



Forum

Accelerating genetic gain through early-stage on-farm sparse testing

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Most African crop breeding programs conduct early-stage selection at very few research stations, which may not reflect smallholder farm conditions. Early-stage on-farm sparse testing utilizes genomic relationships to shift selection from research stations to hundreds of farms in the target population of environments, facilitating increased genetic gain in farmers' fields.

Smallholder farms of less than 2 hectares constitute over 80% of the world's 570 million farms, underpinning the livelihoods of impoverished rural populations. Smallholder farmers and their families represent a significant portion of the 690 million people experiencing daily hunger [1]. Smallholder farming systems are often characterized by low input use and the simultaneous occurrence of multiple stresses, including heat, drought, pests, weeds, and crop diseases. They are also highly susceptible to unpredictable weather extremes associated with climate change [2]. To aid smallholder farmers facing these challenges, Consultative Group of International Agricultural Research (CGIAR) (see Glossary) -coordinated staple crop breeding programs aim to develop improved crop varieties targeted at large populations of farmers working in diverse production environments, referred to as the **target**

**population of environments (TPE)**. The TPE encompasses all farms and future seasons where the varieties produced by a breeding program will be grown.

**Unrepresentative selection environments for developing crop varieties could impede adaptation to low-input smallholder farms**

To ensure high performance of new crop varieties throughout the TPE, the conditions under which selection candidates are evaluated must represent the growing conditions in smallholder farmers' fields. Therefore, plant breeders must design their selection environments to represent the diversity of biophysical conditions and agronomic practices observed on smallholder farms. This remains one of the most fundamental, longstanding challenges in plant breeding. Especially in sub-Saharan Africa (SSA), farm conditions are highly heterogeneous and are often very different from those on research stations, posing an obstacle to simulating on research stations the diversity of on-farm stress factors. For example, smallholder farmers in SSA typically use less than 18 kg/ha of inorganic fertilizer, approximately 20% of what farmers in South Asia apply [3]. Weed management in SSA depends heavily on manual labor, often resulting in significant weed competition. Additionally, many smallholder farmers practice intercropping. Overall, the ecological and socioeconomic heterogeneity among farms in SSA, coupled with the significant difference between crop management on research stations and farmers' fields (especially those managed by women and resource-poor farmers), can result in a low genetic correlation between performance on the research station and on farms, leading to only a fraction of the measured **genetic gain** on-station being realized on-farm [4,5].

**Early-stage testing on research stations could limit genetic gain on smallholder farms**

Especially during the early stages of plant breeding programs, the large discrepancy

Glossary

**CGIAR:** a global research partnership for a food-secure future dedicated to transforming food, land, and water systems in a climate crisis.

**Farm typology:** a classification system used to group farms based on similar characteristics such as size, management practices, socioeconomic factors, or types of crops grown, and livestock raised.

**Genetic gain:** the change in the average genetic value of a population for traits of interest, such as yield, disease resistance, or drought tolerance. Genetic gain is achieved through crossing and selection over successive breeding cycles. It is also known as 'response to selection'.

**Genomic relationship matrix (GRM):** a covariance matrix providing an estimate of the genetic similarity or relatedness among individuals based on shared genomic information, such as the allelic states (genotypes) of SNP markers obtained from DNA microarrays or (reduced representation) genome sequencing.

**Sparse testing:** a multi-environment testing strategy in which not all selection candidates are grown in every testing environment, allowing for broader sampling of locations that represent the target population of environments. Sparse testing requires information on the genetic similarity of selection candidates, such as a GRM, to ensure connectivity between testing environments and facilitate a fair comparison among candidates.

**Target population of environments (TPE):** comprises all farms and future seasons in which the varieties produced by a breeding program will be grown. It is characterized by biophysical conditions, including all biotic and abiotic environmental factors, as well as the agronomic management practices adopted by farmers.

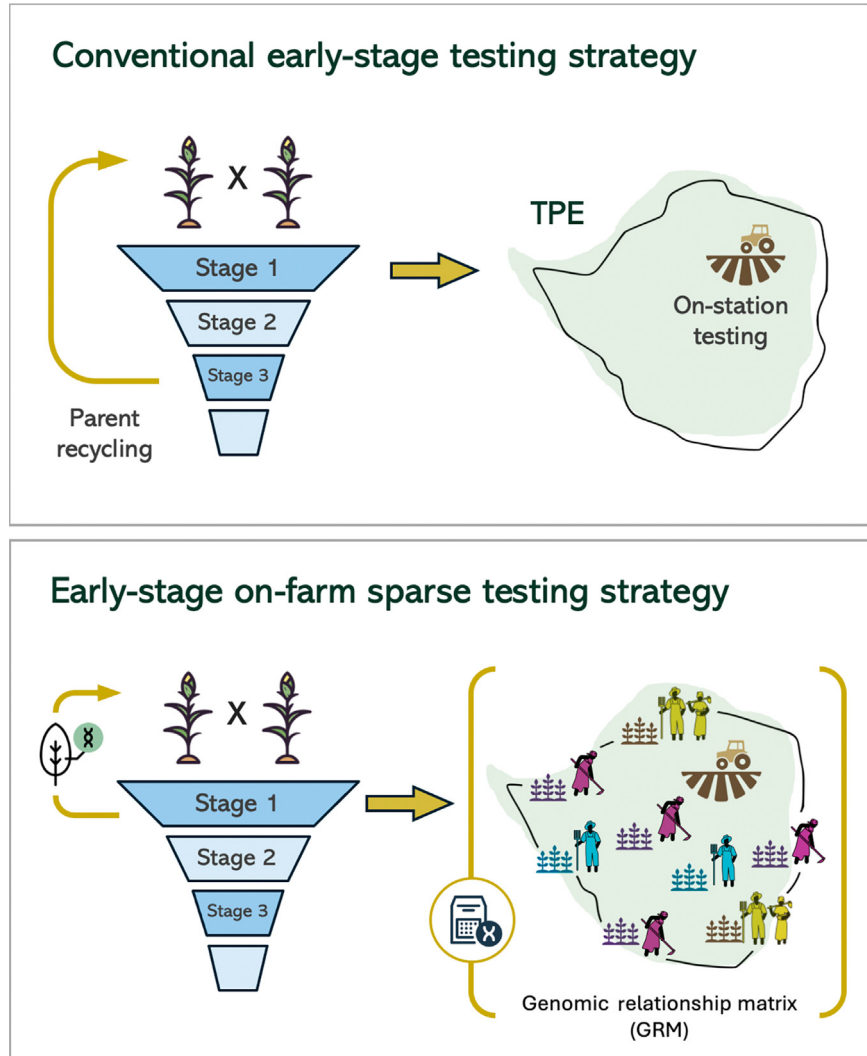
between conditions on research stations and those faced by smallholder farmers poses a significant challenge. Currently, in the majority of CGIAR and National Agricultural Research and Extension Systems (NARES) crop breeding programs, most selection pressure (often >90%) is concentrated at a few well-managed research stations, where thousands of selection candidates are discarded in unreplicated nurseries or initial agronomic trials conducted with little or no replication [6]. This selection strategy is based on the premise that rapidly and inexpensively culling large populations will allow for greater allocation of testing resources to a superior subset of candidates in subsequent stages. However, given the environmental variability

within most African regions, and the management differences between research stations and farms, selecting on only one or a few research stations is unlikely to provide accurate predictions of the on-farm performance across the TPE. Consequently, early-stage testing in an inadequate sample of the TPE under conditions that may not accurately reflect those on smallholder farms imposes a severe bottleneck on early-stage genetic variation. This reality highlights the need for a strategy to evaluate unselected early-stage material at many locations in the TPE under farmer management.

### Early-stage on-farm sparse testing enables selection under realistic growing conditions

Early-stage on-farm **sparse testing** (OFST) shifts a substantial portion of the evaluation process from a few research stations to hundreds of farms, each growing only a few unreplicated selection candidates (Figure 1). This approach offers two fundamental advantages over traditional testing on research stations. First, testing in farmers' fields enables the evaluation of selection candidates under realistic, farmer-managed conditions at the earliest stage of agronomic testing. Second, expanding the number of locations facilitates a more representative sampling of the diverse conditions across the TPE.

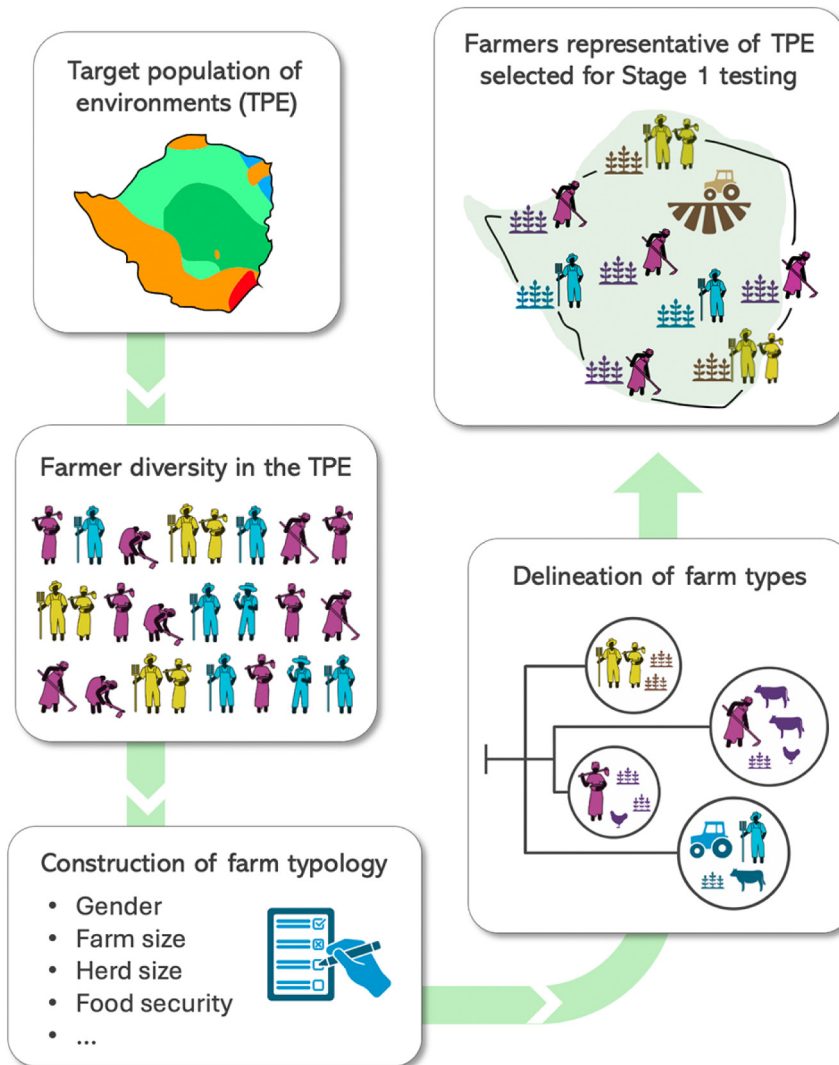
The design of early-stage OFST trials is primarily determined by practical restrictions on smallholder farms, where the capacity to accommodate selection experiments is extremely limited. Therefore, farm-as-incomplete-block (FAIB) designs are employed [4], wherein only three to five selection candidates are allocated to each farm, facilitating the inclusion of resource-poor farmers in the selection process (Figure 2). However, some flexibility in plot numbers per farm may allow larger farmers to grow more genotypes, provided the proportion of farm types remains representative of the TPE.



Trends in Plant Science

**Figure 1. Benefits of early-stage on-farm sparse testing compared to a conventional early-stage testing strategy.** Most African crop breeding programs conduct early-stage selection at only a few research stations managed by breeders (top panel). While this testing strategy may not adequately represent the diverse growing conditions encountered by smallholder farmers across the target population of environments (TPE), selection pressure is often high (indicated by the funnel representing the multiple stages of selection of a crop breeding program). If the genetic correlation between performance on research stations and performance in farmers' fields is low, this testing strategy can impose a severe bottleneck on early-stage genetic variation, leading to only a fraction of the genetic gain measured on-station being realized on-farm. Early-stage on-farm sparse testing (OFST) exploits genomic relationships, usually captured in a genomic relationship matrix (GRM), to shift a substantial portion of the evaluation process to hundreds of farms sampled broadly across the TPE (bottom panel). It is implemented using farm-as-incomplete-block (FAIB) designs where each farmer grows only a few unreplicated selection candidates (usually three to five). Compared to a conventional testing strategy, early-stage OFST allows for the evaluation of selection candidates under realistic, farmer-managed conditions, enables earlier selection of crossing parents using genomic prediction, and facilitates accelerated genetic gains in smallholder farmers' fields. The figure was created with [BioRender.com](https://www.biorender.com) as well as using icons from [Flaticon.com](https://www.flaticon.com) (designers: agus raharjo, Ekli Studio, Freepik).

Furthermore, if the number of genotypes exceeds on-farm testing capacity, a representative subset may be selected [7]. While random allocation of genotypes to farms may suffice, more advanced model-based designs using genomic



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**Figure 2. Capturing the diversity of farmers within the target population of environments.** Smallholder farmers are highly diverse in terms of aspirations, resource endowments, and constraints, even within a community. A critical component in the success of early-stage on-farm sparse testing (OFST) is to ensure that host farmers included in the testing process adequately represent the socioeconomic heterogeneity within the target population of environments (TPE). Without direct processes to target women and resource-poor farmers, both groups can be underrepresented. A stratified sampling approach that incorporates geospatial information and socio-economic data can be used to identify host farms, capturing the farm diversity within the TPE and ensuring a socially inclusive testing network. A **farm typology** is used to describe the heterogeneity across farms and identify patterns. Key drivers of heterogeneity include characteristics around gender of the household head and plot manager, farm size, production orientation, indicators of wealth (such as number of cattle and agricultural assets), and household food security. After the delineation of farm types, farms are selected within each group to ensure that host farmers reflect current diversity within the TPE. Socioeconomic data relevant to handling the heterogeneity of smallholder farming systems by grouping farms of similar characteristics will vary across geographies and crops. While notable, gender is not the sole axis of social difference, and this approach ensures that a range of women farmers are included within the OFST network. The figure was created with [BioRender.com](https://www.biorender.com) and includes a Zimbabwe map of Köppen climate classification from [Wikipedia.com](https://en.wikipedia.org/wiki/Köppen_climate_classification).

relatedness information may improve the distribution of families across the TPE [8]. Early-stage OFST trials using FAIB designs represent a significant advancement over participatory varietal selection (PVS) approaches, which are applied on later-stage material [9], and participatory plant breeding (PPB) methods, which either sample relatively few farmers [10] or rely on bringing farmers to research stations to conduct visual selection [9]. Compared to late-stage PVS and PPB approaches, limited seed availability during early breeding stages and the inclusion of smallholder farmers necessitate relatively small plot sizes.

Early-stage OFST exploits genomic marker relationships between selection candidates, typically captured in the form of a **genomic relationship matrix (GRM)**. This approach enables the marker to serve as the unit of evaluation instead of the individual selection candidate, shifting the focus from replication of the selection candidate to replicating marker haplotypes shared by full-sibs, half-sibs, and other relatives. Information on unreplicated selection candidates is enhanced through observations on numerous closely related family members tested in incomplete blocks across many farms, effectively serving as 'partial replicates'. This enables genomic prediction of a selection candidate's value as a parent or variety across the entire TPE. With the availability of low-cost, mid-density genotyping, early-stage OFST should become feasible for many public breeding programs. Utilizing the GRM necessitates treating genotypes as random effects in a linear mixed model analysis. Likewise, farms are assumed to be randomly sampled from the TPE. This modeling approach resembles genetic evaluations in smallholder dairy farms [11]. The main objective of early-stage OFST is to enhance the prediction of a genotype's mean performance across the TPE for selection purposes. While predicting genotype-by-environment (GxE) interaction effects at the farm level may not yield reliable results,

studying GxE interactions among a few specific subclusters, such as rainfed versus irrigated trials, may be possible.

### Early-stage OFST: a potential game changer in crop breeding for Africa

Early-stage OFST could be a paradigm-shifting approach to enhancing genetic gains in smallholder farmers' fields through several mechanisms, including:

- Improved selection accuracy through decentralized early-stage testing under farmer management, ensuring better sampling and representativeness of both environmental and socioeconomic variation in the TPE.
- Decreased generation interval (faster parent recycling), enabled by enhanced selection accuracy at early testing stages.
- Increased selection intensity facilitated by the GRM, enabling reduced replication, thereby freeing up plots for additional selection candidates.

For early-stage OFST to effectively contribute to the success of a breeding program, it must be recognized that testing in farmers' fields will not replace on-station testing. Instead, on-farm testing complements on-station testing by providing additional insights into traits, particularly yield, influenced by lack of correlation between research stations and on-farm conditions. Conversely, traits such as specific biotic and abiotic resistances, including drought tolerance and disease resistance, may be assessed more efficiently on-station through controlled inoculation and artificial stress conditions. However, even when on-station testing is preferable, a deeper understanding of the TPE gleaned from OFST can help to create managed environments that accurately represent weather, soil conditions, and management practices on smallholder farms.

While combining extensive on-farm and on-station testing is common practice in large-scale commercial breeding programs [12], developing a practical framework for on-farm sparse testing in African smallholder farms will present various unique challenges.

### Critical implementation requirements

Implementing early-stage OFST demands significant resources and high levels of coordination. It relies on a network that brings together CGIAR centers, NARES, and farmers to generate high-quality data from decentralized trials at remote locations. All collaborators must recognize that, unlike late-stage or variety demonstration trials, early-stage material may still display significant undesirable genetic variability. Farmers, in particular, must provide informed consent for the evaluation of unselected materials on their farms, and should receive some form of compensation for any reduced productivity resulting from poor-performing selection candidates. Especially in SSA, the large number of selection candidates in early-stage testing requires inclusion of many farms in FAIBs, given the significant between-farm variation and the limited capacity of smallholder farmers to grow multiple genotypes. To ensure high-quality data collection from FAIB trials, comprehensive training of collaborators and rigorous quality control measures are essential.

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The authors declare no competing interests.

### Declaration of Generative AI and AI-assisted technologies in the writing process

During the preparation of this work the author(s) used ChatGPT (OpenAI) in order to help condense the main text to meet the maximum word count. After using this

tool/service, the author(s) reviewed and edited the content as needed and take(s) full responsibility for the content of the publication.

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