

ORIGINAL ARTICLE

Crop Breeding & Genetics

Yield and climatic parameters in a common bean (*Phaseolus vulgaris* L.) regional trial

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Abstract

Understanding patterns of crop response to environmental factors is critical to simulating target environments in selection environments. In early stages of varietal development, breeding lines are usually developed in centralized facilities. Subsequently, testing continues on a broader array of research stations before dissemination to farmers, fields. Such a system is practiced in common bean (*Phaseolus vulgaris* L.) breeding in East Africa. A regional yield trial called the East Central Africa bean yield trial was distributed in three separate groups that aligned with three breeding pipelines: Andean bush beans (Group 1 or G1), Mesoamerican bush beans (G2), and climbing beans (G3). Forty-three trials met minimal standards of data quality. Trial

Abbreviations: EIAR, Ethiopian Institute of Agricultural Research; Max_RH2M, maximum relative humidity at 2 m; Mean_RH2M, mean relative humidity at 2 m; MET, multi-environment trial analysis; NARO, National Agricultural Research Organization; NASA, National Aerospace Agency; RAB, Rwanda Agriculture and Animal Resources Development Board; STA, single trial analysis; TARI, Tanzania Agricultural Research Institute; VC, variance components; VPD, vapor pressure deficit; YDHA, yield per hectare.

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environments composed of a site, planting date, and its climatic parameters were clustered based on 13 variables of temperature, rainfall, relative humidity, vapor pressure deficit, and altitude. Climatic data were derived from the NASA Prediction of Worldwide Energy Resources (POWER) database, which estimates day-by-day weather for each site. Four climate clusters emerged from this analysis. Climbing bean yield corresponded to climate clusters and heavily responded to high altitude and temperature. Most Andean bush bean environments occupied a centric cluster with few extreme variables. No patterns were observed in the Mesoamerican bush beans. This method should be extended to a larger set of trials and should be used to compare research station environments with farmer production environments.

Plain Language Summary

Common beans are a major staple in East Africa, and this paper presents aspects related to the selection of new varieties suitable to the growing environment and meet the market needs. Genetic improvement of common bean has been conducted in Africa for >40 years with the participation of several partners. Different common bean varieties behave differently under different environmental conditions due to their genetic makeup. Increased crop yield is the primary aim of most plant-breeding programs in Africa. Yield of 214 different varieties, Andean bush types, Mesoamerican bush types, and climbing beans grown in 43 different locations was analyzed to depict patterns of adaptation to different environments. Four climate clusters emerged from the analysis. Climbing beans were found to be more sensitive to climate clusters. High-performing varieties were identified. The study revealed a number of improvements to inform new bean variety targeting in East Africa.

1 | INTRODUCTION

Portuguese traders introduced common bean (*Phaseolus vulgaris* L.) into East and Southern Africa from Latin America at least 300 years ago, and it has become the most important grain legume throughout most parts of the region. The production of dry beans in the region is estimated to be 7 million tonnes, contributing approximately 24% to global production (FAOSTAT, 2019; Farrow & Muthoni-Andriatsitohaina, 2020). East Africa accounts for over 72% of the total production in Africa, with the United Republic of Tanzania having the most significant production of 1.2 million tonnes, followed by Kenya at 1.17 million tonnes and Uganda at 0.98 million tonnes (FAOSTAT, 2019; Farrow & Muthoni-Andriatsitohaina, 2020). Substantial production is also recorded in Burundi, Rwanda, DR Congo, and Ethiopia, among others. Genetic improvement of common bean has been carried out in the region for >40 years, with the participation of several national research programs and the International Centre for Tropical Agriculture (CIAT), which merged with Bioversity International in 2019 to form the Alliance of Bioversity International and CIAT (hereafter referred to as the Alliance). The Alliance facilitates a consortium called the

Pan-African Bean Research Alliance (PABRA) with a membership of 31 countries, which addresses multiple aspects of bean research, including breeding.

Over the past two decades, PABRA's bean breeding program has evolved from a constraint-focused to a client-oriented breeding program (Mukankusi et al., 2023). PABRA adopted a market-led strategy in the early 1990s (Buruchara et al., 2011; Varshney et al., 2019), focusing on major preferred grain market classes and major production constraints. In 2017, the market-led approach was strengthened by adopting the principles of demand-led breeding (Persley & Anthony, 2019) and the bean corridor approach (Pan-Africa Bean Research Alliance [PABRA], 2017). Through these approaches, both regional and country-specific target product profiles (TPPs) have been developed and are guiding breeding decisions (Mukankusi et al., 2019; <https://www.demandledbreeding.org/brochures-fliers>). The Alliance's core bean breeding hubs situated in Colombia (Palmira), Uganda (Kawanda), Malawi (Chitedze), and Tanzania (Selian-Arusha) develop new bean populations and constitute regional yield nurseries as well as constraint nurseries. Similarly, a few national agricultural research (NARs) programs, notably, Kenya (Kenya Agricultural Livestock

and Research Organization), Ethiopia (Ethiopian Institute of Agricultural Research; EIAR), Rwanda (Rwanda Agriculture and Animal Resources Development Board; RAB), Uganda (National Agricultural Research Organization; NARO), Tanzania (Tanzania Agricultural Research Institute; TARI), Republic of South Africa (Agriculture Research Council; ARC), Zambia (Zambia Agricultural Research Institute), and Zimbabwe (Division of Crops Research Department of Research and Specialist Services-Crop Breeding Institute) also develop new bean breeding lines through their own crossing programs and contribute fixed lines to the regional nurseries. The countries receiving nurseries conduct wider testing for suitability and adaptability following a stage gate approach toward variety release and commercialization. The stage gate process is a disciplined way of managing a product from design to delivery through a series of stages (decision-making points/gates) to delivery, and it creates clear opportunities for cross-functional input to come from outside the breeding team (Excellency in Breeding Platform [EIB], 2021).

This approach requires well-defined market segments and breeding pipelines for efficiency. Market segments refer to a group of growers with common variety needs, driven by consumer and processor requirements combined with a set of grower requirements based on where and how the crop is produced (Donovan et al., 2022). For beans, plant growth habit (either climbing type or different forms of bush types) and agroecology are major determinants for bean growers/farmers, while grain/seed color and size are major determinants of consumer and market preference. In addition, genetic diversity in bean is grouped into two major gene pools: Andean and Middle American, or Mesoamerican, based on agroecological adaptation, grain size (Andean with > 40 g/100seeds, Middle American typically medium (25–40 g/100seeds) and small seeds (<25 g/100 seeds), and plant morphology (Singh, Nodari, et al., 1991). This classification is further supported by “DI” genes and F1 incompatibility (Gepts & Bliss, 1985; Viera et al., 1989), phaseolin grain proteins (Gepts et al., 1986), allozymes (Koenig & Gepts, 1989; Singh, Gutierrez, et al., 1991), and DNA markers (Becerra & Gepts, 1994; Haley et al., 1994). Three breeding pipelines that supply several market segments hinged on grain color and can be further subdivided based on regions and countries to guide the program (Table 1). Pipeline 1: The medium and large seeded bush beans adapted to the low- and mid-altitude areas represent 74% of the bean market in Africa (Farrow & Muthoni-Andriatsitohaina, 2020), principally of the Andean and Mesoamerican gene pools. They include one race of Nueva Granada that is defined for the large-grain Andean types, two races of Durango and middle America of the Mesoamerica gene pool, and one Andean race Chile with medium-grain seed size. Admixtures between the two gene pools have also been observed due to inter-gene pool crosses that breeders have conducted over the years.

Core Ideas

- Regional yield trials were deployed to calculate best linear unbiased predictions and best linear unbiased estimations for common bean breeding lines in East Africa.
- Modern climate databases permit greater flexibility in incorporating climatic data in yield analyses.
- Research stations in East Africa can be clustered based on climate. Temperature, vapor pressure deficit, and extreme weather events were major factors.
- Climbing beans respond more to temperature gradients than bush beans.

These types have high commercial value in East Africa and often have a short growing season, making them suitable for many cropping niches where other species do not fit. Breeding efforts have focused on improving resistance to both biotic (majorly diseases) and abiotic stresses (drought and low soil fertility tolerance). High iron seed content and fast cooking time are priority traits in these types. Pipeline 2: Comprised of the small-seeded bush beans of the Mesoamerican gene pool and race Mesoamerica adapted to low and mid altitudes. These represent 10% of the market in Africa (Farrow & Muthoni-Andriatsitohaina, 2020). These beans are often cultivated in the most challenging environments, especially regarding abiotic stress such as drought, high temperature, and soil constraints. As such, abiotic stress tolerance and resistance to biotic stress are a high priority in new varieties. Pipeline 3: The climbing beans represent 16% of the bean market in Africa (Farrow & Muthoni-Andriatsitohaina, 2020). They consist of both Andean and Mesoamerican gene pool: race Peru (Andean gene pool) and races Jalisco and Guatemala (Middle American gene pool). They are labor intensive due to the staking requirement but have high yields and are an important option for intensifying agricultural production where land is limited. Priority traits are the same as the medium and large seeded bush beans.

In addition to seed size and plant growth habit, seed color and color pattern also further subdivide the market segments. A few seed colors and patterns, that is, red-mottled, red, yellow, and sugar/cranberry/speckled, are highly preferred (Table 1).

In this manuscript, the three pipelines will be referred to as Group 1, Group 2, and Group 3, respectively.

The regional trials are aligned to the defined pipelines and offer the possibility of studying the adaptation of breeding lines across a progressively more expansive range of environments. The objective of the current study was to evaluate the

TABLE 1 Common bean market segmentation in Africa.

Breeding pipeline (seed size, growth habit, and agro-ecology)	Major grain color	Est market segment size (Ha)	Regions and countries
1. Medium and large-seeded bush beans adapted to the low and mid altitude areas—principally <i>Andean</i> but may include <i>Mesoamerican</i> types (Total: 5,029,185 ha)	Red mottled	1,968,353	East and Central Africa: Burundi, Democratic Republic of Congo (DRC), Ethiopia, Kenya, Rwanda, Tanzania, South Sudan, Uganda (3,524,059 ha) West Africa: Cameroon and Togo (355,093 ha) Southern Africa: Malawi, Zambia, Zimbabwe, Mozambique, RSA, Madagascar, Angola (1,305,563 ha)
	Sugar/cranberry	1,168,201	
	Yellow	834,565	
	Reds	492,103	
	Purples/Kablanketi	74,608	
	Browns	48,666	
2. Small seed bush beans adapted to low and mid altitudes with heat and drought tolerance—principally <i>Mesoamerican</i> types (Total: 800,755 ha)	Whites	311,772	East and Central Africa: Burundi, DR Congo, Ethiopia, Kenya, Rwanda, Tanzania, Uganda (431,827 ha) West Africa: Cameroon and Ghana (142,304 ha) Southern Africa: Malawi, Zambia, Zimbabwe, Mozambique, RSA, Madagascar, Angola (226,624 ha)
	Reds	299,238	
	Blacks	179,009	
	Browns/khaki	46,949	
	Carioca	21,338	
3. Climbing beans adapted to the mid and high-altitude areas— <i>Majorly Andean</i> but may include <i>Mesoamerican</i> types (Total: 1,029,416 ha)	Red mottled	446,808	East and Central Africa: Burundi, DRC, Ethiopia, Kenya, Rwanda, Tanzania, Uganda (1,029,416 ha)
	Sugar/cranberry	348,427	
	Reds	195,566	
	Yellow	38,613	
	Browns	32,946	
	Whites	16,777	
	Purples/Kablanketi	13,339	

Sources: Mukankusi et al. (2023); Consortium of International Agricultural Research Centers (CGIAR) Global Market Intelligence platform (<https://glomip.cgiar.org/>).

genetic adaptation of breeding lines derived from three breeding pipelines and their response to environmental factors as revealed by a regional bean yield trial in East Africa.

2 | MATERIALS AND METHODS

Over the past 5 years, the breeding program has been reconceptualized in various stages, from product design to seed delivery (Excellency in Breeding Platform [EIB], 2021). Late testing (Stage 6) refers to the testing of lines (developed by partners with crossing programs or partners involved in early generation line testing) in regional and advanced yield trials (AYT) (Table 2). Late testing in the East African context is represented by testing a regional yield trial called the East and Central Africa bean yield trial (ECABYT) and testing of the selections in advanced yield trials by partners in PABRA. Stage 7 (on-farm testing) refers to testing of candidate varieties in a successively more comprehensive range of environments with involvement/engagement of farmers before Stage 8, which addresses formal procedures for legal recognition of lines as accepted varieties and their dissemination.

The ECABYT was grouped into three trials organized according to the three previously described breeding pipelines

of common bean. Research programs in the participating countries evaluated nurseries relevant to the national priorities, preferences, and markets. The trials were typically tested on research stations of partner institutions in the countries, and data were collected and deposited in a shared database employing the breeding management system (BMS) (Integrated Breeding Platform), permitting genotype $\times$ environment ($G \times E$) analysis and response to environmental factors. In addition to standard agronomic and yield data, data for each trial included planting date and latitude and longitude coordinates of testing sites to facilitate associating crop response to environmental factors, including climatic parameters.

2.1 | Materials

Breeding lines that comprised the ECABYT were derived from multiple sources (Table S1). Most lines (50%) originated from the CIAT-Colombia bean program. They were selected by CIAT-Uganda, CIAT-Malawi, and by African national partners including NARO, EIAR, TARI, and National Agricultural Study and Research Institute (INERA-DR Congo) in early testing stages to be part of the regional trial. Other lines stemmed from the crossing programs of EIAR (13%), NARO

TABLE 2 Common stage gate system guiding variety development in the Consortium of International Agricultural Research Centers (CGIAR-NARES) networks.

Stage and gates	Outputs
Stage 1: Product design	Target product profile (TPP): Detailing main traits and any potential trait discovery targets
Stage gate: Product design to trait discovery	Only required if a trait or traits need to achieve a specified target before crossing
Stage gate: Product design to crossing & selection	
Stage 2: Trait discovery	Source germplasm and genetic variants: Identified priority traits, source germplasm lists, data and knowledge on genetic variants of interest and predictions
Stage gate	
Stage 3: Trait deployment	Semi-elite donors: Semi-elite trait donors containing novel variation in demanded recurrent parent backgrounds, data for breeding application including training adjustment
Stage gate	
Stage 4: Crossing and screening	Experimental Products (F1–F2): Individuals from populations that have anticipated higher breeding value defined by TPP, data for training adjustment
Stage gate	
Stage 5: Early testing	Early products (fixed lines F5/F6): Early generation lines with desired breeding value defined in TPP, early generation lines with high realized and predicted breeding value for TPP defined traits, data for training adjustments
Stage gate	
Stage 6: Late testing	Advanced products and candidate varieties (F7 and beyond): Advanced generation germplasm with desired breeding value and/or candidate varieties, data for training adjustments, estimates of genetic gains (preliminary yield trials; PYT, advanced yield trials; AYT and national performance trials; NPT)
Stage gate	
Stage 7: On-farm testing including PVS (researcher and farmer managed)	Candidate varieties: Candidate varieties selected for entry in registration trials, estimates of genetic gains in farmers' fields, data on exotic allele advancement and farmers feed back
Stage gate- to seed systems	
Stage 8: Product registration	Registered variety: Pre-commercial registration trials (Distinctiveness, Uniformity and Stability; DUS, Value for Cultivation tests; VCU), demonstrations, Early Generation Seed; EGS production, licensing

Source: Adapted from Sharifah Syed Alwee (2023).

(1%), INERA-DRC (10%), TARI (1%), RAB (1%), CIAT-Uganda (9%), and CIAT-Malawi (15%). Selection criteria in the development of lines typically involved field resistance to occurring bacterial, fungal, and viral diseases; tolerance to abiotic constraints like drought and edaphic limitations; and general yield advantage over the commercial checks in each country. The trial comprised a total of 214 lines: Group 1: 84 large and medium seeded bush beans (39 red mottled, 10 red, one yellow, 32 sugar, one cream, and one kabblanketi); Group 2: 83 small seeded bush beans (21 white, one red mottled, 47 red, six black, two brown, one cream, one pinto, one purple, one kabblanketi, and one purple mottled); and Group 3: 47 large, medium, and small seeded climbing beans (one red mottled, 13 red, four yellow, 12 sugar, two black, five cream, six pink, one kabblanketi, and three white). For each group, standard checks were defined (Table 3) and included in all trials across countries. The seeds of these lines were compiled and multiplied/bulked at a central location in Uganda under the management of the Alliance bean program staff. Each country

also included additional country checks (ruling commercial varieties) based on their target product profiles (Table 4).

2.2 | Trial design

Across the three groups, 57 trials were established at 22 locations or sites within seven countries. DiGger version 1.0.5 was used to randomize trials using the partially replicated design (Coombes, 2020). Each line appeared once or up to four times in each trial. The trial with the least replications had 45% of the lines repeated, and the one with the highest replications had 98% of the lines repeated more than once. Specifically, Group 1, Group 2, and Group 3 were tested in 16, 15, and 9 sites, respectively, by the national legumes staff of respective agricultural research institutions (Table 5). Seeds for each group were distributed for planting at three locations (low, mid, and high altitudes) within each country in two seasons. A packet of 100 seeds for sowing in a plot was

TABLE 3 Standard checks included in ECABYT2020 (where ECABYT is East and Central Africa bean yield trial) trials.

Group 1		Group 2		Group 3	
Variety name	Grain market class	Variety name	Grain market class	Variety name	Grain market class
CAL96	Large red mottled	SCR15	Small red	MAC44	Large red mottled
RWR2245	Medium red mottled	SCR26	Small red	NABE12C	Large sugar
RWR2154	Large sugar	SCN11	Small black	RWV3006	Large white
UYOLE3	Large sugar	NABE6	Small white	G2333	Small red
RWR2075	Large red	SAB736	Large white	NYIRAMUHONDO	Medium yellow
KATB1	Medium yellow	Jesca	Large purple	Decelaya	Large red
				RWV1129	Large purple

distributed for each test and standard check line. Each country prepared 100 seeds per plot of the country checks, which was included in the trial design. A plot consisted of three rows of 3 m in length. Between-row and plant spacing was 50 and 10 cm for bush, and 60 and 20 cm for climbers with one and two seeds per hill, respectively. All trials were fully rainfed except at Katumani and Thika sites in Kenya, where they were irrigated three times at an estimated rate of 8 mm/day. The management practices for each program varied as below: *Fertilizer application*: In Uganda, NPK 17:17:17 fertilizer was applied by hand at planting at a rate of 125 kg/ha. In Tanzania, DAP 18:46:0 was hand applied at planting as a basal fertilizer at a rate of 50 kg/ha. In Burundi, the fertilizer FOMI IMBURA N-P₂O₅-K₂O-CaO-MgO (9-22-4-13-2) was hand applied during planting at 100 kg/ha. In Kenya, DAP 18:46:0 was applied at planting at 300 kg/ha, and CAN (26:13:13) was applied as a top-dress at the vegetative stage at 200 kg/ha. In Rwanda, decomposed cow dung manure mixed with the soil at a rate of 10 t/ha was applied before planting, and DAP (18:46:0) was also added at 100 kg/ha at planting and top dressing with urea (100 kg/ha) at 3–4 weeks after planting and at flowering. No fertilizer or pest control was applied in Ethiopia and DR Congo. *Weeding*: Hand hoe and hand weeding were performed three times in Uganda, Kenya, Rwanda, and DR Congo and twice in Ethiopia, Tanzania, and Burundi. A selective herbicide, Bentagram, was applied once to suppress weeds before hand-hoe weeding in Kenya only. *Pesticide application*: In Uganda, a pesticide Rocket 44EC (Profenofos 40% + Cypermethrin 4% EC) mixed at a rate of 30 mL per 15 L of water was applied three times during the cropping season. In Tanzania, an insecticide, Duduall profenofos (Profenofos 40% + Cypermethrin 4% EC), mixed at a rate of 40 mL per 20 L of water was applied three times during the cropping season, while in Burundi, Dimethoate 400EC and two fungicides (Benlate and Ridomil) were applied as per the manufacturer's recommendation. In Kenya, pests were controlled using Epic and Escort, considering the manufactures' rates. Diazinon (20 mL in 20 L water) was applied at plant emergence stage and repeated weekly up to 4 weeks. Fungal diseases were controlled using rodazim (20 mL in 20 L)

starting from the 4th week after planting up to physiological maturity at a 2-week interval. In Rwanda, insect pests were controlled by applying supermetrine at 20 mL/20 L of water and rocket: 20 mL/20 L of water. *Staking*: Climbing beans were staked 3 weeks after planting at a rate of four plants per stake in Rwanda, Burundi, and DRC, and three plants per stake in Uganda.

2.3 | Data collection

Study books defining the data parameters to be collected were designed for each partner in the shared BMS program on the CIAT BMS server. Each partner exported the study books, collected, and imported data to BMS based on a standard protocol. Seed harvesting for yield data began when 90% of the pods were discolored. The seeds were sun-dried to 13% moisture content (MC) and sorted before recording total seed weight (g) per plot. Yield per hectare (YDHA) was determined as weight (kg) of harvested seeds divided by effective plot area in m² and multiplied by 10.

2.4 | Data analysis

The field trial data from all testing sites was downloaded from BMS database using the R-package QBMS (Al-Shamaa, 2023). Quality control and data curation were performed to ensure the data were accurate and consistent. Of the 57 trials uploaded to BMS, only 54 (Table S2) were considered for single trial analysis (STA). Three trials were not considered for downstream analysis due to poor data quality.

2.5 | STA and multi-environment trial analysis (MET)

STA and MET were performed in R (R Core Team, 2021) using ASREML package (Butler et al., 2017) and Agri

TABLE 4 Country-specific checks per group.

Group 1			Group 2			Group 3		
Country	Checks	Grain market classes	Country	Checks	Grain market classes	Country	Checks	Grain market classes
Burundi	CODMLB003	Large sugar	Burundi	RWR2245	Medium red mottled	Burundi	Kinure	Medium purple
	IZO2015110	Large yellow		MLB122-98B	Medium carioca		RWV1129	Large kablankei
Ethiopia	F10B.SELNEWBILFA58	Medium yellow	Ethiopia	SER119	Medium red	DR. Congo	MBC23	Large red mottled
							MAC44	Large red mottled
	SAB736	Medium white		NASIR	Medium red		G59/1-2	Small black
	DAB96	Medium cream		Awash Tikure	Medium black		NYIRAMUHONDO	Medium yellow
	SAB632	Large sugar		SCRI5	Medium red		NAMULENGA	Medium cream
	KATB1	Medium yellow		SCN11	Medium black	Rwanda	MBC23	Large red mottled
Kenya	GLP 24	Large dark red kidney		SAB736	Medium white		RWV2350-2B	Large red
	DAB299	Medium red Mottled		Bifort small seeded – 15	Small white		RWV2264	Large yellow
	KATX56	Medium red		Awash Metene	Small white		CAB2	Medium white
	KK Rosecocco 194	Medium red mottled	Kenya	GLP585	Small red		RWV3317	Large sugar
	Embean 14	Medium sugar		Red 16	Medium red		MAC9	Large red mottled
	Faida	Large red mottled		Red 13	Medium red		RWV3006	Large white kidney
	CAL194	Medium red mottled		Katram	Medium red mottled	Uganda	MAC44	Large red mottled
	NUA671	Medium sugar		CAL194	Medium red mottled		NYIRAMUHONDO	Medium yellow
DR Congo	KATB1	Medium yellow		KAT SW-12	Small white		NABE 8C	Large red kidney
	RWR2154	Large sugar		KAT SW13	Small white			
	RWR2245	Medium red mottled		KATB9	Medium red			
Rwanda	RWR2154	Large sugar		GLP1004	Medium kablankei			
	RWR 3194	Large red mottled		GLP1127 (a)	Medium kablankei			
	BOA-1/16	Large red kidney	Rwanda	RWR 3194	Large red mottled			
	Colta	Large yellow		SER16	Small red			
Tanzania	UYOLE03	Large sugar	Tanzania	RCB593	Small red			
	G14369 (JESCA)	Large Kablankei		G14369 (JESCA)	Large kablankei			
	KATB1	Medium yellow		SELIAN97	Medium red			
Uganda	RWR2154	Large sugar		KATB9	Medium red			
	RWR2245	Medium red mottled		Nyeupe-Uyole	Medium white			
	RWR2075	Medium red	Uganda	UBR (92)25	Small white			
	MOORE 8802	Medium yellow		SCR26	Small red			

TABLE 5 Number of trial and location or site names for the East and Central Africa bean yield trial (ECABYT) across six countries.

Country	Number of trials with data	Group 1	Group 2	Group 3
Burundi	18	Bukemba (S1 ^a and S2 ^b) Mparambo (S1 and S2) Murongwe (S1 and S2)	Bukemba (S1 and S2) Mparambo (S1 and S2) Murongwe (S1 and S2)	Bukemba (S1 and S2) Karusi (S1 and S2) Gisozi (S1 and S2)
DR Congo	1			Mulungu (S1)
Ethiopia	6	Arsi Negele (S2) Hawassa (S2) Melkassa (S2)	Arsi Negele (S2) Hawassa (S2) Melkassa (S2)	
Kenya	11	Kakamega (S1 and S2) Katumani (S1 and S2) Thika (S1)	Kakamega (S1 and S2) Katumani (S1 and S2) Thika (S1 and S2)	
Rwanda	14	Gashora (S2) Ngoma (S2) Nyagatare (S2)	Gashora (S1) Ngoma (S1 and S2) Nyagatare (S1 and S2)	Musanze (S1 and S2) Ruhunde (S1 and S2) Rwerere (S1 and S2)
Tanzania	1		Selian (S1)	
Uganda	6	Namulonge (S2) Kawanda (S2)	Namulonge (S2) Kawanda (S2)	Namulonge (S2) Kawanda (S2)

Note: S1^a = First planting within a country (October–January 2020: Murongwe, Karusi, Mulungu, Gashora, Ngoma, Nyagatare, Musanze, Ruhunde, and Rwerere. November–February 2020: Bukemba, Mparambo, Katumani, and Thika. March–June 2021: Selian. April–June 2021: Kakamega).

S2^b = Second planting within a country (March–June 2021: Murongwe, Karusi, Mparambo, Gisozi, Bukemba, and Katumani. April–July 2021: Thika and Kawanda, May–August 2021: NARO-Uganda. September–December 2021: Kakamega. October–January 2021: Gashora, Ngoma, Nyagatare, Musanze, Ruhunde, and Rwerere. July–October 2022: Arsi Negele and Melkassa. August–November 2022: Hawassa).

Utilities (Aparicio & Bornhorst, 2023). Best linear unbiased predictions (BLUPs), best linear unbiased estimations (BLUEs), and heritability were calculated (Tables S2 and S3). Genetic correlations between trials and ($G \times E$) were explored using factor analytic structures and bi plots (Aparicio & Bornhorst, 2023; Isik et al., 2017). Due to the availability of row and column information, spatial models were fitted for all the trials using the approach proposed by Rodriguez-Alvarez et al. (2018). The quality of the data were improved by removing extreme observations based on the principle of three residual standard deviations (SD) and discarding trials with low broad sense heritability (<0.2) to ensure a reliable estimation of the $G \times E$ pattern.

2.6 | Meteorological data collection and analysis

To characterize the climatic conditions of the different environments in which the trials were tested, trial metadata, which included location, year, planting date, and geo-reference coordinates of the sites, was used to capture the climate conditions during the growing season. A time frame based on the planting and harvest dates of the trials was defined. The exact harvest dates were not provided for most of the trials and were thus approximated by adding 90 days to the planting dates. Solar and meteorological data sets were obtained from the NASA Langley Research Center (LaRC) Power Project funded by the NASA Earth Science/Applied Science Program

(Sparks, 2018; <https://power.larc.nasa.gov/>). Data provided by NASA research supports renewable energy, energy efficiency, and agricultural needs. The NASA POWER R package allows easy automation of downloaded NASA POWER global meteorology and climatology data in R software as a tidy data. frame tibble object for analyses and modeling purposes (Sparks, 2018). The downloaded data were used to calculate variables presented in Table 6 and to generate meteorological indices for each site (Table S4). Data were tailored to the trial site and to the growing season from planting to harvest in the given year of the trial. This allows for more precise evaluation of the crop response to environmental parameters and meaningful comparison of response across test sites than using average values across years. Principal component analyses for the climatic indicators were performed using hierarchical k-means clustering to identify groups of environments based on the climatic indicators (Kassambara, 2017a, 2017b; Day & Edelsbrunner, 1984).

2.7 | Comparing bi-plots with meteorological data

Finally, we created the bi-plots of the $G \times E$ interaction from the phenotypic analysis. We compared the phenotypic response with the meteorological data by coloring the vectors in the bi-plots based on the groups given by the hierarchical clustering to highlight the climate cluster into which each trial belonged.

TABLE 6 Parameters accessed or calculated from the power project for analysis of yield data of the ECABYT2020 (where ECABYT is East and Central Africa bean yield trial) bean trial data.

	Abbreviation	Indicator
i.	Max_Tmax	Maximum of maximum temperature
ii.	Min_Tmax	Minimum of maximum temperature
iii.	Mean_Tmax	Mean of maximum temperature
iv.	Max_Tmin	Maximum of minimum temperature
v.	Min_Tmin	Minimum of minimum temperature
vi.	Mean_Tmin	Mean of minimum temperature
vii.	CDD	Maximum number of dry days
viii.	Total_rain	Total precipitation
ix.	Min_RH2M	Minimum of relative humidity at 2 m
x.	Max_RH2M	Maximum relative humidity at 2 m
xi.	Mean_RH2M	Mean relative humidity at 2 m
xii.	VPD	Vapor pressure deficit
xiii.	Altitude	Altitude

3 | RESULTS

3.1 | Single trial analysis

The STA generated BLUEs and BLUPs for each trial for multi-environment trial analyses (MET). Outliers in each trial were identified (Table S2), and 26 data point with residuals of ± 3 SD were excluded from further analyses. Broad sense heritability (H^2) for each trial ranged from 0 to 0.95, and nine out of 54 trials had H^2 of <0.2 (Table S3). A total of 17 trials (Table S5) were excluded from MET because of low H^2 or a strong negative genetic correlation with other trials.

3.2 | Multi-environment trial analysis (MET)

3.2.1 | Analysis of variance and broad sense heritability (H^2)

The variance components (VC) for $G \times E$ were the highest in all the three groups (Table 7). The genotype VC were approximately half of that $G \times E$ in Groups 2 and 3. However, in Group 1, only 6.6% of genotype VC was reported. This was very low compared to the 38.9% for $G \times E$. Group 3 had the highest across environment broad sense heritability (H^2) of 0.58, while Group 1 had the lowest (0.27) (Table 6).

3.2.2 | Genetic correlations

Group 1: The genetic correlations and $G \times E$ plots provide information on trial similarities or differences. Two trials that showed strong negative genetic correlations were identified

TABLE 7 Variance components and broad sense heritability (H^2) from multi-environment trial analysis (MET) analysis.

Effect	Component	Percent (%)	Group
G1 ($H^2 = 0.27$)			
Genotype	16,871.5	6.6	Group 1
Genotype $\times$ environment	99,153.7	38.9	Group 1
Error	87,582.2	34.3	Group 1
Environment $\times$ row	48,673.5	19.1	Group 1
Environment $\times$ column	2748.3	1.1	Group 1
G2 ($H^2 = 0.52$)			
Genotype	66,215.9	10.8	Group 2
Genotype $\times$ environment	128,420.8	20.9	Group 2
Error	210,597.3	34.4	Group 2
Environment $\times$ row	127,111.8	20.7	Group 2
Environment $\times$ column	80,697.7	13.2	Group 2
G3 ($H^2 = 0.58$)			
Genotype	65,650.7	15.7	Group 3
Genotype $\times$ environment	122,200.8	29.3	Group 3
Error	159,501.4	38.2	Group 3
Environment $\times$ row	9,709.4	2.3	Group 3
Environment $\times$ column	60,218.5	14.4	Group 3

and removed from the MET analyses to obtain a more representative genetic breeding value for each genotype. Removal of such trials is justified because they were uniquely distinct within the current data set. Still, more attention may be needed to validate that they do not represent essential production environments that are underrepresented in the current set of testing sites. The magnitude of the $G \times E$ interaction for yield was reflected in the wide range of genetic correlations as expected of a complex trait (Figure 1a). Several high-yielding lines were identified (Table 8). The majority of these were red-mottled in color. Thirty-five lines from this market segment recorded yields higher than the large red-mottled standard check, RWR2245 (Table S6). Considering the yield performance of country checks (Table 4), there were many potential red-mottled lines for further evaluation in each country. On the contrary, no sugar bean recorded yields higher than the large sugar bean standard check, RWR2154, and only one line from this market segment was among the top 10 in yield (Table 8). No superior lines existed in other market segments including large reds and yellows (Table S6).

Group 2: Most trial sites had positive or no correlations between each other for yield (Figure 1b). Four trials that showed strong negative genetic correlations were excluded for MET analyses. Most of the superior yielding lines were originally from CIAT—Palmira. Four red and one black bean out-yielded all the standard and country checks (Table 8). Nine of the top 10 yielding lines belonged to the small red bean market segment (Table S6). Superior yielding small

TABLE 8 Ten most superior yielding lines in each of the three groups compared to checks.

Group 1		Group 2		Group 3	
Genotype	¹ Yield (kg/ha)	Genotype	¹ Yield (kg/ha)	Genotype	¹ Yield (kg/ha)
MEC27	1787.6	BFS32	1999.8	NUV234-3-1	1881.4
² RWR2154	1779.9	SMR126	1974.7	⁵⁶ Kinure	1878.6
MEC8	1746.4	SMC159	1873.6	⁵⁷ MBC23	1775.8
MEC31	1701.1	SCR61	1832.7	⁵⁸ RWV2350-2B	1754.4
MEC6	1686.1	SCN24	1818.0	⁵⁹ MAC44	1745.2
MEC7	1661.5	²⁷ RCB593	1799.7	RWV1348	1732.7
MEC28	1658.3	F9 KIDNEY SELECTION	1796.0	NUV131-2	1726.8
CZ114-5	1644.8	²⁸ RWR 3194	1756.6	CODMLV075	1719.0
MEC20	1611.7	BFS142	1747.5	NUV15-1	1716.7
³ RWR 3194	1602.3	²⁹ UBR (92)25	1730.8	MUHO	1709.9
MEC9	1587.0	SSIN 1309	1727.7	⁶⁰ RWV1129	1709.0
MEC22	1582.3	SSIN 1375	1726.4	CODMLV085	1706.8
⁴ CODMLB003	1576.0	³⁰ SER119	1675.6	IZO201543	1704.5
⁵ F10B.SELNEWBILFA58	1557.6	³¹ GLP585	1617.4	NUV234-3-2	1701.9
⁶ IZO2015110	1534.4	³² RWR2245	1564.5	NUV54	1659.7
⁷ GLP 24	1514.6	³³ MLB122-98B	1531.8	⁶¹ G59/1-2	1628.8
⁸ DAB299	1474.8	³⁴ SCR26	1514.4	⁶² NABE12C	1612.0
⁹ RWR2245	1473.1	³⁵ SER16	1488.8	⁶³ RWV2264	1602.6
¹⁰ RWR2075	1430.9	³⁶ NASIR	1466.1	⁶⁴ NYIRAMUHONDO	1471.1
¹¹ SAB736	1423.2	³⁷ Awash Tikure	1453.4	⁶⁵ G2333	1393.8
¹² KATX56	1417.0	³⁸ SCR15	1445.6	⁶⁶ NAMULENGA	1362.0
¹³ DAB96	1409.2	³⁹ Red 16	1440.7	⁶⁷ DECELAYA	1360.9
¹⁴ CAL96	1408.5	⁴⁰ Red 13	1433.4	⁶⁸ CAB2	1342.1
¹⁵ UYOLE3	1387.4	⁴¹ Katram	1429.4	⁶⁹ RWV3317	1308.7
¹⁶ KK Rosecoco 194	1362.8	⁴² CAL194	1418.3	⁷⁰ MAC9	1295.8
¹⁷ Embean 14	1337.3	⁴³ KAT SW-12	1416.2	⁷¹ NABE 8C	1231.8
¹⁸ Faida	1333.2	⁴⁴ SCN11	1373.3	⁷² RWV3006	1193.9
¹⁹ BOA-1/16	1309.4	⁴⁵ KAT SW13	1369.8		
²⁰ CAL194	1299.1	⁴⁶ SAB736	1363.6		
²¹ Colta	1291.6	⁴⁷ NABE 6	1350.8		
²² G14369	1255.0	⁴⁸ G14369	1334.2		
²³ SAB632	1254.8	⁴⁹ Bifort small seeded - 15	1332.0		
²⁴ NUA671	1247.7	⁵⁰ SELIAN97	1311.6		
²⁵ MOORE 8802	1240.2	⁵¹ Awash Metene	1280.3		
²⁶ KATB1	1215.6	⁵² KATB9	1219.9		
		⁵³ GLP1004	1191.9		
		⁵⁴ Nyeupe-Uyole	1140.7		
		⁵⁵ GLP1127 (a)	1087.0		

Note: ¹Yield in kg/ha presented as best linear unbiased predictions (BLUPs). ^{2,9,10,14,15,22,26}Standard checks that were included in all trials in Group 1, country-specific checks for Group 1 (^{2,9,10,25}Uganda, ^{2,3,19,21}Rwanda, ^{2,9}DR. Congo, ^{4,6}Burundi, ^{5,11,13,23,26}Ethiopia, ^{7,8,12,16,17,18,20,24,26}Kenya, ^{15,22,26}Tanzania). ^{34,38,46,47,48}Standard checks that were included in all trials in Group 2, country-specific checks for Group 2 (^{27,48,50,52,54}Tanzania, ^{28,35}Rwanda, ^{29,34,44,47}Uganda, ^{30,36,37,38,44,46,49,51}Ethiopia, ^{31,39,40,41,42,43,45,52,53,55}Kenya, ^{32,33}Burundi). ^{59,60,62,64,65,67,72}Standard checks that were included in all trials in Group 3, country-specific checks for Group 3 (^{56,60}Burundi, ^{57,58,63,68,69,70,72}Rwanda, ^{57,59,61,64,66}DR. Congo, ^{59,64,71}Uganda).

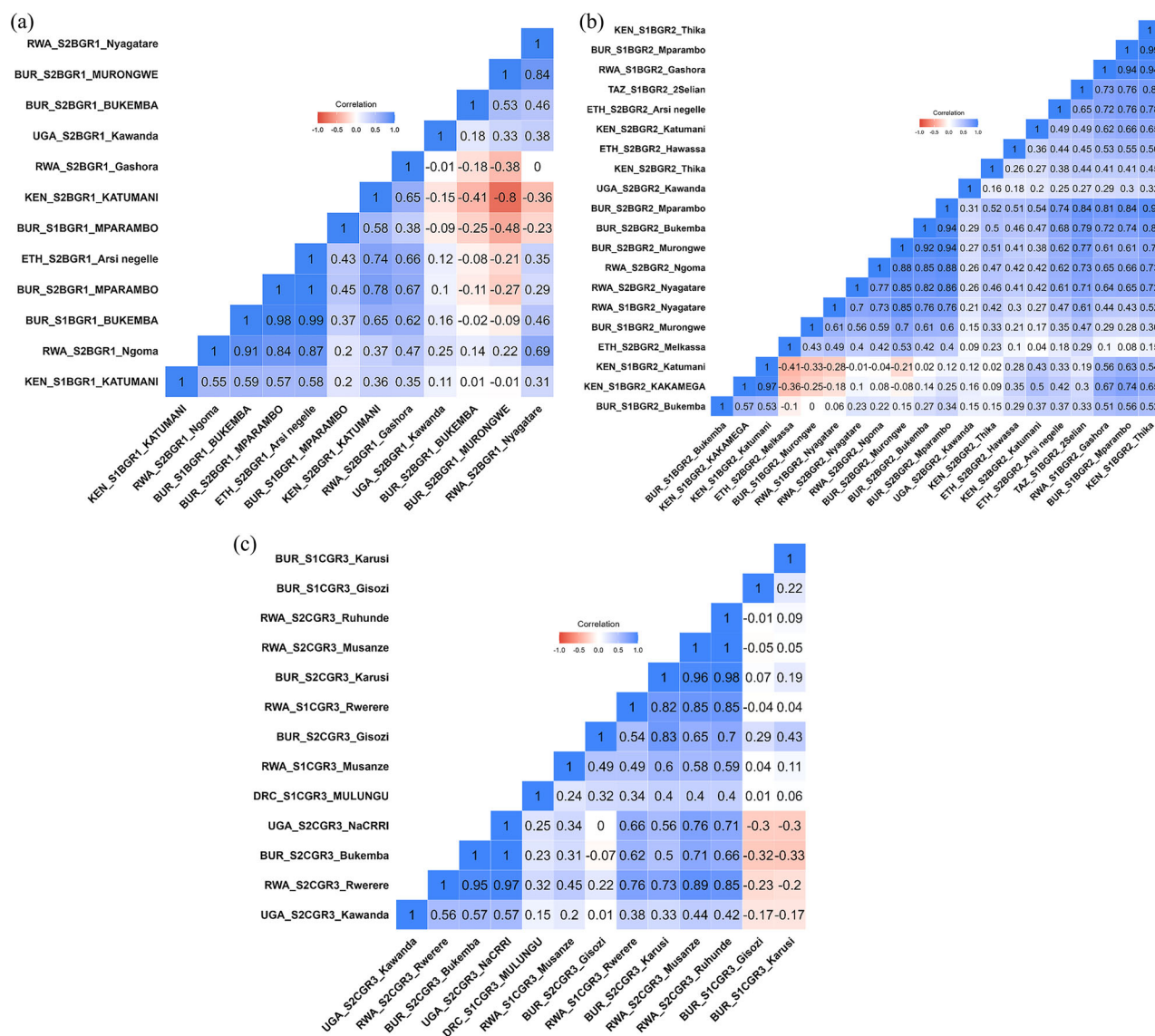


FIGURE 1 Genetic correlations for yield among trials in three groups of lines (Groups 1 [1a], 2 [1b], and 3 [1c]) representing three breeding pipelines.

white beans better than country checks were also present (Table S6). Blacks and other market segments in Group 2 were poorly represented in the combined analyses, and there were few superior lines (Table S6).

Group 3: Most trial sites had positive correlations between each other for yield (Figure 1c). Two trials that showed strong negative correlations in yield were excluded from the MET analyses. One line (NUV234-3-1) from the yellow bean market segment outperformed all the checks, but four checks appeared among the 10 best yielding genotypes (Table 8). Considering the market segments in this pipeline, four yellow beans, three white beans, and 12 red beans, among others yielded better than the standard check for each market segment. The standard checks among the sugar and the red mottled beans were the highest yielding lines (Table S6).

3.2.3 | Environmental clustering

Four climatic clusters were formed when all research sites were analyzed (Figure 2). The first dimension reflected variation in Tmax, Tmin, vapor pressure deficit (VPD), and Min_ and mean relative humidity at 2 m (mean_RH2M). The second dimension explained 18.4% of variation and likewise reflected Min_ and mean of minimum temperature and VPD but was dominated by maximum relative humidity at 2 m (Max_RH2M), which was much more important than mean_RH2M. A high Max_RH2M reflected variation in relative humidity and occasional extremes of rainy weather and could be associated with short-to-medium-length periods of very high humidity that could contribute to disease development, especially fungal diseases.

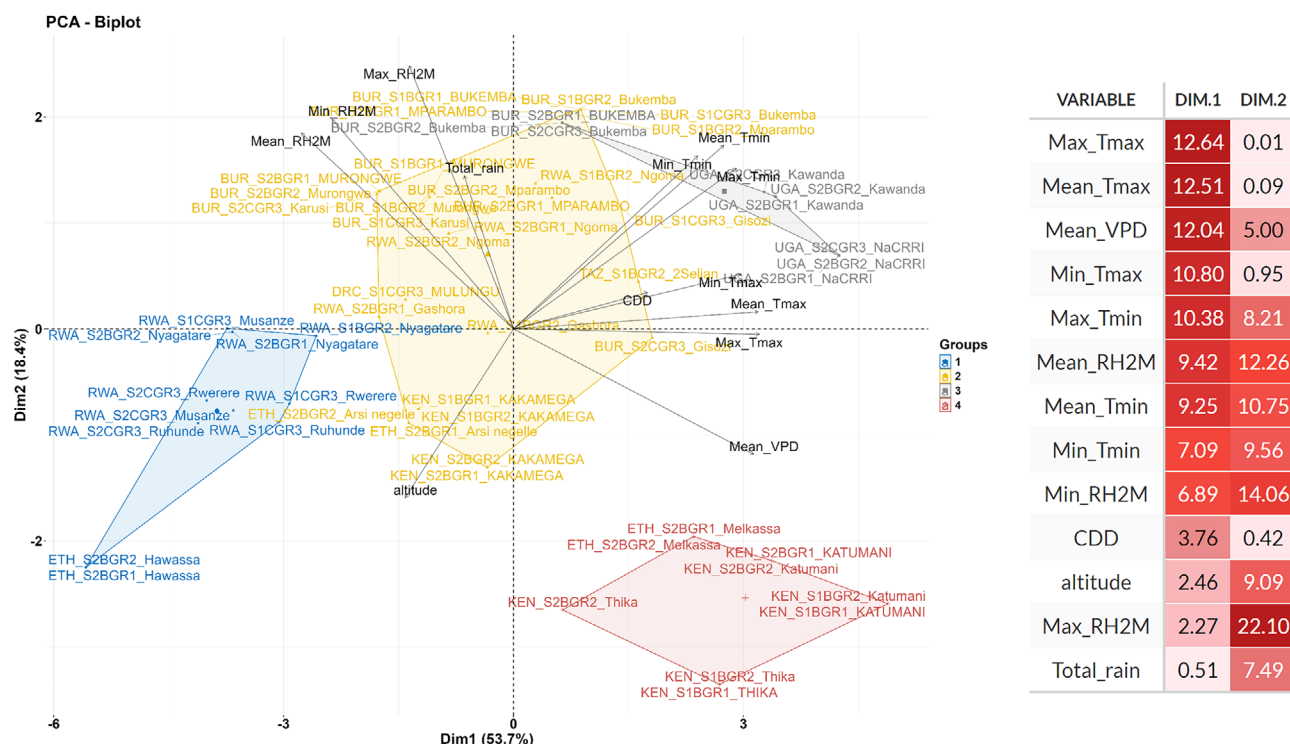


FIGURE 2 Climatic clusters of environments where the East and Central Africa bean yield trial (ECABYT) trials were planted, based on 13 variables. The contribution of each variable to dimensions 1 (Dim1) and 2 (Dim2) is represented in the table to the right.

The yellow cluster tended to be centric on the two dimensions and thus would avoid extreme variables. It was the most significant cluster, representing about 40% of the trials. Three other environmental clusters appeared to be heavily influenced by specific climate vectors. The red cluster with positive values on Dim 1 was represented by two sites in Kenya on the eastern side of the East African highlands (Katumani and Thika), and Melkassa in Ethiopia, with low RH2M and high VPD. Although also associated with lower rainfall, as expected, the effect of total rainfall was less than the other two closely related variables (VPD includes relative humidity in its calculation). One would expect that this cluster would be associated with drought stress. The gray cluster with positive values on Dim 1 seemed to respond primarily to high temperature, and possibly more to Tmin (Max, Min, and Mean), than to Tmax. A blue cluster was opposite the gray cluster and represented high-altitude sites with lower temperature.

3.2.4 | Genotype $\times$ environment interactions

Biplots were created whereby the yield vectors for each trial were colored based on the climate cluster of that test environment. In G1 (Andean bush beans), the greatest number of sites were in the yellow cluster (Figure 3a), which also seemed to be the most common climate among the testing sites. If these sites are in fact representative, this would be the climate of

priority for selection of Andean bush beans. However, this requires confirmation given the small number of trials that met criteria for this analysis. Yield in sites of the yellow and red clusters overlapped, suggesting little to no effect of a drier climate. In fact, most trials in the red cluster had been irrigated, and this apparently was sufficient to counteract the high VPD. Only two trials were in the gray cluster sites, including Kawanda in Uganda and Bukemba in Burundi. These clustered relatively close to each other. Only one site in the blue cluster was included in the analysis.

In Group 2 (Mesoamerican bush beans), the two sites from the gray cluster grouped relatively close to each other, but they did not separate in any way from other climate clusters (Figure 3b). The yields of five trials established in the sites of the red climate cluster were widely distributed across the biplot with no tendency to behave similarly, in spite of the fact that this climate cluster was well differentiated from other climate clusters, and the breeding lines were diverse in yield response. Here again, irrigation of the trials may have compensated for the drier climate. These differences did not elicit a differential response from the crop.

Climbing bean yields (G3) showed the closest relationship with climate clusters (Figure 3c). Yield sites in Uganda (Kawanda and Namulonge) fell in the gray cluster together with Bukemba in Burundi and separated from other sites. Given that the high temperatures and exceptionally high Tmin dominated the gray cluster, this suggests that climbers are

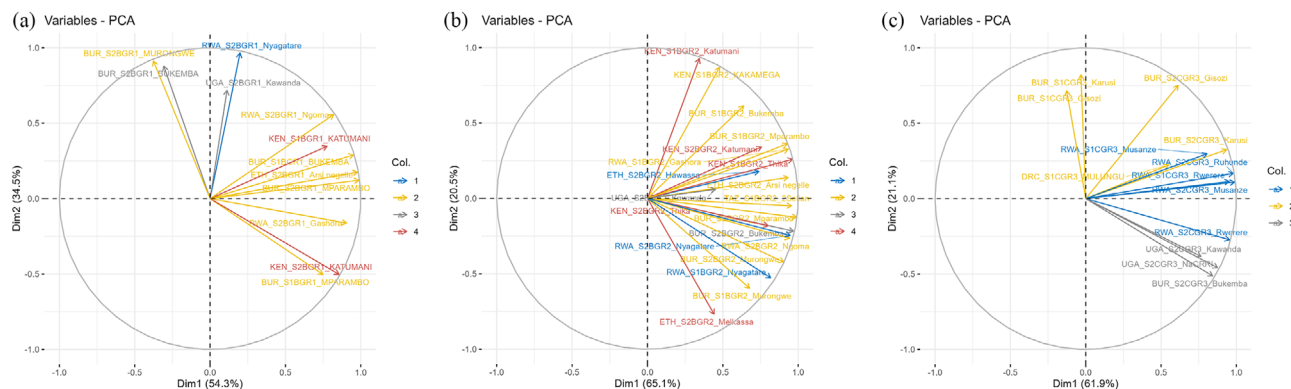


FIGURE 3 Biplot of yields in three trials of the East and Central Africa bean yield trial (ECABYT), identified by color with the climatic cluster of the respective environment.

especially sensitive to high temperatures. Sites in the blue and yellow climate clusters also separated by crop yield. The variables that defined the blue cluster were high altitude and lower temperature, as opposed to the gray cluster with higher temperatures. This again highlights the greater sensitivity of climbers to temperature compared to either the Andean bush beans (G1) or Mesoamerican bush beans (G2), which did not respond differentially on the temperature gradient, except for a tendency for trials in the gray cluster to group together. Climbers were not planted in sites in the red cluster.

4 | DISCUSSION

Among the commonly grown grain legume crops, common beans are the most important, preferred, widely grown, and consumed in Eastern, Central, Southern Africa, and some parts of West Africa, particularly in medium elevation and highland areas (Buruchara et al., 2011). This is a result of their short maturity period (≤ 3 months), high nutritive value, versatility through ease of conversion to cash to meet urgent household needs, relatively long storage and convenience of handling the harvested produce, and compatibility with other crops (maize, cassava, banana, etc.) in many low-input production systems. While the production trends of beans in Africa have been increasing, the crop is very sensitive to climate variability and change. Common bean production is greatly curtailed by several environmental stresses, notably drought, excessive rain/flooding, heat, and cold temperatures, as well as biotic constraints, including field and post-harvest pests and diseases. Some stresses, such as soil degradation, climatic variability, and climate change, are chronic and longer-term, while others are shorter-term and spurred by acute stress (such as those normally linked to emergency interventions).

Increased crop yield is the primary aim of most plant-breeding programs in Africa. Yield performance is deter-

mined by a combination of several traits, notably tolerance to abiotic and biotic stresses, and inherent plant characteristics, including physiological efficiency that guarantee high commercial yield (Kang et al., 2004; Reynolds et al., 2020). In the last decades, consumption traits such as iron (Fe) and zinc (Zn) content and faster cooking time have become essential in addition to the productivity traits (Assefa et al., 2005; Katungi et al., 2015; Kiran et al., 2022; Pixley et al., 2023). Over the years, there has been an overall increase in YDHA of beans, with the most increase being observed in East Africa. Average yield in East Africa has grown from 700 kg/ha in 1960s to over 1000 kg/ha, representing about 43% growth (Food and Agriculture Organization [FAO], 1960–2020). This increase is credited to the high adoption of new improved bean varieties with excellent market potential, and use of good agronomical practices and inputs with the assurance of market (Katungi et al., 2011; Larochelle et al., 2015; Mukankusi et al., 2019). A recent ex-ante analysis conducted in Tanzania and Uganda suggests projected increases in bean demand of 157% and 203%, respectively (Schiek et al., 2021), implying the need for increased production. New varieties with higher yield potential and the ability to withstand stress conditions are hence pivotal for bean adaptation to climate change (Araujo et al., 2015; Beebe et al., 2011).

The high variance component recorded for $G \times E$ across all three groups in this study revealed that the performance of different genotypes varied greatly depending on the environmental conditions. Group 1 showed the highest influence, which makes selection more challenging. While yield performance is presented based on overall group BLUPs, with more data, selection within environmental groups should be explored. Of the popular market classes, the study revealed potential lines for advanced testing in each country for red mottled (Group 1), small red and white (Group 2), and red, yellow, and white (Group 3). While red-mottled occupy the widest hectare in Group 1, sugar and yellow follow, but there were few potential lines. Similarly, superior red-mottled and

sugar bean climbers were limited. Attention to deliver more superior lines in these groups is necessary. The grouping of the test lines into three was based only on seed size and growth habit. This grouping did not consider refined information such as from DNA markers, and thus may not differentiate the yield potential at gene pool level. The grouping lumped the medium and large seeded bush beans together (both Andean and Mesoamerican) in Group 1, and the large, medium, and small in Group 3 for climbers. However, given the selection of certain grain types within each breeding pipeline, the results of classification by grain size corresponded closely to those grain types, and we can say that the great majority of lines in Groups 1 and 2 were Andean and Mesoamerican, respectively. It was observed that the medium-seeded types (mostly Mesoamerican) always outperformed the large types (Andean), a fact that could result in loss of the large-seeded bean types with time through selection if kept in one group. Amongi et al. (2023) reported a 117 kg/ha yield advantage and wider genetic diversity of Mesoamerican beans over the Andean beans. Similarly, higher yield genetic gains have been reported in the small seeded types compared to the large types (Amongi et al., 2022; Mukayiranga et al., 2022). Future regional trials could consider separating the large, medium, and small seeded lines into unique nurseries, that is, (i) large bush, (ii) large climbers, (iii) medium bush, (iv) medium climbers, (v) small bush, and (vi) small-seeded climbers. Future trials should also consider splitting further by grain market class to ensure genetic progress in key demanded bean market classes to respond to the bean corridors (Pan-Africa Bean Research Alliance [PABRA], 2017).

The ECABYT was initiated by the Alliance of Bioversity International and CIAT in the year 2020 to establish a consistent testing mechanism across East and Central Africa Bean Research Network (ECABREN) comprising eight countries to respond to the regional and national demand of bean varieties. The trial is an avenue to wider access of new and elite genetic material for participating in NARS bean breeding programs (including those with limited capacity for variety development). It facilitates regional evaluation of elite lines, generation of useful $G \times E$ data, measurement of breeding network, and country-specific genetic gains and facilitates multiple variety releases, which might attract more investment in the bean seed production due to economies of scale. The analysis of the ECABYT unearthed several insights that can be drawn to help devise stronger testing networks across the whole of PABRA and help to keep pace with the demands of the ever-changing climate.

A unique attribute of the $G \times E$ analysis of the ECABYT was the use of climatic data to explain plant responses. While environmental data (soil and weather) was collected for some trials, it was not used for the analysis because, in most cases, the collected data were inconsistent or sporadic across trials. Instead, the NASA POWER database was employed in this

analysis for uniformity and availability. This database permitted associating crop response with the climatic variables of the same site and season, which gives more confidence in comparisons with crop response than site data averaged over years. Monteiro et al. (2017) proved that NASApower climatic data for agriculture is usable with substantial confidence at regional and national spatial scales.

The environments employed in the regional trial fell into four clusters defined by 13 parameters: one large centric cluster and three additional clusters characterized by high temperatures, low temperatures, and dry conditions with VPD, with maximum relative humidity playing a role in the second dimension. The formation of yield clusters was examined for the three breeding pipelines, and these were compared to environmental clusters. In the biplots of yields, the relationship with the climate clusters is represented by color-coding the vector of each trial for its respective climate cluster. G3 (climbing beans) yield clusters displayed a close relationship with climate clusters along a temperature-altitude gradient. As climbing beans are especially sensitive to temperature, this was logical and expected, but as noted above, this implies that night temperatures may play an especially important role in climber adaptation. Climbing beans are thought to be the most primitive of cultivated beans since the ancestral wild bean is a climbing in nature (Freytag & Debouck, 2002). Common beans are grown over a wide range of altitudes with mean air temperature of 14°C–35°C. Day temperatures of >30°C or >20°C at night result in yield reduction (Porch, 2006; Rainey & Griffiths, 2005). High night temperatures at flowering (and to a lesser degree, high day temperatures) cause flower and pod abortion, reduced pollen viability, impaired pollen-tube formation in the styles, and reduced seed size (Gross & Kigel, 1994; Hall, 2004; Porch & Jahn, 2001). Rising temperatures will affect the altitudinal range of genotypic adaptation, reduce root growth, and accelerate mineralization of soil organic matter, making drought stress more acute (Beebe et al., 2011).

The formation of yield clusters among G1 and G2 trials (Andean bush beans and small seeded Mesoamerican types) showed little relationship to climate clusters. The G2 trials were quite diverse, but the different environmental clusters were distributed almost randomly across the array of yield vectors. To the extent that gray, yellow, and blue climate clusters reflect a temperature gradient, the G2 breeding lines seem to be relatively insensitive to this range of temperatures. The G1 trials likewise showed little relationship to climate, except that the yellow cluster was somewhat more compact, and except for one trial in Murongwe in Burundi, the yellow group separated widely from the two high-temperature gray trials and from the single blue trial.

While materials of the G1 breeding pipeline (medium-large types) are the most demanded in East Africa, several trials were eliminated from the analysis due to very low

heritability. The analysis involved only eleven trials. It is important to expand the number of trials and sites to confirm these preliminary results.

Vectors of yield trials in sites in the red climate cluster similarly were spread widely. This was a surprise, since the red cluster appeared to be very distinct and was characterized by high VPD that would be associated with drought. However, testing lines that supposedly would be variable in drought tolerance did not express a unique pattern of response in the red cluster. Trials at Katumani and Thika were irrigated, but those in Ethiopia were not. In any case, the role of drought tolerance in defining $G \times E$ is still a subject to be studied more carefully. A 60–120-day bean crop requires 300–600 mm of water depending on its environment for maximum production (Allen et al., 1998; White et al., 1994). Water scarcity and abundance, the date of onset of rains, and changes to the length of growing seasons will have direct impacts on the bean crop. In addition, an estimated 50% of bean production in Africa suffers from low phosphorous (P) availability, while 40% may suffer from aluminum (Al) toxicity. Effects of drought and high temperatures are more severe when combined with low P supply and/or Al toxicity (Beebe et al., 2008). In the tropics, high air temperature is often accompanied by high soil temperature in the rooting zone (top 20 cm of soil), leading to poor root formation. Temperatures of air, rooting zone, and subsoil may influence days to flowering, seed germination, and tap or lateral root formation (White & Montes-R, 1993). High temperatures also inhibit N_2 fixation, and bush beans are widely regarded as poor in nodulation and N_2 fixation (Graham & Ranalli, 1997). A recent study, Jha et al. (2023), reports that drought stress-free conditions generally dominate across Ethiopia, Tanzania, and Uganda under historical conditions (50%–80% frequency); however, by 2050, terminal drought stresses of various intensities (moderate, severe, and extreme) would be prevalent in 34% of Uganda, around a quarter of Ethiopia, and 40% of the bean-growing environments in Tanzania. Jha et al. (2023) also suggest that common bean breeding programs should focus primarily on identifying genotypes with tolerance to severe terminal drought, with co-benefits in relation to adaptation to moderate and extreme terminal drought to optimize resource use, and that little to no emphasis on heat stress is warranted by 2050s. The likelihood of more frequent droughts makes understanding the crop response an urgent issue. The task of defining climate clusters that correspond to crop response is central to the definition of target populations of environments (TPE). The results with climbing beans come the closest to identifying such groups of environments, within which key testing sites might be identified for future phenotyping. Nonetheless, the method of employing a regional trial in combination with detailed, on-site climatic data derived from the NASApower database, and for the very trials and seasons, shows promise and should be pursued further. Asfaw et al. (2012) suggest the importance of selection of drought-tolerant material and the relevance of quantitative

trait loci detection in the sites in which the materials will be grown. While field management data were collected; these data were not uniform across the trials, a factor that could impact the $G \times E$ interactions. The extent and intensity of drought stress in various TPEs could be reduced by adequately targeting genotypes, necessitating a differentiated breeding strategy between the TPEs (Jha et al., 2024).

This analysis deals with results obtained on research stations, whereas the target of breeding programs is the farmer's field. Methods described here may be useful to establish relationships between research and farmer environments, at least regarding climate. In some cases, research stations may represent more favorable environments than those where most production take place, especially regarding soil quality and crop management. Ambiguities in the current analysis may be due to environmental factors that are not included in this study. Analysis of environments on a wider scale, especially if soil parameters are considered, may serve to estimate the degree to which research environments correspond to on-farm conditions.

5 | CONCLUSIONS

This study highlights the important role of temperature in bean adaptation. This demonstrates the potential for exploring the application of on-site environmental data for the analysis of crop data and the clustering of environments that can be applied eventually to TPE definition. This requires a larger sample of trials with data of acceptable quality. The possible role of maximum relative humidity in the development of disease and the definition of crop response should be explored. This experience also led to additional improvements for continual and more efficient deployment of the regional trials:

1. It enhances the characterization of testing sites by collecting and using GPS location, soil, temperature, rainfall, and management data in the $G \times E$ analysis, and where possible, it deploys sensors to collect real-time weather data.
2. It adopts a common and standard naming system for advanced lines that include a code for breeding pipeline, grain color, breeding institute, and the line number. This coding system will allow genetic gain estimation for the network and for individual breeding programs utilizing data from the regional trials. This system will allow easy retrieval of data in the BMS to enable joint analysis.
3. Future regional trials could consider separating the large, medium, and small seeded lines into unique nurseries, that is, (i) large bush, (ii) large climbers, (iii) medium bush, (iv) medium climbers, (v) small bush, and (vi) small-seeded climbers to include the aspect of gene pool differences that have an influence on yield and other trait performance.

Future trials should also consider splitting further by grain market class to ensure genetic progress in key demanded bean market classes.

4. It deploys a concrete check strategy with benchmark checks defined for all traits in each target product profile, standard checks defined for essential-improve traits and threshold traits that remains the same through several years, and standard checks that may be defined as the ruling varieties in each country per target product profile responding to the variety replacement strategy.
5. As a future approach, we propose to use extensive on-farm tricot evaluations (on farm Era study) but including older standards to evaluate how well the network has performed over the past 10–20 years over target geographies (Brown et al., 2022).

AUTHOR CONTRIBUTIONS

Winnyfred Amongi: Data curation; formal analysis; investigation; visualization; writing—original draft. **Johan Aparicio:** Data curation; formal analysis; software; visualization; writing—original draft. **Eric Nduwarugira:** Data curation; investigation. **Blaise Ndabashinze:** Data curation; investigation. **Kijana Ruhebuza:** Data curation; investigation. **Reuben Otsyula:** Data curation; investigation. **Shamir Misango:** Data curation; investigation. **Eliezh Kamau:** Data curation; investigation. **Davis Karanja:** Data curation; investigation. **Wincaster Mutuli Makoani:** Data curation; investigation. **Anuerite Uwera:** Data curation; investigation. **Shida Nestory:** Data curation; investigation. **Stanley Nkalubo:** Data curation; investigation. **Eunice Kesiime:** Data curation; investigation. **Abel Moges:** Data curation; investigation. **Kidane Tumsa:** Data curation; investigation. **Teshale Mamo:** Supervision; visualization. **Steve Beebe:** Validation; visualization; writing—review and editing. **Clare Mukankusi:** Conceptualization; methodology; supervision; writing—review and editing.

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

DATA AVAILABILITY STATEMENT

All data needed to understand, evaluate, and build upon the reported research are in this article and its supplementary information Tables. Raw trial data were curated in Breed-

ing Management System (BMS) of the Alliance of Bioversity International and CIAT, and they are available upon request.

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SUPPORTING INFORMATION

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