the effective selection, acceptance, and production of new cotton varieties in Zimbabwe through the integration of farmer engagement methodologies in cotton variety development

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ABSTRACT

Any breeding program's success depends on the active cooperation of important stakeholders or technology recipients. Since cotton (Gossypium hirsutum L.), a multipurpose crop, is farmed throughout most of the world, various parties must be involved in the process. Participatory Variety Selection (PVS) is a "client-oriented" research methodology used in Zimbabwe's national variety development programme. Five advanced genotypes and one commercial variety that was widely grown by farmers were used in the procedure that involved the evaluation of several advanced cotton genotypes by farmers in various cotton growing areas. They were raised in a mother-baby experiment setting. The goal of the study was to improve the identification and selection of best-performing cotton through the combination of farmers' and researchers' selection criteria.genotypes in various growth environments. The study found that large bolls (> 5g), uniform boll split (to avoid numerous picks), short interboll distance (many bolls per fruiting branch), uniform short height (1.0-1.2m), more bolls per plant (>30), and low pest damage were among farmers' desired cotton qualities (bollworms and Jassid). During voting and focus group discussions, the farmers identified SN-96-5, 830-01-3, and 645-98-11 as their top performing genotypes. The farmers recorded 206 votes, 130 votes, and 129 votes, respectively, for each of these genotypes. Statistics were applied to the total seed cotton yield data from the researcher-managed (Mother Trial) and farmer-managed (Baby Trial) plots. The study's findings, which showed significant variations in genotype, environment, and interaction (Table),5) identified genotype SN-96-5 as the top performing genotype (P=0.04, P=0.001, and P=0.035, respectively). SN-96-5 was the most optimal, high-yielding, and reasonably stable genotype, according to AMMI and GGE biplots. Thus, it is advised that Zimbabwean producers release and use SN-96-5 for commercial purposes.

INTRODUCTION

In Zimbabwe, smallholder farmers grow the important cash crop known as cotton (Gossypium hirsutum L.).Due to its agricultural and industrial worth and the numerous products and byproducts it produces, cotton is a crop that is planted all over the world.

For the past ten years, smallholder farmers in Zimbabwe have noticed a reduction in the yields of seed cotton. As a result, various viewpoints have been expressed regarding the causes of yield decline, with some of them including the effects of climate change, the lack of improved varieties, and inadequate crop management techniques, including alternatives for managing pests, diseases, and agronomic factors [1].Due to this, the country's cotton production has decreased.influencing the stability of the national income and foreign exchange. Yet, the consequences of climate variability, such as extended mid-season dry spells, high temperatures, and severe disease and insect pressures, have had an impact on many countries that grow cotton. Despite the efforts of both public and commercial breeding programmes to reduce such unfavourable conditions through the creation of new kinds, delayed development has resulted in cotton producers becoming overly dependent on the old types, which are unable to survive the effects of climate change. Farmers in Zimbabwe are still cultivating outdated kinds that were introduced in 1998 and 2006, which poses a problem for the country's cotton production. It follows that Farmers have few alternatives for using modern, enhanced cotton genotypes that are tolerant of climatic variations. Through its efforts to implement the intervention strategies outlined in the Crops Research, Biodiversity, and Variety Development Sub-Program Performance Management Program (Government of Zimbabwe, Sub-program, Crops Research, Biodiversity, and Variety Development Template, 2021), where some improved advanced cotton varieties have been developed, the national breeding programme has been able to halt the situation.Review of the literature and the study's objectives In order to empower farmers and increase variety adoption, the national breeding programme has modified its variety trialling into a researcher-farmer collaboration [2]. This is in line with the National Development Plan 1 and the country's vision 2030, which clearly outline the need to strengthen on-farm trials and improve stakeholder participation [3]. It is noted in the document that it takes time to persuade farmers to accept new technology, which results in a slower adoption of new and better technologies.Like Kolech et al. [4], who reported that despite the development of new high-yielding and late blight-tolerant potato varieties, there has been less adoption of new types than anticipated. and the cotton industry faces the same situation. Fentahun et al[5] .'s participatory research on cotton included testing eight newly released cultivars. The research's findings highlighted the significance of taking farmers into account when choosing cultivars that thrive in their producing zones. This brings up important participatory research fundamentals that can be

significantly taken into account when assessing cotton varieties for early and prompt adoption by farmers. The project, which aimed to enhance the bonds already in place between farmers and researchers, establishes a framework for farmer involvement, which will in turn foster a sense of belonging and ownership for the research results produced [6]. This indicates that such strategies will increase farmers' motivation to practise innovation in their farming and cropping techniques. Farmers should be actively involved in cotton research so that they feel and understand what is happening become involved in the process of determining which technologies are most appropriate for their farming settings. This justifies significant improvements in productivity and production, leading to more sustainable agricultural changes and improved livelihoods. During the 2020–21 growing season, six cotton genotypes, including five advanced experimental lines and one commercial check variety (commonly grown by smallholder farmers), were assessed on farmers' fields in four important cotton production regions: Masakadza (Middleveld Region), Dande, Chibuwe, Tokwane, and Matikwa (Lowveld Region). Tables 1 and 2 respectively contain information on the site and genotype.The trial's Mother-Baby Method was used in its execution, and a Randomized Complete Block Design was used to duplicate the six genotypes twice (RCBD). Researchers chose the genotypes based on how well the candidates performed in multiple locations. In the baby experiment, each plot was planted in 8 rows measuring 8 metres long, but in the mother trial, each plot was planted in 6 rows measuring 6 metres long. We used a 0.3m intra-row spacing and a 1m inter-row spacing. This produced 208 plants per 64m2 plot, and the 36m2 net plot's seed cotton yield data was used for analysis.Data on total seed cotton yields were gathered from each site and subjected to an across-site analysis of variance (ANOVA) using Genstat 18th Version, with mean separation using the Least Signifi cance Difference (LSD) at a 5% probability level.The Genotype-Genotype x Environment (GGE) biplots and the Additive Main Effects and Multiplicative Interaction (AMMI) model were used for the stability analysis of the seed cotton yield. Due to the use of graphical presentations based on environment-centered Principal Component Analysis and double-centered Principal Component Analysis for GGE and AMMI, respectively, the two statistical analysis models are similarly identical [14]. The statistical analysis for the GGE and AMMI was carried out using Genstat 18th version. The AMMI analysis tries to explain the genotypic means, environmental means and their\sscores, stability value, genotypic and environmental average effectiveness and genetic stability. The average environment coordination (AEC) approach is used

in the GGE biplot to evaluate the seed cotton yield stability, optimum genotypes, specific adaptability, mega-environments, and winning candidates.

Participatory Variety-based descriptive statistics Candidate genotype SN-96-5 received the greatest score and was ranked first overall across all sites, with a total of 206 votes, according to selection by voting, which was conducted at each site [13]. Candidate genotype 645-98-11 was rated third after scoring a total of 129 points, whereas candidate genotype 830-01-3 was ranked second with 130 total points.In an effort to understand why farmers selected these top three possibilities out of a total of six genotypes, a Focus Group Discussion (FGD) was held. Most farmers reported that candidate SN-96-5 received high marks for having a significant number of large bolls, with an average of 35 per plant, as well as for experiencing uniform boll splitting, which is a crucial positive.Farmers require this quality in a variety. In addition to ensuring well-matured bolls in the first split, uniformity in boll splitting also allows farmers to endure fewer picks. the additional arguments made by farmers in favour of the same candidate contained low bollworm levels and a short interboll distance, which were both justified by the number of fruiting sites per sympodial branch.relative to other candidates, harm. Hence, when all of the justifications for choosing candidate genotype SN-96-5 were combined, they demonstrably demonstrated that the variety was more productive than the others [18]. At Dande and Chibuwe, where it was ranked first, and at Masakadza, Matikwa, and Tokwane, where it was ranked second, the candidate was the genotype that had won the race.Due to its uniform boll split and generally medium to big bolls, candidate genotype 830-01-3 was ranked second. The candidate produced 17 bolls on average per plant. According to the farmers' justifications, genotype 830-01-3 outperformed other genotypes in terms of overall yield.Third-placed candidate genotype 645-98-11 was praised by farmers for its medium height uniformity, medium-sized bolls, and short interboll distance. The check variety CRI-MS2 was one of the lowest three contenders, coming in at number four with 101 points, followed by candidate 83-01-4 at number five with 96 points, and candidate 85-01-1 at number three with 27 points. Farmers typically have several needs, but they can't all be met by a single variety, which is why diverse suites of varieties are chosen [19,20].According to an across-site analysis of variance, there were significant differences in the yield of seed cotton for the genotypic, environmental, and interaction effects (Table 4) (P = 0.04, P = 0.001, and P = 0.035, respectively). For genotypic, environmental, and interaction effects, the sum of squares

contributed 14%, 32%, and 12%, respectively, to total variation. This indicates that the environment contributed more to the performance difference among the varietals.Matikwa received the highest score, which equates to 2277kg/ha, followed by Chibuwe, Dande, and Masakadza with scores of 2046kg/ha, 2050kg/ha, and 1281kg/ha, respectively. When compared to CRI-MS2 and 83-01-4, which had mean yields of 2014kg/ha and 2008kg/ha greater than the overall average of 1971kg/ha, SN-96-5 had the greatest mean yield for seed cotton at 2415kg/ha.PC1 and PC2 each contributed 67.75% and 20.55%, for a combined contribution of 88.30%. The most desirable genotype, SN-96-5, was identified by the GGE comparison biplot as being close to the first concentric circle (Figure 2). The mean genotypic yield performance and stability were displayed in the GGE ranking biplot, demonstrating that SN-96-5 is a stable candidate with a high yield. This was made clear by its location on the far right following the Average Environment Coordinate (AEC) and by the fact that its perpendicular line to the Average Environment Axis is often somewhat short (Figure 3).Two macro environments—one with just a Tokwane site, the other with Masakadza, Dande, Chibuwe, and Matikwa—were shown on the GGE Scatter plot. SN-96-5 was conclusively the winning genotype for it.as it was situated on the vertex of that sector of the polygon's second segment. Findings based on IPCA 2 values in comparison to Total Seed The optimal genotypes for cotton mean yields (Figure 5) were the SN-95-6, 83-01-4, and check CRI-MS2 varieties .Biplot AMMI. This demonstrated the genotypes' stability and excellent yield. Based on their geographic locations, the genotypes 645-98-11, 830-01-3, and 85-01-1 were unstable and low-yielding. Matikwa, Dande, Tokwane, and Chibuwe were high yielding and highly interacting locations, making them ideal for genotypes with specialised adaptations.

Conclusion

The study demonstrated the significance of farmer preferences in Zimbabwe when choosing varieties for adoption and output. In particular, the study showed that farmers' involvement in various evaluation and selection processes, together with the researchers' selection criteria, result in relevant and reliable findings. Based on statistical data analysis (Mother-Baby Trial Data), the genotypes SN-96-5, 83- 01-4, and check CRI-MS2 showed higher adaptability and stability, while genotypes SN-96-5, 830-01-3, and 645-98-11 were observed and chosen as the best by farmers through Participatory Variety Selection (Use of farmer-preferred attributes). Due to genotype SN-96-5's producing performance and wider adaptability throughout

the test conditions, it is advised for commercial release.Even if the findings of the farmer evaluation via voting and focus group discussion revealed a similar trend for the best variety, Nonetheless, the author contends that greater analysis and development of technological methods for use by farmers in selecting the best varieties based on a certain characteristic is required. For instance, farmers may decide that a variety is the best based on large bolls (which are more weight-related), but if the bolls are weighed on a scale, they may not be as large as the farmers claim. This will result in a scientific conclusion that is easier to verify.

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