerican) [8, 13]. The gene pools refer to the domestication centres of wild beans identified by using the phaseolin seed protein [20], different allozymes [21–23], and various classes of molecular markers [24–26]. These markers are still useful in understanding the common bean germplasm; for example, the phaseolin protein molecular marker was utilized by Arunga and Odikara [24] to designate Kenyan French beans into the two common bean gene pools. Furthermore, various DNA assays (random amplified polymorphic DNAs and sequence characterized amplified regions) linked to the major rust resistance genes have been developed and utilized in the identification of resistance genes and for marker-assisted selection [8]. The classification of the common bean germplasm is important in rust resistance breeding because combining genes from both gene pools is a major strategy in integrated management of the disease [27, 28]. The objectives of this study were, therefore, to determine the distribution and factors influencing the occurrence of bean rust in Kenya and to identify cultivars with genes that confer resistance to this fungus.

2. Materials and Methods

The study entailed a field survey to assess the prevalence, severity, and factors influencing the occurrence of rust in cultivated common beans in five counties in Kenya. Secondly, field and greenhouse trials were carried out to evaluate a panel of common bean genotypes for resistance to rust.

2.1. Evaluation of Incidence, Severity, and Factors Influencing Occurrence of Bean Rust

2.1.1. Study Area. The study was conducted during the second cropping season (September 2020–January 2021) in five counties located in six major agroecological zones in Kenya. The zones are located in the warm lower humid midlands (LM1–LM4), cool upper midlands (UM1), and lower highlands (LH1) of western and central Kenya. The counties represent major bean production areas in Kenya. The sampled fields were at an altitude ranging from 1027 to 2429 m above sea level. Overall, a total of 150 fields were targeted in central Kenya (Embu and Kirinyaga Counties) and in western Kenya (Uasin-Gishu, Bungoma, and Kakamega Counties).

2.1.2. Sampling Design. The survey targeted smallholder farmers with field sizes averaging 1.2 ha[29] that formed the study units, and each field was visited once. Purposive and simple random sampling based on intensity of bean production, crop stage, and spatial and ecological location was used, targeting 30 fields in each county. Fields with bean plants at flowering to pod-formation growth stages were selected randomly at intervals of five to 10 km along the main roads. Following the methodology of Odogwu et al. [30], the size of each sampled field was estimated and the crop stage established. Equidistant steps following an inverted "*V*" outline were made at the edge of the field from which the sample plants were selected. At each predetermined pace, the plant nearest to the right foot was taken as the sample unit. Assessment of disease was done on 20 plants of the same cultivar sampled within each field. Evaluations were done on a cultivar found in a sample field. Whenever necessary, the number of randomly selected single plants per field was adjusted to suit the field size and crop distribution.

2.2. Data Collection and Analysis. Bean rust incidence was recorded from 20 sampled plants of the same cultivar within the sample field. Rust disease severity was rated using a modified CIAT 1– 9 scale, adopted from Van Schoonhoven and Pastor-Corrales [31]. This scale considers nine infection types, where 1 = no visible pustule, 2 = pustules covering 1% of leaf area, 3 = few pustules covering 2% of leaf area, 4 = intermediate pustules covering 5% of leaf area, 5 = small pustules covering 8% of leaf area, 6 = pustules covering 10% of leaf area, often surrounded with chlorotic halos, 7 = large pustules covering 15% of leaf area, surrounded with chlorotic halos, 8 = large pustules covering 20% of leaf area surrounded with chlorotic halos, and 9 = very large pustules covering more than 25% of leaf area, often with defoliation. A disease score of 1–3 was regarded as resistant, 4–6 as intermediate, and 7–9 as susceptible.

The global positioning system (GPS) readings of latitude, longitude, and altitude were recorded for each field using a GPS map camera lite application (version 1.0.7). In addition, information regarding factors affecting disease prevalence was recorded in a field book based on the

farmers' responses. These factors included the cropping system (intercrop or sole crop), common bean cultivar under production, seed source (farmer-saved seeds, local market, or certified seed from merchants), previous crop planted, and other cultural practices (fungicide use, crop debris management, crop spacing, and management of volunteer plants). At harvest maturity, seeds were collected from the visited farms for the purpose of screening for resistance to rust. Infected common bean leaves were collected from each sampled field for subsequent single-spore isolation and multiplication for further screening for rust resistance.

The GPS survey data from each sample location on field coordinates were used to develop the bean rust disease severity map. Rust incidence and severity data were subjected to analysis of variance using GenStat [32] Discovery Edition 14.0 statistical software. In this analysis, location (counties), cropping system, cultivar, source of seeds, debris management, previous crop, fungicide use, and management of volunteer plants were considered fixed factors. Multiple mean comparisons for rust disease incidence and severity for all fields surveyed were performed using Tukey's studentized range test at $\alpha = 0.05$.

3. Germplasm Screening for Resistance to Bean Rust

3.1. Experimental Site. Evaluation of the resistance profiles of the genotypes under field and greenhouse conditions was conducted at the University of Embu research field, located at a latitude of 0°30′S and a longitude of 37°27′E. The area's mean temperature is 19°C, with a maximum of 25°C and a minimum of 10°C, and an average annual rainfall of 1,120 mm [33].

3.2. Plant Materials. The common bean germplasm used in this study comprised of 77 bean genotypes obtained from farmers in the surveyed counties, which represented major bean-growing areas in western and central Kenya, the Kenya Agricultural and Livestock Research Organization (KALRO) seed unit, and the French bean improvement program at the University of Embu. The common bean genotypes consisted of 13 landraces, 20 French bean cultivars, 29 dry bean cultivars, 3 breeding lines, and 12 bean rust differential cultivars. Codes UN1 to UN8 were used to identify the eight landraces that were unnamed. GLP X92 (susceptible to rust) and the 12 differential cultivars/lines were used as checks because information on their resistance genes and gene pools was available [8].

3.3. Field Experimental Layout and Data Collection. The field experiment was conducted from May to July 2021, during the long-rain cropping season. The experiment was set up as a randomized complete block design with three replicates. Twenty-one seeds from each entry were sown in a 2-meter-long row, with inter and intrarow spacing of 30 cm and 10 cm, respectively. A susceptible cultivar, GLP X92, was planted as a spreader row after every five entries at a relatively high plant density to ensure increased disease pressure. Disease inoculation was based on natural infection. Bean rust disease severity was recorded using the modified CIAT 1– 9 disease rating scale adopted from Van Schoonhoven and Pastor-Corrales [31].

3.4. Screening for Resistance under Greenhouse Conditions. Ten viable bean rust isolates obtained during the survey were purified through single-spore isolation [8]. An individual unopened pustule including a 25 mm^2 surrounding leaf tissue for each isolate was separately cut and the spores were collected and transferred to susceptible seedlings of cultivar GLP X92. The single-pustules were collected and multiplied on the susceptible variety for three consecutive cycles and then characterized into physiological races using a set of 12 differential cultivars, according to Steadman, Pastor-Corrales, and Beaver [34]. Four races identified as 29-1, 29-3, 61-1, and 63-1 and an additional set of mixed isolates was used to evaluate the response of the germplasm to bean rust.

Ten seeds of each common bean germplasm panel and 12 differential series (as standard checks) were sown on seedling trays filled with sterile soil and laid out in a randomized complete block design with three replicates. The disease inoculum was introduced on 8–10-day-old plants with about two-thirds of the primary leaves expanded by hand spraying viable *U. appendiculatus* urediospores at a concentration of 2.0×10^4 urediospores per ml of distilled water. Inoculated plants were then transferred to a screenhouse maintained at 20 ± 1°C and a relative humidity >95% under a 12-hour light/dark regime for approximately 48 hours, after which the plants were transferred to a greenhouse at 20 ± 5°C for about 14 days.

Bean rust severity was rated using a 1–6 scale, where 1 = no visible pustule (immune), 2 = necrotic spots without sporulation, 3 = sporulating pustules <300 μm in diameter, 4 = sporulating pustules with a diameter of 300–500 μm, frequently surrounded by chlorotic halos, 5 = sporulating pustules with a diameter of 500–800 μm, frequently surrounded by chlorotic halos, and 6 = sporulating pustules larger than 800 μm in diameter frequently surrounded by chlorotic halos [34]. Cultivars with reaction values of 1–3 were categorized as resistant and 4–6 as susceptible. The most prevalent infection grade was chosen in case of several infection grades.

3.5. DNA Analysis for Gene Pool Affiliations. Young leaves were collected from each of the 77 common bean genotypes, and DNA was extracted using the Mahuku DNA extraction protocol [35]. The phaseolin protein SCAR marker was used in PCR amplification [35]. A 10 μl reaction volume in FrameStar® Break-A-Way PCR tubes containing 1X Dream Taq buffer (containing 2 mM $MgCl_2$), 0.2 mM dNTPs, 0.5 μM of each reverse and forward primer, 0.1 U Taq Polymerase (Thermo Fisher Scientific), and 1.5 ηg/μl of genomic DNA were used. The PCR procedure was as follows: an initial denaturation step at 94°C for 3 min, followed by 35 cycles of the following three steps: denaturation at 94°C for

10 s, 55°C annealing for 40 s, an extension at 72°C for 2 min, and a final extension step at 72°C for 5 min. To each PCR product, 2 μl of 6x DNA loading dye (NEB) was added. A 50 bp DNA ladder (https://www.thermofisher.com/order/catalog/product/10416014) was loaded in the first well; then, PCR product contents were loaded in subsequent wells on a 1.5% agarose gel prestained with 5 μm of ethidium bromide in 1x sodium borate buffer and run at 100 volts for 3 hours. The DNA bands were then viewed under ultraviolet light (UVP® GelDoc-it system) and scored for the presence of either two or three fragments of different sizes.

4. Results and Discussion

4.1. Prevalence, Incidence, and Severity of Bean Rust. Bean rust disease was observed across the five surveyed counties, with varying degrees of incidence and severity. Rust severity scores ranged from 1 to 9, with an incidence between 0 and 100%. The mean rust severity map revealed the distribution of rust across the surveyed counties (Figure 1). Incidence and severity of bean rust varied significantly ($P < 0.001$) among counties (Table 1) and the altitude (Table 2) of the regions. The overall mean rust incidence for the counties surveyed was 55.2%, with an overall mean severity of 3.03. The mean rust recorded was as follows: Bungoma (prevalence 100%; incidence 70.8%; severity 3.99), Uasin Gishu (prevalence 96.7%; incidence 61.20%; severity 3.12), Kakamega (prevalence 100%; incidence 57.30%; severity 3.00), Kirinyaga (prevalence 93.3%; incidence 48.3%; severity 2.69), and Embu (prevalence 83.3%; incidence 38.3%; severity 2.34). In this study, the incidence and severity of common bean rust varied by location, depending on environmental conditions and crop husbandry practices. The high incidence and severity of bean rust may be attributed to the agronomic practices adopted in the studied production areas among smallholder farmers. For instance, due to the use of susceptible cultivars and poor bean residue management, the bean rust incidence and severity were high in some individual fields studied in Bungoma, Kakamega, and Uasin Gishu counties, which could be explained by specific cultural activities compounded by high relative humidity due to high rainfall received in the counties in 2020 [36]. Lower bean rust incidence and severity were recorded in low altitude areas of <1,200 m above sea level, especially in lower parts of Embu County that occasionally receive low rainfall and high temperatures, which do not favor the occurrence of bean rust disease. Areas with altitudes of more than 1,200 m above sea level had a high bean rust incidence and severity. This may be attributed to high rainfall and relative humidity that favors infection and development of bean rust disease [12].

4.2. Effects of Cultural Practices on Bean Rust Prevalence and Severity. Some common bean production practices significantly influenced the incidence and severity of bean rust in the surveyed regions (Tables 3 and 2). This inference is consistent with the previous findings that show that the environment is a major factor affecting the distribution of biotic stressors on pulse crops [37]. Production of common beans as a sole crop or intercrop did not influence disease incidence or severity. Similarly, the source of seeds used for planting and previous crops grown had no significant influence on the incidence and severity of bean rust in the surveyed counties. The insignificant influence of the cropping system, source of planting material, and previous crop grown on prevalence of bean rust may be explained by the fact that bean rust could be influenced by the interaction of a set of factors such as ideal environmental conditions, host plant susceptibility, and high virulence of the pathogen.

Table 1: Incidence and severity of bean rust in western and central Kenya.

County	Number of fields surveyed	Bean rust[1]	
		Incidence (%)	Severity
Bungoma	30	70.83[a]	3.99[a]
Uasin Gishu	30	61.17[b]	3.12[b]
Kakamega	30	57.33[c]	3.00[bc]
Kirinyaga	30	48.33[d]	2.69[cd]
Embu	30	38.33[e]	2.34[d]
Mean		55.20	3.03

[1]Means within the same column followed by the same letter are not significantly different from one another ($P < 0.05$). a, b, c, and d following the values are supposed to show the differences in the means.

Fungicide use significantly ($P < 0.01$) affected the incidence and severity of bean rust, with reduced disease in fields sprayed with fungicides such as Dithane M45® (Mancozeb) and Funguran® (copper hydroxide-770 g/kg). However, the occurrence of rust in some fields in the surveyed counties in the central region despite fungicide treatment suggests ineffective application of fungicides or possibly that the pathogen in those areas has developed resistance to the fungicides being used. This finding emphasizes the need to evaluate the effectiveness of the available fungicides for efficacy and informed use of fungicides in the management of bean rust among smallholder farmers.

Incidences and severity of bean rust were cultivar-dependent, with the most susceptible cultivars being Kisii, Sungura, GLP-24 (Canadian Wonder), and Kablanketi, whereas the most resistant cultivars were Vanilla, Embean 14, and KAT B11. Limited cultivar selection among common bean farmers in Kenya, resulting in the use of cultivars susceptible to rust, contributed to high-rust incidence and severity in the surveyed counties. The significant influence of common bean cultivars under production on the occurrence and severity of bean rust observed in fields cultivated with landraces and commercial cultivars is due to their inherent genetic structure. Common bean cultivars have been reported to have a range of resistance to bean rust disease depending on their genetic composition under field conditions [19, 38].

Strategies used in the management of common bean residues, management of volunteer plants, and crop spacing had significant effects on mean rust incidence and severity ($P < 0.05$). The bean rust pathogen cannot survive without its common bean host, being an obligate parasite [28], and this could explain the significant influence of different strategies

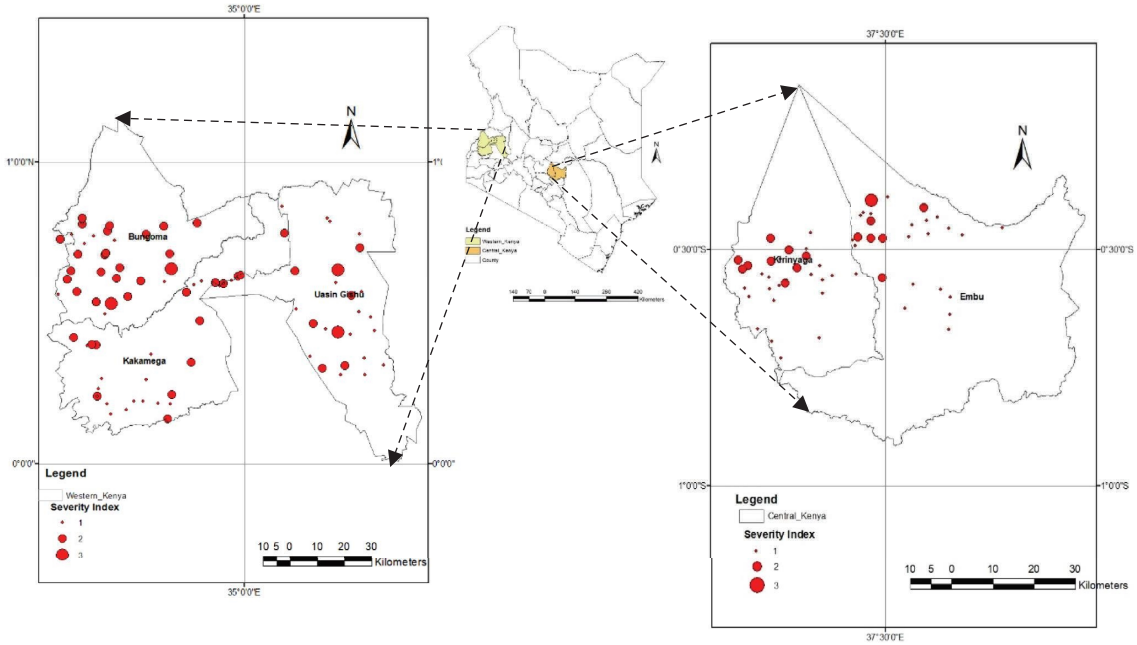

Figure 1: The map of Kenya showing disease severity scores of the fields in the counties surveyed. Score of 1 represents resistant, 2 represents intermediate reaction, and 3 highly susceptible to rust.

Table 2: Factors affecting incidence and severity of bean rust in western and central Kenya.

Factor	Factor classification	Bean rust[1]	
		Incidence (%)	Severity
Altitude	1200–1800 masl	58.33[a]	3.19[a]
	>1800 masl	57.24[a]	2.98[a]
	<1200 masl	14.50[b]	1.34[b]
Cropping system	Sole crop	55.70[a]	3.09[a]
	Intercrop	54.20[a]	2.92[a]
Fungicide use	No fungicide spray	57.30[a]	3.14[a]
	Fungicide spray	35.00[b]	1.91[b]
Seed source	Certified seed agents	49.50[a]	3.05[a]
	Local market	56.20[a]	3.06[a]
	Saved seed	54.70[a]	2.96[a]
Management of volunteer plants	No management	57.10[a]	3.12[a]
	Soil incorporation	52.90[b]	2.91[a]
	Herbicide spray	30.00[c]	1.65[b]
Debris management	Trash-lines	77.50[a]	4.05[a]
	Compost manure	65.33[b]	3.48[a]
	Burn	62.77[b]	3.41[a]
	Leave on soil surface	59.50[b]	3.33[ab]
	Livestock feed	47.47[c]	2.64[b]
	Soil incorporation	45.00[c]	2.38[c]

[1]Means followed by the same letter within a column are not significantly different from one another ($P < 0.05$). a, b, and c following the values are supposed to show the differences in the means.

used by farmers in managing volunteer plants and bean debris on bean rust incidence and severity. Bean plant debris may bear viable rust spores, and this influences the occurrence and severity of bean rust. Using bean debris in making trash-lines, preparing compost manure, and leaving it on the soil surface significantly contributed to the high incidence and severity of bean rust in farmers' fields compared to those who reported to practice soil incorporation and had significantly lower rust. These findings agree with the recommendation for the elimination of bean residue through strategies such as soil incorporation to aid in the management of bean rust disease. High mean rust incidence

Table 3: Effect of cultural practices on incidence and severity of bean rust in the study areas.

Source of variation	[1]DF	Incidence [2]MS	Severity MS
Cropping system	1	74.8ns	0.958ns
Altitude	2	8887.8***	15.835***
Cultivar	23	1039.3**	3.722**
Seed source	2	225.5ns	0.191ns
Previous crop	10	794.2ns	2.923ns
Residue management	3	2017.8**	5.026*
Fungicide use	1	6300.6***	19.364**
Management of volunteer plants	2	1251.0***	3.623***
Crop spacing	19	1193.7***	2.030**

[1]DF: degree of freedom. [2]MS: mean square values with *, **, and *** implying significance at $P = 0.05$, $P < 0.01$, and $P < 0.001$, respectively; ns: not significant at 0.05 probability level.

and severity were observed at close spacing, possibly due to increased relative humidity and enhanced pathogen inoculum spread, which could favor bean rust development.

4.3. Bean Rust Races. Four bean rust races 29-1, 29-3, 61-1, and 63-1 were obtained from single spores (Table 4). Races 29-1, 29-3, and 61-1 were previously reported in Kenya [18, 39], and this highlights their predominance and importance in genotype screening for resistance in breeding programs. The common bean rust race 63-1 identified in this study has not been previously documented in Kenya, and this points out the necessity for comprehensive collection and characterization of bean rust isolates into physiological races using sequence analysis and BLAST technology.

4.4. Profiles of Common Bean Resistance to Rust Based on Field and Greenhouse Evaluations. Field and greenhouse screening of the common bean germplasm in Kenya revealed high variability in response to rust (Table 5). The low disease pressure under field conditions could be attributed to a low initial inoculum, high chances of disease escapes, and unfavourable environmental conditions in the field [40]. This variability in host resistance to different races of bean rust indicates the possibility of resistance genes inherent in the genotypes. Genotypes such as MU#13, UN2-Darkgreen, UN6-Nakholo, Kat X56, and KMR-11 (Angaza) exhibited high resistance under field and greenhouse conditions and are therefore potential parental genotypes in common bean breeding for the region. According to Wagara and Kimani [41], genotype variability in response to bean rust can be exploited in common bean improvement programmes as sources of resistance. As similarly reported by Arunga [42] and Kamiri et al. [43], MU#13, a local French bean breeding line, is resistant to a number of bean rust races and anthracnose. This genotype can be exploited in French bean improvement for disease resistance to counter local races. However, there is a need for the characterization of these resistance sources and the development of high-throughput molecular markers to aid in marker assisted breeding for rust resistance.

Table 4: Characterization of bean rust isolates based on their reaction on the 12 differential cultivars.

Isolate ID	Andean gene pool						Mesoamerican gene pool						Race	Gene pool
	1	2	3	4	5	6	7	8	9	10	11	12		
Uas1	S	R	S	S	S	R	S	R	R	R	R	R	29-1	Andean
Kak17	S	R	S	S	S	R	S	R	R	R	R	R	29-1	Andean
Emb27	S	R	S	S	S	R	S	R	R	R	R	R	29-1	Andean
Kir14	S	R	S	S	S	R	S	S	R	R	R	R	29-3	Andean
Emb4	S	R	S	S	S	R	S	S	R	R	R	R	29-3	Andean
Kir24	S	R	S	S	S	S	S	R	R	R	R	R	61-1	Andean
Kak11	S	R	S	S	S	S	S	R	R	R	R	R	61-1	Andean
Uas16	S	R	S	S	S	S	S	R	R	R	R	R	61-1	Andean
Bun13	S	R	S	S	S	S	S	R	R	R	R	R	61-1	Andean
Bun25	S	S	S	S	S	S	S	R	R	R	R	R	63-1	Andean

S: susceptible, R: resistant, 1: early gallatin, 2: redlands pioneer, 3: montcalm, 4: Pompadour Checa 50, 5: golden gate wax, 6: PI260418, 7: great northern 1140, 8: aurora, 9: Mexico 309, 10: Mexico 235, 11: Compuesto Negro Chimaltenango (CNC), and 12: PI181996.

A consistent reaction to bean rust was observed among the differential cultivars harbouring *Ur-3*, *Ur-3+*, *Ur-5*, *Ur-11*, *Ur-14*, and *Ur-CNC* resistance genes under field conditions and to races 29–1, 29–3, 61–1, and 61–3 as well as mixed isolates. This emphasizes their importance in breeding for resistance to bean rust in Kenya. Most genotypes exhibited a susceptible reaction to rust, and this may be attributed to the broad pathogenic variability of *U. appendiculatus*, as similarly reported by Hillocks et al. [44]. Therefore, there is a need for pyramiding resistance genes into common bean germplasm as a breeding strategy in bean rust disease management. Additionally, multiyear/multiseason evaluation for bean rust resistance across different altitudinal ranges in central and western Kenya would be necessary for targeted deployment of resistance genes.

A sample with a profile of two fragments of 249 bp and 270 bp was considered as belonging to the Mesoamerican gene pool, and a sample with three fragments of 249 bp, 264 bp, and 285 bp was considered to belong to the Andean gene pool [45]. Based on this, 37 genotypes were classified as Mesoamerican, whereas 40 genotypes belonged to the Andean gene pool. Common bean genotypes of Andean origin such as Enclave, Kat X56, Kablanketi, and KMR 11 (Angaza) and Mesoamerican genotypes such as MU#13, Manakelly, and UN6-Nakholo were resistant to all the races evaluated. However, the Andean genotypes Hawaii, Julia, Amy, Samantha, and UN3-Yellow small were susceptible to all the Andean bean rust races. Paralleled common bean host reactions relative to the bean rust pathogen suggest host-pathogen coevolution, which explains the occurrence of *Uromyces appendiculatus* as a biotroph comprising different pathotypes. Generally, genotypes of the Mesoamerican gene pool exhibited high resistance to bean rust compared to those of the Andean gene pool, supporting probable pathogen coevolution with the common bean host. Furthermore, the Andean genotypes as well as some Mesoamerican genotypes were susceptible to the Andean races used in this study, complementing the findings by Acevedo et al. [38]. High resistance among the Mesoamerican genotypes

Table 5: Reaction of common bean germplasm to bean rust under field and greenhouse conditions.

S/no.	Genotype	Growth habit[a]	Seed size[b]	Gene pool[c]	Field disease reaction[d]	Greenhouse screening				
						Mixed isolate	29-1	29-3	61-1	63-1
1	MU#03	I	S	MA	R	S	R	S	S	S
2	MU#13	I	S	MA	R	R	R	R	R	R
3	Rosebella	I	L	A	R	S	R	S	R	S
4	KMR 11 (Angaza)	II	L	A	R	R	R	R	R	R
5	Embean14 (Mwende)	I	L	MA	IR	S	R	R	R	R
6	Rosecoco (GLP 2)	I	L	A	R	S	S	R	S	S
7	GLP-585 red haricot	I	S	MA	IR	S	S	R	S	S
8	GLP X92	II	L	MA	S	S	S	S	S	S
9	GLP-24	I	L	A	R	R	R	R	R	S
10	Kablanketi	II	S	A	R	R	R	R	R	S
11	Kat/B1 (Katheka)	I	L	A	IR	S	R	S	R	R
12	Kat X56	I	L	A	R	R	R	R	R	R
13	KK Rosecoco-194	I	L	A	R	S	R	S	R	S
14	KK8	I	L	A	IR	S	R	S	S	S
15	New rose coco	I	L	MA	R	S	S	S	R	R
16	Rio rojo	I	L	A	IR	S	R	R	R	S
17	Tasha	I	L	MA	R	R	R	R	S	S
18	Wairimu dwarf	I	M	MA	S	S	R	S	R	S
19	AB 136	II	M	MA	R	R	R	R	R	S
20	Cornell 49-242	II	M	MA	R	S	R	S	S	S
21	G 2333	II	M	MA	IR	S	R	R	R	S
22	Kaboon	I	L	A	IR	S	R	S	S	S
23	MDRK	I	L	A	IR	S	S	S	S	S
24	Mexico 222	I	M	MA	S	S	S	S	S	S
25	Mexico 54	II	M	MA	R	S	S	S	R	S
26	Mitchelite	II	S	MA	S	S	S	S	S	S
27	Ouro negro	II	M	MA	R	R	R	R	R	R
28	Perry marrow	I	L	A	R	S	S	S	S	S
29	PI 207262	II	S	MA	IR	S	S	R	S	S
30	TO	II	M	MA	IR	S	S	R	S	S
31	TU	II	M	MA	IR	S	S	S	R	S
32	Widusa	I	M	A	S	S	S	S	S	S
33	Aurora	II	M	MA	R	R	R	S	R	R
34	CNC	II	M	MA	R	R	R	R	R	R
35	Early Gallatin	I	M	A	IR	S	S	S	S	S
36	Golden gate wax	II	L	A	IR	S	S	S	S	S
37	Great northern 1140	II	M	MA	S	S	S	S	S	S
38	Mexico 235	II	M	MA	R	R	R	R	R	R
39	Mexico 309	II	M	MA	R	R	R	R	R	R
40	Montcalm	I	L	A	IR	S	S	S	S	S
41	PC-50	I	L	A	IR	S	S	S	S	S
42	PI 181996	II	L	MA	R	R	R	R	R	R
43	PI 260418	II	L	A	IR	S	R	R	S	S
44	Redlands pioneer	I	L	A	R	S	R	R	R	S
45	Amy	I	S	A	S	S	S	S	S	S
46	Blazer	I	M	A	IR	S	S	S	S	S
47	Boston	I	S	A	R	S	R	R	R	S
48	Edge	I	S	A	R	R	R	S	R	S
49	Enclave	I	S	A	R	R	R	R	R	R
50	Fanaka	I	S	A	IR	S	S	R	S	S
51	Hawaii	I	S	A	IR	S	S	S	S	S
52	Julia	I	S	A	S	S	S	S	S	S
53	Konza	I	S	A	R	S	R	R	R	S
54	Lomami	I	S	A	S	S	S	R	S	S
55	Manakelly	I	S	MA	R	R	R	R	R	R
56	Mara	I	S	A	R	R	R	R	R	S
57	Moonstone	I	S	A	IR	S	R	S	S	S
58	Samantha	I	S	A	IR	S	S	S	S	S
59	Seagull	I	S	A	IR	S	R	S	S	S

Table 5: Continued.

S/no.	Genotype	Growth habit[a]	Seed size[b]	Gene pool[c]	Field disease reaction[d]	Greenhouse screening				
						Mixed isolate	29-1	29-3	61-1	63-1
60	Serengeti	I	S	A	IR	S	R	R	S	S
61	T19	I	M	MA	R	S	R	R	S	R
62	Teebus	I	M	MA	S	S	S	R	S	R
63	Teresa	I	S	A	IR	S	R	S	S	R
64	Vanilla	I	S	A	IR	S	R	R	S	R
65	GBK 032805	I	M	MA	S	S	S	S	S	S
66	GBK 032928	I	M	MA	IR	S	S	S	R	R
67	Kamusele	II	S	A	IR	S	S	R	R	S
68	MCM 1015	II	S	MA	R	R	R	R	S	R
69	MCM 2001	II	M	MA	R	R	R	R	R	S
70	MCM 5001	II	S	MA	IR	R	R	R	R	S
71	UN 1-khaki small	II	S	MA	IR	S	S	S	S	R
72	UN 2-dark-green round	II	M	A	R	R	R	R	R	R
73	UN 3-yellow medium	II	M	A	IR	S	S	S	S	S
74	UN 4-yellow small	II	S	MA	S	S	S	S	S	S
75	UN 5-Libya	I	S	MA	S	S	S	R	S	S
76	UN 6-nakholo	I	L	MA	R	R	R	R	R	R
77	UN 8-Tanzania	I	L	MA	IR	S	R	R	S	R

S/no. 1–3: breeding lines, 4–32: dry bean cultivars, 33–44: differential cultivars, 45–64: French bean cultivars, 65–77: landraces. [a]growth habit; I: determinate; II: indeterminate. [b]Seed size; S: small; M: medium; L: large. [c]Gene pool; A: Andean; MA: Mesoamerican. [d]Field disease reaction; R: resistant; IR: intermediate reaction; S: susceptible.

emphasizes their usefulness in gene introgression to aid in the integrated management of bean rust in Kenya.

5. Conclusions

Bean rust is prevalent in central and western Kenya. The choice of resistant cultivars for production, the management of crop residue, and the use of fungicides can desirably be used in managing bean rust diseases. Farmers need to be informed on the appropriate cultural practices to employ in reducing the incidence and severity of common bean rust. The use of resistant cultivars can be utilized in managing bean rust instead of fungicides, which are expensive and potentially hazardous to the environment. Cultivars such as Kat X56, Enclave, and KMR-11 can be used by farmers, considering their high resistance to bean rust. Breeding for resistance can utilize local germplasm such as UN-2, UN-6, MU#13, Kat X56, and KMR-11, as well as one or more of the Mesoamerican genes such as Ur-3, Ur-3+, Ur-5, Ur-11, Ur-14, and Ur-CNC in common bean improvement.

Data Availability

Some of the data used to support the findings of this study are included in the article. Additional data are available from the corresponding author upon request.

Disclosure

While the research reported here was funded by Kirkhouse Trust, the design, execution, and interpretation of the research remain wholly the responsibility of the authors.

Conflicts of Interest

The authors declare that there are no conflicts of interest regarding the publication of this paper.

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