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Climate change, disease dynamics, and breeding responses in common bean (*Phaseolus vulgaris* L.) production in Tanzania: a systematic review (2005–2025)

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Common bean (*Phaseolus vulgaris* L.) plays a significant role in Tanzanian agriculture, sustaining food security and rural livelihoods for millions of smallholder farmers. However, its production is increasingly jeopardized by climate change and variability, most notably drought, heat stress, and flooding which has intensified both the frequency and severity of devastating diseases and insect pests. This systematic review, conducted in accordance with PRISMA 2020 guidelines, synthesizes findings from 103 peer-reviewed studies published between 2005 and 2025, drawing from leading scientific databases and institutional repositories focused on Tanzania. Results indicate that over 65% of documented disease outbreaks are attributable to climate extremes, which significantly influence pathogen virulence, life cycles, and host vulnerability. Drought was found to correlate with a 30–50% increase in wilt disease incidence, while heat waves accelerated disease progression in approximately one-third of cases with estimated yield loss of up to 40% by 2050. Flooding, though less frequently addressed, was identified as an emerging and insufficiently studied factor in soil- and water-borne diseases. Breeding initiatives in Tanzania have advanced drought, heat tolerance and resistance to diseases, yet more than 70% of programs continue to focus on single-stress resistance, with limited integration of multi-stress or participatory approaches. The adoption of genomic-assisted selection methods remains promising within national breeding efforts. This review underscores the necessity of transitioning toward climate-smart breeding frameworks, integrating multi-stress resilience, robust disease surveillance, and participatory research to enhance the sustainability and productivity of common bean cultivation under changing climatic conditions.

KEYWORDS

breeding strategies, climate variability, disease dynamics, drought, flooding, heat stress, multi-stress tolerance, participatory breeding

1 Introduction

Common bean (*Phaseolus vulgaris* L.) is an important crop for food security and rural livelihoods in Tanzania, providing essential dietary protein, micronutrients, nutritional fibre, carbohydrates, minerals, vitamins and household income for millions of small-holder farmers especially where high carbohydrates foods are consumed (Islam et al., 2024). It is cultivated across diverse agro-ecological zones, ranging from highland regions with bimodal rainfall to semi-arid lowlands prone to erratic climatic events (Buruchara et al., 2010; Hillocks et al., 2006). Despite its agronomic and socio-economic importance, bean production remains highly vulnerable to climatic change and variability, particularly drought, heat waves, and flooding, which have intensified over the past two decades (Akpo et al., 2021; Lema and Majule, 2009). Climatic stressors reduce bean yields directly through physiological disruption and indirectly by altering plant disease dynamics. In several bean-growing areas, especially in East Africa, there were formerly sporadic diseases such as anthracnose (*Colletotrichum lindemuthianum*), angular leaf spot (*Pseudocercospora griseola*), Bean Common Mosaic Virus (BCMV), common bacteria blight (*Xanthomonas axonopodis* pv. *Phaseoli*), Leaf rust (*Uromyces appendiculatus*) and root rots (*Pythium* spp.) which have become more frequent, severe, and geographically widespread (Binagwa et al., 2019a,b; Hillocks et al., 2006). These shifts are strongly associated with altered precipitation regimes, elevated night-time temperatures, and an increasing frequency of extreme weather events, which collectively affect both host susceptibility and pathogen life cycles, creating favourable conditions for pathogen proliferation and transmission (Kimaro et al., 2015; Mwangi et al., 2021).

The collaborations between Tanzanian national and the regional breeding programs most notably the Tanzania Agricultural Research Institute (TARI) and the Alliance of biodiversity International and CIAT (ABC) have made significant strides in developing common bean varieties with enhanced tolerance to drought and heat stresses. Nonetheless, these efforts often fall short in addressing the complex interactions between multiple climatic stressors and disease pressures. Integration of pathogen resistance traits into multi-stress selection pipelines remains limited, and current disease surveillance and forecasting systems are under-resourced and insufficiently coordinated with breeding priorities (Kuwabo et al., 2023; Tryphone and Bilaro, 2022). Given the urgency of building climate-resilient agricultural systems, there is a critical need for an evidence-based synthesis of how climate variability is reshaping disease dynamics in common bean production. While scattered studies have investigated individual diseases or climatic factors, a comprehensive, systematic analysis that explicitly links disease ecology with breeding interventions in the Tanzanian context is lacking (Jarvis et al., 2012; Johansson et al., 2024; Ramirez-villegas and Philip, 2015).

Although several reviews have examined crop diseases and climate change more broadly, they often provide generalized regional conclusions with limited Tanzania-specific synthesis and limited linkage to breeding pipelines and practical response options. This review addresses that gap by systematically consolidating Tanzania-based evidence on disease occurrence and associated climatic factors, and by critically evaluating breeding efforts and adaptive strategies targeting both disease resistance and climate-related stresses. The review systematically synthesized the existing

literature on the intersection of climate change and variability, bean disease infection dynamics, and breeding strategies in Tanzania. Specifically, it seeks to: (i) analyse how different dimensions of climate change and variability influence the incidence, severity, and distribution of common bean diseases; (ii) document reported disease outbreaks and identify emerging epidemiological trends; (iii) assess the extent to which breeding programs have incorporated climate and disease resilience traits; and (iv) identify research gaps and propose strategic recommendations for future breeding and management towards improving common bean productivity. Framed within the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 methodology, this review ensures transparency, reproducibility, and analytical rigor, offering a timely resource for researchers, breeders, policymakers, and development actors working at the intersection of climate change, plant health, and food systems resilience.

2 Methodology

2.1 Eligibility criteria

Studies were considered eligible if they:

- i Evaluated the impacts of climatic stressors including drought, heat, flooding, and rainfall variability on common bean (*Phaseolus vulgaris* L.) production in Tanzania.
- ii Investigated the correlation between climate change and variability and the epidemiology of common bean diseases within Tanzanian agro-ecological contexts.
- iii Documented the incidence, emergence, or patterns of major common bean diseases in Tanzania, drawing from empirical field observations and reported outbreaks.
- iv Assessed breeding interventions and strategies developed in response to climate-induced and disease-related challenges in common bean production.

Publications were included if they were:

- i Published between January 2005 and March 2025,
- ii Written in English, and
- iii Provided primary empirical data, experimental results, or substantial methodological insights.

Exclusion criteria included: (i) studies not focused on Tanzania only, (ii) research on crops other than *Phaseolus vulgaris*, (iii) papers lacking discussion of climate or disease interactions, and (iv) editorials, opinion pieces, or inaccessible full-text records.

2.2 Information sources

A comprehensive literature search was conducted across peer-reviewed databases (Web of Science, Scopus, Google Scholar) and institutional repositories (CGIAR, CIAT, FAO, AGRICOLA, and Tanzania Agricultural Research Institute archives). To ensure completeness, backward snowballing was applied by reviewing the reference lists of key articles. The search was conducted between January and March 2025, and all retrieved records were systematically logged.

2.3 Search strategy

Search strings combined controlled vocabulary and free-text terms with Boolean operators. Examples included:

- i “climatic variability AND common bean diseases AND Tanzania”
- ii “drought OR heat stress AND *Phaseolus vulgaris* AND disease incidence”
- iii “breeding for climate resilience AND common bean AND Tanzania”

Search queries were adapted for each database. All retrieved records were imported into Mendeley Desktop for reference management and de-duplication prior to screening.

2.4 Study selection

The selection process occurred in two stages. First, titles and abstracts were screened independently by two reviewers against

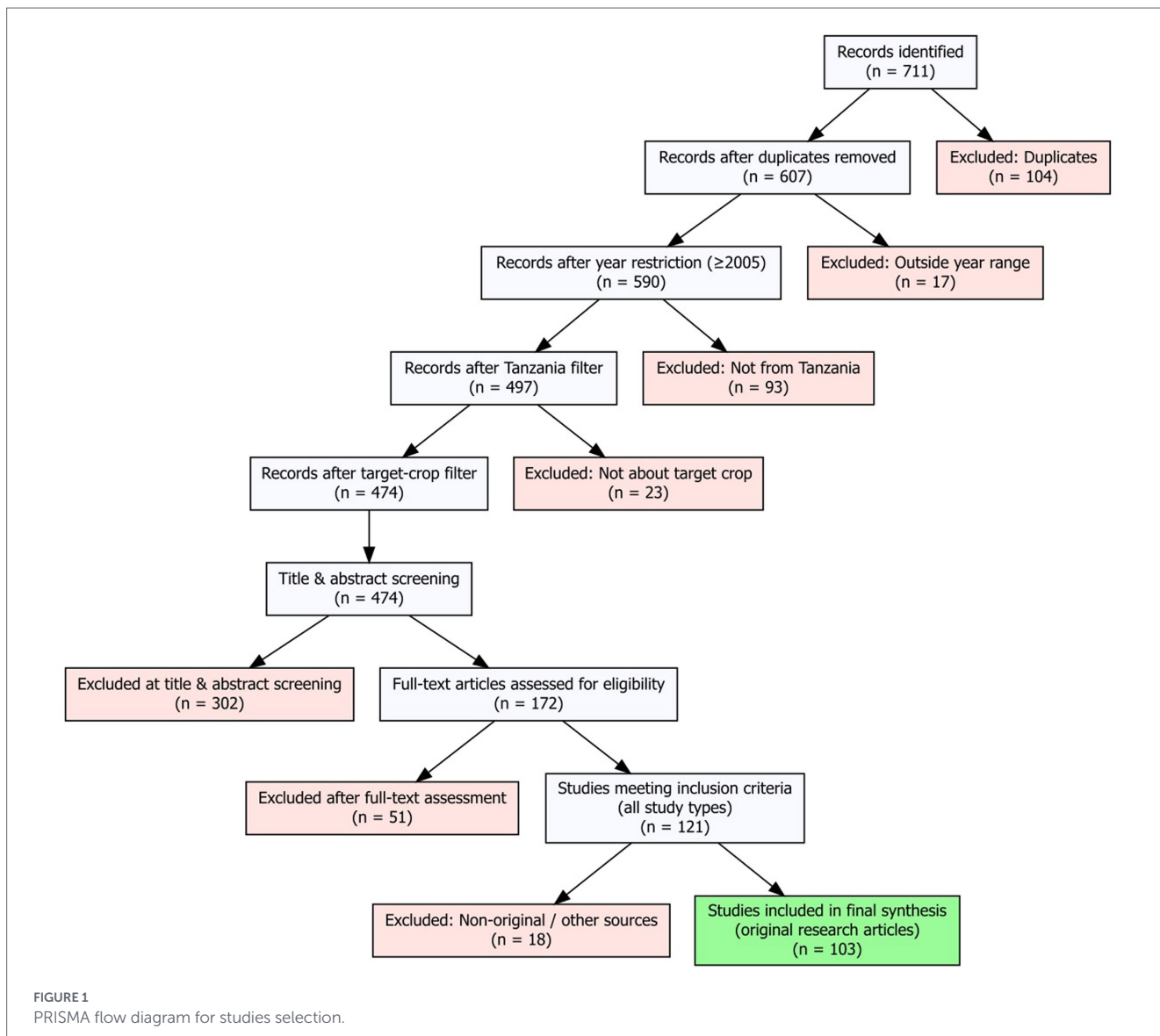
the eligibility criteria. Second, full texts of shortlisted articles were assessed to confirm inclusion. The overall process is summarized in a PRISMA 2020 flow diagram, documenting the number of records identified, screened, excluded, and retained for synthesis (Figure 1).

2.5 Data extraction and synthesis

Data extraction followed a standardized template that was piloted and refined during preliminary screening. Key variables included: author(s), year, study location, climatic stressor(s), disease(s) reported, methodological design, and breeding responses. Supplementary notes were recorded to capture contextual insights.

Extracted data were synthesized using thematic analysis, which organized findings into six domains:

- i Impacts of climate change and variability on disease dynamics
- ii Heat-related disease patterns
- iii Drought-induced disease changes



- iv Effects of flooding and waterborne pathogens
- v Documented disease outbreaks in Tanzania
- vi Breeding strategies for climate resilience research

Themes were iteratively refined to ensure analytical depth and to capture cross-cutting issues.

2.6 Data synthesis

Given the heterogeneity of study designs, a narrative synthesis formed the primary analytical approach. Thematic synthesis grouped findings into six domains: (i) climate change and disease interactions, (ii) heat-related disease patterns, (iii) drought-induced disease changes, (iv) flooding and waterborne pathogens, (v) spatiotemporal disease outbreaks, and (vi) breeding strategies for climate resilience research.

2.7 Data analysis

All analyses were conducted in R version 4.5.0 (R Core Team, 2025). Data import, cleaning, transformation, and visualization used tidyverse components, including dplyr, tidyr, stringr, forcats, purrr, lubridate, tibble, and ggplot2. Excel input and output used readxl and writexl. Variable names were standardized with janitor. Figures were produced with ggplot2, labels were positioned with ggrepel, scales were adjusted with scales, multi-panel layouts used patchwork, and vector graphics were exported with svglite and ggsave functions.

3 Results

3.1 Distribution of studies

3.1.1 Trends of studies

Between 2005 and 2025, research output showed three clear peaks in 2015, 2019, and 2024, each accounting for about 13–14%

of total publications, while earlier years (2005–2012) had only a few studies annually. Breeding emerged as the dominant focus with around half of all studies, particularly strong in 2019, followed by disease research ($\approx 39\%$) which surged in 2024, while climate-related studies were least represented ($\approx 25\%$) and never exceeded two per year (Figure 2). These patterns suggest that scientific attention has primarily centred on breeding and disease management, with climate aspects related to common beans remaining underexplored, and that periodic surges in output are likely linked to shifts in funding priorities, emerging threats, or policy-driven research agendas.

3.1.2 Climatic stressors

Studies were categorized by primary climatic stressors (heat, drought, flooding, and variable climatic factors). For each category, frequencies and proportions with 95% confidence intervals were computed as indicated in Table 1.

3.1.3 Diseases reported

To identify the most significant common bean diseases reported in Tanzania, a frequency analysis was conducted using data extracted from 103 systematically reviewed studies. Each mention of a specific disease within a study was counted as one occurrence, regardless of whether multiple mentions appeared in the same document. The frequencies were then aggregated across all sources to generate a ranked list of the most frequently cited diseases. A total of 94 distinct diseases were mentioned. The counts were converted into relative frequencies and percentages to assess the prominence of each disease. The cumulative percentage was also calculated to show the proportion of total mentions captured by the leading diseases. The top ten diseases were visualized using horizontal bar charts, highlighting *anthracnose* (12.8%), *common bacterial blight* (10.6%), and *angular leaf spot* (9.6%) as the most dominant, followed by *bean common mosaic virus* (8.5%), *leaf rust* (7.5%), and *root rots* (7.5%). Less frequently reported but noteworthy diseases included *haloblight* (6.4%), *bean common mosaic necrotic virus* (3.2%), *white mould* (2.1%), and *ascochyta leaf spot* (1.1%) as presented in Figure 3.

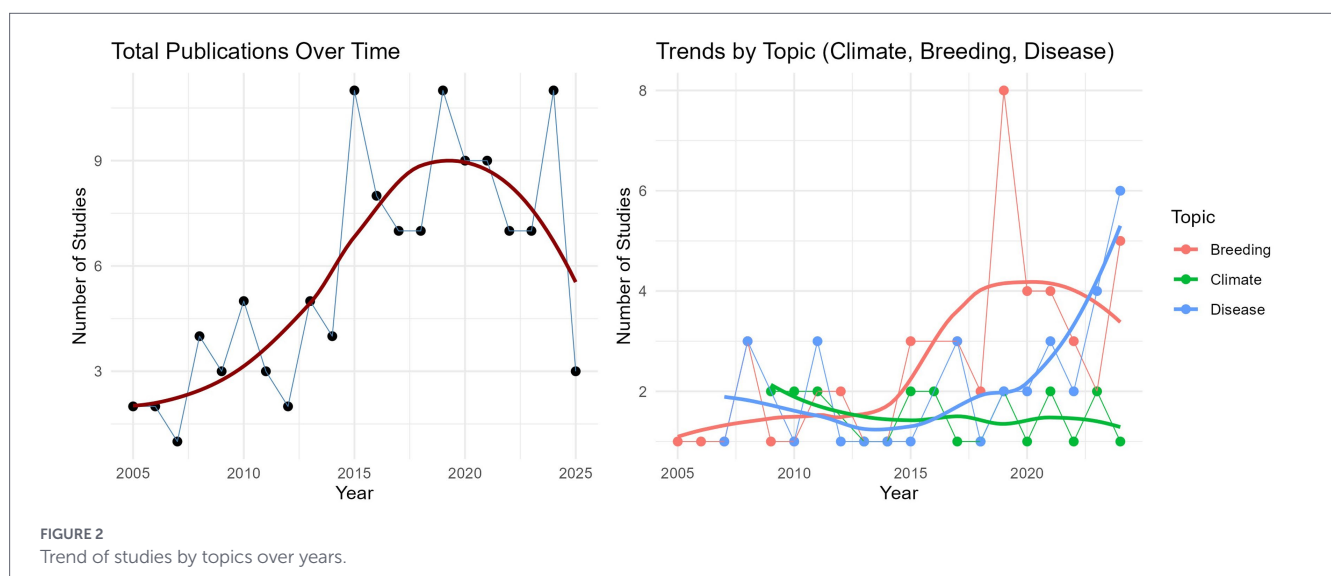


TABLE 1 Summary of studies by climatic stressors.

Stressor	Number of studies	Percent	CI
Heat	8	6.6%	3–13%
Drought	17	14.0%	9–21%
Flooding	9	7.4%	4–14%
Variable climatic factors	23	19.0%	13–27%

3.1.4 Breeding strategies investigated

Breeding methods used in the reviewed studies indicate a clear dominance of molecular-based approaches. Molecular techniques, including marker-assisted selection (MAS) and quantitative trait loci (QTL) mapping, were the most frequently reported, accounting for 26.3%, highlighting the growing importance of genomic tools in modern plant breeding. This was closely followed by integrated approaches combining conventional pedigree/phenotypic selection with molecular techniques (21.1%) and purely conventional methods (21.1%), showing that breeders still rely heavily on classical approaches (21% vs. 26%), particularly in resource-limited contexts. Screening and evaluation trials were also commonly reported (18.4%), reflecting their role in preliminary identification of resistant or high-performing genotypes before advancing them to molecular characterization. A smaller proportion of studies had no clear methods used (unspecified or other methods) (3 mentions, 7.9%) and participatory/demand-led/adoption-oriented approaches (2 mentions, 5.3%). The least represented were statistical $G \times E$ models (AMMI/GGE), reported only once (2.6%), indicating limited use of advanced genotype-by-environment interaction modelling in the reviewed studies as shown in Figure 4.

3.2 Impact of climate change and variability on bean diseases

Climate change and variability drives shift in distribution, intensity, and timing of bean diseases in Tanzania. Climate change refers to long-term shifts in average climate conditions and extremes, while climate variability refers to shorter-term seasonal and year-to-year fluctuations around those averages that influence the timing and severity of outbreaks. Changes in rainfall onset and cessation, together with seasonal drought, increase foliar disease pressure and raise root-rot risk in lowlands agro-ecologies (Jackson et al., 2018; Jha et al., 2023; Luhunga and Songoro, 2020). Anthracnose and related foliar problems intensify in wetter periods and humid canopies, consistent with multi-location surveys and reviews by Kadege et al. (2022, 2024b) and Masunga et al. (2020). However, the reported loss due to anthracnose is below 10% in Tanzania (Kadege et al., 2024a). Leaf rust disease populations show broad virulence across tropical-subtropical sites, reinforcing the need for wide-spectrum screening and responsive scouting (Jochua et al., 2008). Moreover, bacterial blight severity also rises under variable moisture and heat above 20 °C (Beebe et al., 2016), linking epidemic development to seasonal signals and causing a yield loss up to 40% in Tanzanian common bean production (Aman et al., 2023). These trends reduce the reliability of fixed calendars for bean production and call for adaptive surveillance tied to seasonal outlooks.

3.2.1 Heat-related disease dynamics

High temperatures during sensitive stages shorten safe windows and accelerate epidemic development. Climate and field analyses support hot-site screening linked to disease performance rather than temperature alone (Jha et al., 2023; Kadege et al., 2024a). Heat alone is estimated to cause a yield loss of up to 40% by 2050 (Ramirez-villegas and Philip, 2015). Combined stress environments reduce yield stability and heighten vulnerability to opportunistic infections, which argues for joint evaluation of heat with disease pressure (Mazengo and Tryphone, 2019). Elevated temperatures also intensify expression of bacterial blight in common beans, underscoring the need to test resistance under multi-stress conditions (Aman et al., 2023).

3.2.2 Drought-driven pathogen interactions

Water-deficit stress predisposes beans to root rots and necrotrophs. Multi-environment trials show yield retention in selected drought-tolerant lines, but disease risk still increases when dry spells coincide with disease inoculum presence (Karantin et al., 2019). Genotype \times environment studies on *Pythium* confirm that disease outcomes shift with moisture variability (Binagwa et al., 2019a,b). Rainfall-based risk work links disease surges to sequences of dry-wet events and highlights drainage and sanitation as core packages even in drought-prone zones (Farrow et al., 2011; Namayanja et al., 2014). These findings support integrating drought \times pathogen screening into advancement of bean breeding pipelines.

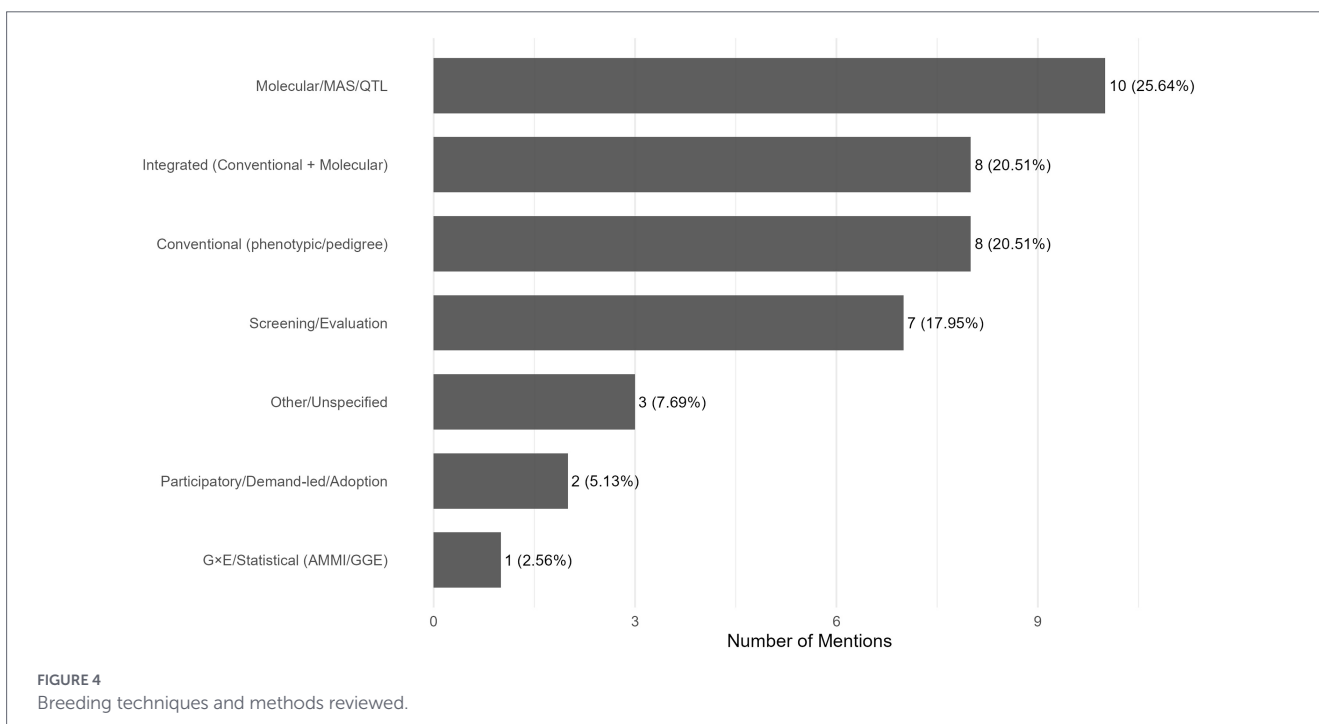
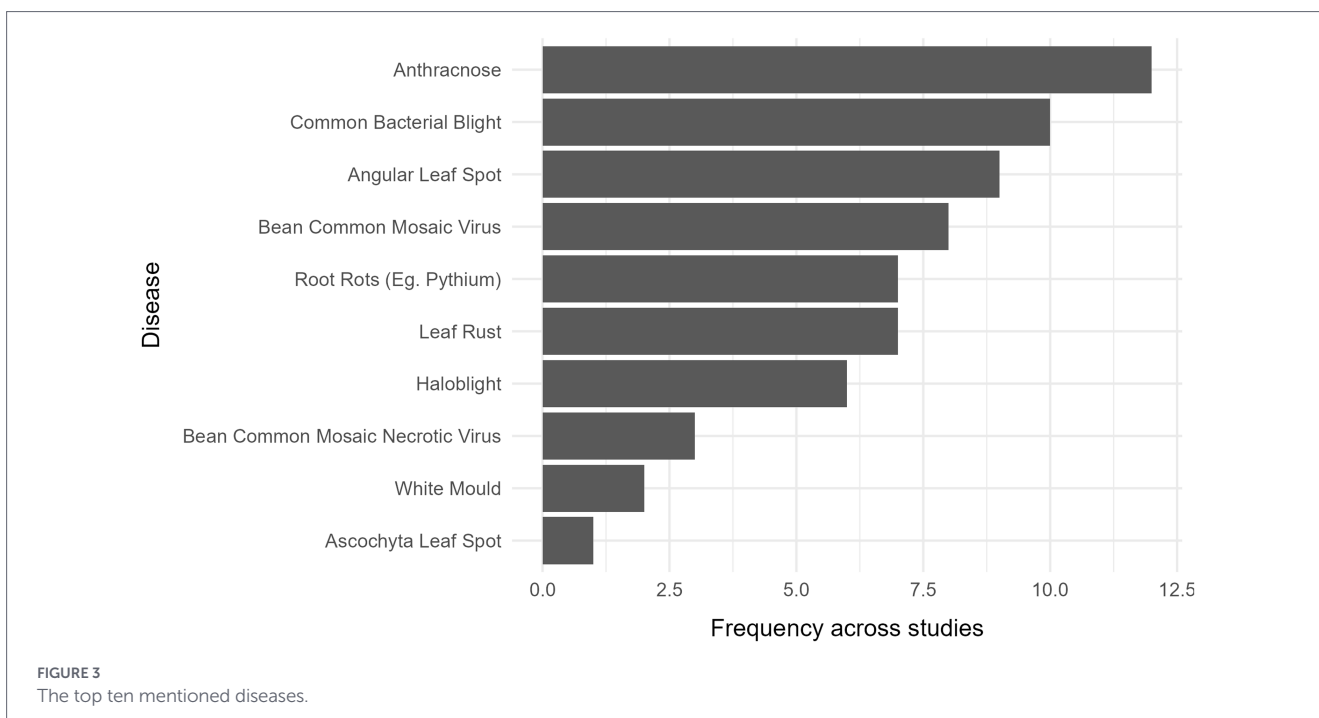
3.2.3 Flooding and waterborne pathogens

Flooding and waterlogging favor *Pythium* and allied root rots and raise foliar disease risk during humid periods. Analyses that track consecutive wet days explain stand losses and guide location and drainage actions in lowlands (Farrow et al., 2011). Resistance sources and QTL on Pv07 and Pv08 provide a path to waterlogging and root-rot resilience (Binagwa et al., 2019a,b; Namayanja et al., 2014; Soltani et al., 2018). Reviews and location tests emphasize pairing tolerant genetics with residue management and site-specific drainage to limit epidemic spread after heavy rains (Kadege et al., 2022). To distil these findings, Table 2 summarizes the major climatic factors influencing bean diseases, their impacts, and adaptive solutions.

3.3 Common bean disease occurrences and management in Tanzania

3.3.1 Historical and contemporary patterns of disease outbreaks in Tanzania

Outbreak patterns have shifted over the past two decades. Anthracnose, angular leaf spot, leaf rust, and common bacterial blight remain the most frequent problems in major bean-growing zones. Surveys and race studies confirm high anthracnose diversity across Tanzania, with widespread in the Southern Highlands and other production belts (Kadege et al., 2024b; Kazimoto et al., 2022; Masunga et al., 2020). Leaf rust populations show substantial virulence diversity across tropical and subtropical environments, reinforcing the need for broad resistance screening for example, a total of 380 *U. appendiculatus* isolates were differentiated into 65 virulence phenotypes on bean lines derived for rust resistance genes (Jochua et al., 2008). Field and



screenhouse work also links root rots and bacterial diseases to stressed environments, tightening the climate–disease link in lowland and mid-altitude systems (Aman et al., 2023; Binagwa, et al., 2019a).

Geographic risk profiles are broadening. Race surveys and multi-location evaluations report disease pressure beyond historical hotspots, with anthracnose, rust, and root rots now recorded across a wider set of districts than earlier extension reports suggested (Kadege et al., 2024b; Masunga et al., 2020). Regional climate analyses for Tanzania document more frequent extremes and changing rainfall onset/cessation, which aligns with the observed intensification of foliar and root diseases in-season (Jackson et al., 2018; Jha et al., 2023; Luhunga and Songoro, 2020).

With time and climate change, pathogen aggressiveness and host resistance are co-evolving. Recent breeding and Genome-wide association studies (GWAS) outputs identify strong and shifting selection on resistance loci, especially for anthracnose, with donor lines and resistance panels informing pyramiding strategies (Kadege et al., 2024a; Kazimoto et al., 2022; Kuwabo et al., 2023). Release of multiple-disease-resistant materials for Tanzanian conditions (for example, Kikatiti) reflects this response, though on-farm disease pressure still varies with seasonal climate anomalies (Aman et al., 2023; Nchimbi-Msolla et al., 2024).

TABLE 2 Climatic factors and their impact on bean crop.

Theme/ problem area	Affected variables	Proposed/observed solutions	Citations
Temperature and rainfall variability	Yield, cropping cycles, soil fertility	Climate-smart practices (mulching, intercropping, early planting), improved forecasts	Johansson et al. (2024), Mkonda et al. (2018), and Nassary (2025)
	Erratic rainfall and temperature extremes destabilize cropping calendars and increase pathogen pressure.		
Drought stress	Yield, genotype stability, root health	Drought-tolerant varieties (SER16, BFS60), moisture conservation, indigenous knowledge	Jha et al. (2023), Kabote et al. (2024) and Mazengo and Tryphone (2019)
	Drought remains the most consistent stressor, severely increasing bean vulnerability.		
Flooding and waterlogging	Germination, root disease incidence, pathogen spread	Drainage, raised-bed farming, flood-focused CSA practices	Chang'a et al. (2010) and Soltani et al. (2018)
	Floods aggravate root rots and foliar outbreaks; site-specific management is essential.		
Heat stress	Yield, phenology, pathogen aggressiveness	Heat-tolerant varieties, shading, adjusted planting schedules, cover crops	Grosholz (2023), Kagalawe et al. (2011), and Luhunga and Songoro (2020)
Physiological heat effects	Flowering, pollen viability, seed set	Screening for reproductive tolerance, controlled irrigation	Elia (2013) and Mligo et al. (2022)
	Heatwaves accelerate disease cycles and suppress host immunity, compounding yield losses.		
Climate-pest/disease connection	Rust, anthracnose, and pest outbreaks	Marker-assisted breeding, integrated pest management (IPM), gene pyramiding	Katunzi (2013) and Ojoyi (2017)
	Climate stress amplifies pest and disease burdens; resistant varieties are critical for resilience.		

3.3.2 Climatic influences and disease dynamics

Rainfall timing and intensity shape disease pressure in beans. Late or erratic onset shifts planting and exposes crops to peak pathogen periods during flowering and pod fill (Jackson et al., 2018; Luhunga and Songoro, 2020). Seasonal drought patterns align with yield losses and higher disease risk in East Africa, reinforcing the need to set planting windows to avoid stress peaks (Jha et al., 2023). Simulated and observed rainfall analyses link root rot risk to consecutive wet days and heavy events, especially in lowlands (Binagwa, et al., 2019a; Farrow et al., 2011; Namayanja et al., 2014).

High humidity and frequent rain increase foliar epidemics. Reports from Tanzania show anthracnose and angular leaf spot intensifying under wet conditions, consistent with multi-location race surveys and reviews (Kadege et al., 2022, 2024a; Masunga et al., 2020). Leaf rust populations display broad virulence, so humid, high-canopy fields require wide-spectrum resistance and vigilant scouting (Jochua et al., 2008).

Dry spells alter virus problems through vector-host dynamics. Regional work documents diverse virus complexes in Tanzanian beans, including Potyvirus and Begomovirus groups; disease expression tracks seasonal stress and vector activity (Mwaipopo et al., 2021). Bacterial blight severity also increases under heat and variable moisture, which complicates calendar-based control (Aman et al., 2023).

3.3.3 Pathogen diversity, resistance genes, and breeding progress

Pathogen populations affecting beans in Tanzania are diverse and virulent. Anthracnose surveys and race studies reported wide variation across production zones, with strong disease pressure in the

Southern Highlands and northern sites (Kadege et al., 2024a; Masunga et al., 2020). Rust populations also show broad virulence across tropical and subtropical environments, which supports wide-spectrum screening and regional monitoring (Jochua et al., 2008). Viral landscapes in Tanzanian bean systems include Potyvirus and Begomovirus groups, confirming multi-pathogen contexts that vary with season and site (Mwaipopo et al., 2021).

Genetic sources of disease resistance in common beans are thoroughly documented and play a crucial role in breeding programs aimed at combating major bean diseases in Tanzania. For anthracnose, significant progress has been made through the mapping and validation of Co-gene loci in diverse common bean materials. These loci serve as reliable genetic anchors for breeding and selection, ensuring that new bean varieties maintain stable and effective resistance across different environments (Geffroy et al., 2008). In the case of angular leaf spot, detailed phylogenetic research has revealed a distinct Afro-Andean genetic structure within pathogen populations (Serrato-Diaz et al., 2020). This understanding has been instrumental in guiding the deployment of Phg resistance loci and associated molecular marker sets, which are now used to select and breed for durable resistance to angular leaf spot in Tanzanian germplasm (Serrato-Diaz et al., 2020). For common bacterial blight, the identification of quantitative trait loci (QTL) such as SAP6, along with the development of closely linked molecular markers, has greatly improved the effectiveness of selection and evaluation under local Tanzanian conditions (Duncan et al., 2011; Tryphone et al., 2012). Recent efforts have expanded upon these foundational discoveries by screening advanced breeding lines under simultaneous pressure from multiple diseases. These screenings ensure that the resistance traits remain effective and relevant in the locally adapted germplasm, helping to sustain bean production even as disease pressures evolve (Aman et al., 2023).

Breeding progress combines association genetics with multi-environment testing. GWAS on anthracnose resistance identified significant loci in yellow-seeded panels, strengthening marker-assisted selection, and cross-validating field scores (Kuwabo et al., 2023). Evaluations in Tanzania report concurrent gains in disease resistance and yield components, with lines selected across contrasting locations (Kadege et al., 2024a,b). A multi-disease-resistant cultivar (Kikatiti) released for Tanzania shows broad adaptation, reflecting sustained selection across pathogen and site gradients (Nchimbi-Msolla et al., 2024). Introgression efforts add to this pipeline by moving resistance into farmer-preferred backgrounds (Kazimoto et al., 2022).

3.3.4 Integrated disease management and climate adaptation

Integrated disease management is essential for protecting bean crops in Tanzania as climate conditions become increasingly unpredictable. Combining resistant varieties with improved agronomic practices, timely monitoring, and strategic seasonal planning has proven to significantly reduce disease losses. Recent studies from Tanzania and neighbouring regions demonstrate that these approaches are effective across diverse environments and changing climate and disease patterns.

3.3.4.1 Deploy resistant germplasm as the first line

Anthracnose, Angular leaf spot (ALS), and Common bacterial blight (CBB) resistance loci enable selection and pyramiding in Tanzanian materials (Duncan et al., 2011; Geffroy et al., 2008; Serrato-Diaz et al., 2020; Tryphone et al., 2012). Recent GWAS and location testing refined selection targets and validated lines under local pressure (Kadege et al., 2024a; Kuwabo et al., 2023). Multiple-disease resistant releases for Tanzania show broad adaptation across sites (Nchimbi-Msolla et al., 2024).

3.3.4.2 Strengthen field hygiene and cultural practices

Rotate away from legumes in high-risk fields. Use residue management, clean seed, and tool sanitation to lower primary disease inoculum. Intercropping and mulching support climate-smart goals while suppressing splash dispersal and soil moisture swings (Myers and Kmiecik, 2017; Nyasimi et al., 2017; Taba-Morales et al., 2020).

3.3.4.3 Plan for disease, drought, heat, and floods together

Drought-tolerant genotypes such as SER16 and BFS60 stabilize yield, but root rots still rise under stress, so pair tolerance with sanitation and drainage effects (Binagwa et al., 2019a; Karantin et al., 2019; Mazengo and Tryphone, 2019). The QTL linked to flood tolerance and *Pythium* resistance guide choices for lowland sites (Namayanja et al., 2014; Soltani et al., 2018). Where heat spikes, adjust planting dates and canopy management to reduce foliar epidemics that track humidity surges (Jha et al., 2023; Kadege et al., 2022). Late or erratic rains shift exposure to peak pathogen pressure. Use district-scale forecasts to set planting windows and fungicide or bactericide decision points (Jackson et al., 2018; Jha et al., 2023; Luhunga and Songoro, 2020). Root rot risk rises with clusters of wet days; drainage and field access plans limit stand loss (Farrow et al., 2011).

3.3.4.4 Strengthen surveillance and extension

Use simple rainfall-based risk rules and field scouting to trigger action. Link village-level observations to advisory messages through local platforms that already deliver climate-smart agriculture content (Kabote et al., 2024; Nyasimi et al., 2017). Regional breeding and PABRA networks provide the pipeline for resistant seed and technical backstopping (Beebe et al., 2011; Clare et al., 2022). Table 3 describes the main identified diseases and their corresponding resistant genes and cultivars.

3.4 Crop improvement for disease and climate resilience in Tanzania

Climate change and climate variability in Tanzania are altering disease risk in common bean by shifting rainfall onset and cessation, increasing the frequency of wet and dry spells, and raising temperatures during sensitive growth stages. These changes affect canopy humidity, leaf wetness duration, and soil saturation, which in turn modify pathogen infection cycles and host susceptibility. For example, wetter and more humid periods increase foliar disease pressure, while lowland areas with poor drainage face higher root rot risk following prolonged wet conditions or repeated wet spells (Jackson et al., 2018; Jha et al., 2023; Luhunga and Songoro, 2020). Heat can shorten safe production windows and accelerate epidemic development, and it can also intensify symptom expression for common bacterial blight, which strengthens the case for evaluating resistance under heat and combined stress conditions rather than under disease pressure alone (Aman et al., 2023; Jha et al., 2023; Kadege et al., 2024a; Mazengo and Tryphone, 2019).

3.4.1 Conventional and participatory breeding approaches

Conventional and participatory breeding have delivered varieties and advanced lines that align well with farmer priorities such as grain type, cooking quality, and marketability, which remains essential for adoption and seed diffusion (Binagwa et al., 2019a; Hillocks et al., 2006; Letaa et al., 2015). However, the market focused selection can miss climate driven disease risk. As rainfall becomes more erratic and wet spells cluster, foliar diseases can surge in humid canopies and root rots can increase in lowlands and poorly drained fields (Jackson et al., 2018; Jha et al., 2023; Luhunga and Songoro, 2020). Under these conditions, a variety that performs well in a typical season may fail in an anomalously wet season if resistance is not durable, or if it was not tested under those wet canopy conditions. Participatory selection remains a major strength, but its adaptive value under climate change depends on where trials are run. Farmer panels should be placed deliberately in drought prone sites, hot sites, and flood risk lowlands so that farmer preferred traits are assessed alongside disease resistance under the climate conditions that drive outbreaks. This aligns with the broader recommendation in the manuscript that resilient variety development must combine farmer preference screening with climate informed trial placement and monitoring.

Tanzanian bean improvement built on station selection and farmer participation. Early releases such as Selian 05, Uyole 04, Lyamungu 90, Jesca, and Kabanima matched grain type, cooking quality, and market traits, which drove uptake across highland and semi-arid zones (Hillocks et al., 2006; Kanyeka et al., 2007). Regional

TABLE 3 Identified diseases and resistant genes and cultivars.

Disease	Main pathogen(s)	Key genes/QTL	Resistant varieties/lines	Notes	Citations
Anthraxnose (ANTH)	<i>Colletotrichum lindemuthianum</i>	Co-1, Co-2, Co-3, Co-4, Co-5, Co-6, Co-8, Co-12-Co-16, Co-Pa; clusters on Pv01, Pv03–Pv05, Pv07	NUA 48, NUA 64, RWR 2154; Sweet Violet, VTT 923-23-10; donors G2333, AB136; YBC278 (GWAS hit)	42 races reported in TZ; race 3,610 virulent in SH; race 2 widespread; recommend resistant cultivars + integrated management	Geffroy et al. (2008), Kadege et al. (2022, 2024a,b), Kanyeka et al. (2007), Kazimoto et al. (2022), Kuwabo et al. (2023), and Masunga et al. (2020)
Angular leaf spot (ALS)	<i>Pseudocercospora griseola</i>	Phg-1/Co-14, Phg-2, Phg-3/Co-34; markers include Pv06, SU91 (Pv08)	Sources AND 277, Mex 54, Ouro Negro; pyramiding ongoing	TZ isolates include Afro-Andean clade; divergence requires careful gene deployment	Fourie et al. (2015), Chilagane et al. (2013), Luseko et al. (2016), and Serrato-Diaz et al. (2020)
Common bacterial blight (CBB)	<i>Xanthomonas</i> spp.	SAP6 (Pv10), SU91 (Pv08), other CBB-QTL	VAX lines; Kikatiti (moderate CBB via SAP6); advanced lines with CBB resistance	Marker–phenotype correlations enable MAS; VAX backgrounds show dominant resistance	Aman et al. (2023), Duncan et al. (2011), Nchimbi-Msolla et al. (2024), and Tryphone et al. (2012)
Halo blight (HB)	<i>Pseudomonas syringae</i> pv. <i>Phaseolicola</i>	HB4.2 (Pv04, broad), HB5.1 (Pv05, race-specific)	Donors PI 150414, CAL 143, cv. Rojo	Combine HB4.2 + HB5.1 for durability; yield risk tied to HB5.1 races	Fourie et al. (2015) and Tock et al. (2017)
Rust	<i>Uromyces appendiculatus</i>	Ur-3, Ur-4, Ur-6, Ur-11	Kikatiti (Ur-3/Ur-11); differential sets for surveys	Tropical/subtropical fields show higher virulence diversity; sample many sites	Jochua et al. (2008) and Nchimbi-Msolla et al. (2024)
BCMV/BCMNV	Potyvirus	I (dominant), bc-3 (recessive)	Kikatiti, Mshindi, AO 29–3-3A, 13A/59-98-3×3-3A, KT020	Multi-disease lines validated; molecular screening with SW13 (I) and ROC11 (bc-3)	Aman et al. (2023), Mwaipopo et al. (2017), Mwaipopo et al. (2021), and Nchimbi-Msolla et al. (2024)
Powdery mildew (PM)	—	Candidate CNL/TNL clusters on Pv04; candidate genes on Pv10; RLKs on Pv11	—	Defense-related genes near significant SNPs from GWAS	Binagwa et al. (2021)
Pythium root rot	<i>Pythium</i> spp.	QTL on Pv08 (≈59–62.3 Mb) and Pv07 (≈4.7 Mb); links with flooding tolerance	ADP-014, ADP-080 (resistant); RWR 1946/2075/719 (donors); ADP-429/–604 (tolerant)	Single dominant gene reported in BILEA sources; strong G × E	Binagwa et al. (2019a), Farrow et al. (2011), Namayanja et al. (2014), and Soltani et al. (2018)
Viral landscape (NGS)	Begomo-, Poty-, Carlaviruses	—	—	NGS identified viruses across zones; mechanical transmission confirmed	Mwaipopo et al. (2021)
Integrated mgmt/ climate context	—	—	—	Biological, chemical, and cultural measures; climate change shifts pest pressure; need better rainfall sensing	Beebe et al. (2011), and Farrow et al. (2011), Grosholz (2023), Islam et al. (2024), Nyasimi et al. (2017), and Taba-Morales et al. (2020)

assessments show adoption responds to local preferences, input access, and market signals (Katungi et al., 2009; Letaa et al., 2015). Program records document successive releases and scaling efforts that improved productivity and seed quality (Binagwa et al., 2018;

Kalyebara and Buruchara, 2008). Participatory variety selection linked farmer panels with trial advancement, improving placement and shortening feedback loops (Binagwa et al., 2019a,b). However, there is limited efforts breeding for climatic pressure adaptability compared

to other market traits. Some of reported efforts includes genotyping for flooding (Soltani et al., 2018) and drought (Sadohara et al., 2024) resistant Tanzanian germplasm. Different breeding activities have been conducted for viral, bacterial and fungal diseases as described in Table 4. However, many breeding targets have historically emphasized market and agronomic traits, and there is still limited routine selection for combined climate stresses and climate-associated disease pressures.

3.4.2 Molecular and marker-assisted selection

Molecular breeding and marker assisted selection can be presented as an adaptive response as it allows breeders to keep resistance in the background while climate variability increases disease unpredictability. In Tanzania, anthracnose, angular leaf spot, common bacterial blight, rust, and virus diseases remain dominant, and their outbreaks are increasingly shaped by rainfall variability and heat (Aman et al., 2023; Jha et al., 2023; Kadege et al., 2024b; Masunga et al., 2020). Under wetter and more humid periods, anthracnose and related foliar problems intensify, which means that deploying anthracnose resistance loci is not just a genetic achievement, it is a direct adaptation to the rainfall patterns that extend leaf wetness and sustain epidemics (Kadege et al., 2022, 2024b; Masunga et al., 2020). For angular leaf spot and other foliar pathogens that respond strongly to canopy humidity, MAS allows the use of resistant donor sources and the tracking of resistance across multiple genomic regions, including performance across loci on Pv01 to Pv07 in multi-location work (Kadege et al., 2024a,b; Kuwabo et al., 2023). ALS work also confirms Afro-Andean population structure, guiding Phg locus use and marker choice for Tanzanian isolates (Luseko et al., 2016; Okii et al., 2019;

Serrato-Diaz et al., 2020). This matters under future climates because rainfall variability can intensify splash dispersal and maintain humid canopy periods, increasing the odds that susceptible varieties experience repeated infection cycles.

For common bacterial blight, the climate link should be made explicit. Bacterial blight severity rises under variable moisture and heat, and elevated temperatures can intensify expression, so resistance screening and deployment should be validated under warm conditions to ensure resistance remains effective when heat waves occur (Aman et al., 2023; Beebe et al., 2016). The CBB, QTL such as SAP6 and linked markers support introgression and field validation in local backgrounds for this disease (Duncan et al., 2011; Tryphone et al., 2012). Virus resistance provides another clear example of breeding as adaptation. Routine marker checks for I and bc-3 help maintain resistance while breeding lines are advanced into new environments where climate variability can shift planting windows and disease exposure patterns (Aman et al., 2023; Mwaipopo et al., 2021; Nchimbi-Msolla et al., 2024). For abiotic stress, a QTN for seed yield on Pv03 that also confers heat tolerance, and additional QTNs on Pv01, Pv05, and Pv10 linked to early maturity and yield under water limitation, can be interpreted as adaptive as they reduce yield instability when drought and heat become more frequent and when stress shortens the safe production window (Sadohara et al., 2024). Flooding tolerance and root rot resilience should also be tied directly to climate drivers. Flooding and waterlogging favour Pythium and allied root rots, and rainfall based triggers using consecutive wet days help explain stand losses in lowlands (Farrow et al., 2011). A QTL region on Pv08 associated with multiple beneficial traits offers a practical marker assisted route for targeting both flooding tolerance and Pythium root rot resistance,

TABLE 4 Breeding strategies and their impacts in crop productivity.

Focus area	Methods/techniques used	Key traits/genes	Notable varieties/lines	Citations
Conventional breeding	On-station screening; evaluation, multi-location trials, PVS	Yield stability; seed type; broad resistance	Selian 05; Uyole 04; Lyamungu 90; Jesca; KatB1; KatB9	Binagwa et al. (2019b), Hillocks et al. (2006), and Kanyeka et al. (2007)
Molecular breeding	GWAS; MAS; SNP/QTL mapping	Anthracnose (Co-1, Co-3, Co-15, Co-16); CBB (SAP6); BCMV (I); BCMNV (bc-3)	YBC278; VAX lines; derivatives from APA × KT020	Aman et al. (2023), Duncan et al. (2011), Kuwabo et al. (2023), and Mwaipopo et al. (2021)
Drought resilience	Multi-environment trials; stress indices (YI, STI)	Early maturity; deep rooting; WUE	SER16; BFS60; KG104-72; RCB233	Jha et al. (2023), Mazengo and Tryphone (2019), and Tryphone and Bilaro (2022)
Heat resilience	Introgression; physiological screening; hot-site trials	Pollen viability; stay-green; canopy cooling	Early crosses; experimental lines	Jha et al. (2023) and Kadege et al. (2024a)
Flooding tolerance	QTL mapping; controlled flooding trials	Root aeration; hypocotyl elongation; survival QTL (Pv07, Pv08)	ADP-014; ADP-080; ADP-429; ADP-604	Farrow et al. (2011), Namayanja et al. (2014), and Soltani et al. (2018)
Multi-disease resistance	Gene pyramiding; MAS; G × E trials	Anthracnose (Co); ALS (Phg); Rust (Ur); BCMV/ BCMNV (I, bc-3)	NUA 48; NUA 64; RWR 2154; Kikatiti	Kadege et al. (2024b), Kazimoto et al. (2022), Masunga et al. (2020), and Nchimbi-Msolla et al. (2024)
Integrated frameworks	Genomic selection; participatory breeding; modeling	Multi-stress adaptation; climate resilience; farmer-preferred traits	CIAT-PABRA/Alliance pipeline	Beebe et al. (2011), Clare et al. (2022), and Taba-Morales et al. (2020)

which is increasingly relevant where clustered rains and poor drainage create repeated waterlogging events (Farrow et al., 2011; Soltani et al., 2018).

3.4.3 Breeding for climate resilience

Climate variability increases the likelihood that farmers face multiple diseases within a single season because the same year may include humid periods that favour foliar epidemics and saturated soils that favour root rots. In this context, multi-disease resistance becomes a climate adaptation strategy because it buffers yield when climate anomalies shift which disease dominates in a given location and season (Farrow et al., 2011; Jackson et al., 2018; Soltani et al., 2018). Drought remains the most consistent constraint. Multi-environment trials and index-based selection identify stable performers such as SER16 and BFS60 that retain yield under stress and mature early (Mazengo and Tryphone, 2019). Seasonal drought patterns in East Africa support sowing windows that avoid stress peaks and reduce downstream disease pressure (Jha et al., 2023). Hot-site evaluations show the need for heat screens that preserve foliar disease performance during flowering and pod fill (Jha et al., 2023; Kadege et al., 2024a). Flood-prone lowlands face root-rot surges; QTL on Pv07 and Pv08 and tolerant donors guide selection for waterlogging and *Pythium* resilience (Binagwa et al., 2019a,b; Namayanja et al., 2014; Soltani et al., 2018). Rainfall-based risk models link clusters of wet days to stand loss, which supports drainage investments and site choice during variety placement (Farrow et al., 2011). In future work, the adaptive value of “climate resilience” breeding will be strongest when drought, heat, and flooding screening are routinely paired with disease pressure so that selected lines are proven under the combined stress profiles that are becoming more common.

3.4.4 Multi-disease resistance and climate–disease interactions

Multiple-resistant materials suited to Tanzanian conditions are available, including releases and advanced lines combining resistance to anthracnose, rust, common bacterial blight, and BCMV or Bean mosaic common necrotic virus (BCMNV) with acceptable yield and grain traits (Binagwa et al., 2018; Kadege et al., 2024a). Kikatiti provides a clear example of broad adaptation with stacked resistance in national testing and release (Nchimbi-Msolla et al., 2024). However, race surveys report wide anthracnose diversity and strong virulence variation for rust, which signals that resistance durability cannot be assumed across locations and seasons (Jochua et al., 2008; Masunga et al., 2020). Under increasing climate variability, this diversity becomes more consequential because shifting seasonal conditions can favour different pathogen populations over time. These findings support race-aware screening, rotation and pyramiding of resistance sources, and post-release surveillance in hotspot environments so that breeding remains responsive to evolving disease risks (Jochua et al., 2008; Masunga et al., 2020).

3.4.5 Toward integrated breeding pipelines

In general, breeding pipelines are transitioning toward integration of farmer-preferred traits with MAS and GWAS outputs, and stability analyses to inform release decisions (Philipo et al., 2021; Tryphone and Bilaro, 2022). Regional networks and institutional reviews also outline practical routes for scaling seed, agronomy, and markets while keeping

disease and climate risks in view (Beebe et al., 2010, 2011; Clare et al., 2022; Katungi et al., 2019; Taba-Morales et al., 2020). However, current programs remain limited in their ability to address climate–disease challenges in a systematic way. Key gaps include limited routine screening under combined stress, for example heat or drought paired with pathogen pressure, insufficient evidence on resistance stability under variable moisture and heat across contrasting agro-ecologies, and weak linkage between climate risk indicators, disease surveillance, and advancement or placement decisions (Aman et al., 2023; Farrow et al., 2011; Jha et al., 2023; Tryphone and Bilaro, 2022).

Addressing these gaps requires a conceptual shift toward climate–disease trait bundling, in which breeding targets are explicitly designed to mitigate climate-driven disease pressures rather than treating stresses in isolation. A practical workflow is feasible: first confirm farmer acceptance in target ecologies; then use routine marker confirmation for key resistance stacks such as Co, Phg, SAP6-linked regions, and virus resistance loci; and finally test multi-site stability across drought-prone, heat-prone, and flood-risk environments, with seasonal outlooks guiding trial placement and varietal recommendation domains (Clare et al., 2022; Philipo et al., 2021; Tryphone and Bilaro, 2022). In this framing, loci and QTLs are not reported only as discoveries. Their value is demonstrated when they stabilize yield and resistance in the specific climate anomalies that increasingly drive disease losses in Tanzanian bean systems (Farrow et al., 2011; Sadohara et al., 2024; Soltani et al., 2018).

4 Discussion

The findings show the need to reframe common bean (*Phaseolus vulgaris* L.) improvement in Tanzania around climate change and variability and rising disease pressure. Beans anchor food and nutrition security in the highlands. Production now faces concurrent drought, heat, flood risk, and shifting pathogen profiles. Breeding and management must respond as a single, integrated system.

4.1 Climate variability as a driver of production instability

Rainfall is less reliable and extremes are more frequent in key bean zones of Tanzania. District-level analyses report changes in onset, cessation, and heavy-rain events that affect planting windows and in-season disease risk (Jackson et al., 2018; Luhunga and Songoro, 2020). Regional drought analyses link seasonal patterns to yield loss and management timing, which supports stress-avoidance planting calendars (Jha et al., 2023). Drought limits leaf expansion and yield stability in local trials, while high temperatures during flowering reduce reproductive success (Mazengo and Tryphone, 2019). Heavy and clustered rains raise root-rot risk in lowlands, consistent with models and field evidence (Binagwa et al., 2019a; Farrow et al., 2011; Namayanja et al., 2014).

Climate anomalies intensify disease pressure. Race surveys and monitoring confirm wide anthracnose diversity and broad rust virulence in tropical and subtropical environments (Jochua et al., 2008; Masunga et al., 2020). Reports of flood-linked root rots and wetter-season foliar disease align with observed rainfall shifts (Binagwa et al., 2019a; Farrow et al., 2011). Virus complexes identified by next-generation sequencing add further pressure and vary with season and site (Mwaipopo et al., 2021). These patterns reduce the reliability of static calendars and single-stress recommendations.

4.2 Advances and shortcomings in breeding efforts

Collaborations among TARI, the ABC network, and partners have raised genetic gain and adoption. Landmark releases matched grain type, cooking quality, and market traits and spread through participatory testing and scaling programs (Binagwa et al., 2018; Binagwa et al., 2019b; Hillocks et al., 2006; Kalyebara and Buruchara, 2008; Kanyeka et al., 2007; Letaa et al., 2015). Drought-focused testing identified stable performers such as SER16 and BFS60 using stress indices and multi-environment trials (Mazengo and Tryphone, 2019).

Through the remained gaps, heat and flood tolerance still receive limited routine screening despite growing relevance in lowland and hot-spot sites (Lema and Majule, 2009; Soltani et al., 2018). Separation of abiotic and biotic pipelines leads to entries that perform in trials but falter in variable farmer environments. Wider use of site-specific testing and placement tied to seasonal outlooks would reduce this gap (Jha et al., 2023; Philipo et al., 2021).

4.3 Emerging opportunities in molecular breeding

Resistance loci provide strong anchors. Co genes for anthracnose, Phg loci for angular leaf spot, and QTL such as SAP6 for common bacterial blight support selection in Tanzanian backgrounds (Duncan et al., 2011; Geffroy et al., 2008; Serrato-Diaz et al., 2020; Tryphone et al., 2012). GWAS and multi-location testing identified resistant, yellow-seeded materials and clarified site effects, including YBC278 performance across several chromosomes (Kadege et al., 2024a, 2024b; Kuwabo et al., 2023). Virus resistance based on the I gene and bc-3 is part of advanced line evaluation and release (Aman et al., 2023; Mwaipopo et al., 2021; Nchimbi-Msolla et al., 2024). Building genomic-data workflows and routine marker checks into advancement would accelerate pyramiding and reduce release risk.

4.4 Institutional integration and knowledge gaps

Risk information is not yet fully linked to breeding decisions. Rainfall and early-warning products exist for Tanzanian districts but are underused in bean variety placement and scouting plans (Jackson et al., 2018; Luhunga and Songoro, 2020). Root-rot risk models show practical triggers based on consecutive wet days, yet many programs lack field protocols to act on them (Farrow et al., 2011). Extension content on climate-smart agriculture and seed dissemination can close part of this gap where platforms operate (Clare et al., 2022; Nyasimi et al., 2017; Taba-Morales et al., 2020). Program documentation also highlights constraints in diagnostics and coordination across breeders, pathologists, and climate services (Islam et al., 2024). Linking these streams would improve the timeliness of responses and the durability of resistance.

4.5 Towards climate- and disease-resilient bean systems

Priorities emerging from this review are clear and actionable:

- i Multi-stress phenotyping. Evaluate candidate lines under combined drought, heat, flood, and pathogen pressure in

representative Tanzanian sites (Mazengo and Tryphone, 2019; Philipo et al., 2021; Soltani et al., 2018).

- ii Climate–pathogen prediction. Use seasonal outlooks and simple rainfall rules to schedule sowing and guide scouting where foliar diseases and root rots peak (Farrow et al., 2011; Jha et al., 2023; Luhunga and Songoro, 2020).
- iii Participatory pipelines. Retain farmer panels to secure grain type, cooking quality, and market fit during advancement and release (Hillocks et al., 2006; Letaa et al., 2015).
- iv Genetic stacking at scale. Pyramid Co, Phg, and CBB QTL with I and bc-3 using routine marker checks; verify stability across contrasting sites before wide release (Duncan et al., 2011; Kadege et al., 2024a; Kuwabo et al., 2023; Nchimbi-Msolla et al., 2024; Tryphone et al., 2012).

5 Conclusion and recommendations

5.1 Conclusion

Recent research covering 2005–2025 clearly shows that climate change is reshaping disease patterns in common bean production throughout Tanzania. The most significant climate factors are unpredictable rainfall, such as shifts in the start and end of rainy seasons and frequent wet or dry spells and rising temperatures with more extremes. These changes affect disease outbreaks by influencing crop stress, canopy humidity, leaf wetness, and soil saturation, which in turn alter when and how severe epidemics become. The risk of bean diseases in Tanzania is increasing in complexity and unpredictability. Foliar diseases are more intense during wetter, humid conditions, while lowland regions with poor drainage are increasingly exposed to root diseases. There is marked diversity among pathogens and their aggressiveness, meaning that resistance effective in one area may not work elsewhere as climate and disease populations shift. This underscores the need for flexible farming calendars and robust disease monitoring that respond to changing seasonal conditions.

Tanzanian breeding programs have advanced through conventional, participatory, and molecular approaches, aiming for varieties resistant to multiple diseases. However, these efforts still lag the escalating disease pressures caused by climate shifts. Key gaps include limited screening for resistance under heat, drought, and waterlogging combined with pathogens, insufficient data on resistance performance across Tanzania's diverse agro-ecologies, and a lack of climate-informed selection in trials and recommendations. Seed multiplication and distribution often do not keep up with the release of new varieties, slowing progress. Given these findings, bean breeding in Tanzania must become more proactive and adaptive. Breeding should prioritize combining climate resilience with strong disease resistance developing varieties that withstand major diseases as well as drought, heat, and temporary flooding, validated across different regions and seasons. Effective strategies include establishing nurseries that simulate both abiotic stress and disease pressure, conducting multi-location trials, using advanced genetic tools to combine resilience and resistance, and monitoring new varieties after release. Collaboration among breeders, pathologists, climate experts, seed suppliers, and extension officers, while focusing on farmer-preferred traits, is crucial

for protecting yields and supporting Tanzanian food security in a changing climate.

5.2 Recommendations

These recommendations present an integrated and implementable pathway for advancing climate-smart common bean improvement in Tanzania. They are intentionally sequenced to mirror the breeding-to-delivery continuum: first, defining target production environments and priority stress combinations; second, generating evidence through integrated multi-stress phenotyping and pest/disease screening; third, strengthening selection and advancement decisions through marker-assisted gene stacking and improved genomics–phenomics data systems; and finally, supporting deployment and sustained impact through participatory selection, climate-informed agronomic management, and coordinated seed-system partnerships. Surveillance, early warning, and measurable indicators are treated as enabling functions across these stages. In this way, each recommendation builds on the preceding one, linking problem characterization to varietal development and, ultimately, to adoption and performance monitoring under real farming conditions.

- i To enhance resilience and productivity in common bean production under changing climate and disease pressures, a comprehensive approach is advocated. It is essential to mainstream multi-stress phenotyping by evaluating candidate varieties under combined conditions of drought, heat, flooding, and key pathogens at representative sites. This process should involve both screen-house challenges, particularly for root rots, and targeted field tests during flowering at hot sites. Such integrated assessments ensure that varieties are robust across a spectrum of relevant stresses.
- ii Utilising seasonal climate outlooks is vital for effective variety selection and crop management. District-level forecasts should inform the setting of sowing windows and the development of scouting plans. Simple rainfall-based triggers can be employed to guide decisions on drainage interventions and foliar disease management, thereby reducing the risk and impact of disease outbreaks and climate extremes across bean-growing regions.
- iii Implementing resistance gene stacking using molecular markers further strengthens crop resilience. By pyramiding resistance genes such as Co, Phg, and CBB QTL together with virus resistance loci like I and bc-3 and subsequently verifying these stacks with marker checks at key advancement points and following multi-site testing, breeders can ensure multi-disease resistance in new bean lines.
- iv To support these breeding efforts, building capacity in both genomics and phenomics is crucial. This involves establishing routine genotyping workflows and, where possible, high-throughput phenotyping systems. Additionally, developing data management platforms that integrate field performance scores, weather data, and molecular marker information will facilitate more informed and rapid decision-making.
- v Strengthening surveillance and early warning systems is also recommended. Linking field scouting, basic diagnostic tools, and rainfall monitoring into a straightforward alert system will enable breeders, extension staff, seed partners, and potentially farmers to respond quickly to emerging threats. This proactive approach supports timely interventions and minimises crop losses.
- vi Flood resilience should be prioritised by expanding the selection for waterlogging tolerance and resistance to pathogens such as *Pythium*. Tolerant lines should be paired with appropriate drainage solutions and tailored agronomic practices suited to specific sites, ensuring that these varieties perform optimally under adverse conditions.
- vii Keeping farmer preferences at the centre of breeding programmes is imperative. Participatory selection should be carried out in target ecologies, with close monitoring of important traits such as grain type, cooking time, and marketability, alongside assessments of disease resistance and climate adaptability. This approach ensures that released varieties are well aligned with end-user needs and preferences.
- viii Alignment of seed systems and supportive policies is necessary to accelerate the distribution of resilient varieties. Efforts should focus on the rapid multiplication of quality seed, efficient delivery mechanisms, and fostering public–private partnerships. Funding should support multi-year testing networks, and climate services should be fully integrated into national breeding strategies.
- ix Adopting a structured, three-gate workflow will improve the efficiency and effectiveness of variety development. The first gate involves securing farmer acceptance in target production zones. The second gate is the confirmation of resistance gene stacks through marker analysis. The third gate ensures multi-site stability, with variety placement informed by seasonal forecasts and basic post-release surveillance to monitor ongoing performance.
- x Finally, it is important to establish clear indicators to monitor the development and release of new varieties. These should include tracking the time required for variety release, stability of performance across stress-prone sites, adoption rates in different zones, and reductions in losses during extreme seasons. Such metrics will help refine advancement processes and optimise variety placement each year, ensuring continued progress in climate-smart bean breeding.

Data availability statement

This study did not generate any new primary datasets. All data analyzed in this article are derived from previously published or publicly available sources, which are cited in the reference list. Any further information can be obtained from the corresponding author upon reasonable request.

Author contributions

MD: Conceptualization, Data curation, Formal analysis, Writing – original draft, Writing – review & editing, Software, Methodology. PB: Resources, Conceptualization, Investigation, Project administration, Writing – review & editing, Funding acquisition, Methodology. BM: Conceptualization, Writing – review & editing, Funding acquisition,

Methodology. DM: Funding acquisition, Conceptualization, Writing – review & editing, Methodology. SM: Funding acquisition, Writing – review & editing, Conceptualization, Methodology. LC: Conceptualization, Writing – review & editing, Funding acquisition, Methodology. SN-M: Conceptualization, Writing – review & editing, Validation, Supervision.

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