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# Anthracnose Disease in common Bean (*Phaseolus vulgaris*): Perspectives, Management Practices and Breeding for Resistance in the sub-Saharan Africa

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***Abstract*— Anthracnose disease, inflicted by the fungus Colletotrichum lindemuthianum, remains among the most devastating diseases of common bean (Phaseolus vulgaris) in the SSA, where production is challenged by high pathogen diversity, recurrent epidemics, and limited access to clean seed. This review synthesises current perspectives on pathogen biology, epidemiology, and virulence complexity in SSA, emphasising the predominance of highly variable races that challenge durable resistance. Existing management practices, including cultural measures, biological, and chemical methods. These offer partial and often inconsistent control due to resource limitations and the pathogen's rapid spread. Consequently, Host Plant Resistance (HPR) remains the foundation for sustainable management of anthracnose. We critically examine progress in breeding programs in the sub-Saharan Africa (SSA), highlighting the introgression and pyramiding of major Co resistance genes through conventional crossing, backcrossing, and increasingly, MAS approaches. However, the durability of these resistance genes is threatened by emerging virulent strains, narrow genetic bases in breeding pipelines, and inconsistent phenotyping environments across national breeding programs. Opportunities for improvement include strengthening race characterization, exploiting Andean–Mesoamerican diversity, integrating genomic selection, and harmonizing regional screening networks. Overall, effective mitigation of anthracnose in SSA will require coordinated breeding efforts, improved seed systems, and the deployment of diversified and locally adapted resistant cultivars.**

***Keywords*— *Anthracnose, Common bean, SSA, Genomic selection, HPR***

## I. INTRODUCTION

Common bean (Phaseolus vulgaris L.) is one of the vital legumes produced in Sub-Saharan Africa(SSA). The crop is well known for its contributions to the socio-economic welfare of the smallholder communities in the developing countries. Common bean acts as a principal source of protein content (19.7 - 24.24.3%), complex carbohydrate (50-65%), dietary fibre (23-32 g/100g), vitamins and minerals such as iron (Fe) and zinc (Zn), and calories (7.3%) in the human diet [1;2]. Additionally, the common bean provides indirect job opportunities and income to those who engage in the bean value chain. For instance, 16% of Zambians, 2.8% Ethiopians, and 75% of Tanzania's smallholder farmers are involved directly in bean production [3;5]. Total bean production in the SSA is approximately 7 million tons, which is equivalent to 24% of the global beans produced annually [6]. Country-wise, significant production is witnessed in Tanzania, Ethiopia, Kenya, and Uganda [7;8]. But the quantity produced per hectare (~0.8 t/ha) in these countries yet lies far below the attainable experimental yield (>2 t/ha) [9]. Many findings have reported higher potential yield of common bean attainable in research studies including [10] indicating a potential yield of 2- 3 tons/ha can be attained, [7] reported a yield range of 2.5- 5 t/ha to be achieved in research stations, and [11] positing a potential yield of up to 6 t/ha, showcasing the highest achievable experimental yield under strictly controlled environment.

The noticed potential deviations can primarily be suggested by some factors constraining common bean production, attributing factors include the issues of soil fertility degradation, poor quality of seed, drought incidences, and the mysterious impacts of pests and diseases. For instance, the study by [12] showcased a yield loss of up to 70% under drought and nutritional stress. Ref [13] reported a potential yield loss of 40-100% due to fungal, bacterial, and viral diseases in the Tanzanian common bean production fields. Fungal diseases such as angular leaf Spot (ALS) caused by Pseudocercospora griseola and anthracnose disease (caused by Colletotrichum lindemuthianum), are the most devastating diseases of common bean. The study by [14] reported a 20-80% yield loss attributed to ALS infection in Ugandan bean cropping fields. However, anthracnose itself has the potential to cause a grievous yield loss of 90-100% under drastic infection. Many research findings have reported this loss in countries like Zambia, Malawi, Tanzania, Cameroon, and Ethiopia [15;16;17;18;19]. Understanding the cause and effect of this disease on the common bean. This study aims to critically review and synthesize knowledge on anthracnose disease, as well as propose a long-term solution towards the disease in SSA.

## II. BIOLOGY AND EPIDEMIOLOGY OF ANTHRACNOSE

Anthracnose is a hemibiotrophic fungus exhibiting both biotrophic and necrotrophic phases during infection. The fungus shows a higher level of virulence mainly due to its environmental adaptability, wide host tissue range, pathogen dynamics and frequent occurrence of new races. Studies by [20;21] reveal that the disease inoculum may survive in crop debris, soils and in the infected bean seeds for up to five years. Disease proliferation is highly evident during cool and wet seasons. The disease affects all the above-ground parts of common bean inclusive of stems, leaves and pods[15;22]. Its symptoms appear as dark brown to black necrotic lesions on stems and abaxial leaf veins, most salient symptoms are visualized on pods where sunken lesions with reddish brown borders develop [5].According to the ref [6] anthracnose can survive best at >92 relative humidity and a temperature range of 13- 26oC, with an optimum of ~17oC.

Numerous races of anthracnose have been listed in many countries in sub-Saharan Africa. Of all countries in the region, Zambia is reported to have the largest number (58) of physiological races, followed by Tanzania and Uganda (57 races each) [23;25]. A detailed list of races of anthracnose is documented in Table 1. The presence of many races often complicates breeding for durable resistance. In SSA, infrequent pathogen characterization in many parts of the region hampers targeted resistance breeding [25;26]First, confirm that you have the correct template for your paper size.

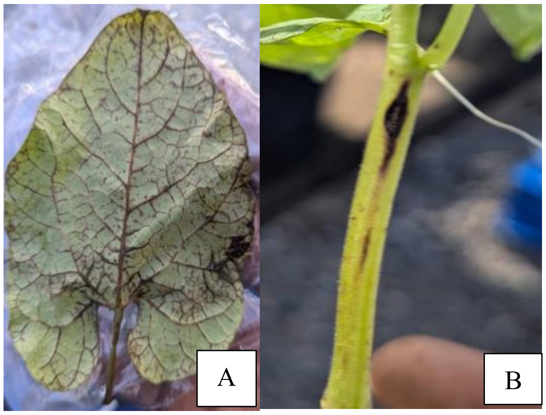

Fig. 1. Anthracnose symptoms on bean leaf (A) and stem (B) (*Source*: Field observation)

Fig. 2. Anthracnose symptoms on bean pods (*Source*: Field observation)

TABLE I. DIVERSITY OF COLLETOTRICHUM LINDEMUTHIANUM RACES IN SUB-SAHARAN AFRICA

| **Country** | **Total no. of races** | **Abundant race** | **Highly virulent race** | **References** |
|---|---|---|---|---|
| Burundi | 10 | 401, 485 | 401, 485 | [5];[46] |
| Ethiopia | 18 | 9, 272, 1011, 2260 | 2073, 2225, 2260, 3047 | [47] |
| Kenya | 7 | 38, 55 | 38 | [48] |
| South Africa | 13 | 3, 7, 81, 83, 89, 263 | 7, 81, 83, 89, 263 | [48][27] |
| Tanzania | 57 | 0, 2 | 3610 | [49][7] |
| Uganda | 57 | 167, 2047, 4095 | 1024, 1536, 1538, 1856, 1857, 1989, 2023, 2039, 2045, 2047, 3086, 4033, 4095 | [50];[51][11] |
| Zambia | 58 | 247 | 247 | [10];[29] |

## III. MANAGEMENT OF ANTHRACNOSE IN COMMON BEAN PRODUCTION FIELDS

Underscoring the impact of anthracnose disease in common bean production fields, different management strategies have frequently been used to set-down disease severity and optimize common bean yields. Such strategies include;

### *A. Cultural Control Practices*

These includes, crop rotation, use of clean seed, and sanitation helping to reduce inoculum pressure by omitting pathogen-hosts [6].

### *B. Use of Bio-control*

This involves the use of formulated essential microbes and plant extracts to suppress anthracnose disease. The technique has been used in some parts of the SSA, including Ethiopia and Tanzania. In Ethiopia, for instance, the method has been reported to achieve ~60 % reduction in infected pods (from ~79 % down to ~31 %) and reduce yield loss from ~70 % to ~46 % using Trichoderma spp (*Trichoderma harzianum*, and *T. viride*), and *Pseudomonas fluorescens for seed treatment and foliar application.* [37]. Another study by [38] reported a 350 kg/ha increase in common bean yield due to the application of *Azadirachta indica* and *Lippia javanica*. at 10% w/v. plant extracts. But the effective use of these bio-controls has been impaired by many restraints, limited farmers' awareness and access to the biological organisms, inadequate knowledge on the proper use and handling procedures of the organisms and uncertainties of climate change, causing potential depression of beneficial microbe species [23].

### *C. Chemical Control*

The use of fungicides has been paramount in suppressing anthracnose inoculum in during seed treatment and foliar spray in the field. Most commonly used synthetic fungicides include seed treatment with Benomyl or Carbendazim (500-1000 ppm), which has shown high precision in the in-vitro inhibition of *Colletotrichum lindemuthianum* growth [39]. Foliar applications of protective multisite fungicides such as Mancozeb and systemic triazole fungicides such as Difenoconazole have been shown to reduce anthracnose incidence and severity, thereby improving yield and 100-seed weight [24;40]. More recently, foliar sprays of a QoI (strobilurin) fungicide Azoxystrobin, have reduced the area under disease progress curve (AUDPC) by ~63 % in bean anthracnose trials [37]. Fungicides can be effective but remain economically and logistically challenging for smallholder farmers.

### *D. Integrated Disease Management (IDM)*

This is another management approach mostly used in the SSA. The method involves creating a strategic control package with different tactics such as cultural, biological and chemical control methods, with the intent of thwarting pathogen impacts on crops, preventing pathogen resistance to a single control program, and reducing chemical exposure on crops and the environment [23]. The method has shown a promising control of anthracnose in some parts of the SSA, including Ethiopia. For instance, a study by [41] reported a combination of seed treatment with *Pseudomonas fluorescens*, *Trichoderma harzianum*, *T. virid* (10g/kg seed), foliar fungicides (mancozeb 2 kg/ha, mancolaxyl 3.5 kg/ha), and a range of cultural practices to improve yield from 1.01 t/ha to 1.79 t/ha and reducing disease severity form ~79% to 31%. Despite its holistic focus, the adoption of IDM by smallholder farmers has been significantly constrained by poor access to reliable recommendations, credit constraints, labour-intensive and on-time availability of quality control materials [42;43].

### *E. Host Plant Resistance (HPR).*

This refers to the process of developing and utilizing crop varieties that possess genetic traits enabling them to avoid, tolerate, or suppress infection by pathogens. It is a meticulous option for minimizing the use of synthetic fungicides in the control of anthracnose disease in common bean. Resistant bean varieties carry genes (Co-genes) capable of recognizing and counteracting pathogen infection, thereby preventing the characteristic lesions and defoliation that lead to yield decline [44]. The following are the key elements of HPR for the successful management of bean anthracnose disease.

- Qualitative Resistance (Gene-for-Gene Resistance). Resistance is controlled by one or a few major resistance (R) genes, often referred to as Co- genes. It follows the gene-for-gene model, where a specific common bean resistant gene (R) interacts with a corresponding pathogen avirulence gene (Avr) [45]. This type of resistance provides high but race-specific resistance, meaning it protects against certain races of *C. lindemuthianum* but may fail if a new race emerges that can overcome that gene. Examples, Co-1, Co-2, Co-3, Co-4, Co-5, Co-6, Co-10, and Co-42 have been identified in different bean gene pools (for instance, Michelite cultivar carries Co-1, providing resistance to certain races [44]. The approach also proffers a quick and strong response, and makes it easy to identify resistant genes explicitly with MAS.
- Quantitative resistance (Polygenic / Minor gene resistance). This is the form of resistance in which a bean crop possesses many resistant genes, working additively together to withstand the unpleasant impacts of anthracnose disease. It focuses on quantitative traits with a small additive effect, thus offering a broad-spectrum and more durable resistance across different pathogen strains. This type of resistance requires a structured pyramidal breeding process to offer valuable and long-term disease management [46;47]. Quantitative resistance to anthracnose in beans has been mapped to multiple chromosomes, with QTLs for spore production. A popular example of a bean cultivar falling under this category is the G2333 with genes such as Co−42, Co−5, Co−7 (or Co−35), which is often used as a donor parent in anthracnose-based breeding programs [35].
- Classical-Molecular breeding integration. Traditional breeding is now enhanced by molecular tools such as: Marker-Assisted Selection (MAS), which uses DNA markers linked to Co-genes or QTLs for early selection. Gene Pyramiding involves combining multiple R genes or QTLs into one genotype for broader and more durable resistance, and the Genomic Selection (GS) approach employs genome-wide markers to predict resistance performance without phenotyping every generation [46]. Example: Pyramiding Co-1 and Co-42 genes offers a wider protection range than either alone.
- Screening and deployment. Resistance screening involves greenhouse and field evaluations against multiple races of *C. lindemuthianum*, and the use of differential cultivars to identify race-specific responses. Once identified, resistant varieties are deployed to farmers' fields, reducing dependence on fungicides and lowering inoculum pressure in the environment. Periodic monitoring of pathogen populations is crucial to detect any virulent race that might overcome deployed resistance [36].

Of all the management approaches discussed herein, HPR remains the most sustainable solution for the control of anthracnose in common bean. The approach can attain a sustainable control of up to 100% when a race-specific variety is used [30]. The method is gaining prominence in many parts of the SSA due to its potential ability to control the disease, easy adoption by local farmers, cost-effectiveness and the associated environmental and health safety. Yet durability is often undermined by the breeding techniques used, pathogen variability and genotype × environment interactions. [26]. Several resistant varieties have been identified in SSA; some of these are listed in Table 2 below.

TABLE II. SOME OF THE ANTHRACNOSE RESISTANT BEAN VARIETIES RELEASED IN THE SSA AND THEIR RESPECTIVE COUNTRY OF RELEASE

| **Variety/Cultivar** | **Country of Focus/Use** | **Anthracnose Resistance Genes** | **References** |
|---|---|---|---|
| G2333 | Rwanda, Uganda, Tanzania (used as donor parent) | Co−4$^{2}$, Co−5$^{2}$, Co−7 (or Co−3$^{5}$) | [13];[45] [11] |
| Umubano (Derived from G2333) | Great Lakes Region (example; Rwanda) | Co−4$^{2}$, Co−5, Co−7 | [10] |
| NABE 10C (Derived from G2333) | Uganda | Co−42, Co−5, Co−7 | [10] |
| NUA 48, NUA 64, TARIBEAN 3, TARIBEAN 4, TARIBEAN 6, Selian 14, Selian 15 | Tanzania | Unspecified | [5][30] |
| AB 136 | Tanzania (used as donor parent) | Co−6, Co−8 | [52][45] |
| K 132 | Kenya, Uganda | Unspecified | [9] |
| Kiangara, Kirundo, RWR 10, MCM 2001 | Kenya | Unspecified | [52] |

## IV. COMMON BREEDING TOOLS AND METHODS IN THE SSA

Breeding efforts in SSA are primarily driven by the interplay between international organizations, private local agri-techs and public based agricultural institutions. These actors operate vital breeding programs focusing on overcoming the challenges posed by the high pathogenic variability of *C. lindemuthianum,* while meeting local market and consumer preferences. The list of key actors in the SSA breeding program is presented in Table 3 below.

TABLE III. MAJOR ACTORS AND PLATFORMS IN SSA BREEDING FOR ANTHRACNOSE

| **Organization** | **Description** |
|---|---|
| Alliance Bioversity International-CIAT/PABRA | Provide germplasm, diagnostics, training, and regional coordination; they're central to distributing resistant germplasm and protocols across national programs. |
| National Agricultural Research Systems (NARIS) | In countries such as Uganda, Rwanda, Zambia, Ethiopia, Kenya and Zambia run on-farm and station screening, variety evaluation and release pipelines; many collaborate with CIAT and other CGIAR partners. |
| University and research collaborations | (regional GWAS and mapping efforts, example., the Yellow Bean Collection GWAS) are increasing genomic inputs into breeding in SSA. |

### *A. Breeding Objectives and Strategies for Improving Common Bean Resistance to Anthracnose*

- Incorporation of Resistance Genes (Major Gene Resistance): The fundamental strategy involves identifying and introgressing major resistance genes (Co genes) for *Colletotrichum*, from known donor sources into locally adapted, but susceptible, elite varieties. Some of the frequently used donor parents in SSA crosses include, G2333 which is a Mesoamerican originated genotype known to carry multiple resistance genes, including alleles of Co-4$^{2}$, Co-5$^{2}$, and Co-7. It provides broad-spectrum resistance [7]. AB136 is another Mesoamerican source carrying resistance genes, including Co-6. Other differential cultivars are such as Cornell 49-242 and TU are also sometimes recommended or used as resistance donors [7;53].
- Pathogen Variability Studies (Understanding the Threat): A critical component of the breeding strategy is the continuous study of the pathogenic variability and race distribution of *C. lindemuthianum* across different agro-ecological zones. Studies in countries like Uganda, Ethiopia, and Zambia consistently reveal a high number of highly virulent and diverse races (example, races 2047, 4095, 4031) within small geographical areas [25;35]. This understanding guides breeders to select appropriate donor parents that provide resistance to the most prevalent and/or virulent local races, ensuring the new varieties will be effective in the target environment.
- Focus on Multiple Trait Improvement: Anthracnose resistance is typically integrated into a holistic breeding program that aims for multi-trait varieties. Resistance must be combined with traits preferred by farmers and consumers to ensure adoption, some of these traits include, high yield potential, tolerance to other major biotic stresses (like Angular Leaf Spot, Common Bacterial Blight, and Bean Common Mosaic Virus), abiotic stress tolerance (such as

drought and heat tolerance, and low soil fertility) and the preferred grain types (colour, size, market class, like red speckled, mottled, or small-seeded black beans).

### *B. Breeding Tools and Methods*

In SSA breeding efforts focus on deploying both race-specific major genes and quantitative resistance through QTLs and gene pyramiding, combined with marker-assisted selection (MAS), GWAS/genomic approaches and introgression from diverse Andean/Mesoamerican and wild germplasm [12]. Modern SSA breeding programs increasingly pair conventional crossing and multi-environment phenotyping with molecular tools (GWAS and marker panels) and participatory variety selection to deliver broadly-adapted, durable resistance that fits farmers' preferences [13]. Ongoing perspectives emphasize genomics-enabled pyramiding of broad-spectrum resistance, better pathogen monitoring (race diversity), and stronger seed-system uptake to translate resistance into impact under variable climates in SSA [14]. Some of the frequently used breeding approaches to thwarting the unpleasant impact of anthracnose in the SSA are detailed hereunder.

- *Plant Introduction Method.* Plant introduction (also called germplasm introduction or exotic/foreign introduction) is the practice of bringing plants or seed (usually accessions, landraces, improved lines or released varieties) from other geographic regions or gene banks into a target country/region for evaluation and use. In breeding programmes, introduction can be categorized intro primary (introduced fits are released directly as varieties in the foreign area) and secondary (the introductions are subjected to subsequent evaluations or used as donor parents to improve local varieties). The method has frequently been used in countries like Tanzania, Uganda and Rwanda, where donor parents like G2333 and AB136 [7;56]. For instance, the study by [16] evaluated 11 introduced Brazilian bean genotypes and found that G2333, TU, Kaboon, K13, SEL1308, and BRS Cometa were the most effective lines against anthracnose.
- *Introgression of resistance genes (Conventional breeding).* Breeding programs, particularly those in the Pan-Africa Bean Research Alliance (PABRA) framework (which includes CIAT and National Agricultural Research Systems - NARS), continue to use conventional breeding methods like hybridization and backcrossing to introgress known resistance genes. This strategy forms the backbone of the breeding programs, focusing on transferring known, effective anthracnose resistance genes (Co-genes) into locally adapted and market-preferred varieties [17].

  The approach has been used in countries like Uganda, where the National Agricultural Research Organization (NARO) has incorporated resistant genes into locally developed lines, such as 136/2(8) and 142/4(4). Specifically, 136/2(8) contains the Co-4$^3$ gene, and 142/4(4) contains the **Co-5** gene [9]. These are crosses involving high-yielding, susceptible Ugandan lines like K132 or Nabe13 and resistance donors like G2333 (Co-4$^2$, Co-5$^2$, Co-7) and AB136 (Co-6, Co-8). In Ethiopia, some of the most resistant germplasm tested includes varieties like Awash Melka, which had the lowest disease severity of 45% in a field evaluation, compared to a high of 58% in the susceptible check variety Awash-1. The varieties Awash-2 and Awash-Melka are consistently high-yielding and adapted, suggesting they carry effective resistance or tolerance mechanisms [18]. Some of the most commonly used donor parents in anthracnose breeding programs in SSA are listed in Table 4.
- *Gene pyramiding Technique.* Pyramiding is a powerful breeding strategy whereby more than one resistance gene is deliberately combined into a susceptible but agronomically or commercially preferred variety to achieve broader and more durable resistance than would be possible with a single gene. In the context of common bean (Phaseolus vulgaris) resistance to anthracnose, this approach is of particular importance because the pathogen is highly variable, with many races and strains capable of overcoming single-gene resistances [46;66]. For example, it is well documented that the Co-gene family (Co-1, Co-2, Co-3, Co-4, Co-5, Co-6, etc.) confers race-specific resistance, but that gene breakdown is frequent when used singly without complementary genes [67].

  In sub–Saharan Africa (SSA) bean breeding programmes, one widely used donor parent is the cultivar G2333. This cultivar carries what is considered a "powerful pyramid" of anthracnose-resistance genes: specifically, Co-42, Co-52, and Co-7 (sometimes referenced as Co-4$^2$, Co-52, Co-7, depending on nomenclature) and has shown broad resistance across many races of the pathogen [35]. Another critical donor in SSA breeding is the cultivar AB136, which has been shown to carry Co-6 and a recessive allele Co-8 [68]. By using these donor parents in crosses with susceptible but preferred varieties, breeders aim to stack multiple resistance genes in a single genotype, thereby increasing the spectrum of resistance (i.e., number of races the line resists) and reducing the risk of resistance breakdown if new virulent races emerge.

  The pyramiding process typically involves marker-assisted backcrossing (MABC) or pedigree breeding augmented with DNA markers linked to the resistance genes. For example, in the case of G2333, genes Co-5 and Co-42 have been introgressed into Andean climbing bean germplasm using PCR-based markers (SAS13, SAB3, etc.) [69]. Once donor ×

recurrent parent crosses are made, subsequent backcrosses and selfing reduce the donor background while retaining the resistance genes. Progenies are then selected for the presence of the target genes, plus good agronomic traits (yield, seed type, consumer preference) [70]. In SSA, this means taking a market-preferred variety (example, with accepted seed colour, size, growth habit) and converting it from susceptible to resistant via gene pyramiding.

The main rationale of pyramiding in this patho-system is the high pathogenic variability of *C. lindemuthianum*, which means that a single resistance gene may work initially but is prone to being overcome by new races or strains in different environments. As one review puts it: "given the occurrence of so many genes associated with resistance to different strains of the same race of *C. lindemuthianum,* gene pyramiding is a recommended strategy to obtain durable resistance." [71]. In SSA contexts, where bean production often spans multiple agro-ecologies and where pathogen races may differ by site, the need for broad-spectrum resistance across sites and races makes the pyramiding approach even more compelling.

However, pyramiding is not without its challenges. Some studies indicate that there can be a yield or agronomic penalty associated with stacking multiple resistance genes, especially if linkage drag or negative pleiotropic effects are not addressed. For example, a study in Uganda found that lines carrying Co-42 + Co-5 + Co-9 showed very low disease severity but had some negative correlations with seed weight and number of seeds per plant [72]. Furthermore, the selection process is time-consuming and must ensure that the pyramided lines still meet farmers' preferences for seed type, growth habit, and adaptation. Multi-location testing is essential because pathogen race composition and environmental conditions vary across SSA and affect how well the resistance holds up [71].

TABLE IV. LIST OF DONOR PARENTS FREQUENTLY USED

| Donor Parent | Resistance Gene(s) | Region/Use |
|---|---|---|
| G2333 | Co-4$^2$, Co-5$^2$, Co-7 | SSA (introduced via CIAT/PABRA collaborations) [60;61]. |
| YBC278, YBC130, YBC267 | Putative QTLs linked on Pv01, Pv04, Pv08 | Eastern and Southern Africa [10]. |
| Mexico 222 | Co-1, Co-3 | African breeding and reference panels; [43]. |
| PI-207262 | Broad-spectrum; exact Co gene not characterized | Donor parent in NARS breeding programs[44]. |
| AB136 | Polygenic resistance (multiple loci) | Introgression and backcrossing in African national programs [7;50;65] |

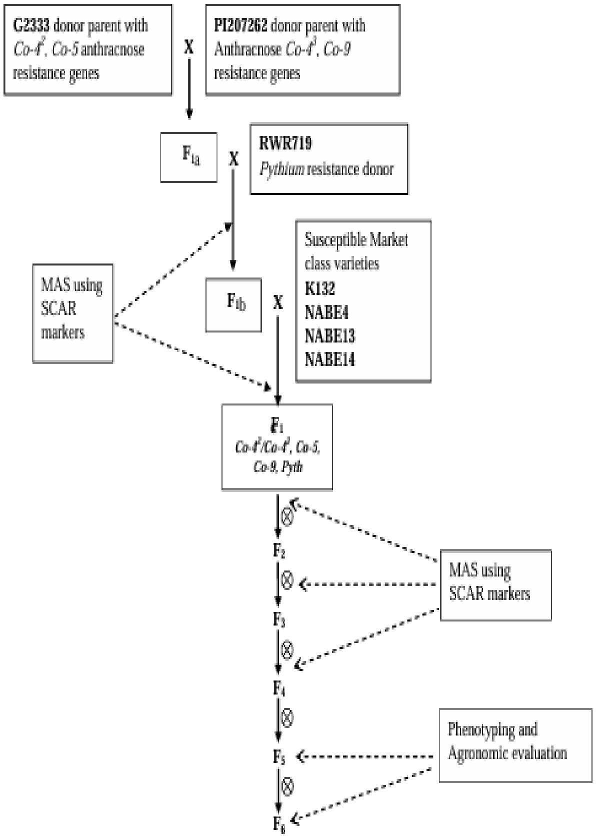

Fig. 3. Anthracnose Gene pyramiding workflow (*Source*; ref [19])

### C. *Molecular Tools and Genetic Characterization for Anthracnose Resistance*

The use of molecular tools, especially Marker-Assisted Selection (MAS), is crucial for accelerating the breeding process and ensuring the successful transfer of multiple genes (pyramiding). MAS is the most prominent method used in advancing anthracnose resistant common bean varieties in the SSA. Many breeders are actively using Sequence Characterized Amplified Region (SCAR) markers tightly linked to major Co-genes for MAS [7;74]. For instance, the marker SAB3 is used for selecting the Co-5-gene whereas SBB14 (or SAS13) is used for selecting the Co-$4^2$-gene [21].

- *MAS efficiency.* In one MAS study using a backcrossing scheme in a PABRA-affiliated program, the SAB3 and SBB14 markers were applied to progeny. This resulted in a successful selection of progenies, with SAB3 and SBB14 showing positive reactions in 33% and 44% of the $BC_2F_1$ plants, respectively, confirming the presence of the desired resistance genes at a very early stage [21].
- *New loci identification.* This strategy adopts a set of Next Generation Sequencing technologies like Genotyping-By-Sequencing (GBS) or Whole Genome Sequencing (WGS) to instantly discover novel genes associated with resistance to anthracnose disease in common bean. WGS for instance, uses high density SNP markers to scan the DNA sequences of the entire genome [8][22]. NGS technologies are frequently linked with genomic techniques like Genome-Wide Association Studies (GWAS) to confer the association between genetic variants (SNPs) and the observable phenotypic characters.

  GWAS are being conducted on local germplasm, such as the Andean Diversity Panel (which includes lines adapted to East Africa). These studies have identified major Quantitative Trait Loci (QTLs) for resistance on chromosomes Pv01, Pv02, and Pv04, which helps breeders discover and utilize new, locally-effective resistance genes like the single dominant gene Co-1 on Pv01 [48;76]. Indicated in *table 4* below, is the GWAS study indicating potential SNPs linked to anthracnose resistance genes in the yellow common bean collection.

TABLE V. SNP MARKERS SIGNIFICANTLY LINKED TO ANTHRACNOSE RESISTANCE IN YELLOW BEAN COLLECTION

| **Trait** | **Chr** | **SNP** | **Position (bp)** | **P-value** | **$R^2$ (%)** |
|---|---|---|---|---|---|
| Race 5 | Pv04 | Chr04_40179029 | 4,017,029 | 1.50E-06 | 12.6 |
| Race 19 | Pv04 | Chr04_2140558 | 2,140,558 | 1.10E-11 | 24.7 |
| Race 39 | Pv02 | Chr02_49318523 | 49,318,523 | 7.40E-10 | 30.1 |
| Race 39 | Pv05 | Chr05_15211384 | 15,211,384 | 1.19E-07 | 13.3 |
| Race 39 | Pv07 | Chr07_27321363 | 27,213,163 | 7.15E-07 | 14.2 |
| Race 51 | Pv04 | Chr04_2140558 | 2,140,558 | 7.60E-10 | 18.8 |
| Race 81 | Pv01 | Chr01_49584097 | 49,584,097 | 6.20E-08 | 41.2 |
| Race 183 | Pv04 | Chr04_1067693 | 1,067,693 | 3.40E-11 | 22.5 |
| Race 1050 | Pv01 | Chr01_49583965 | 49,583,965 | 1.90E-12 | 27.5 |
| Race 1105 | Pv01 | Chr01_49584097 | 49,584,097 | 1.10E-10 | 21.4 |

Chr=Chromosome, bp=base pair, E= exponential
*Source*: https://doi.org/10.1371/journal.pone.0293291.t003

### D. *Participatory Variety Selection (PVS) and Adoption in SSA*

Participatory Variety Selection (PVS) has emerged as a valuable approach for integrating farmer knowledge and preferences into common bean breeding programs across Sub-Saharan Africa (SSA). However, despite its noticeable benefits in enhancing adoption and ensuring locally adapted varieties, several issues continue to stunt its effectiveness, explicitly in breeding for anthracnose resistance. As cited by [24], one of the central challenges lies in the need to balance scientific breeding objectives with diverse farmer preferences. While breeders emphasize traits such as resistance to *C. lindemuthianum* and yield stability, farmers often prioritize market-related traits such as seed colour, size, and cooking quality. This disconnection sometimes results in limited adoption of improved resistant varieties, even when their agronomic performance is superior.

Another persistent issue is the lack of gender responsiveness within PVS processes. Studies such as those by [65;77;78], highlight that women and men farmers frequently differ in their trait preferences, with women often focusing on cooking quality, ease processing, and household use, while men prioritize marketability and yield. When these gendered preferences are overlooked, PVS trials risk producing recommendations that favour one group over the other, thus undermining equitable adoption. Incorporating gender analysis and inclusion frameworks in participatory selection is therefore critical for ensuring that newly released anthracnose-resistant varieties respond to the needs of all user groups.

In addition, environmental variability and pathogen diversity present major technical challenges in conducting PVS for anthracnose resistance. As noted by [5], anthracnose is a highly variable disease with numerous physiological races across Africa *table 1.* A variety that performs well under one ecological condition or against a specific pathogen race may be susceptible elsewhere [27]. This variability complicates farmer-led evaluations because on-farm trials often span diverse environments with differing disease pressures. Consequently, PVS results may be inconsistent or not easily scalable across regions unless harmonized protocols and multi-location testing strategies are adopted.

Resource and logistical constraints further hinder the successful implementation of PVS programs. A study by [15] emphasized that while PVS escalates the uptake of resistant lines, its effectiveness depends on continuous interaction between researchers, extension agents, and farmers. Unfortunately, many national breeding programs in SSA operate under limited funding and human resources, leading to poorly coordinated on-farm trials and inadequate documentation of farmer feedback. As a result, valuable experiential knowledge from farmers is sometimes lost before being integrated into breeding decisions. Sustained institutional support and funding mechanisms are thus required to strengthen feedback loops between breeders and farming communities.

Finally, the Pan-Africa Bean Research Alliance (PABRA) model provides valuable insights into both the successes and ongoing issues of scaling PVS in SSA. While PABRA has institutionalized participatory approaches within its bean improvement framework, challenges remain in standardizing data collection, ensuring long-term farmer engagement, and disseminating outcomes across national programs [28]. Many PVS trials remain localized, with results not always comparable or integrated into regional breeding pipelines [26]. Strengthening collaboration among institutions, harmonizing PVS methodologies, and leveraging digital data tools could enhance the efficiency and scalability of participatory breeding for anthracnose resistance.

### *A. Phenotypic Screening and Trait Association*

Rigorous phenotypic screening of breeding material in local disease hot-spots is indispensable for validating the broad-spectrum efficacy of breeding lines intended for durable resistance to *C. lindemuthianum* in common bean. Multi-race hotspot screening where breeding materials are challenged with a cocktail or panel of locally important races, reproduces the complex pathogen pressures found in farmers' fields and therefore provides realistic selection pressure. For example, in Zambia, a comprehensive survey and characterization of *C. lindemuthianum* detected exceptionally high race diversity (58 distinct races among 103 isolates), underscoring the need for multi-race screening to identify truly broad-spectrum resistance. Earlier work in Zambia also showed that specific blends of races and broad race panels reveal differing resistance patterns among genotypes, confirming that single-race screens can overestimate field durability [29]

In many SSA countries, breeders routinely pair hotspot, multi-race screening with multi-environment agronomic evaluation so that disease resistance is advanced together with yield stability and farmer-preferred traits. In Tanzania, multi-location evaluations identified advanced lines (NUA 48 and NUA 64) that combined anthracnose resistance with superior agronomic performance, these lines demonstrated a 56% yield advantage over commercial checks in on-farm trials and were notable for stable grain yields and favourable traits such as plant vigour and appropriate maturity [30]. Genome-wide association studies and targeted phenotyping in regional collections have also helped to link phenotypic resistance with molecular markers and known resistance loci, improving selection efficiency [13].

Country examples across SSA further illustrate the value and diversity of phenotypic screening approaches. In Ethiopia, field trials conducted under natural infestation at research centres (including Sirinka) recorded wide variation in anthracnose severity among tested varieties, demonstrating the importance of screening under natural hotspot conditions to capture realistic disease pressure and genotype responses [31]. In South Africa, surveys and glasshouse pathogenicity work found multiple distinct races among isolates collected from major bean-growing provinces. They identified only a few landraces and differentials with consistent resistance across the tested set, reinforcing the need for multi-race panels and cross-site testing [32]. In Kenya and Uganda, national programs and recent participatory on-farm screenings have documented variable responses among locally important varieties and breeding lines, and have highlighted how farmer management and micro-environmental differences influence observed resistance and yield outcomes [13].

The combination of multi-race hotspot screening and multi-environment trials has also produced genotypes that balance stress tolerance and disease resistance. For instance, in Zambia some pinto and drought-tolerant genotypes showed both acceptable seed yields under water stress and resistance to several races of *C. lindemuthianum* [25;36]. These integrated performance profiles are especially valuable in SSA, where drought, poor soils and diverse pathogen populations co-occur.

Despite these advances, important challenges remain. *First,* high pathogen diversity and geographic variation in race composition mean that lines resistant in one country or zone can be susceptible in another, the Zambian studies documented co-occurrence of isolates virulent on both Andean and Middle American gene pool cultivars and showed that no single isolate overcame certain combinations of pyramided genes, emphasizing complex local interactions [10]. *Second*, genotype × environment (G×E) interactions are often large, in the Tanzanian multi-location study environment explained a large share of variation for both anthracnose infection and grain yield, implying that even genotypes with strong resistance require careful across-site validation [30],. *Third*, the scale of robust screening, many races, many sites and multiple seasons, places heavy demands on resources, infrastructure, pathogen surveillance and technical capacity in many national programs across SSA; this constrains how widely and frequently truly representative hotspot screening can be executed [48;81].

To address these limitations, recent regional work recommends combining hotspot multi-race screening with harmonized protocols, shared differential sets and molecular diagnostics, together with targeted on-farm validation and integration of farmer-preferred traits. Automated and high-throughput phenotyping platforms, combined with molecular markers for known Co genes, are also being piloted to increase screening throughput and objectivity [33]. Continued investment in coordinated pathogen surveillance and cross-country trial networks will be essential if gene pyramids and newly developed lines are to deliver broadly durable anthracnose resistance across the highly heterogeneous landscapes of SSA.

## V. KEY MANAGEMENT CHALLENGES IN THE SSA

### *A. High pathogen diversity and incomplete surveillance*

Recent work in Zambia found 58 distinct races of *C. lindemuthianum* from just 103 isolates, many of them previously unreported, indicating very high pathogen diversity [10]. In Ethiopia, surveys revealed 17 physiological races, including some that overcome widely used resistance genes (such as, G 2333's Co-genes), suggesting co-evolution and frequent emergence of virulent pathotypes [34]. In the Tanzanian context, race characterization remains limited. Earlier work highlighted that the limited number of differential cultivars used and patchy geographical coverage constrain understanding of local race structure [35]. These gaps mean breeders may unknowingly deploy varieties that lack resistance to local or newly emerging races, and choosing which Co-genes (major resistance genes) to pyramid becomes problematic.

### *B. Capacity and infrastructure gaps*

According to a review of common bean genomics in Africa, many national agricultural research systems (NARS) lack routine molecular genotyping platforms, modern phenotyping nurseries, and trained staff, slowing down marker-assisted selection (MAS) for anthracnose [8]. For example, a molecular marker-assisted backcrossing program in Rwanda (introgressing Co-genes) reports challenges in sustained genotyping due to limited infrastructure and funding [36]. The long-term sustainability of MAS pipelines is hampered when NARS lack the capacity to maintain laboratories, consumables, and skilled human resources.

### C. Resource Allocation and Sustainability

Breeding programs in SSA often juggle multiple priorities such as drought tolerance, bio-fortification (iron and zinc), and disease resistance, leading to competing resource demands**.** The Tropical Legumes II (TL II) project (covering several SSA countries) identified that limited breeder capacity and funding cycles make it hard to sustain long-term anthracnose-specific pipelines beyond donor-funded phases [37]. Seed systems and delivery also pose bottlenecks: even when resistant lines are developed, poor access to quality seed (especially breeder and foundation seed) constrains adoption [38].

### *D. Complexity of matching resistance to local market classes*

Many resistance sources, such as climbing types or lines carrying Co-genes, are not in the preferred market-adapted seed classes like local landraces or bush types, so breeders need to perform extensive backcrossing. A Tanzanian study successfully introgressed Co-genes into popular local varieties (Masai Red, Soya Njano), but the process was time-consuming. $F_2/F_3$ segregation, moderate heritability, and multi-location testing are necessary [87]. Additionally, phenotypic evaluation under local environments (G × E) shows that resistant lines may face yield or other agronomic trade-offs, making selection more challenging. For instance, in Tanzania, the study by [51] found that the environment contributed approximately 59% of the variation in anthracnose severity, complicating reliable selection.

### *E. Race specificity of major genes and durability problems*

Many Co-genes confer **race-specific** resistance, without pyramiding (stacking multiple Co-genes) and without continued pathogen surveillance, resistance can break down when new races appear. This is well recognized in African breeding programs [8]. The genetic diversity within *C. lindemuthianum* populations also complicates matters. Some studies suggest intra-race variability, meaning even supposedly broad-spectrum Co-genes may fail on certain isolates [39]. A review on pathogen management in Africa highlights that limited understanding of local pathogen biology (infection cycles, survival and spread) undermines durable resistance breeding [40].

## VI. CONCLUSIONS

Anthracnose disease remains a major limitation to common bean production in sub-Saharan Africa due to high pathogen variability, favourable environments, and weak seed value chains and management systems. While cultural, biological, and chemical controls provide partial mitigation, host plant resistance (HPR) is the most sustainable and widely applicable strategy, supported by advances in gene introgression, pyramiding, and marker-assisted selection. However, the durability of resistance is undermined by evolving virulent races, limited pathogen surveillance, narrow genetic diversity, and strong genotype × environment interactions. Key gaps include inadequate race characterization, limited use of genomic tools, and insufficient integration of farmer and market preferences into breeding programs. Moving forward, strengthening regional surveillance systems, expanding genomic-enabled breeding, improving multi-location screening, and reinforcing seed systems and participatory approaches will be critical to developing and delivering durable, widely adopted anthracnose-resistant bean varieties in SSA.

## VII. PRACTICAL RECOMMENDATIONS

### A. *Expanding coordinated pathogen surveillance*

A harmonized race-typing protocol should be developed to fortify the development of a regional database of isolates so that breeders may target the most relevant *Co genes* for each agro-ecology.

### B. *Making KASP/SNP panels routine*

Adopting validated KASP assays for key Co loci and quality control (QC) markers so MAS becomes scalable. Partnering with regional genotyping service providers or shared CGIAR centres to lower per-sample genotyping costs.

### C. *Pyramiding resistance and validating in hotspots*

Stacking multiple resistance genes and testing lines under multi-race nurseries and natural hotspot sites to improve durability.

### D. *Investing in capacity building and laboratory networks*

Regional training in disease phenotyping, race typing, and molecular breeding will multiply the effect of existing resources (CIAT/PABRA/NARS collaborations are a good model).

### E. *Early integration of PVS and marker profiling*

This will ensure breeder-selected lines best meet consumer acceptance requirements to improve adoption and impacts

### F. *Integrating genomic selection*

This approach improves genetic gain, boosts prediction accuracy, and shortens breeding cycles by focusing on high-density molecular markers (often SNPs) with minor additive effects. The technique is also time-efficient, reduces phenotypic burden, and is highly adaptable, allowing its use in natural hotspot areas.

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