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Banana fibre yield and recovery in diversified farming systems of Uganda: Protocol, allometry and determinants

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ABSTRACT

The use of fibre from banana pseudo-stems is gaining traction globally. However, reliable tools for determination of banana fibre stocks and their determinants are lacking. We developed widely applicable allometric models for rapid evaluation of plant-level banana fibre yield and probed determinants for yield and recovery. A total of 346 pseudo-stems were purposively sampled from on-station and farmers' fields across four banana genomes (*AAA, AAA-EA, AAB, ABB*) at pre- and post-flowering growth stages. Fibre was mechanically extracted, sun-dried, stored and weighed to determine fibre yield and recovery, whose determinants were assessed using generalized mixed-effects models. Genome-specific allometric models for estimating fibre yield, based on variables measured within (*in-situ*) and outside the field (*ex-situ*), were fitted using multiple linear regression analysis. Mean dry fibre yield was 146 g plant^{-1} while recovery was 0.8%, highest in genomes *AAA* and *AAB*, respectively. Half of the ten developed models had a prediction accuracy (adj. R^2) ranging from 65% to 79%, highest for *AAA-EA* and *general* models for *in-situ* and *ex-situ* conditions, respectively. Genetic and morphological pseudo-stem traits were the top determinants of yield and recovery, while physiological and phenological traits were specific to yield and recovery, respectively. Assuming 0.8% fibre recovery and current machine efficiencies, seven pseudo-stems yield 1 kg of dry fibre. The dominant genome *AAA-EA* is a potential source of raw material as fibre traits were similar to genomes *AAB* and *ABB*, which are currently preferred for high fibre output by fibre producers.

1. Introduction

Successful transition to a bio-based economy is strongly dependent on a sustainable supply of sufficient amounts of raw material from biological resources. However, biomass availability remains the principle challenge affecting the global transition towards a bioeconomy to date (Antar et al., 2021; Chidozie et al., 2025). As such, there is growing interest in the utilization of biomass from agricultural residues to widen the source of raw material for the growing bio-based industry (IRENA, 2023; Kumar et al., 2022). The global fibre industry is no exception to this bioeconomic transition considering its renewed commitments to mitigate climate change through the use of alternative sustainable sources of raw material with wide industrial applications (Adhia et al., 2021; AL-Oqla et al., 2015; TextileExchange, 2024).

Utilization of natural fibres from agricultural residues, including banana (*Musa spp.*) pseudo-stem fibre, is becoming an attractive pathway to a sustainable fibre industry world over (Duque-Acevedo et al., 2020; Jayaprakash et al., 2022; Kumar et al., 2022). However, most of the options for natural fibre from agricultural residues have barely been exploited and banana pseudo-stem fibre is not an exception to this (Amrutha et al., 2019). Currently, there is a knowledge gap on the available, attainable, and potential fibre quantities from banana pseudo-stem residues and their associated production factors. In addition, there is a lack of reliable and efficient tools to rapidly quantify and periodically monitor banana fibre stocks in diverse cropping systems. The latter hinders the assessment of the spatio-temporal distribution of

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different biomass stocks needed to ascertain sustainable supply of raw material for the growing bio-based industry (Yang et al., 2021). In turn, it creates a bottleneck affecting innovation in research and marketing of bio-based products for emerging regional bioeconomies, like the one in East Africa (Kamusingize et al., 2025a).

The banana pseudo-stem (hereafter referred to as the stem) is a cylindrical structure of tightly compacted elongated leaf stalks, called sheaths, that rise from the soil and carry the leaves upwards while offering mechanical support to the plant (Speijer and De Waele, 1997). The sheaths contain vascular bundles made up of several thread-like structures (fibrils) that form the fibrous material commonly known as banana fibre, categorised among leaf fibres (Kozłowski and Mackiewicz-Talarczyk, 2020; Subagyo and Chafidz, 2020). In the Great Lakes region of East Africa, where Uganda is located, banana fibre is sourced from edible *Musa* genotypes cultivated for fruit production. These genotypes are hybridized from two wild *Musa* species, namely *Musa acuminata* and *Musa balbisiana,* and include diploids, triploids and tetraploids (Simmonds and Shepherd, 1955). In this study, we focus on the triploid genotypes in genome groups *AAA*, *AAA-EA*, *AAB,* and *ABB*, commonly sourced for banana fibre in Uganda (Kamusingize et al., 2025a). The potential for fibre yield and recovery, as key banana fibre traits, is poorly understood in edible bananas compared to other industrial crops grown for fibre, e.g. abaca (*Musa textilis*) (Bales et al., 1981; Bande et al., 2013) and cotton (Johnson et al., 2002; Ul-Allah et al., 2021). In this study, we define banana fibre yield as the total amount of fresh or dry fibre, in grams, extracted per stem. Fibre recovery is the proportion, in percentage, of the extracted dry fibre obtained from the fresh biomass of the extracted stem.

Beyond the effect of genotype (Paramasivam et al., 2022; Uma et al., 2007), banana fibre yield and recovery from *Musa spp*. is also dependent on stem phenology, growing conditions, and extraction techniques (Divya et al., 2016; Kozlowski et al., 2005). Considering phenology, banana fibre can be extracted from plants at all stages of growth, i.e., vegetative, flowering, and at bunch harvest stage, as long as the plant is at least 1.8 m tall, i.e., the current minimum requirement for stems purchased for fibre extraction in Uganda (Kamusingize et al., 2025a). However, harvesting stems before bunch harvest poses risks on food security for banana-dependent communities. In this study, we were particularly interested in exploring the influence on fiber yield and recovery of pre- and post- flowering stems. In relation to growing conditions, banana stems, like banana fruits, are also affected by various biotic and abiotic constraints that are detrimental to the quantity and quality of biomass. These constraints include pest damage, such as banana weevils (*Cosmopolites sordidus*) (Rukazambuga et al., 1998), diseases like fusarium wilt (*Fusarium oxysporum f. sp. cubense* (FOC) (Bastasa and Baliad, 2005; van Westerhoven et al., 2022), and environmental factors like drought (Nansamba et al., 2022; Taulya, 2013) affecting moisture content of the plant. Therefore, in addition to genetic and phenological traits, we also sought to explore the influence of morphological, physiological (moisture content), and plant health (FOC disease severity and weevil pest damage) traits on fibre yield and recovery.

Addressing sustainability aspects associated with the altered utilization of banana stems for fibre is also important to minimize the negative effect on other competing stem uses (Kamusingize et al., 2025a), especially continuous nutrient export which affects the productivity of the cropping system (Kema and Drenth, 2018; Rietveld et al., 2022). Therefore, next to assessing fibre recovery at plant level, we also considered it important to understand the variation in fibre recovery at sheath level with the aim of identifying plausible fibre extraction zones within the stem with the highest recovery. Leveraging such high fibre recovery zones for fibre extraction provides for recycling sheaths of low fibre recovery in the field as mulch. Therefore, we included sheath position among the morphological determinants of fibre recovery at sheath level.

Another key challenge to understanding these banana fibre traits relates to the lack of robust biomass assessment tools. In Uganda, banana fibre producers use visual assessments of the size and type (girth, height, and genotype), and fresh weight of the stem when purchasing stems for fibre extraction (Kamusingize et al., 2025a). Such methods are subjective and may result in poor assessments of the attainable fibre output, in turn affecting the price per stem paid to farmers. Use of allometric models, as a non-destructive technique, is considered effective for rapid assessment of crop biomass in the field (Niklas, 2004). However, there are hardly any studies on allometric models for predicting fibre yield in commonly grown fibre crops, such as cotton, ramie, hemp, and jute. Earlier attempts in this regard focused on leaf biomass in general, e.g. for sisal (Vuorinne et al., 2021). For banana, existing allometric models were developed to estimate bunch weight (Wairegi et al., 2009) and general plant biomass (Kamusingize et al., 2018; Nyombi et al., 2009), but not for fibre yield (Jayasinghe et al., 2022). The only existing allometric models developed to estimate fibre yield are for close relatives of banana, such as abaca (Armecin and Coseco, 2012) and *Ensete (Ensete ventricosum)* (Yemataw et al., 2021). However, these models are unsuitable for use in the genetically diversified banana cropping systems of Uganda (Gold et al., 1998; Karamura, 1999). The study by Armecin and Coseco (2012), conducted in the Philippines, considered only one genotype, *Musa textilis Nee* and a very small sample size of 15 plants. The study by Yemataw et al. (2021), conducted in Ethiopia, concluded that leaf and petiole length of the first outer green leaf, and plant height were the best predictors for fibre yield (adj. R^2: 0.35–0.57). Besides showing low predictive power, these predictor variables are not easy to measure in the field before plant harvest, i.e. *in-situ.* Beyond *in-situ* conditions, there are no studies that offer fibre yield predictors for stems already harvested from the field, i.e., for *ex-situ* conditions, a key tool we considered necessary to guide fibre producers during stem purchase. We considered easy-to-measure above-ground stem morphological traits (i.e., girth, height, fresh weight, and number of sheaths) as potential predictors of banana fibre yield, for both *in-situ* (i.e., within field) and *ex-situ* (outside the field) conditions.

In summary, with the growing potential of the banana fibre industry in East Africa, it was of paramount importance to develop accurate and informative allometric models for estimating fibre yield by different user groups (Jayasinghe et al., 2022). It was also important to understand the determinants underlying banana fibre traits at plant level to better target interventions for increasing fibre production. Specific to banana fibre extraction techniques, whether manual retting, mechanical, chemical or biological, the extraction protocols used to obtain the fibre in previous assessments (Armecin and Coseco, 2012; Bekraoui et al., 2022) were neither clear nor reproducible. Hence, a standardized fibre extraction protocol was needed for the reproducibility of study findings. Therefore, as a novel contribution of our study, we addressed these afore-mentioned limitations paving way to harness the potential of edible bananas for fibre production at scale.

This study, therefore, aimed at developing robust allometric models for rapid evaluation of plant-level fibre yield based on predictors that are easy to measure, and probing the underlying determinants for both yield and recovery in diversified banana production systems of Uganda. Specifically, we: (i) Quantified extractable dry fibre yield and recovery in banana stems of different genomes and at different growth stages; (ii) Derived allometric models for predicting extractable dry banana fibre yield, and (iii) Assessed underlying determinants for banana fibre yield and recovery. We hypothesised that banana fibre yield and recovery are not only dependent on the genome group but also on the growth stage of the plant (objective i). A second hypothesis was that the mean differences between observed and predicted dry fibre yields are negligible across genomes assessed in diverse banana cropping systems for both *in-situ* and *ex-situ* conditions (objective ii). Thirdly, we hypothesized that beyond the genetic and phenological traits of the plant, fibre yield and recovery were also strongly influenced by stem morphological, health and physiological traits (objective iii). For simplicity, we restricted morphological traits to *ex-situ* predictors when assessing determinants of

yield and recovery at plant level, and sheath position for recovery at sheath level.

The rest of the paper is organized as follows: 2 describes the data sources and methods used to arrive at the study findings presented in 3. Implications of these findings are discussed in 4 and concluding remarks presented in 5. Additional information on Sections 2 and 3 is presented in supplementary material attached.

2. Materials and methods

2.1. Site description

The study was conducted in major banana growing areas of Uganda, specifically Southwestern, Western, and Central regions (Ochola et al., 2022) (Fig. 1). In Central region, data were collected mainly from on-station banana breeding blocks of the National Banana Research Program at the National Agricultural Research Laboratories (NARL-Kawanda) Institute, Wakiso district (Fig. 1C). A few genotypes missing at NARL-Kawanda were sampled from a nearby farmer's field. On-station fields were considered due to availability of sufficient stems of different genotypes, growing under similar conditions, required for model calibration. In Western and Southwestern regions, data were obtained from farmers' fields in Rwimi (Fig. 1A) and Birere (Fig. 1B) sub-counties located in Bunyangabu and Isingiro districts, respectively. Banana production systems across these sites experience different biophysical, agronomic management, and socio-economic characteristics (Table A.1). Therefore, data obtained on-farm were used to validate how well the allometric models, calibrated with on-station data, captured underlying variability across regions.

2.2. Data collection

Data underlying this study were collected in 2023 and are available in the 4TU research data repository (Kamusingize et al., 2025b).

2.2.1. Fibre extraction protocol

Fibre extraction was done through a mechanical process, commonly used in Uganda (Kamusingize et al., 2025a), using a locally fabricated diesel engine-powered decorticating machine (Model R175A, with maximum rating output of 7Hp/2600 RPM). This study built on existing information on the commonly used mechanical process of extracting banana fibre (Bekraoui et al., 2022) and developed a more robust and reproducible protocol, particularly for research purposes. We added new elements to the protocol based on results of preliminary assessments (Appendix A.2), stakeholder consultations, field observations, and literature review.

Preliminary assessments involved determining the most suitable point to cut the stem for extraction. The aim was to facilitate smooth separation of sheaths without splitting the stem into two halves, a common practice in Uganda which results into unequal parts of a given sheath, some too small to extract in the machine. In addition, this practice makes it difficult to identify sheath position, a variable that was of interest in this study. We considered cutting the stem at 30 cm height above the root collar as the most ideal point (Appendix A.2.1).

We then established a standardized dry fibre state to minimize variation in data due to the hygroscopic nature of banana fibre, i.e. the tendency to regain moisture after drying (Subagyo and Chafidz, 2020). Most banana fibre studies considered sun drying (Bekraoui et al., 2022; Madhushani et al., 2022; Mumthas et al., 2019), yet oven-dried weight was the standard method in biomass-related allometric studies (Picard et al., 2012). Therefore, this study tested the difference in moisture content of dry fibre samples under different drying treatments, i.e., sun drying and in storage for 24 hrs, 48 hrs, 72 hrs, and 96 hrs in reference to the oven dried standard method (Govett et al., 2010). Oven drying was done on already sun-dried and stored samples at 60 °C for 8 h to dry the samples to a constant weight in a laboratory at NARL-Kawanda. These oven drying conditions were considered ideal to avoid negatively impacting the quality of the samples (Houghton et al., 2009). Based on the findings (Appendix A.2.2), the protocol considered dry weight in storage at room temperature, after sun drying, recorded after at least three days.

The improved step-by-step protocol for extracting decorticated banana fibre is presented in Fig. 2. Detailed considerations and limitations for each step are provided in supplementary material (Appendix A.2.3). No fibre pre-processing method, such as washing, was done before sun drying to remove impurities, such as gum and traces of non-fibrous material, often contained in banana fibre produced by a decorticator machine (Subagyo and Chafidz, 2020).

2.2.2. Plant sampling and measurement

Banana plants were purposively selected and tagged before destructive sampling. These included genotypes representing four genome groups and different purposes: *AAA* (*Bogoya / Gros michel*) and *AAB* (*Sukari ndizi*) as dessert bananas; *ABB* (*Kayinja / Pisang awak*), a juice banana; and *AAA-EA* (*Mbwazirume*, *Musakala*, *Nakitembe*, *Mujuba*, *Enshenyi,* and *Enzirabahima*), the cooking (*matooke*) bananas. We considered plants at two phenological growth stages, i.e., pre-flowering and post-flowering. The pre-flowering stage was characterized by emergence of a cigar leaf,[1] and the post-flowering stage by either a visible flower bud or bunch. In both growth stages, only plants $\geq$ 1.8 m height were selected. A total of 30 plants per growth stage per genome was obtained for the on-station sampling, except for the *AAB* genome group with 27 plants at pre-flowering stage due to scarcity. On-farm, 5 plants per growth stage per genome per site were obtained from 37 farmers' fields (20 fields in Birere and 17 in Rwimi). Overall, 346 stems were extracted, including 237 from on-station for quantification of fibre yield and recovery and allometric model calibration. One hundred and nine (109) stems were obtained from farmers' fields for model validation only. These stems combined resulted in a total of 5060 dry fibre sheath samples.

Prior to destructive sampling, stem morphological traits, i.e., girth (at root collar, at 30 cm, and 100 cm height above the soil surface) and height (total and extractable) were recorded *in-situ* as potential fibre yield predictors. All other variables were recorded *ex-situ*, including stem fresh weight, number of sheaths and their position and fresh weight, extracted fresh and dry weight of fibre, and severity of weevil pest damage and fusarium wilt disease (Rhizome Discoloration Index – RDI score). Stem height was considered as the length from the root collar to the point of insertion of the uppermost pair of leaves. Height of the extractable stem was the length from the 30 cm point above the root collar to the point of attachment of the oldest live pair of leaves. Sheath position was systematically assigned in ascending order from outwards towards the central core of the stem. The plant health indicators were assessed based on existing field assessment guidelines (Rukazambuga et al., 1998; Viljoen et al., 2017). Additionally, a representative composite sub-sample (250 g) of stem fresh biomass was obtained from residues of the fibre extraction process (Fig. 2, Step 5) and oven dried at 105 °C for 24 h to estimate stem moisture content using the oven method at the NARL-Kawanda laboratory.

2.3. Data processing and analysis

Data were processed and analysed following a systematic approach (Fig. 3) detailed below.

Prior to analysis, volume of the extractable stem, as a proxy for stem volume, was computed using the formula of a cylinder, given the cylindrical form of the banana stem (Sango et al., 2018; Speijer and De Waele, 1997), with girth at 30 cm height above root collar and extractable height. Combining predictors is used in allometric modelling

[1] The description of cigar leaf is at https://www.promusa.org/Banana+leaf

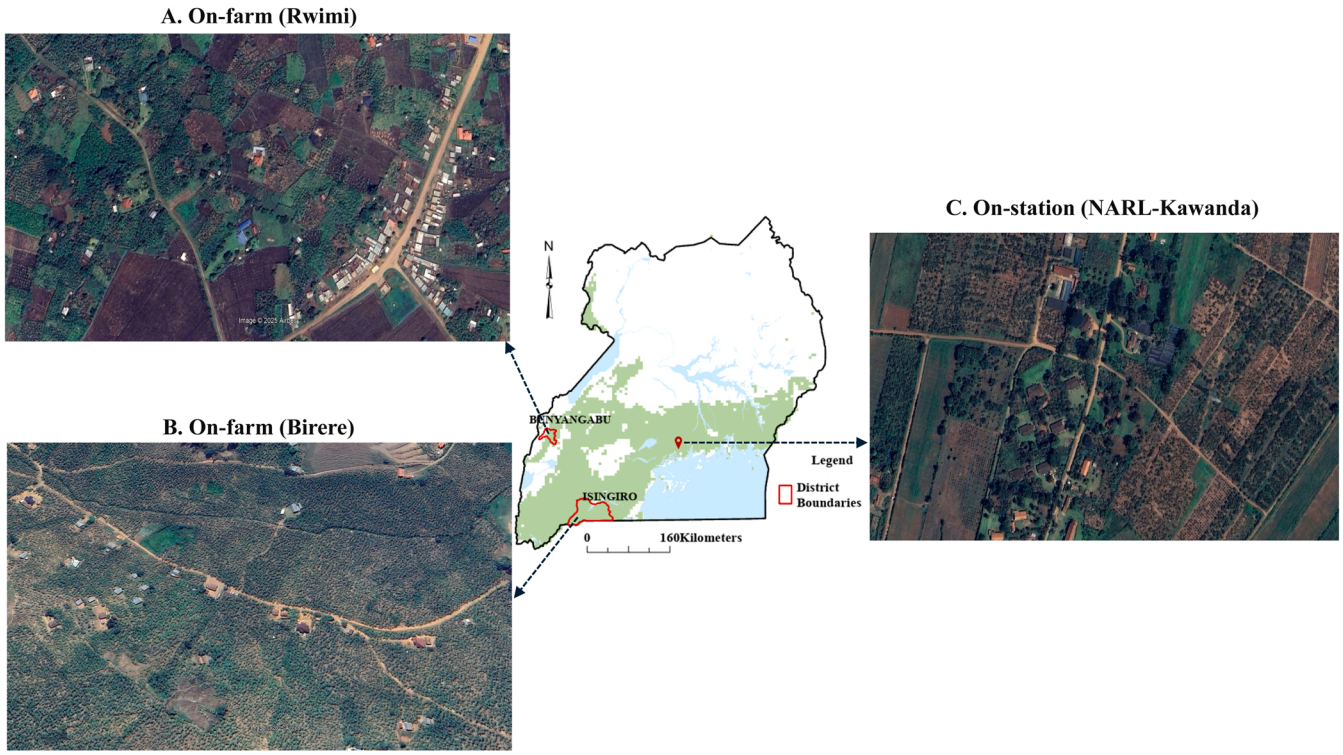

Fig. 1. Banana distribution map of Uganda (Ochola et al., 2022) showing landscapes of diversified banana cropping systems selected as study sites for allometric model calibration (on-station) and validation (on-farm). Representative landscape images were obtained using Google Earth pro imagery taken in 2024. Landscapes shown for Rwimi and Birere are for Kadindimo and Kahenda villages, respectively. Kandindimo shows diverse cropping land uses while banana monoculture fields dominate in Kahenda. Map lines delineate study areas and do not necessarily depict accepted (sub)national boundaries.

to improve model prediction accuracy (Vuorinne et al., 2021) or deal with issues of multi-collinearity (Wairegi et al., 2009). Fibre recovery at sheath level was computed by dividing the dry fibre yield per sheath by its fresh weight (Silla et al., 2019). Fibre recovery at plant level was computed as the sum of dry fibre yield per plant divided by the fresh weight of the extracted stem. All variables were checked for data

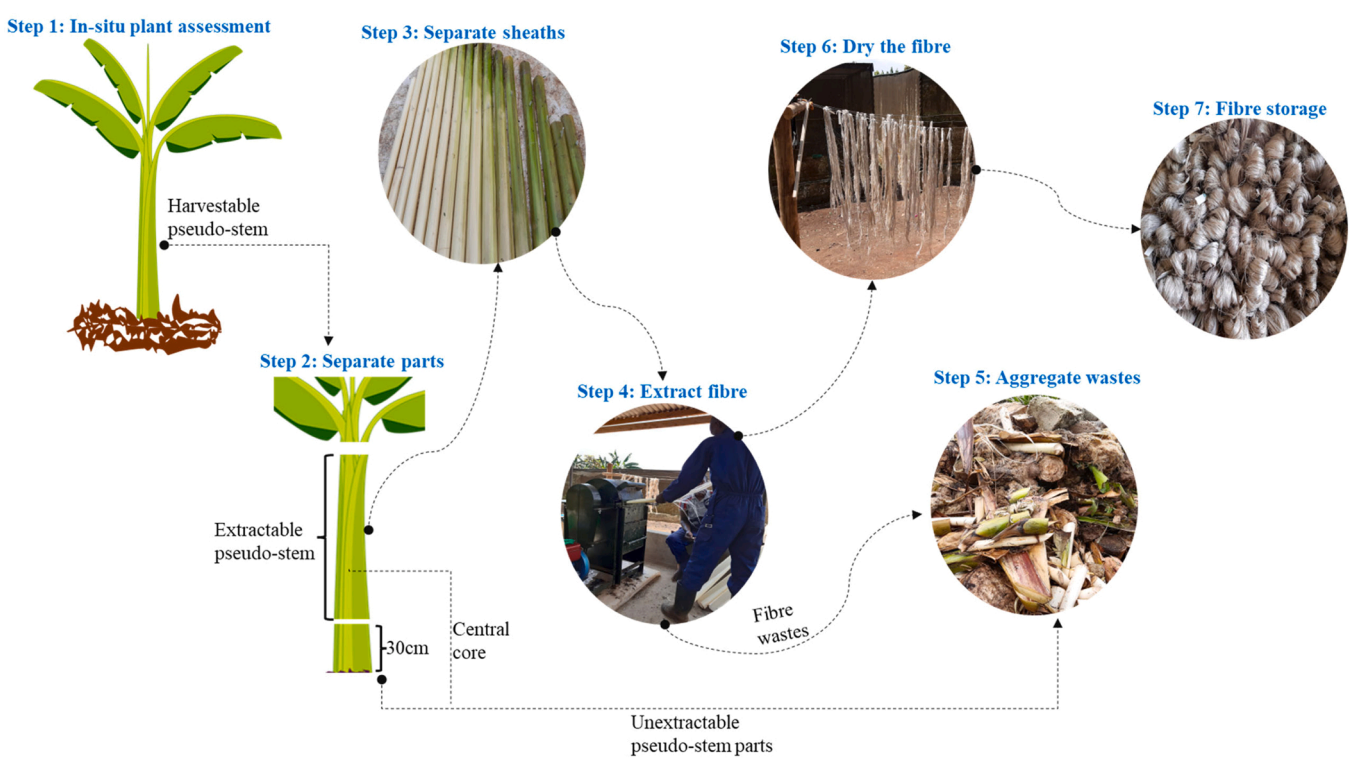

Fig. 2. An improved generalized step-by-step protocol for extracting decorticated banana fibre.

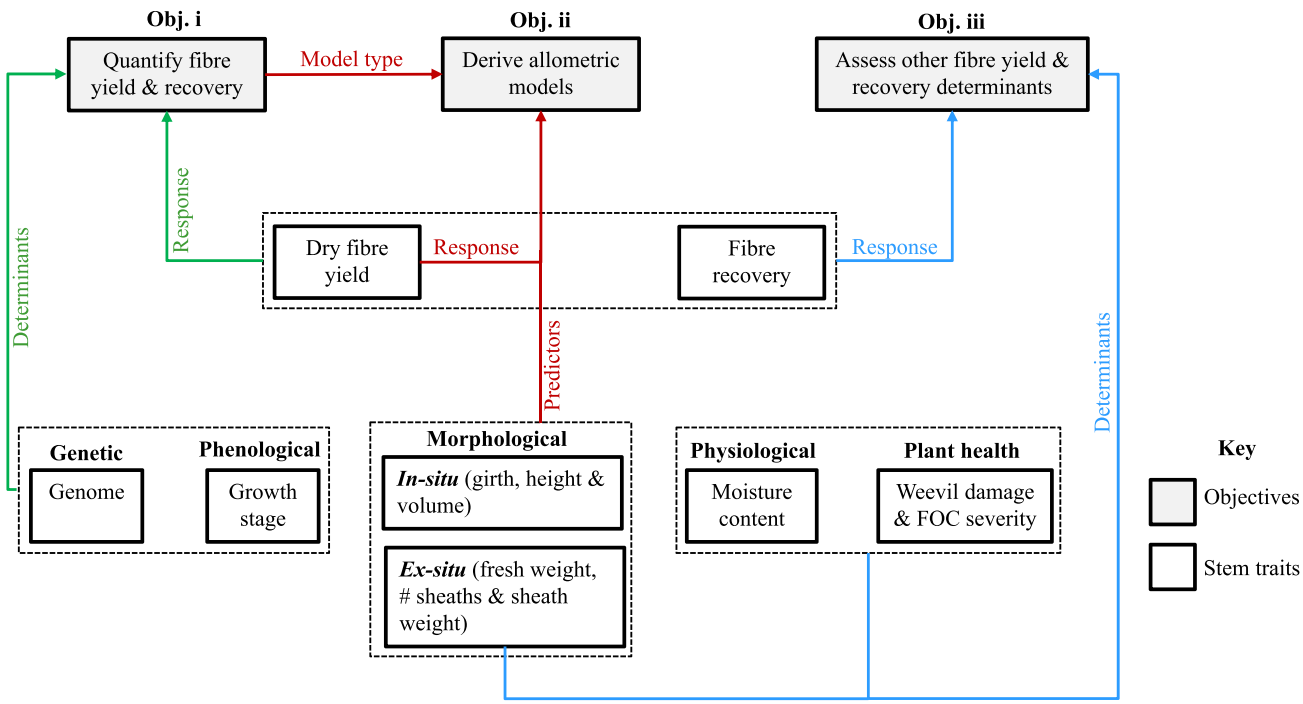

Fig. 3. Schematic flow diagram showing the data analysis procedure for each objective. The colour coding of connecting lines shows the data requirements per objective, i.e., green (Objective i), red (objective 2) and blue (objective 3). Whereas sheath position was one of the morphological determinants for fibre recovery at sheath level it was not part of the potential predictors of fibre yield, thus not included in the figure.

anomalies, such as missing values and outliers, prior to analysis.

Data analysis was executed in R (v4.3.1) software. Descriptive and multivariate methods were used to summarize stem traits and visually explore relationships between dry fibre yield or recovery with other variables. Specific to stem traits, Principal Component Analysis (PCA) in packages *FactoMineR* and *Factoextra* (Kassambara and Mundt, 2017; Lê et al., 2008) was used to summarise and visualize the correlations of variables across genomes. Prior to testing any hypothesis, the *Shapiro-wilk* test for normality was conducted on the response variables, i.e. fibre yield or recovery. Using on-station data only, generalized linear mixed-effects models, in packages *lme4* with link function *gamma* (Bates et al., 2015) for fibre yield and *glmmTMB* with link function *beta* (Brooks et al., 2017) for fibre recovery, were used to statistically test the effect of genome and growth stage on dry fibre yield or recovery, with field ID as a random effect (Objective i) (Model 1).

$$Model\ 1: \ Dry\ fibre\ yield\ (g)\ or\ Fibre\ recovery\ (\%) \sim Genome + Growth\ stage + (Genome \times Growth\ stage) + (1|Field\ ID) + \varepsilon$$

To derive allometric models for predicting dry banana fibre yield (Objective ii), we used on-station data for model calibration and on-farm data for model validation following a stepwise approach. In the first approach, fixed factors with significant effects from Model 1 were used to determine the type and number of predictive models needed. Deriving predictive models by these factors was intended for practitioners in the fibre industry to easily know the right model to select for estimating fibre yield based on the plant genetic and phenological characteristic of choice. In the second approach, we separately selected predictors of dry fibre yield, for both *in-situ* and *ex-situ* conditions, following a set of criteria: a) a Pearson correlation matrix was used to select potential variables showing moderate to high, and significant correlation coefficients (≥ 0.3) with dry banana fibre yield; b) independence among predictors to minimize cases of collinearity using the Variance Inflation Factor (VIF) method, considering predictors with a VIF < 10 (Vittinghoff et al., 2012); and c) significant individual predictors or their combination with the highest coefficient of determination (adj. R^2) based on the *all-possible* variable selection approach in package *Olsrr* (Hebbali and Hebbali, 2017) using a multiple linear regression model. In the third approach, we fitted various types of regression models, including linear, polynomial, exponential, logarithmic, and power models, to identify the best-fitting predictive model. Finally, after calibration with the on-station data, model selection was based on its prediction accuracy, i.e., how well a model predicted independent on-farm data during validation. All potential models were evaluated using statistical metrics, such as adj. R^2, root mean square error (RMSE), and visual diagnostics (1:1 identity line and residual plots). We selected models with the highest adj. R^2, a close alignment of predicted values to the 1:1 line, and residuals randomly scattered around the reference line. Finally, using on-farm data only, we evaluated the differences in means of dry fibre yield between observed and predicted values for the selected models with a paired *t*-test statistic to test the second hypothesis. The Wilcoxon non-parametric test was used for cases where the data were not normally distributed.

To assess determinants of fibre yield and recovery (Objective iii), all numeric explanatory stem traits were scaled using the function *scale()* in R and later checked for collinearity prior to hypothesis testing. Then, generalized mixed-effects models were used to test the influence on fibre yield or recovery of potential determinants as fixed effects, varying at plant (Model 2) and sheath (Model 3) level, with field ID and plant number as random effects where necessary.

$$Model\ 2: Fibre\ yield\ (g)\ or\ Fibre\ recovery\ (\%)_{plant} \sim Weevil\ damage + Fusarium\ score + Moisture\ content + No.\ extracted\ sheaths + Extractable\ stem\ fresh\ weight + (1|Field\ ID) + \varepsilon$$

$$Model\ 3: Fibre\ recovery_{sheath} \sim Weevil\ damage + Fusarium\ score + Moisture\ content + Sheath\ position + (1|Plant_No/Field_id) + \varepsilon$$

Across all statistical models, we used the *Anova* function in the *car* package (Fox and Weisberg, 2018) to estimate the level of significance associated with the fixed effects from mixed-effects model results.

Finally, a *Tukey's* post *hoc* test, using the package *emmeans*, was used to identify significant pairwise differences in fibre yield or recovery across genomes and growth stages.

3. Results

3.1. General stem characteristics

In general, the two first components of a PCA for the banana stem traits assessed explained 73% of the total variation (Fig. 4). Across all genomes, mean and standard deviation of fresh and dry fibre yield per plant were 512 ± 242 g and 146 ± 66 g, respectively (Table B.1). Fibre recovery per plant was 0.8 ± 0.3% of fresh biomass of the extracted stem. With this recovery, seven plants, on average, are needed to obtain 1 kg of dry fibre. Specifically, in Fig. 4, genome *AAA* stood out with high values for traits, such as girth, height, weight, and fibre yield. In contrast, genome *AAB* showed low values for these traits but exhibited high levels of FOC disease severity and fibre recovery. Genome *AAA-EA* demonstrated high levels of moisture content, while genome *ABB* did not display any extreme values in the traits assessed. Banana weevil damage, being negligible (0–5%), was not particularly correlated with any genome. Therefore, despite observing high and low values in stem traits for genomes *AAA* and *AAB*, respectively, there was no single trait that showed similar values or distinctly differentiated all the four genomes.

3.2. Extractable dry fibre yield and recovery

Overall, average dry fibre yield per plant, aggregated across growth stages, ranged between 121 g for *AAB* and 205 g for *AAA* (Fig. 5 and Table B.1). Between growth stages, the mean dry fibre yield was 147 g and 145 g for post- and pre-flowering stages, respectively (Table B.2). Within-genome variability in fibre yield was also wide in plants of the *AAA* genome, especially those at post flowering stage, and small in plants for the *AAB* genome compared to other genomes (Fig. 5). Fibre yield differed significantly across genomes and only marginally (non-significant) between growth stages (Fig. 5, Table 1 and Table B.3). The interactive effect of genome and growth stage was non-significant (Table 1). Based on these results, we developed ten allometric models to predict dry fibre yield, i.e., a general model combining all genomes, and one model per genome for both *in-situ* and *ex-situ* conditions separately.

The mean fibre recovery per plant ranged between 0.6% and 1.4%, being highest in genome *AAB* and stems at pre-flowering stage compared to other genomes and stems at post flowering stage (Fig. 6, Table B.4). Similarly, within genome variability in fibre recovery was also wide in plants of the *AAB* genome, especially those at pre-flowering stage, compared to other genomes (Fig. 6). Unlike fibre yield, recovery was significantly different across genomes and growth stages, and the interaction effect was also significant (Fig. 6, Table 2). Further exploration with pairwise comparisons (Table B.5) showed that recovery was significantly higher in the *AAB* genome compared to the others. Significant differences between growth stages were observed in *AAB* and *AAA* genomes.

At sheath level, the overall mean and standard deviation of fibre recovery across genome and growth stage was 1.2 ± 0.5%, with highest values observed in *AAB* for both growth stages compared to other genomes (Fig. 7A and Table B.6). Similar to fibre recovery at plant level, within-genome variability in fibre recovery at sheath level was also wide in plants of the *AAB* genome, compared to other genomes (Fig. 7A). Within the stem, however, we observed minimal variations in fibre recovery with increasing sheath position (Fig. 7B), indicating the absence of a high fibre recovery zone worth targeting during fibre extraction. Similar to fibre recovery at plant level, recovery at sheath level was also

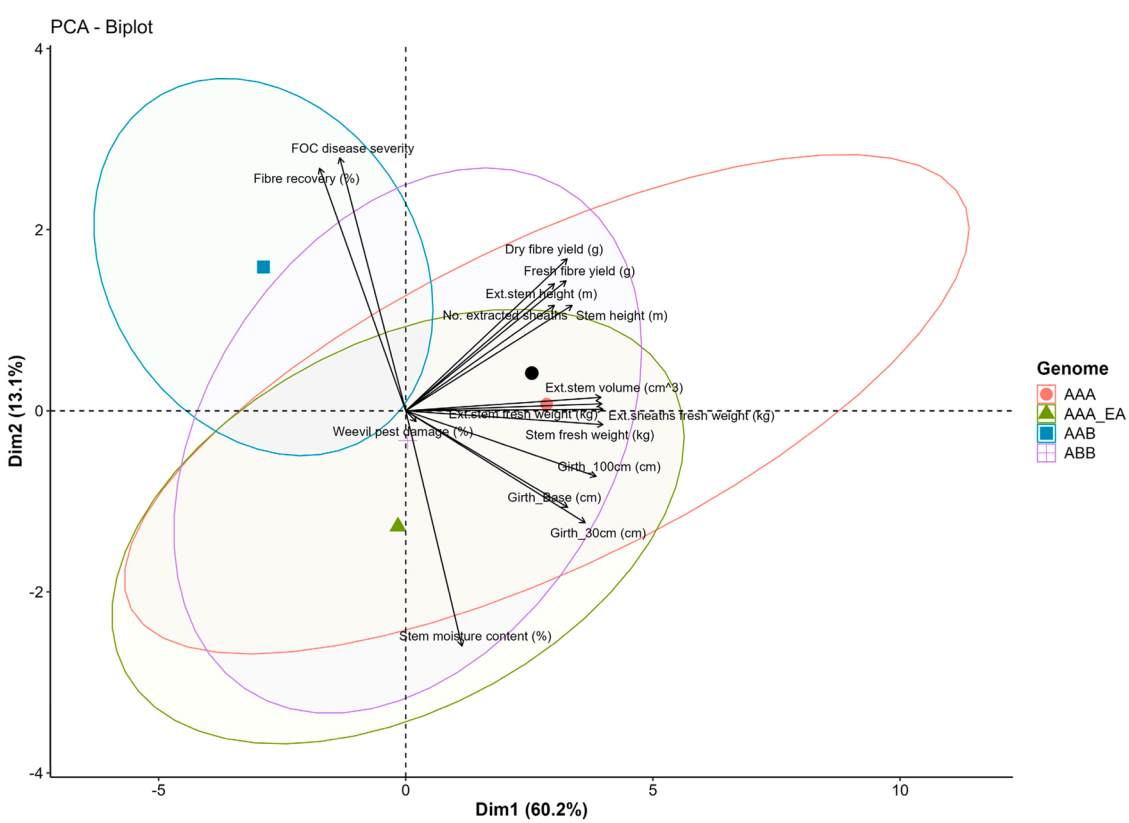

Fig. 4. Results of the principal component analysis (PCA) showing the amount of variability explained across genomes by banana stem traits assessed, and the correlation of these traits with genomes using data sourced from on-station only. The black dot shows the centroid position of all genomes combined. Other coloured shapes are the centroids for the specific genomes, i.e., red circle (*AAA*), green triangle (*AAA-EA*), blue square (*AAB*) and a purple square (*ABB*).

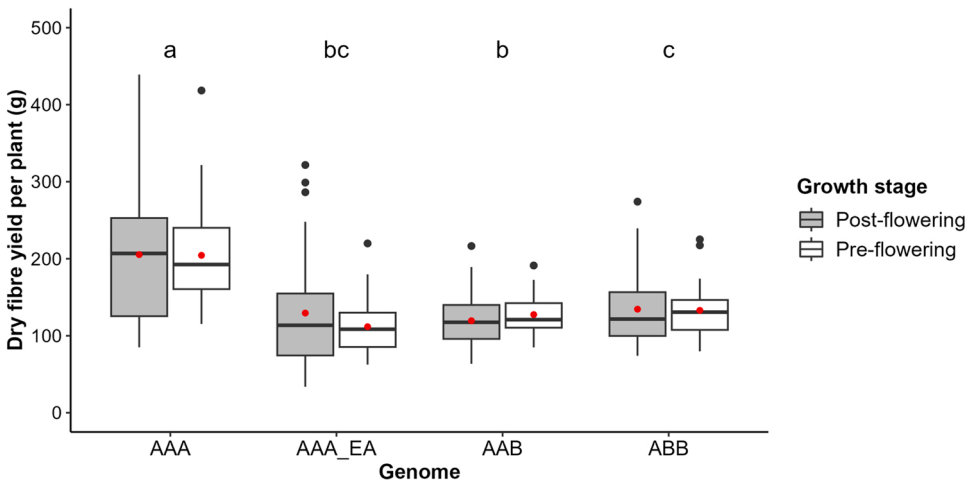

Fig. 5. Variation in yield per plant of extracted dry banana fibre across genomes and plant growth stages of banana stems sourced from on-station. The red dot denotes the mean value per genome and growth stage while the letters indicate significant differences in mean yield between genomes aggregated across growth stages.

Table 1
Anova results of the generalized linear mixed effects model of dry banana fibre yield per plant (g) across genome and plant growth stage for banana stems sourced from on-station. Df refers to the degrees of freedom while p-values indicate the significance level.

Fixed effect	Chisq	Df	p
Genome	74.11	3	**< 0.001**
Growth stage	4.99	1	**0.025**
Genome × Growth stage	5.55	3	0.136

significantly different across genomes, plant growth stages, and their interaction (Table 3).

In summary, whereas both banana fibre yield and recovery vary significantly across genomes, only recovery varies significantly across plant growth stages. Sheath position plays a minimal role in determining fibre yield along the banana stem.

3.3. Allometric models for predicting extractable dry banana fibre yield

3.3.1. Selection of predictors

Exploration, through correlation matrices, of the relationships between variables (Fig. B.2) for both *in-situ* and *ex-situ* conditions showed differences in Pearson correlation coefficients between dry fibre yield and potential predictors (Table 4). Highest coefficients were observed for all genomes combined and the *AAA-EA* genome for *in-situ* and *ex-situ* conditions, respectively. The predictors selected for model calibration had correlation coefficients ranging between 0.56 – 0.75 and 0.57 – 0.82 for *in-situ* and *ex-situ* conditions, respectively, but also met all other criteria described in 2.3. In summary, predictors varied across models for *in-situ* conditions, while for *ex-situ* conditions, the predictors '*Extractable fresh weight*' and '*number of extracted sheaths*' were the most important across board.

Table 2
Anova results of the generalized linear mixed effects model of banana fibre recovery per plant (%) across genome and plant growth stage for banana stems sourced from on-station. Df refers to the degrees of freedom while p-values indicate the significance level.

Fixed effect	Chisq	Df	p
Genome	86.8	3	**< 0.001**
Growth stage	50.0	1	**< 0.001**
Genome × Growth stage	31.9	3	**< 0.001**

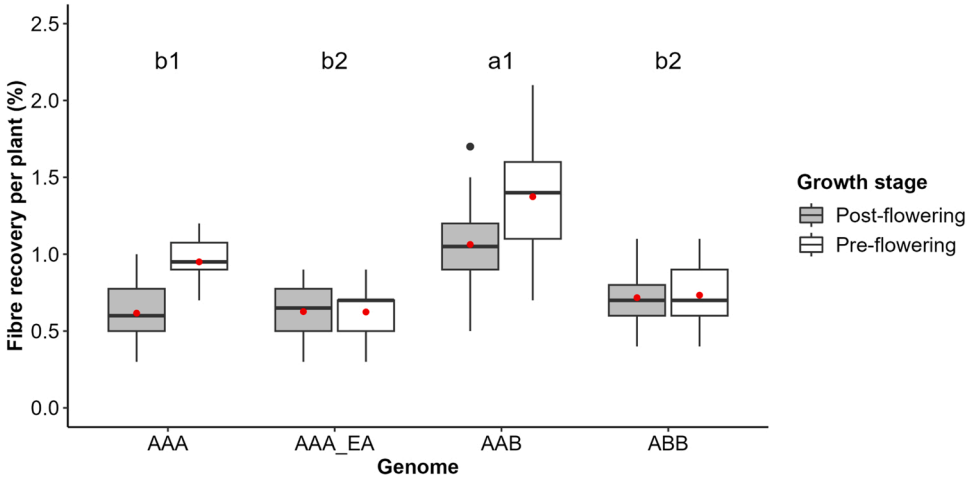

Fig. 6. Variation in banana fibre recovery per plant across genome groups and plant growth stages for banana stems sourced from on-station. The red dot denotes the mean value per genome and growth stage while the values above each group of boxes denotes the significant difference. Letters indicate differences in fibre recovery between genomes. Numbers indicate differences between growth stages within a genome where 1 means significantly different and 2, not different.

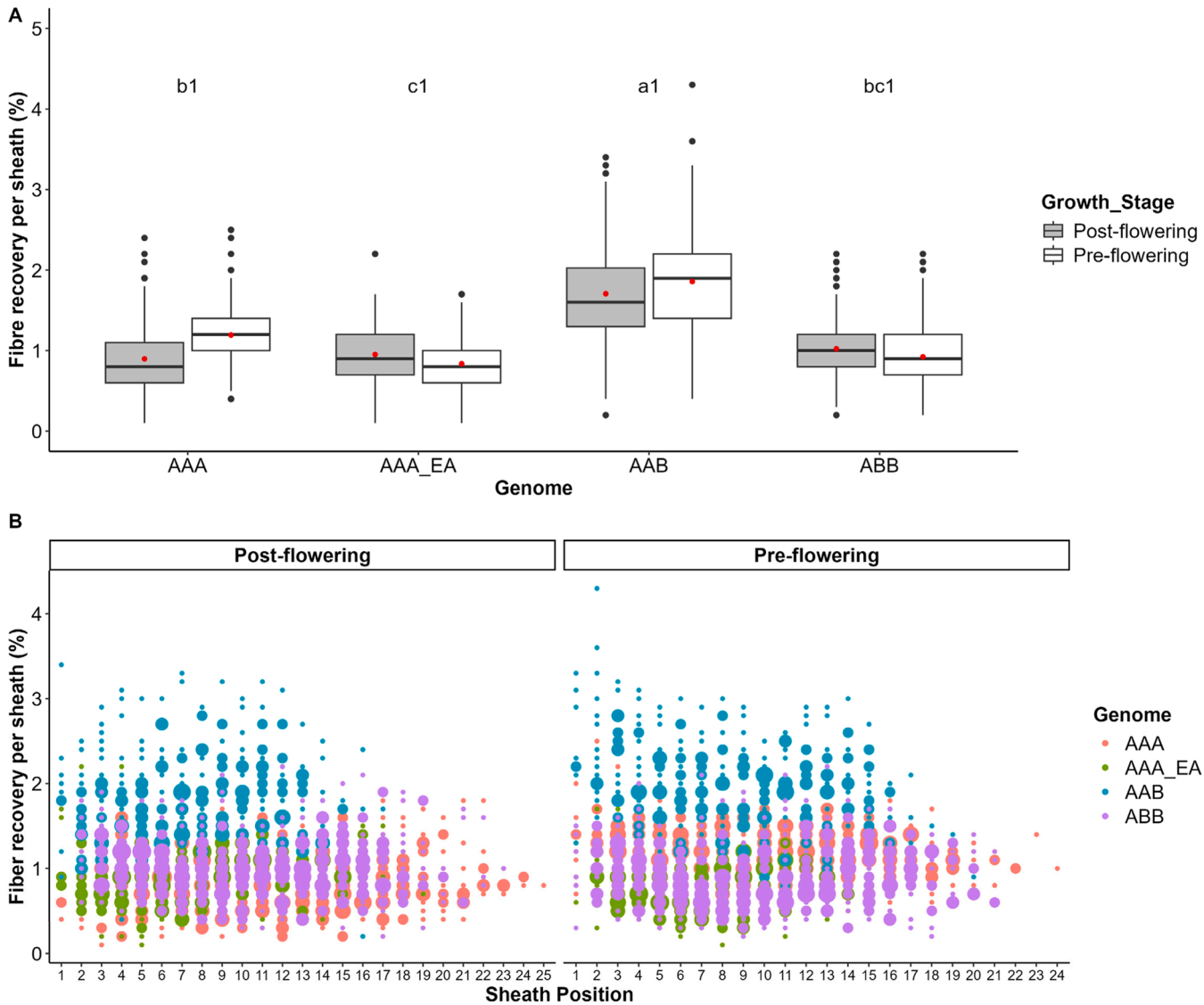

Fig. 7. Variation in fibre recovery per sheath (%) across genome and plant growth stage (A), and variation between fibre recovery and sheath position within the banana stem from outwards towards the central core (B). In figure A, the red dot denotes the mean value for fibre recovery per sheath while the values above each group of boxes denotes the significant difference. Letters indicate difference in fibre recovery between genomes. Numbers indicate difference between growth stages within a genome where 1 means significantly different. In figure B, the size of the dot denotes the number of points at the same sheath position with the same value of fibre recovery. The smallest dot represents 2 sheaths, and the biggest dot represents 8.

Table 3
Anova results of the generalized linear mixed effects model of banana fibre recovery per sheath (%) across genome and plant growth stage for banana stems sourced from on-station. Df refers to the degrees of freedom while p-values indicate the significance level.

Fixed effect	Chisq	Df	p
Genome	918.4	3	**< 0.001**
Growth stage	119.4	1	**< 0.001**
Genome × Growth stage	169.0	3	**< 0.001**

3.3.2. Model calibration and validation

We evaluated five allometric model types (linear, polynomial, exponential, logarithmic, and power) during the calibration and validation process (Table B.7 and Figs. B.3 to B.7). 40% of the selected models were based on linear functions (Table 5). Half of the selected models had a prediction accuracy (adj. R^2) ranging from 65% to 79%, highest in *AAA* and *General* models for *in-situ* and *ex-situ* conditions, respectively (Fig. 8). Poor model accuracy (adj. R^2) was observed in *AAB* models, with highest values at 15% and 37% for *in-situ* and *ex-situ* conditions, respectively. Below are the equations for the allometric models selected and their coefficients (Table 5) for both *in-situ* and *ex-situ* conditions:

$$\text{Simple linear}: y = a + b\,x \tag{1}$$

$$\text{Multiple linear}: y = a + b_1x_1 + b_2x_2 \tag{2}$$

$$\text{Power}: \ln(y) = a + b_1.\ln(x_1) + b_2.\ln(x_2) \tag{3}$$

$$\text{Logarithmic}: y = a + b.\ln(x) \tag{4}$$

$$\text{Logarithmic}: y = a + b_1.\ln(x_1) + b_2.\ln(x_2) \tag{5}$$

$$\text{Exponential}: \ln(y) = a + b_1x_1 + b_2x_2 + b_3x_3 \tag{6}$$

Where: y denotes the predicted dry banana fibre yield, a is the intercept, and b is the coefficient of the predictor variable x. Power, logarithmic and exponential functions are presented as linear models

Table 4
Pearson correlation coefficients between potential predictors for model calibration and dry banana fibre yield (g) for banana stems sourced from on-station. In bold are the predictors selected for each calibration model per condition. ns denotes predictors not significantly associated with dry banana fibre.

		Genome				
Condition	**Predictor variable**	**General**	**AAA**	**AAA-EA**	**AAB**	**ABB**
In-situ	Girth at base (cm)	**0.59**	0.62	0.41	**0.63**	0.53
	Girth at 30 cm (cm)	0.61	**0.75**	0.53	0.68	0.60
	Girth at 100 cm (cm)	0.68	0.75	**0.70**	0.68	**0.67**
	Total height (m)	0.67	0.54	0.77	0.23 ^{ns}	**0.56**
	Extractable height (m)	**0.62**	0.55	**0.67**	0.07 ^{ns}	**0.59**
	Extractable volume (cm^3)	0.75	0.70	0.77	0.66	0.70
Ex-situ	Total fresh weight (kg)	0.74	0.70	0.78	0.63	0.68
	Extractable fresh weight (kg)	**0.74**	**0.68**	**0.82**	**0.57**	**0.68**
	No. extracted sheaths	**0.73**	**0.76**	**0.81**	**0.58**	0.60
	Extracted sheaths fresh weight (kg)	0.77	0.75	0.82	0.68	0.67

with logarithmic transformed variables.

Across sites, the observed mean dry fibre yields collected from farmers' fields (Table 6) were generally higher than on-station for all genomes (Table B.1). Fibre yields were higher by 16 – 54% and 6 – 45% in Birere and Rwimi, respectively. Model accuracy varied considerably across sites (Table 6), with 80% and 60% of the genomes showing similar mean values ($p > 0.05$) between predicted and observed fibre yields in Birere, and 60% and 100% in Rwimi, for *in-situ* and *ex-situ* conditions, respectively.

3.4. Determinants of fibre yield and recovery

In addition to the genetic trait (Table 1), physiological and morphological effects explained part of the variation in fibre yield at plant level (Table 7 and B.8). Contrary to fibre yield, the variation in fibre recovery at plant level was significantly explained by morphological traits only (Table 7 and B.9), in addition to genetic and phenological traits (Table 2). Also, whereas an increase in stem fresh weight positively increased fibre yield, it resulted in a negative effect on fibre recovery (Table 7). At sheath level, variation in fibre recovery was significantly explained by all traits, i.e., morphological, physiological, and plant health traits (Table 7 and B.10), in addition to the genetic and phenological traits (Table 3). Notably, plant health traits showed divergent effects in explaining the variation in both fibre yield and recovery at plant and sheath levels, i.e., a negative effect of weevil damage and positive effect of FOC disease severity (Table 7). However, these traits were not significant at plant level. Overall, genetic and morphological pseudo-stem traits were the top determinants of yield and recovery, while physiological and phenological traits were specific to yield and recovery, respectively.

4. Discussion

4.1. Variability in banana fibre yield and recovery

Dry banana fibre yield per plant of edible bananas, ranging between 121 g to 205 g, was in the same range as that of other *Musa* species, like abaca (117 g – 573 g) (Armecin and Coseco, 2012), of which fibre is the main product. This fibre yield is associated with plant morphological traits, e.g. girth, height, weight, and number of sheaths related to biomass yield in general. Our findings also show that fibre yield of *AAA-EA* genome is similar to that of *AAB* and *ABB* genomes. This is contrary to stakeholder perceptions in Uganda who prefer the latter for their high fibre yield compared to *AAA-EA* genome (Kamusingize et al., 2025a). However, considering the high susceptibility of the *AAB* and *ABB* genomes to biotic stresses, such as fusarium wilt disease (Kema and Drenth, 2018; van Westerhoven et al., 2022), there is great potential in

Table 5
Regression coefficients of selected allometric models for predicting dry banana fibre yield per plant for *in-situ* and *ex-situ* conditions.

Genome	Condition	Model type	Equation	Predictor	Estimate	Standard error	t-statistic	p	Confidence interval (2.5 – 97.5%)		
General	In-situ	Power	3	Intercept	-0.58	0.47	-1.23	0.220	-1.52	–	0.35
				Girth at base (cm)	1.14	0.12	9.85	< 0.001	0.91	–	1.37
				Extractable height (m)	0.83	0.09	8.94	< 0.001	0.65	–	1.01
	Ex-situ	Multiple linear	2	Intercept	-41.92	12.83	-3.27	0.001	-67.21	–	-16.64
				No. extracted sheaths	8.97	1.11	8.07	< 0.001	6.78	–	11.16
				Extractable fresh weight (kg)	3.03	0.35	8.71	< 0.001	2.34	–	3.71
AAA	In-situ	Simple linear	1	Intercept	-228.12	51.29	-4.45	< 0.001	-330.79	–	-125.45
				Girth at 30 cm (cm)	6.47	0.76	8.52	< 0.001	4.95	–	7.99
	Ex-situ	Multiple linear	2	Intercept	-93.19	43.15	-2.16	0.035	-179.59	–	-6.79
				No. extracted sheaths	15.09	3.43	4.41	< 0.001	8.23	–	21.95
				Extractable fresh weight (kg)	1.61	0.83	1.93	0.059	-0.06	–	3.28
AAA-EA	In-situ	Logarithmic	5	Intercept	-711.69	117.42	-6.06	< 0.001	-946.92	–	-476.46
				Girth at 100 cm (cm)	181.40	32.81	5.53	< 0.001	115.68	–	247.11
				Extractable height (m)	172.10	34.11	5.05	< 0.001	103.76	–	240.43
	Ex-situ	Power	3	Intercept	0.32	0.36	0.89	0.378	-0.40	–	1.04
				No. extracted sheaths	1.13	0.18	6.21	< 0.001	0.77	–	1.49
				Extractable fresh weight (kg)	0.55	0.10	5.49	< 0.001	0.35	–	0.75
AAB	In-situ	Logarithmic	4	Intercept	-432.76	93.12	-4.65	< 0.001	-619.38	–	-246.14
				Girth at base (cm)	137.99	23.10	5.97	< 0.001	91.71	–	184.28
	Ex-situ	Logarithmic	5	Intercept	-156.40	51.52	-3.04	0.004	-259.69	–	-53.11
				No. extracted sheaths	75.17	23.30	3.23	0.002	28.45	–	121.89
				Extractable fresh weight (kg)	37.53	12.57	2.99	0.004	12.33	–	62.73
ABB	In-situ	Exponential	6	Intercept	3.16	0.29	10.85	< 0.001	2.57	–	3.74
				Girth at 100 cm (cm)	0.04	0.01	4.73	< 0.001	0.03	–	0.06
				Total height (m)	-0.46	0.22	-2.04	0.046	-0.91	–	-0.01
				Extractable height (m)	0.40	0.17	2.42	0.019	0.07	–	0.74
	Ex-situ	Simple linear	1	Intercept	45.43	13.12	3.46	0.001	19.16	–	71.70
				Extractable fresh weight (kg)	4.68	0.66	7.08	< 0.001	3.36	–	6.00

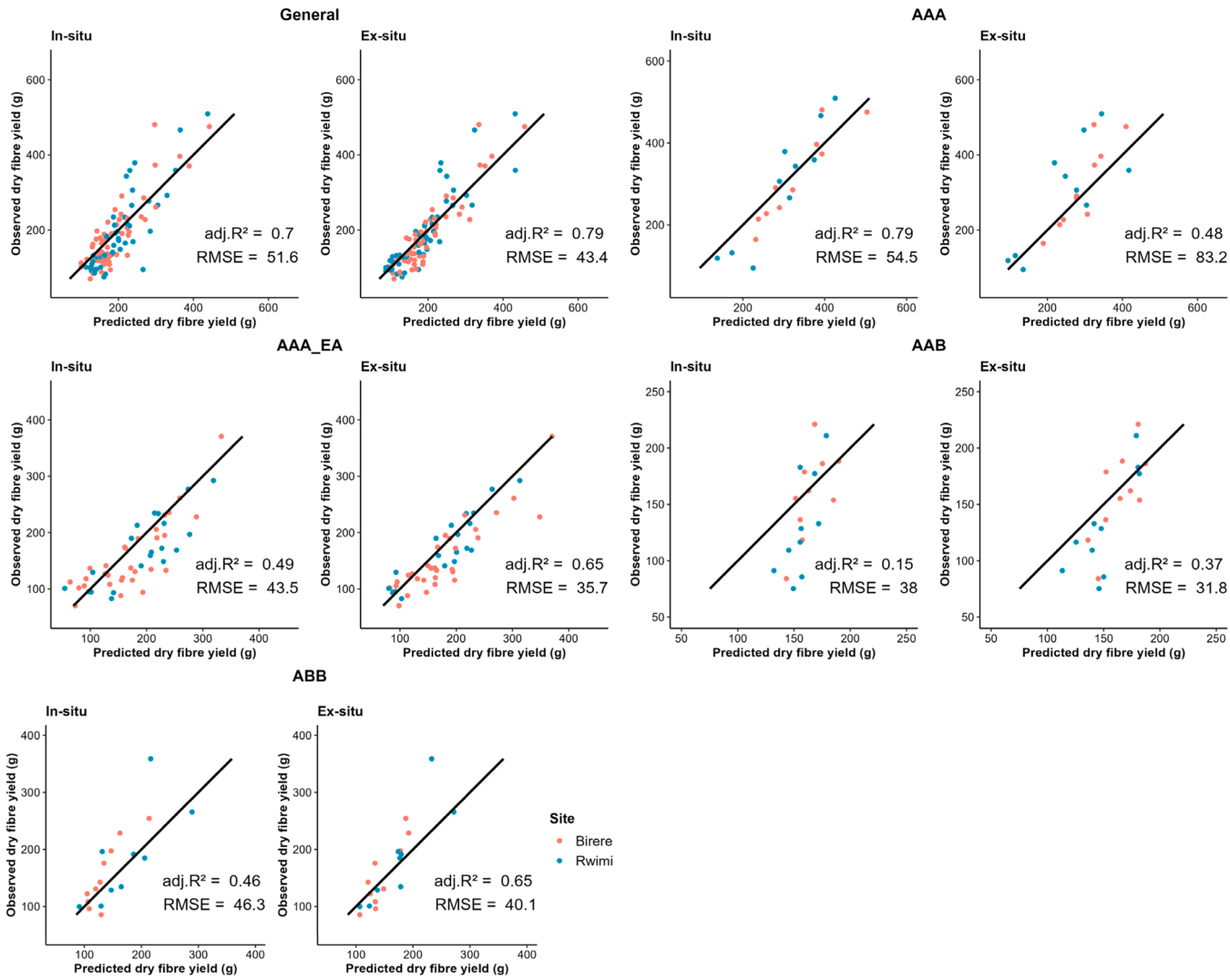

Fig. 8. Performance accuracy of selected allometric models, per genome or for all genomes combined, when used for predicting dry banana fibre yield per plant for *in-situ* and *ex-situ* conditions. The black line (the 1:1 identity line), adj. R^2 (the coefficient of determination), and RMSE (the root mean square error) are metrices used to assess model performance.

harnessing cooking-type (*AAA-EA*) bananas as a reliable source of raw material for the growing fibre industry. Besides, the latter are the dominant genetic group in banana cropping systems of the Great Lakes region of East Africa (Brown et al., 2017; Kema and Drenth, 2018). In addition, deliberate effort has been incurred over years, through breeding and agronomic research, to improve their productivity and address biotic and abiotic production constraints compared to other banana genomes (den Braber et al., 2021; Kimunye et al., 2021; Nyombi et al., 2010; Taulya, 2015; Tumuhimbise et al., 2018; Uwimana et al., 2020; Wairegi and van Asten, 2011).

Overall, fibre recovery per plant ranged between 0.6% and 1.2% comparable to that of abaca in the Philippines (1.62%) (Armecin and Coseco, 2012) and culinary banana cultivars in India (0.24 – 1.15%) (Uma et al., 2007). Contrary to our findings at genome level, recovery was highest in *ABB* (2.49%) genome and lowest in *AAA* (1.10%) for genotypes *Karupuravalli* and *Grand Naine*, respectively, in another study conducted in India (Paramasivam et al., 2022). In our study, genotypes *Gros michel* and *Pisang awak* were assessed for genomes *AAA* and *ABB*. Therefore, it is possible that fibre recovery also differs at genotype level despite similarity in genome groups, a knowledge gap for future studies. Across genomes, the low fibre recovery observed in this study could be attributed to the high moisture content of the fresh banana stems, averaging at 91% (Table B.1), and the low efficiency of the fibre extractor machine used (Kamusingize et al., 2025a). However, despite its inefficiency, the mechanical method of extracting fibre using a fibre decorticator remains the commonest technology used at commercial scale since its fibre production throughput per day is 20–30 times higher than that of the manual retting process (Akatwijuka et al., 2024; Uma et al., 2007). Furthermore, a comparison with other fibre extraction methods shows that this method is a better alternative to chemical methods due to its high fibre yield (Madhushani et al., 2022), but not to the biological approach (Das and Kalita, 2022). The latter, however, is limited by a long time of fibre throughput, and in some cases, the process involves soaking stems in large volumes of water to activate microbial activity (Mumthas et al., 2019; Tahir et al., 2011), leading to a high water footprint which is environmentally unsustainable. Despite the fact that some review studies have documented the merits and demerits of the different methods and their effect on fibre quality (Akatwijuka et al., 2024; Badanayak et al., 2023; Mumthas et al., 2019), comparative studies of their effect on fibre yield and recovery ratio are limited. Therefore, future studies could explore the mechanisms of various extraction methods and establish optimal extraction processes that can be adopted by the industry.

Table 6
Mean differences in observed and predicted dry banana fibre yield of on-farm data for the selected allometric models. p values in bold show non-significant differences between the values. +denotes results of the test-statistic done using Wilcoxon's non-parametric test following significant ($p > 0.05$) normality results of the Shapiro test. All other results are based on a paired *t*-test statistic. SD is the standard deviation. n is the number of stems harvested.

Genome	Site	Condition	n	Mean dry fibre yield (g) ± SD		p
				Observed	Predicted	
General	Birere	Ex-situ	60	182.4 ± 90.4	193.8 ± 71.9	0.008+
		In-situ			188.2 ± 68.1	**0.129+**
	Rwimi	Ex-situ	49	190.9 ± 101.4	186.9 ± 80.4	**0.968**
		In-situ			201.6 ± 69.8	0.033
AAA	Birere	Ex-situ	10	315 ± 110.8	292.8 ± 63	**0.286**
		In-situ			328.9 ± 87.1	**0.339**
	Rwimi	Ex-situ	10	297.5 ± 144.4	245.2 ± 105	**0.096**
		In-situ			296.2 ± 93.5	**0.952**
AAA-EA	Birere	Ex-situ	30	155.5 ± 63.5	179.8 ± 71.3	0.000
		In-situ			172.5 ± 65.8	0.025
	Rwimi	Ex-situ	20	170.3 ± 61.7	177.1 ± 66.7	**0.275**
		In-situ			192.3 ± 68.6	0.025
AAB	Birere	Ex-situ	10	158.5 ± 39	164 ± 17.2	**0.565**
		In-situ			164.8 ± 14.8	**0.545**
	Rwimi	Ex-situ	10	131.1 ± 45.6	150.5 ± 23.4	**0.075**
		In-situ			157.1 ± 13.5	**0.056**
ABB	Birere	Ex-situ	10	154.2 ± 57.5	146.1 ± 29.7	**0.473**
		In-situ			135.4 ± 33	**0.100**
	Rwimi	Ex-situ	9	184.6 ± 84.3	175.7 ± 51.7	**1.000**
		In-situ			173.4 ± 58.8	**0.820**

Table 7
Anova results of the generalized linear mixed-effects model of banana fibre yield per plant (g), fibre recovery per plant and sheath (%), and potential determinants for banana stems sourced from on-station. Df refers to the degrees of freedom while p values in bold indicate significant differences. The signs – and + indicate the nature of influence a given determinant has on a given fibre trait.

Fibre trait	Plant trait	Fixed effect	Chisq	Df	p	Influence
Yield per plant	Health	Weevil pest damage (%)	1.9	1	0.164	-
		Fusarium disease severity index	1.9	1	0.168	+
	Physiological	Stem moisture content (%)	6.6	1	**0.01**	+
	Morphological	No. extracted sheaths	47.8	1	**< 0.001**	+
		Extractable stem fresh weight (kg)	37.1	1	**< 0.001**	+
Recovery per plant	Health	Weevil pest damage (%)	1.7	1	0.197	-
		Fusarium disease severity index	2.8	1	0.096	+
	Physiological	Stem moisture content (%)	0.5	1	0.46	+
	Morphological	No. extracted sheaths	30	1	**< 0.001**	+
		Extractable stem fresh weight (kg)	101.8	1	**< 0.001**	-
Recovery per sheath	Health	Weevil pest damage (%)	47.6	1	**< 0.001**	-
		Fusarium disease severity index	298.7	1	**< 0.001**	+
	Physiological	Stem moisture content (%)	29.7	1	**< 0.001**	-
	Morphological	Sheath position	53.1	24	**< 0.001**	na

4.2. Determinants of banana fibre yield and recovery

Across the board, genome and morphological traits were the most important determinants for both fibre traits, while physiological and phenological traits were specific to yield and recovery, respectively. Specific to genome, other studies reported similar findings where fibre yield varied significantly with cultivar, e.g. for bananas in India (Uma et al., 2007) and hemp in Italy (Amaducci et al., 2008). Unfortunately, unlike for other commonly cultivated fibre crops, such as ramie (Wang et al., 2021), cotton (Yang et al., 2020), abaca (Ereful et al., 2022), and flax (Mokshina et al., 2020), there are hardly any advanced genomic studies on edible bananas specific to fibre. Yet, understanding plant genetic traits and underlying mechanisms responsible for banana fibre yield and recovery is necessary to support selective breeding efforts for fibre-rich genotypes required by the industry. A starting point in this direction could be building on the findings of a recent genomic study by Zhou et al. (2024) that analysed the potential gene-related regulatory mechanisms of fibre quality traits, cellulose and lignin, for broader banana genome classifications, i.e., *M. balbisiana*, *M. acuminata,* and the *T-genome* for abaca. A key conclusion of this study was that the gene expression patterns were closely related to the mechanical properties of the fibres and varied among different banana varieties during growth and development.

Unlike genome, plant growth stage was not a determinant of banana fibre yield. In contrast, banana fibre producers in Uganda preferred older stems perceived to yield more and better-quality fibre (Kamusingize et al., 2025a). However, the similarity exhibited in fibre yield across growth stages was not surprising because the fibre is extracted from stem sheaths which are removed periodically upon full or partial senescence during agronomic management routines as the plant grows. During plant development, initiation of new sheaths ceases at flowering stage (Stover and Simmonds, 1987) signalling a transition from vegetative growth to reproductive development. This growth characteristic and agronomic practice could partly explain the higher variability in fibre yield observed in stems at post- than pre-flowering stage (Fig. 5). Therefore, as fibre yield of stems at post-flowering stage benefits from other stem traits, such as sheath length, those at pre-flowering stage benefit from the larger number of sheaths present by the time of extraction. However, this study did not specifically investigate the effects of the number and length of the sheaths on fibre yield for stems at varying growth stages; hence, this remains a research gap for future studies.

Distinct from fibre yield, recovery at plant level was significantly different across growth stages in two genome groups and generally

higher in pre-flowering plants. This could be attributed to the lignification process and underlying mechanisms that affect lignin synthesis and its deposits in cell walls to enhance mechanical support of plant organs during development (Boudet, 2000; Zhou et al., 2024). Therefore, as high lignin content makes the fibre more rigid and stiff (Das and Kalita, 2022), fibre in younger plants, which contain less lignin, is easier to extract, resulting in a higher recovery.

Specific to plant health, our field observations showed that sheaths heavily damaged by banana weevils, common in *AAA-EA* stems (Fig. B.8), were susceptible to breakage during fibre extraction. However, the level of weevil pest damage observed in the corm was low, and the variable hardly determined fibre yield or recovery, although it exhibited a negative effect across the board, including at sheath level. Unfortunately, no robust tools exist for assessing weevil pest damage at stem level beyond the current ones targeting the corm (Rukazambuga et al., 1998; Viljoen et al., 2017), a key research gap for future studies. In contrast to pest damage, an increase in FOC disease severity resulted in a positive effect on both fibre yield and recovery. This was contrary to our expectation of a negative effect, as fusarium wilt is a key constraint to banana production in general (Kema and Drenth, 2018). Therefore, the disease mechanism underlying this observation is worth investigating to mitigate risks of disease spread, especially through recycling of fibre extraction waste arising from harvesting diseased stems assumed to contain more fibre.

4.3. Allometric models for predicting dry banana fibre yield

Half of the ten allometric models developed predicted fibre yield on farmers' fields moderately well (adj. R^2: 65–79%). This gives confidence in the validity of the models derived in this study. However, these model prediction values are lower than those reported for abaca (R^2: 92%) (Armecin and Coseco, 2012), but higher than ensete (adj. R^2: 35–57%) (Yemataw et al., 2021). The low accuracy of our models is attributed to the variation in the growing environments from which we sourced the stems compared to the abaca study (Armecin and Coseco, 2012). In the latter, plant sampling for model calibration and validation was done in one location on plants of the same cultivar at the same growth stage. In fact, for our models to achieve this level of prediction accuracy was a remarkable achievement considering multiple sources of variability. Therefore, our models can be reliably applied on diverse genotypes growing under different pedo-climatic conditions. Additionally, the model coefficients could be used to develop more complex crop growth or yield simulation models for understanding fibre traits in edible bananas, a current knowledge gap.

Also, the poor model performance (adj. $R^2 < 0.4$) exhibited by genome *AAB* for both *in-situ* and *ex-situ* conditions is worth mentioning. It is not clear why both models overestimated fibre yield from farmers' fields. Perhaps, the method we used to calibrate the models with data sourced from on-station and validate them with on-farm data was not appropriate for this specific genome. Our field observation showed that on-station fields were, in general, poorly managed compared to farmers' fields. For *AAB*, specifically, on-station fields were old, weedy, and many suckers (≥ 4) were maintained per mat. High sucker densities increase plant competition for resources which may result in an overall negative effect on biomass production. To improve model prediction accuracy, future research could consider developing the models using, e.g. bootstrapping methods on a pooled dataset to capture diverse sources of variability, including biophysical and agronomic management factors.

Our results also showed that dry fibre yield can be estimated *in-situ* with different predictors per genome and *ex-situ* with predictors that are similar across genomes. Similarly, *in-situ* predictors for fibre yield estimation in other *Musa* species, ensete (Yemataw et al., 2021) and abaca (Armecin and Coseco, 2012), also varied. Specific to edible banana, the selected *in-situ* predictors are similar to those of other biomass studies which reported a strong correlation between pseudo-stem biomass and girth (Wairegi et al., 2009). For *ex-situ* conditions, our results confirm that fibre yield can best be predicted with two key predictors, i.e., the fresh weight of the extractable stem and the number of sheaths. Interestingly, considering the fresh weight of the extractable stem was an emerging practice among fibre producers in Uganda to determine stem price (Kamusingize et al., 2025a). However, predicting biomass using predictors assessed after plant harvest is not a common practice in plant allometry studies. Therefore, we consider this a novel contribution from our study that is useful for decision making, particularly for fibre industry players interested in estimating a return on investment during stem purchase.

5. Conclusion

Successful transition to a bio-based economy is strongly dependent on a sustainable supply of sufficient amounts of raw material from biological resources, such as natural fibre from agricultural residues, and reliable tools to periodically monitor such biomass stocks. However, these aspects remain a key knowledge gap in developing bioeconomies, such as Uganda's banana fibre sector. In this study, we quantified extractable dry fibre yield and recovery in banana stems of different genomes and at different growth stages, derived allometric models for rapid evaluation of plant-level dry banana fibre yield, and probed determinants for both yield and recovery. Our findings on fibre yield and recovery were comparable to those of other *Musa* species commonly grown for industrial fibre, such as abaca. The allometric models proved robust for use in diverse pedo-climatic environments. Genetic and morphological pseudo-stem traits were the top determinants of yield and recovery, while physiological and phenological traits were specific to yield and recovery, respectively.

Our results on fibre yield show great potential in harnessing fibre from the dominant cooking-type bananas (*AAA-EA)* as a major source of raw material for the growing industry since their fibre yield was comparable to genomes *AAB* and *ABB* currently most preferred by fibre producers. The high inefficiency (<1% fibre recovery) of the fibre extraction machines poses challenges as a high number (7) of banana stems is required to produce one kg of fibre. In addition, as plant growth stage does not matter for fibre yield, there is no need to cut stems before bunch harvest. In order to safeguard the food security of banana-dependent farming households while promoting the exploitation of fibre production, policy interventions may be needed to prohibit stem harvest for fibre before flowering. Perhaps the most important novel contribution of our study lies in a well-documented fibre extraction protocol, and, for the first time, allometric models to predict dry banana fibre yield. These models, developed for both *in-situ* and *ex-situ* conditions, are intended to serve interests of diverse stakeholder groups in the banana fibre industry, such as researchers or fibre producers purchasing stems for fibre extraction. However, a refinement of the allometric models with low predictive accuracy, e.g. *AAB,* is necessary to provide tools for genome-specific fibre studies. Finally, the information generated in this study contributes to a better understanding of banana fibre as a raw material for the budding banana fibre industry in Uganda. It also lays foundation for furthering research and business in such emerging plant-based fibres with less global focus yet great potential.

CRediT authorship contribution statement

Katrien Descheemaeker: Writing – review & editing, Validation, Supervision, Resources, Methodology, Conceptualization. **Daphine Kamusingize:** Writing – review & editing, Writing – original draft, Visualization, Project administration, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Esther Ronner:** Writing – review & editing, Validation, Supervision, Resources, Methodology, Conceptualization. **Godfrey Taulya:** Writing – review & editing, Validation, Supervision, Resources, Methodology, Conceptualization. **Priver Namanya:** Writing – review & editing, Supervision, Project administration, Funding acquisition,

Conceptualization. **Hugo Dorado Betancourt:** Writing – review & editing, Visualization, Validation, Resources, Methodology. **Jerome Kubiriba:** Writing – review & editing, Supervision, Project administration, Funding acquisition, Conceptualization.

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.indcrop.2026.123442.

Data availability

Link to the data is added below and also referenced under the materials and methods section.

Data underlying the publication "Banana fibre yield and recovery in diversified farming systems of Uganda: Protocol, allometry and determinants." (4TU.ResearchData)

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