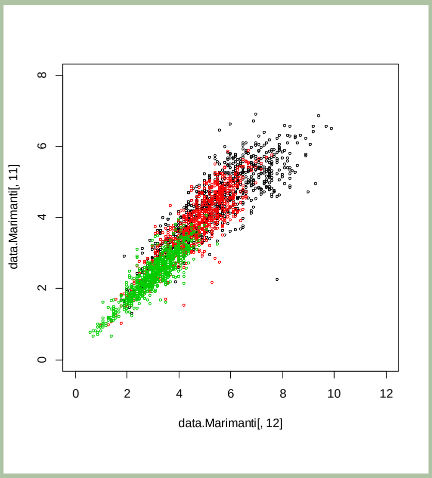
GENETIC PERFORMANCE AND PLUS TREE TRAITS TABLE FOR *MELIA VOLKENSII* IN THE DRYLANDS OF KENYA

TECHNICAL NOTE



GENETIC PERFORMANCE AND PLUS TREE TRAITS TABLE FOR *MELIA VOLKENSII* IN THE DRYLANDS OF KENYA.

Technical Note

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Cover Photos:
Clockwise: Assessment of Marimanti *M. volkensii* progeny test site, Marking selected 2nd generation tree, Figure of Melia growth data, Measuring of diameter (Photographs by J. Kariuki)

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Foreword

Kenya Forestry Research Institute (KEFRI) has been collaborating with the Japan International Cooperation Agency (JICA) in a series of projects for more than 35 years related to social forestry development in the ASAL areas of eastern Kenya. From the projects implemented so far, appropriate tree species for the region have been identified based on their adaptability and acceptance by the local communities. Among the species screened, *Melia volkensii* was prioritized as the most suitable for further development especially for commercial forestry in the drylands. *M. volkensii* is an indigenous tree species that is highly rated for its fast growth and multiple uses. The species is used for production of high quality timber, fodder, medicine and as bee forage.

In 2012, a project titled "Project on development of drought tolerant trees for adaptation to climate change in drylands of Kenya (2012～2017)" was initiated and has been implemented with the aim of enhancing KEFRI's research capacity in breeding of drought tolerant trees. In 2016 to 2021, another project "Capacity Development Project for Sustainable Forest Management in Kenya" was implemented. This project continued with some of the tree breeding activities initiated by the project on "Development of drought tolerant trees"

During implementation of the two projects, KEFRI collected candidate plus trees of *M. volkensii* and evaluated their genetic performance for growth, stem form, flower and fruits bearing and health status through establishment of seed orchards, establishment of progeny tests and their evaluation for the last six years. The genetic performance of the plus trees has been evaluated and the results presented in this report as Plus Tree Traits Table. The traits table summarizes growth, reproductive and disease tolerance parameters across the test sites. The Plus tree traits table will contribute to orchard improvement through rogueing of inferior families leading to more improved seed from the orchards. The results will also guide selection for further breeding programs in subsequent Melia breeding generations ultimately leading to establishment of more productive Melia commercial plantations in Kenya.

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Director, KEFRI

Tohru Nakashizuka
(Toru Asano)

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Director General of FFPRI

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1. Introduction

In Kenya, the arid and semi-arid areas (ASALs) occupy 80% of the country's land area and are home to over 10 million people who are predominantly pastoralists and agro-pastoralists. The drylands are endowed with abundant natural resources, with more than 70% of national livestock population, and 90% of the wild game that supports much of the tourism sector. The population pressure on drylands is caused by immigration of farming communities from the high potential areas, changing lifestyles of the local inhabitants, bioprospecting and minerals exploration. Consequently, drylands are increasingly being recognized as the new frontier for Kenya's development.

The climatic conditions in the drylands are generally hot, with low, erratic and poorly distributed rainfall. Annual rainfall ranges from 150 mm to 750 mm and occurs in one or two peaks around April and November. The potential evapotranspiration is higher than precipitation. Effects of climate change, which is a permanent shift in the traditional climate patterns, are also expected to exacerbate the already harsh climatic conditions in drylands. It is projected that in the next 100 years, the average temperature in the East Africa region could increase by 3 ^{o}C, as a result of climate change. The frequency and intensity of extreme climatic events such as droughts and floods will also increase, and the arid and semi-arid lands (ASALs) will be most affected.

Kenya is more susceptible to impacts of climate change due to frequent and recurrent droughts, over dependence on rain-fed agriculture and the limited economic capacity. The effects of climate change are already being felt in Kenya and the Government has given official recognition of the current and potential impacts of climate change through the preparation of a policy on disaster management and also in the Vision 2030. Among the goals of the Vision include; formulating adaptation programs on climate change and desertification in ASALs. The National Forest Program 2016-2030 recommends expansion of commercial trees in ASALs and establishment of tree improvement programme for the drylands.

In the past 34 years, the Japan International Cooperation Agency (JICA) has collaborated with Kenya Forestry Research Institute (KEFRI) and Kenya Forest Service (KFS) in social forestry development in the ASAL areas of eastern Kenya. From the projects implemented so far, the appropriate tree species for the region have been identified based on their adaptability and acceptance by the local communities. Among these, *Melia volkensii* was prioritized as the most suitable for further development. *M. volkensii* is an indigenous tree species that is highly rated for its fast growth and multiple uses. The species is used for production of high quality timber, fodder, medicine and as bee forage.

In 2012, a project titled "Project on development of drought tolerant trees for adaptation to climate change in drylands of Kenya (2012～2017)" was initiated and has been implemented with the aim of enhancing KEFRIs research capacity in breeding of drought tolerant trees for Kenya's drylands and development of an extension system to promote planting of indigenous trees in ASALs. Furthermore, KEFRI had implemented "Social Forestry for Adaptation to Climate Change (2014 to 2018)" as a third country training program, which has been supported by JICA since 1995. From 2016 to 2021, another project "Capacity Development Project for Sustainable Forest Management in Kenya" was implemented. This project was a continuation of the breeding project for development of drought tolerant trees.

The objective of tree breeding is to supply genetically superior materials that are adapted to target planting areas, solve specific problems and produce desired products. To achieve this objective, tree breeding is mainly consists of "determining variation patterns, assessing the intensity and cause of variation, packaging the variation into desirable trees, and mass production of the improved individuals" (Zobel and Talbert, 1984).

In the first project on breeding for drought tolerance (2012-2017), KEFRI selected 100 Candidate Plus Trees (CPTs) of *M. volkensii*, collected their propagules and established seed orchards. Progeny trials to evaluate genetic worth of the CPTs in terms of growth, flower and fruits bearing and health status were also established but evaluated in the second project. In this report, we compile results of analysis of the genetic performance of plus trees and present them as traits table.

The results of genetic analyses and the resulting traits table will contribute to orchard improvement through rogueing of inferior families leading to more improved seed from the orchards. The results will also guide selection for further breeding programs in subsequent Melia breeding generations ultimately leading to establishment of more productive Melia commercial plantations in Kenya. We provide brief description for the materials, measurement of traits, and analysis methods used before presenting the plus-tree traits table.

2. Selection of Melia Candidate Plus Trees and establishment of clonal seed orchards

2.1 Candidate Plus Tree selection

One hundred (100) Candidate Plus Trees (CPTs) of *Melia volkensii* were selected from 2012 to 2013 across arid and semi-arid areas the Kenya. The CPTs were selected in various regions within the species' natural range using a set of criteria (Table 1). The locations where CPTs were selected is depicted in Figure 1. The selection process involved reconnaissance in sites of natural occurrence of the species, followed by actual selection within the viable Melia populations (at least 30 individuals). Individual CPTs selection involved identification of potential candidate tree, assessment of the selected tree and its five nearest neighbours (check trees). The purpose of assessing the candidate *M. volkensii* tree and the check trees was to confirm superiority of the plus tree in comparison with the neighbouring Melia trees. In addition to documentation of geographic location of the CPTs (GPS), vegetation type, soil type and climatic conditions of the site was done. Candidate plus tree selection was based on stem straightness, growth vigor, branch size and number and health (Table 1).

Candidate Plus Trees were selected in the following regions (transects): Mutha-Inyali, Katulani-kavisuni, Voi-Mwatate, Voi-Galana, Embu-Ishiara-Gatunga, Embu-Dams, Mwea Special, Mwingi-Nuu, Mwingi-Tseikuru, Isiolo-Meru, Garissa-Bangale, Garba-Wamba and Wamba-Marsabit.

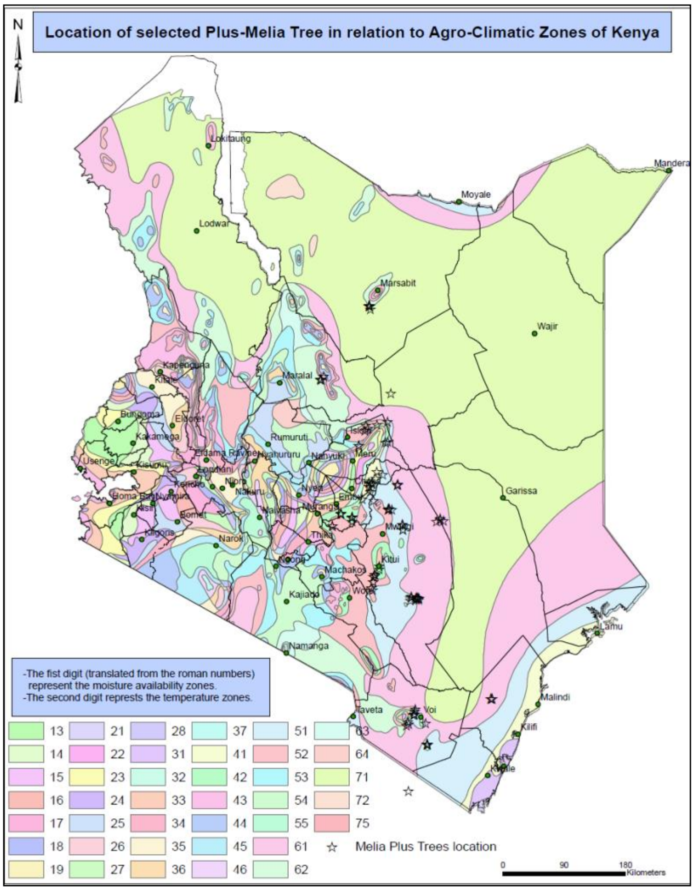


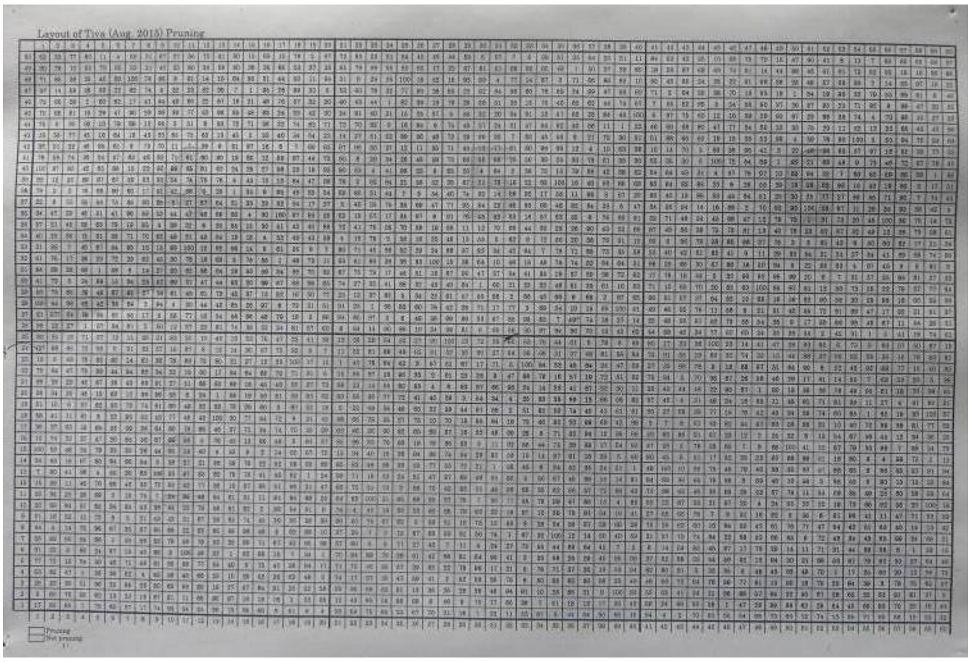
Figure 1: *Melia volkensii* Plus tree selection sites in Kenya

Table 1: Selection Criteria for *Melia volkensii* CPTs

No	Criteria
1	A tree in the dominant or co-dominant crown class (at or above the general tree canopy level) compared with the surrounding trees;
2	Superior in height and diameter growth in comparison to surrounding 5 trees
3	High growth vigour in comparison to surrounding 5 trees
4	Good tree form (Straight straightness and light branching habit)*
5	Light-medium branching, less steep angled branches
6	Not crooked or twisted stems/branches, No spiral grain
7	Free from insect pests and free of any signs of diseases

2.2 *Establishment of seed orchards*

Rootstocks of *M. volkensii* were raised at the KEFRI Kitui nursery for 4 months. Scions from the 100 CPTs trees were collected and taken to the nursery for grafting onto the rootstocks. Eighty (80) scions were obtained from each of the selected plus trees and 72 grafted onto Melia rootstocks in September 2012 using the top grafting method. The grafted seedlings were raised and managed in the nursery through watering, root pruning and disease control for 4 months until early December. The seed orchards were established from 2013 at Kitui and Kibwezi, using the grafted seedlings. In each orchard, 100 clones of plus trees each with 5 ramets were planted in 6 blocks resulting to 3,000 seedlings per site. The spacing was 6 m x 6 m (Figure 2).



Layout of Tiva (Aug. 2015) Pruning

Pruning
Not pruning

Figure 2: Layout of Melia Orchard in Tiva, Kitui

3. Establishment of *Melia volkensii* progeny tests

Seed for establishment of progeny tests was collected from the seed orchards, and from the original CPTs in the field for orchard families that had not started seeding. The seedlings were raised at KEFRI Kitui nursery in 2015 and used to establish 4 main progeny and 4 sub-progeny tests.

The eight progeny tests were located in four eco-regions (wet and cool (in the north), semi-wet and semi-cool (middle), semi-dry and semi-hot (middle), and dry and hot (south)) based on climate and the distribution range of *M. volkensii* (Figure 3). The progeny tests were of two types, main and sub-progeny tests, located in Marimanti (main) and Gaciongo (sub), Makima (sub) in the North; Tiva (main) and Kibwezi (main) and Ikithuki (sub) in the middle areas and Kasigau (main) and Voi (sub) in the south.

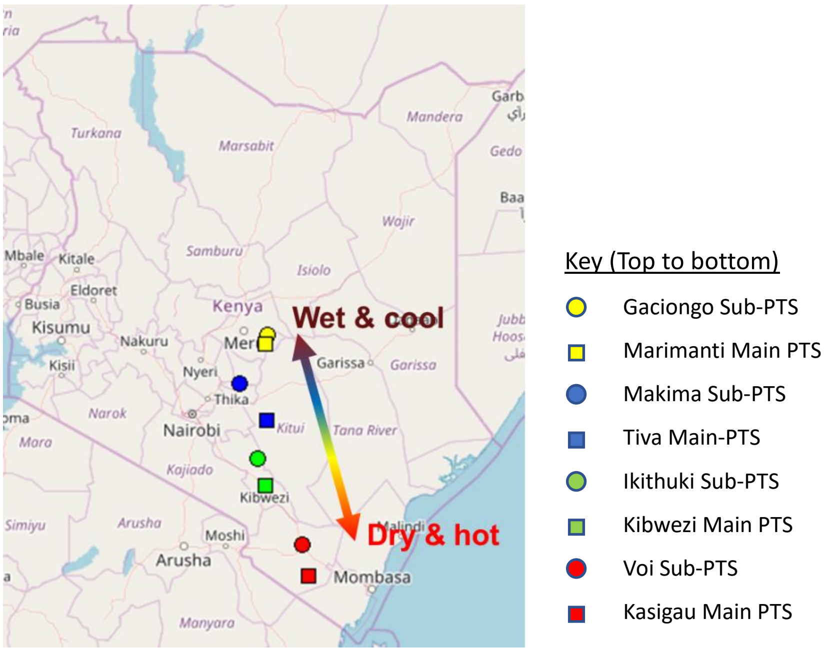


Figure 3. Climatic range in locations of progeny tests
(The dots represent progeny test sites across the region)

4. Phenotypic and genetic analysis of growth, tree form, fecundity and health at progeny trials

Tree height, Diameter at Ground Level (DGL) and Diameter at 50cm (D_{50}) were assessed one month after planting. Tree height, Diameter at Breast Height (DBH) and D_{50} were assessed twice a year starting at 6 months to age 5 years. Height was measured using a measuring rod while diameter was assessed using calipers and diameter tape. Stem straightness was evaluated using a subjective score rating of a 5-point scale: 1 = most twisted, 5 = straightest starting at age 4 years. Tolerance to fungal disease were measured with a subjective rating with a 2-point scale: 1 = no disease, 2 = diseased starting at 4 years. Fecundity was also assessed at year on a 4-point scale 1-None, 2-flowers, 3-fruits and 4-fruits and flowers starting at age 4 years. The analysis was done using data from the main progeny tests.

4.1 General growth trends

The average growth for height of trees at about 5 years ranged from 3.4 m to 11.2 m for Marimanti, 3.9 m to 11.4 m for Tiva, 3.8 m to 9.7 m for Kibwezi and 3.7 m to 9.8 m for Kasigau. In diameter growth the values ranged from 3.1 cm to 20.8 cm for Marimanti, 4.1 cm to 21.6 cm for Tiva, 3.1 cm to 18.1 cm for Kibwezi and 4.6 cm to 17.7 cm for Kasigau. However, due to wide variation, the mean values trends per site are shown in Figures 4 (height) and 5 (diameter).

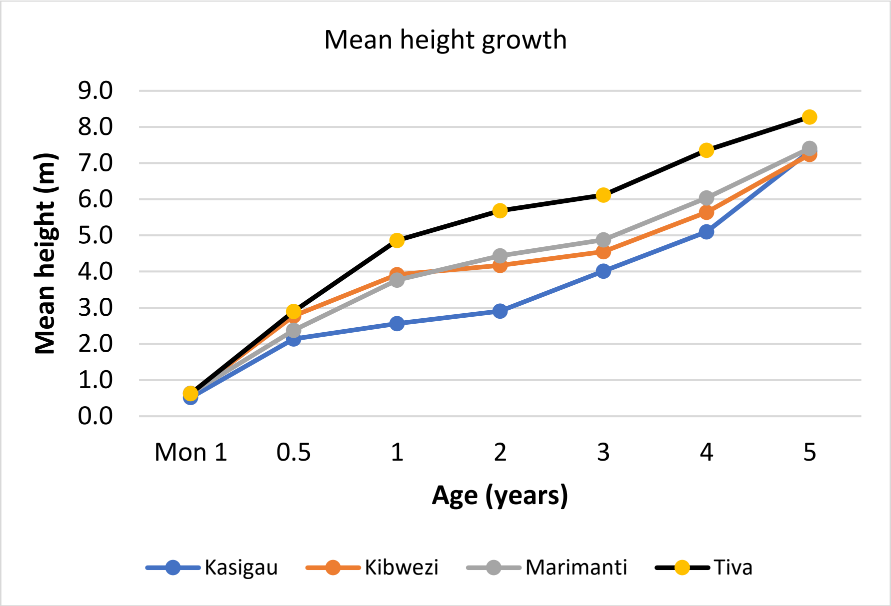


Figure 4. Mean height of *Melia volkensii* at 4 progeny test sites

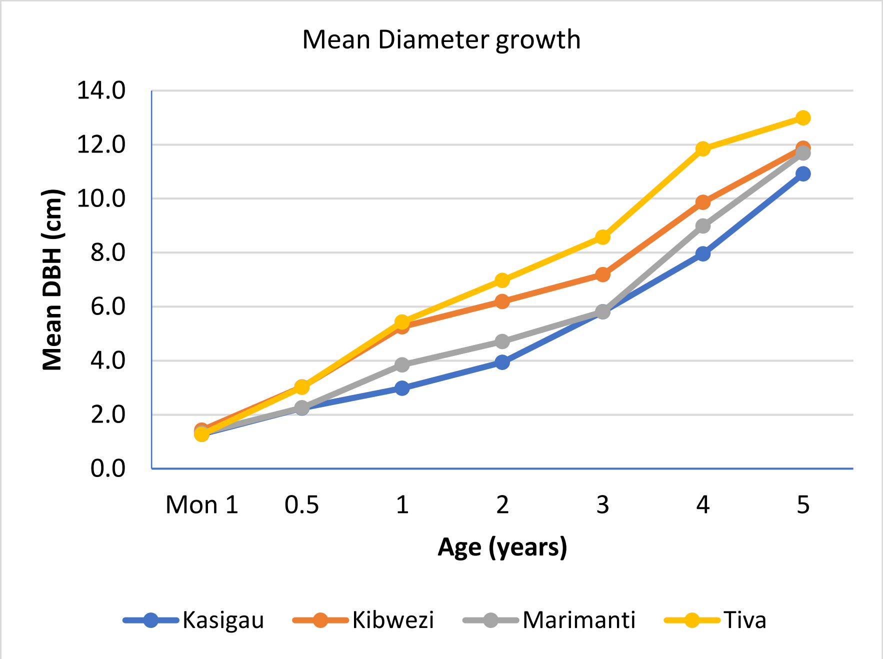
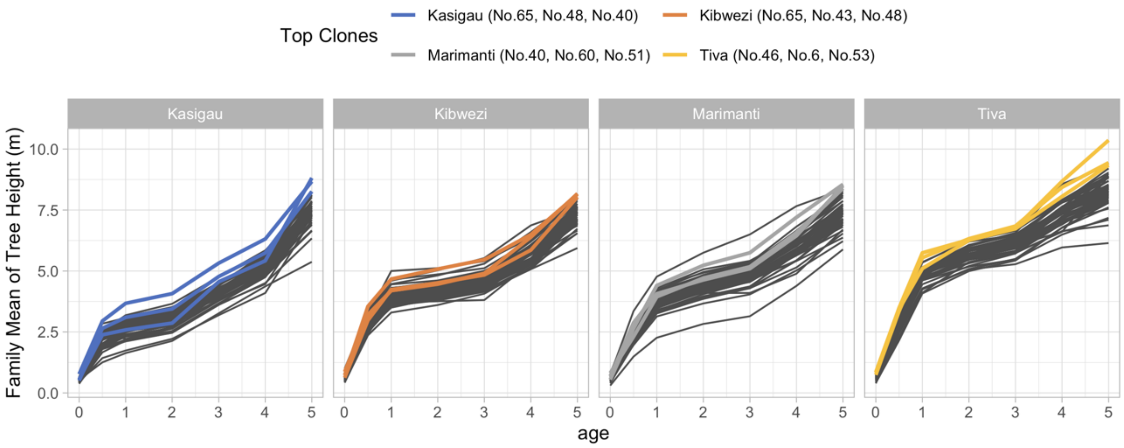


Figure 5. Mean diameter of *Melia volkensii* at 4 progeny test sites

4.2 Best performing clones by site in terms of tree height and DBH

The family height and DBH mean of each clone at each site is shown in Figures 6a and 6b. The best performing clones in height and DBH were different among sites and traits are shown on top of Figures 6a and 6b.

(a) Tree Height



(b) DBH

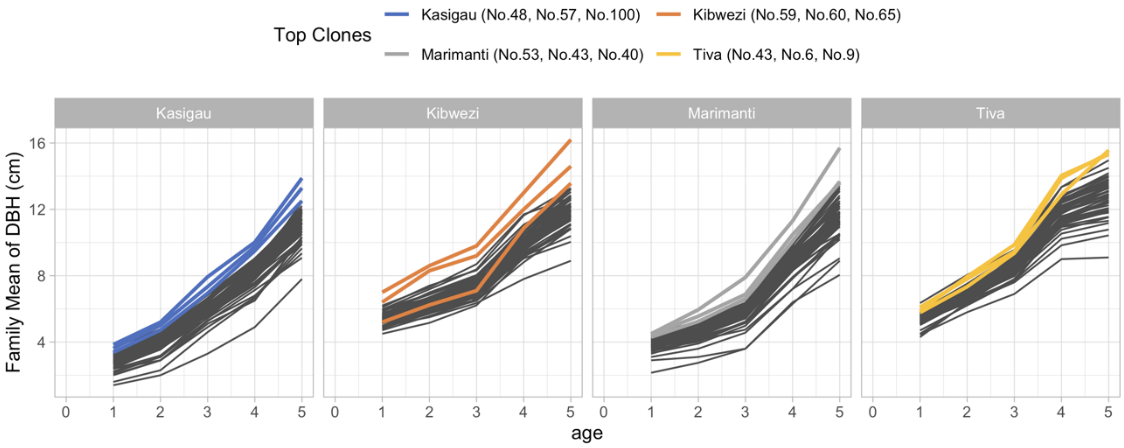


Figure 6. Family mean growth of *Melia volkensii* for each clone at 4 PT sites

(Top 3 clones at age 5 for each site were presented with color.)

4.3 Calculation of stem volume

Since there are no stem volume equations available for *M. volkensii*, we used stem volume equation for *M. azedarach* in Japan (Forestry Agency Japan, 1970) as shown below:

$$V = 10^{-4.199274} \times DBH^{1.8007256} \times H^{0.98511581}$$

Where V is stem volume of a tree (m^3), DBH is diameter at breast height (cm), and H is tree height (m).

The volume obtained from above equations fall in the middle of conic volume and cylindrical volume calculated from tree height and DBH (Figure 7). Since the two species are in the same genus and exhibit similar characteristics, usage of this equation is appropriate until an original stem volume equation is constructed for *M. volkensii* in future. Stem volumes were calculated using this equation in subsequent analysis.

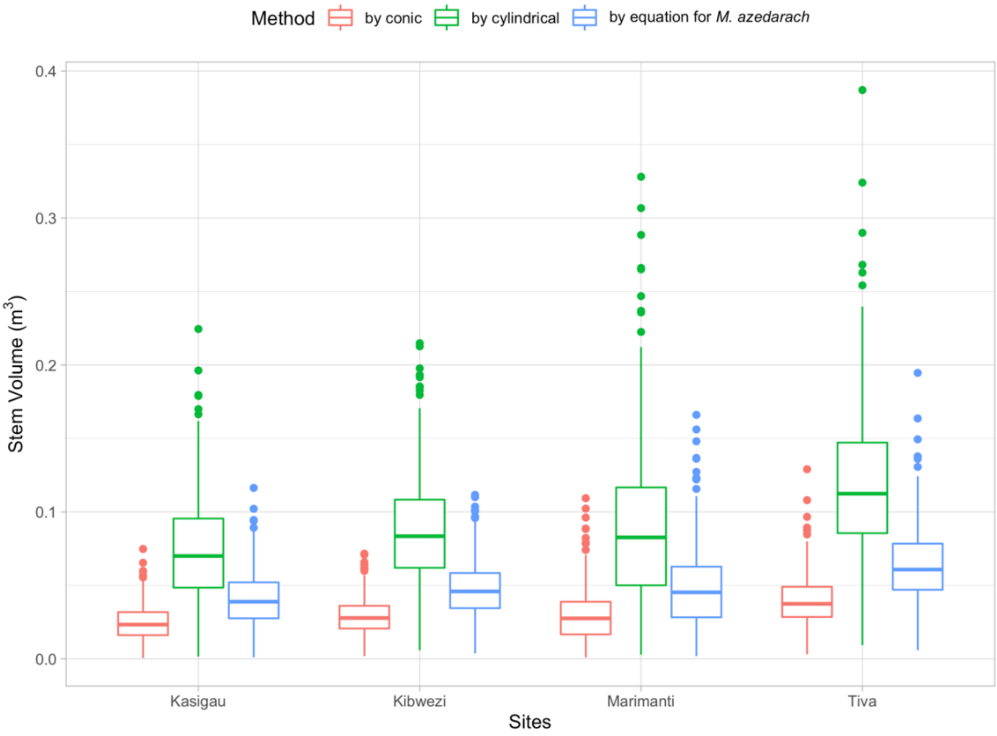


Figure 7. The difference in stem volume among progeny test sites and different calculation methods

(The boxplot shows individual stem volumes at age 5).

The difference of family mean of stem volume increased with age. The top clones were different among sites. The best performing clones in terms of stem volume in Kasigau were clone No 46, 77 and 65, in Kibwezi clones No. 59, 60 and 65, in Marimanti clone no 40, 43 and 53 and in Tiva clone no 6, 43 and 46 (Figure 8).

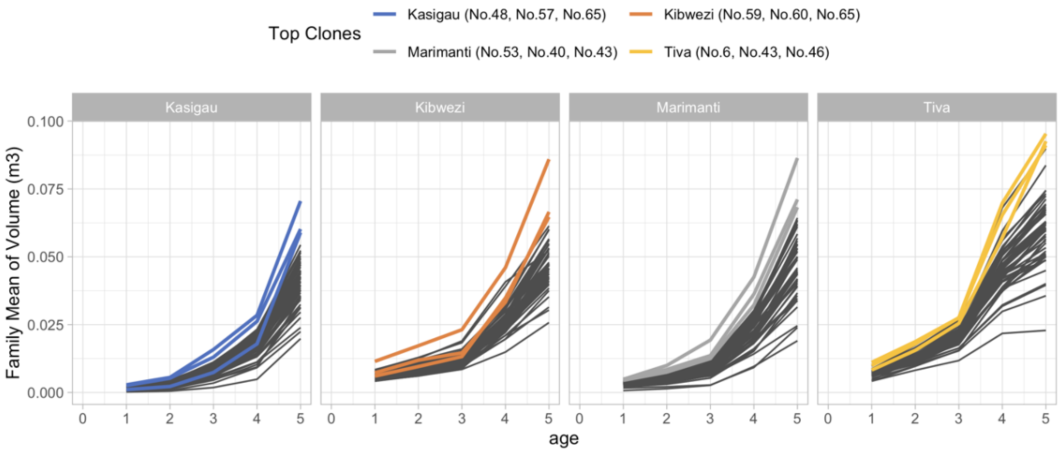


Figure 8. Family mean stem volume of *Melia volkensii* for each clone at 4 progeny test sites

(Top 3 clones at age 5 for each site were presented with color)

The performance shown above contains site effect. However, selection of clones for breeding 2nd and subsequent generations will be subject to the ranking presented in plus tree traits table (Section 6). The top 3 families presented per site should not be taken as recommendation for planting in the areas.

5. Genetic analysis of phenotyped traits

5.1 Data cleaning

We used the 4 main progeny test sites data for analysis, because the number of planted progeny trees for each plus trees were small (5 to 1, mostly 2) in sub-progeny sites. For genetic analysis of growth data at age 5, data collected from damaged trees (broken top, infected, and so on) were removed. The outliers were checked by tree height-DBH ratio and the data which the ratio was > 2 or the ratio < 0.2 were removed. The numbers of trees are different among mother plus trees.

Progenies of 69 out of the collected 100 CPTs were planted in the main progeny test sites. After data cleaning, the available growth data were from 2,664 progeny trees of 55 plus trees planted in four main progeny tests were used in the analysis.

5.2 Evaluation of fecundity and disease tolerance

The number of progeny trees which flowered were 46 which translated to 1.3% of the total trees in 4 main PTS at age 5 years. The number of trees with fruits were 477 representing 13.5% of total trees in 4 main PTS at age 5 years. The fruits bearing rate of the progenies of each CPT for each site, and their relationship among sites are presented in Figure 9. Even between Kibwezi and Marimanti, where relatively higher fruits bearing rates were observed, the correlation coefficient was low (r = 0.193).

The number of progeny trees which were infected by fungal disease were 240 representing 6.8% of all trees in 4 main PTS at age 5 years. The rate of infected trees for the progenies of each plus-tree at each main site, and their relationship among sites are presented in Figure 10. The infection rates were biased to zero, and the relationship is weak among sites.

The genetic parameters and breeding values were not estimated for fruit bearing and infection rates because of their zero biased distribution and low relationship among PTS sites. The rate for each clone calculated for all trees across 4 main-sites were used for the evaluation value for each plus tree.

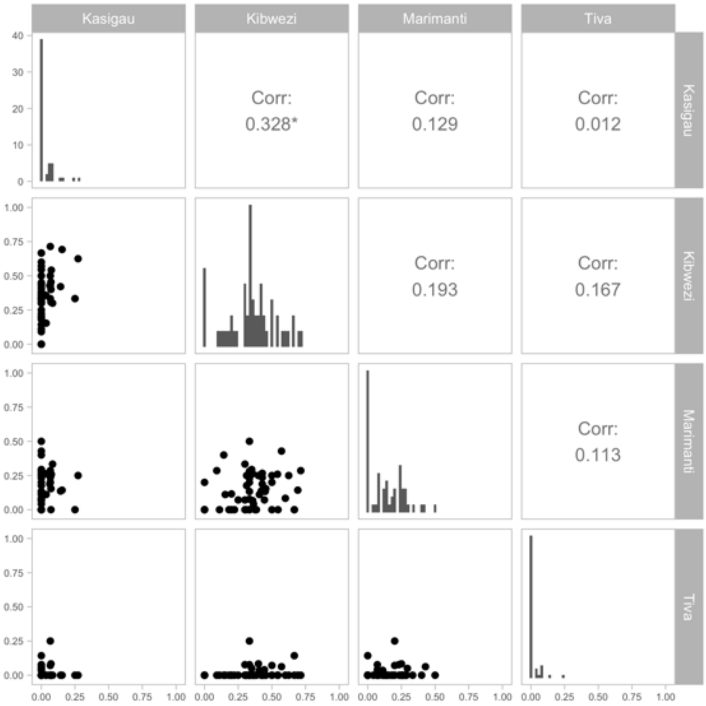


Figure 9. The relationship of fruits bearing rate of the open-pollinated progenies of plus trees among sites.

(Points in lower triangle panel shows the fruits bearing progeny tree rate of each plus tree).

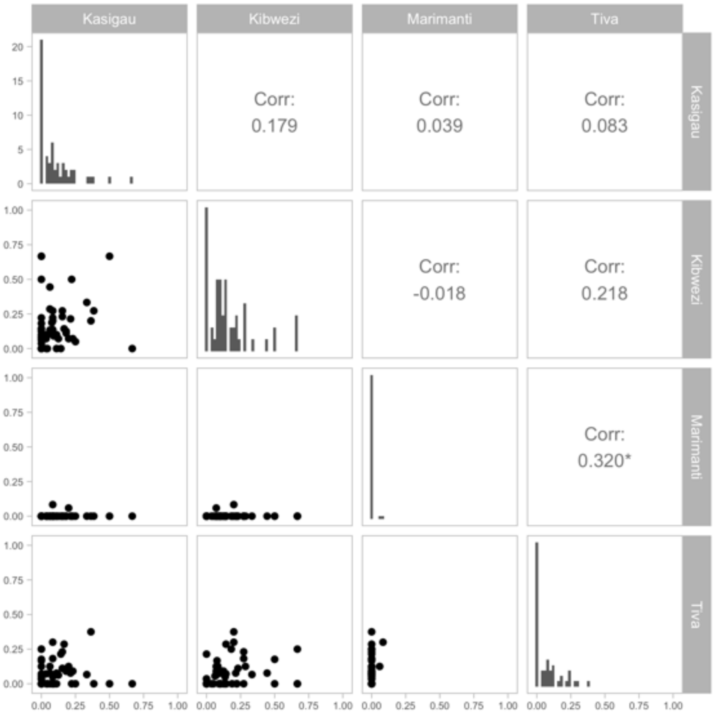


Figure 10. Rate of plus tree infections among sites.

(Points in lower triangle panel show the rate of infection among progenies of each plus tree).

5.3 Genetic parameters for growth and tree form traits at each site and genetic correlation among sites.

Genetic parameters were analyzed for tree height, DBH, stem volume, and tree form at age 5 for each PTS site, using following mixed linear model:

$$y_{ijk} = \mu + B_i + F_j + p_{ij} + e_{ijk}$$

where y_{ijk} is the phenotypic value for target trait, μ is the mean, B_i is the fixed effect of replication i, F_j is the random effect of mother plus tree (general combining ability (GCA) of mother clone) j , p_{ij} is random effect of plot by replication i and clone j, and e_{ijk} is random residual effects. Tree form traits were treated as interval scale in this analysis whereas they were measured on ordinal scale. Variance components were estimated from the linear model by REML method, and heritability for each site and trait were obtained using following equation:

$$h^2 = \frac{4 \cdot \sigma_f^2}{\sigma_f^2 + \sigma_p^2 + \sigma_e^2}$$

Where h^2 is individual narrow-sense heritability, σ_f^2 is family variance, σ_p^2 is plot variance, and σ_e^2 is residual variance. The BLUP of GCA of mother tree clones were also obtained using above mixed linear model. The breeding value of each CPT was calculated as twice the GCA for each mother plus tree for each site. The genetic correlations among sites were calculated as correlation coefficients of breeding values of CPTs per site.

The heritability values are shown in Figure 11. Tree height showed highest heritability. The heritability of stem form was low, but showed that tree form is a heritable trait in *M. volkensii*. Tiva, where average growth was best, showed the highest heritability compared to other sites.

The genetic correlations among sites for tree height and stem volume are presented in Figure 12. All combinations showed positive relationships. The genetic correlation of tree height between Tiva and Marimanti showed highest genetic correlation (r = 0.602). Tree height showed higher genetic correlations than stem volume in most combination of sites.

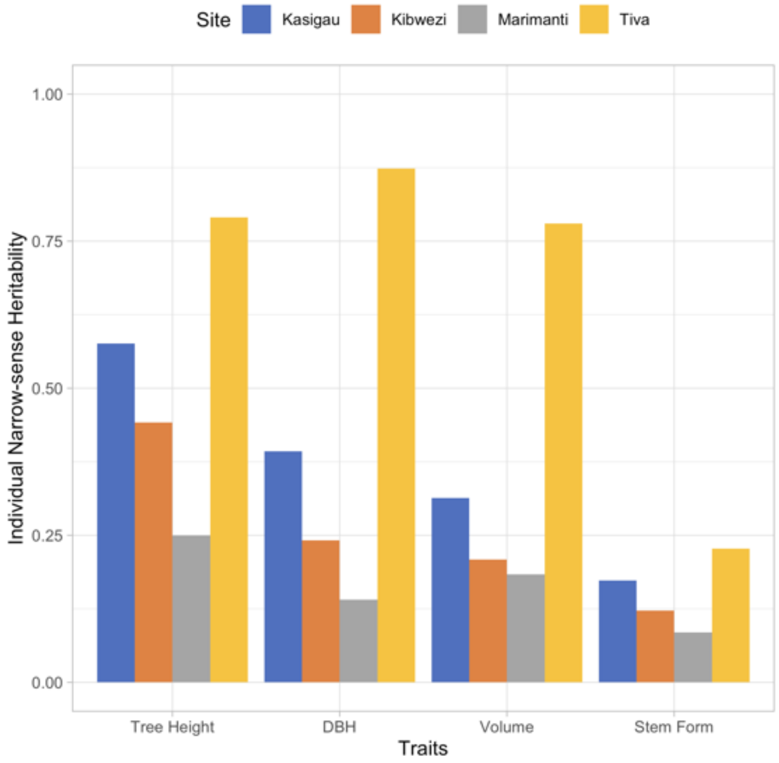


Figure 11. The narrow sense heritability of growth and tree at age 5

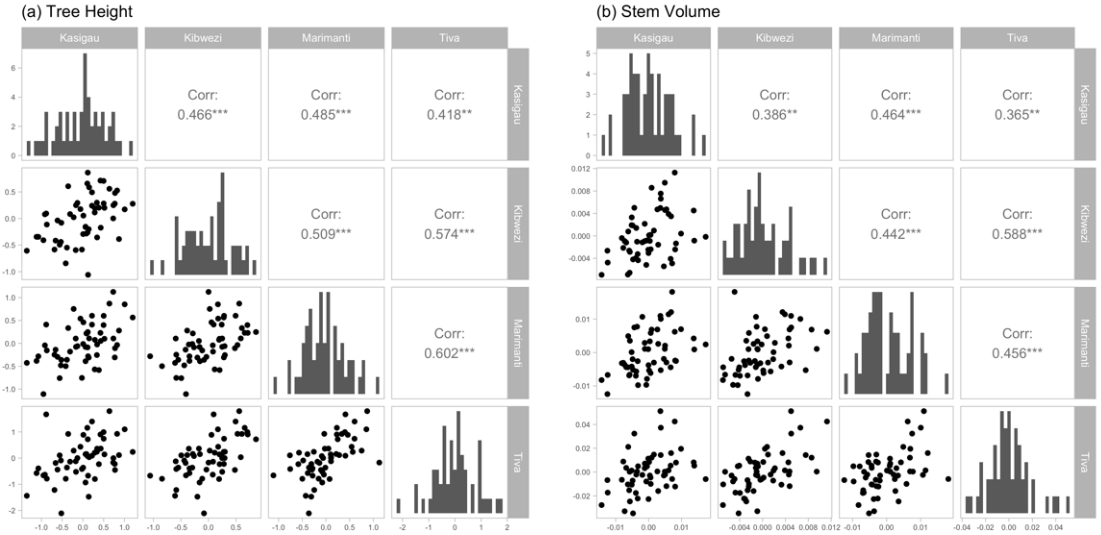


Figure 12. The genetic correlations of tree height and stem volume among sites.

(Each point shows the breeding value of CPT at each site at age 5 yrs.).

5.4 The effect of seed source on performance the traits

There are two seed sources, from seed orchard and from the original trees in the field, as described in section 3. The effects of seed source for each site and each trait were tested at age 5 years. We prepared data set for each site that have clones including both seed sources.

The number of clones included in tests were 22.6 on average. A log likelihood ratio test was adopted for the two linear models as explained in 5.4. The effect of seed source was added to the model as fixed effects. The p-values were over 0.05 for all traits and sites. This indicates that the effects of seed source for the tested traits in *M. volkensii* were small and non-significant and therefore were not included in subsequent analysis.

5.5 Prediction of breeding values across sites

Genetic parameters were analyzed for tree height, DBH, stem volume, and tree form at age 5 years across sites, using following mixed linear model:

$$y_{ijkl} = \mu + E_i + EB_{ij} + F_k + EF_{ik} + p_{ijk} + e_{ijkl}$$

Where y_{ijkl} is the phenotypic value for target trait, μ is mean, E_i is fixed effect of site i, EB_{ij} is the fixed effect of replication j in site i, F_k is the random effect of mother plus tree k (general combining ability (GCA) of CPT) , $EF_{ik}$is the effect of interaction between site i and mother clone k (genotype by environment interaction), p_{ijk} is random effect of plot by replication j and clone k at site i, and e_{ijkl} is random residual effect. The individual narrow sense heritabilities were estimated using the following equation:

$$h^2 = \frac{4 \cdot \sigma_f^2}{\sigma_f^2 + \sigma_{sf}^2 + \sigma_p^2 + \sigma_e^2}$$

Where h^2 is individual narrow-sense heritability, σ_f^2 is family variance, σ_{sf}^2 is family by site variance, σ_p^2 is plot variance, and σ_e^2 the residual variance. The breeding value of each CPT was calculated as twice the GCA for each CPT per site. The analysis was executed using breedR package (Muñoz and Sanchez 2020) in statistical package R (R Core Team 2021).

The narrow sense heritabilities are shown in Figure 13(a). Tree height showed highest heritabilities (0.476) compared to other assessed traits. The heritability of stem form was low, but genetic improvement would be possible. The ratios of variance components are shown in Figure 13 (b). The variance components of family by site interaction in tree height was small, showing small effects of environment on ranking of tree height across the sites. The effects of family by site interaction were larger for DBH and stem volume compared to tree height. There is a possibility that some families are more suited to different eco-region based on genetic correlation among sites (Figure 12) and the ratio of family by site interaction variance to family variance (Figure 13). However, the selection of superior plus tree groups adapted for all eco-region would be possible. Several progeny sites would be required for each eco-region to clarify the effects of genotype by eco-region interaction in the *M. volkensii* breeding program.

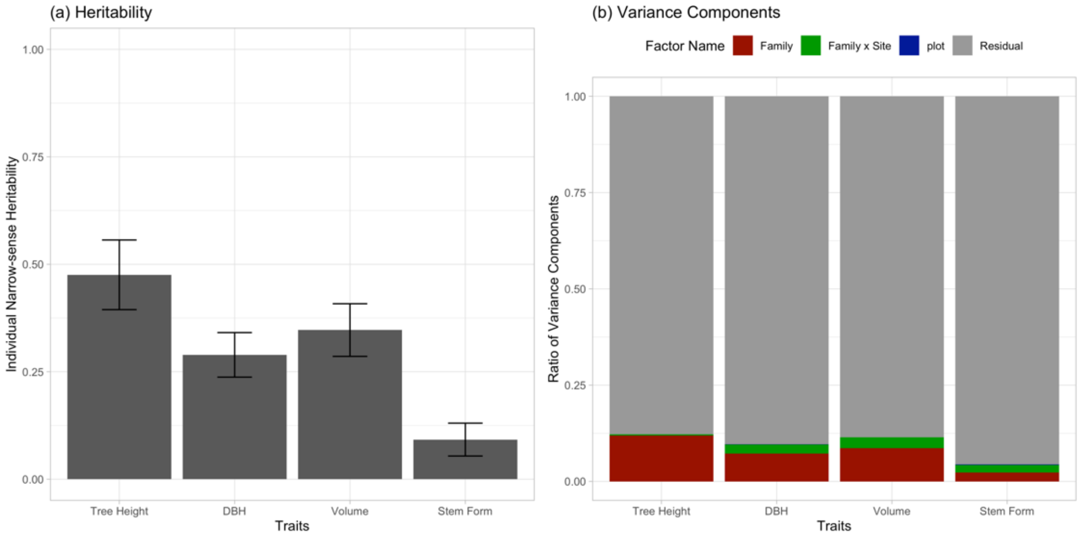


Figure 13. Heritabilities and variance components estimated across main progeny test sites

The relationship among breeding value, growth traits, tree form, ratio of fruits bearing trees, and ratio of disease infected trees are presented in Figure 14. Stem form showed higher positive correlation of around 0.6 with growth traits – height and DBH. The correlation among the ratio of fruits bearing trees and growth traits, and among disease infected rate and growth rate was low.

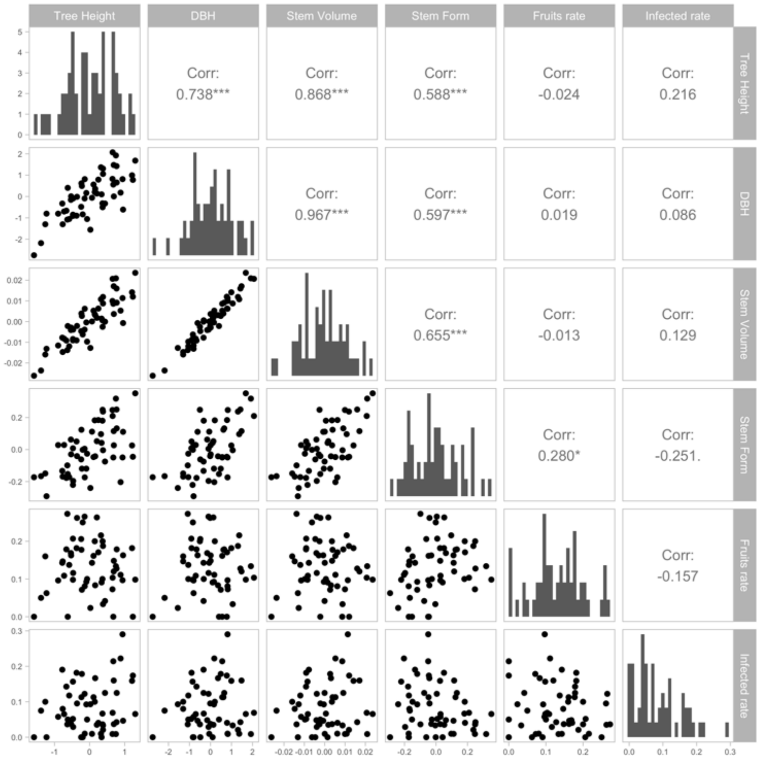
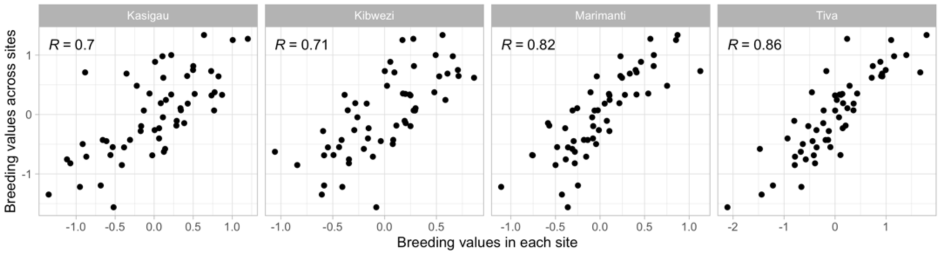


Figure 14: The relationship among breeding value of growth traits and tree form, across-sites fruits bearing rate and infection rate.

The relationship between breeding values predicted at each site and breeding values predicted across sites were shown in Figure 15 for tree height and stem volume. The correlation coefficients were higher for tree height. The correlations were high, but in some site showed smaller values under 0.7. This means the selected clones based on breeding values predicted across sites have the possibility that shows smaller performance than expected.

a) Tree Height



b) Stem Volume

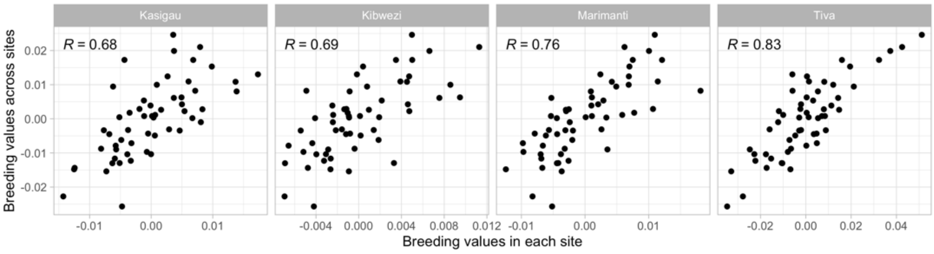


Figure 15: The relationship between breeding values predicted in each site and breeding values predicted across sites.

(a): Tree height, b): Stem volume.

5.6 Simulation of genetic improvement of seed orchards

The expected genetic gain by selection of superior clones and rouging inferior ones from seed orchards were calculated based on breeding values for each trait:

$$G_a = \frac{\sum_{i=1}^{m} B_k}{m} - \frac{\sum_{i=1}^{n} B_k}{n}$$

Where G_a is genetic gain, m is number of selected plus trees, n is number of pre-selected plus trees, B_k is breeding values of k the clone. B_k is ordered to descending order of breeding values. The selection rate is m/n. The relative gain was calculated by:

$$G_r = \frac{G_a}{M}$$

Where G_r is relative gain, M is general mean (average of fixed effects across sites). The assumptions were: random mating among all trees, no pollen contamination from outside sources, and equal contribution to pollen and seed production among all clones in a seed orchard. The genetic gain by selection of top 50% of clones for each trait are shown in Table 2. By rogueing seed orchards by 50% of inferior clones, the stem volume in the stand at age 5 years will be improved by about 0.0082 m^3, and its rate to general mean is about 16%. This shows that stem volume in plantations would be improved by about 16 % if the seed is obtained from rogued seed orchards compared to if the seed is from orchards with all 55 plus trees. For tree height, the genetic gain is 0.54 m, and will be improved by about 7%.

The genetic gains by changing selection rate are presented in Figure 16. When top 16% of clones (top 9 clones) are selected, volume would be improved about 33% at stand age 5. Because the genetic correlations are positive among traits (Figure 12), when the superior clones are selected based on the breeding value of volume, tree form would be also improved to some extent.

Table 2. Genetic gain by the selection of top 50 % of clones age 5 across PTS sites

Trait	Genetic Gain	General Mean	Relative Genetic Gain
Tree Height	0.54 m	7.56 m	7.13 %
DBH	0.75 cm	11.9 cm	6.29 %
Volume	0.0082 m^3	0.0490 m^3	16.77 %
Stem Form	0.12	3.52	3.33 %

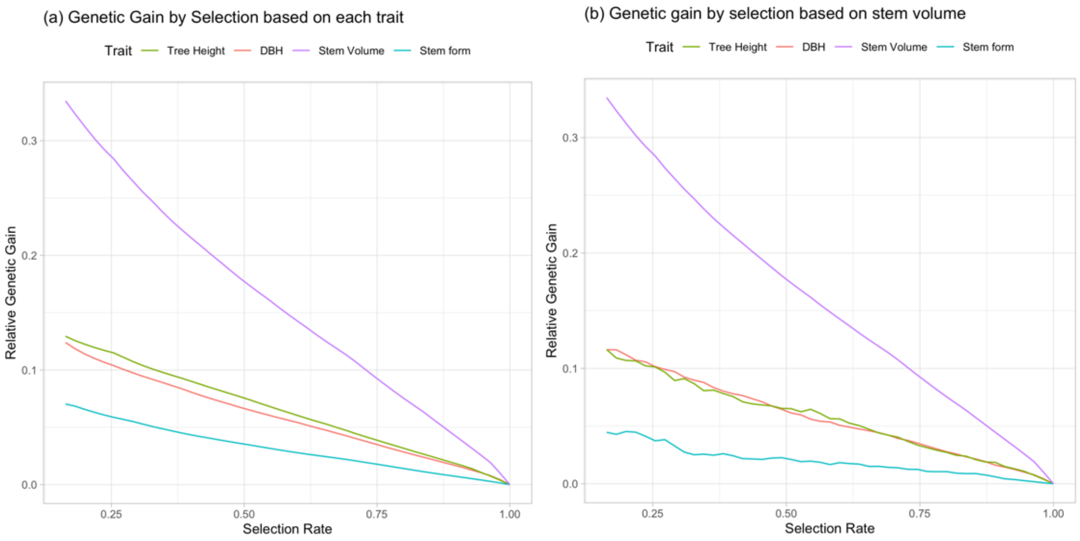


Figure 16. Genetic gain with different selection rates.

(Selection rate means the rate of selected clones. (a) Selections were based on each trait. (b) Selections were based on stem volume.)

6. Plus tree traits table

The plus tree traits across all sites are presented in Table 3. The number of CPTs listed in the Table are 55 clones, and ordered by the deviations from average breeding values of stem volume. Data obtained from 4 main CPTs at age 5 was used. The calculation of breeding values is described in section 5.5. The plus tree trait table that shows breeding values ordered by the deviations from the average for each site are presented in Table 4.

This plus trees traits table will contribute to orchard improvement through rogueing of inferior families leading to more improved seed from the orchards. After deciding on the rogueing intensity (%) to be used the orchards, the table can be used to determine which families are to be removed. Similarly, it can be used in determining families to select forward for second and subsequent breeding generations.

Table 3. Plus Tree traits table across sites

Clone	Stem Volume*		Tree Height*		DBH*		Stem Form*		Fruits**	Fungal Disease**	Assessed Trees***
	m^3	rank	m	rank	cm	rank	index	rank	rate	rate	number
No. 6	0.0246	1	1.337	1	1.800	3	0.368	1	0.10	0.07	57
No. 9	0.0210	2	0.749	8	1.931	2	0.310	2	0.13	0.01	111
No. 7	0.0199	3	0.618	14	1.960	1	0.176	7	0.10	0.07	52
No. 43	0.0173	4	0.688	11	1.481	5	0.110	13	0.12	0.16	21
No. 49	0.0172	5	0.814	7	1.572	4	0.275	3	0.13	0.04	45
No. 51	0.0153	6	1.253	3	1.129	8	0.056	19	0.18	0.16	36
No. 48	0.0130	7	1.273	2	0.889	11	-0.021	27	0.00	0.17	18
No. 53	0.0124	8	0.980	5	0.933	10	-0.021	28	0.10	0.29	20
No. 29	0.0109	9	0.336	19	1.180	7	0.197	6	0.19	0.02	46
No. 11	0.0108	10	0.321	21	1.370	6	0.091	15	0.22	0.01	100
No. 3	0.0100	11	0.648	12	0.823	12	0.239	4	0.07	0.01	107
No. 46	0.0094	12	0.708	10	0.647	15	-0.031	32	0.00	0.21	11
No. 40	0.0082	13	0.731	9	0.533	17	0.095	14	0.18	0.13	48
No. 57	0.0080	14	0.346	18	0.960	9	-0.027	30	0.03	0.03	29
No. 4	0.0063	15	0.244	22	0.785	14	0.175	8	0.17	0.04	118
No. 8	0.0061	16	-0.145	31	0.799	13	-0.176	49	0.08	0.01	96
No. 60	0.0054	17	0.886	6	0.185	24	-0.193	50	0.11	0.22	14
No. 19	0.0043	18	0.068	27	0.427	20	-0.081	39	0.16	0.11	54
No. 58	0.0039	19	0.190	23	0.444	19	-0.026	29	0.08	0.17	10
No. 20	0.0029	20	-0.279	36	0.485	18	0.084	16	0.18	0.11	54
No. 22	0.0028	21	0.642	13	-0.104	30	0.009	25	0.15	0.04	52
No. 14	0.0026	22	0.106	25	0.086	25	0.145	10	0.20	0.10	44
No. 65	0.0022	23	0.374	16	0.192	23	0.054	20	0.09	0.00	11
No. 33	0.0018	24	-0.262	35	0.370	21	-0.149	44	0.07	0.18	46
No. 70	0.0011	25	0.483	15	-0.183	32	-0.039	33	0.04	0.13	42
No. 74	0.0008	26	-0.047	29	0.316	22	-0.081	38	0.09	0.09	48
No. 16	0.0008	27	0.184	24	-0.018	27	0.027	24	0.25	0.04	54
No. 61	0.0005	28	1.000	4	-0.467	38	0.138	11	0.16	0.05	41
No. 5	0.0004	29	0.352	17	-0.355	35	0.164	9	0.10	0.07	83
No. 2	0.0002	30	0.071	26	-0.043	28	0.111	12	0.14	0.01	101
No. 100	-0.0010	31	-0.579	44	0.549	16	-0.117	42	0.00	0.05	38
No. 31	-0.0031	32	-0.403	37	-0.138	31	-0.070	37	0.26	0.10	37
No. 34	-0.0033	33	-0.448	40	-0.014	26	-0.172	48	0.12	0.03	66
No. 10	-0.0034	34	-0.549	42	-0.049	29	-0.046	35	0.16	0.04	76
No. 13	-0.0034	35	0.330	20	-0.617	40	0.211	5	0.20	0.04	53
No. 1	-0.0043	36	-0.231	34	-0.446	36	-0.053	36	0.21	0.00	33
No. 27	-0.0045	37	-0.554	43	-0.208	33	0.043	22	0.17	0.05	77
No. 17	-0.0049	38	-0.186	32	-0.220	34	-0.028	31	0.27	0.12	41
No. 37	-0.0062	39	-0.196	33	-0.825	45	-0.001	26	0.25	0.00	8
No. 55	-0.0071	40	-0.682	46	-0.556	39	0.060	18	0.11	0.07	42
No. 76	-0.0079	41	-0.429	39	-0.756	44	0.044	21	0.21	0.05	55

Clone	Stem Volume*		Tree Height*		DBH*		Stem Form*		Fruits**	Fungal Disease**	Assessed Trees***
	m^3	rank	m	rank	cm	rank	index	rank	rate	rate	number
No. 23	-0.0088	42	-0.821	50	-0.449	37	-0.160	47	0.14	0.19	33
No. 32	-0.0090	43	-0.497	41	-0.938	46	-0.230	54	0.10	0.16	40
No. 12	-0.0097	44	-0.687	47	-0.730	43	-0.194	51	0.18	0.14	71
No. 21	-0.0104	45	-0.107	30	-1.129	47	-0.045	34	0.10	0.05	55
No. 30	-0.0104	46	-0.851	51	-0.654	41	0.061	17	0.10	0.06	48
No. 91	-0.0117	47	0.067	28	-1.414	53	-0.200	53	0.02	0.09	37
No. 97	-0.0123	48	-1.194	52	-0.693	42	-0.262	55	0.06	0.00	16
No. 59	-0.0130	49	-0.428	38	-1.256	51	0.042	23	0.10	0.20	8
No. 41	-0.0130	50	-0.627	45	-1.182	49	-0.200	52	0.14	0.12	45
No. 36	-0.0144	51	-0.755	49	-1.254	50	-0.153	46	0.15	0.07	69
No. 24	-0.0148	52	-1.218	53	-1.152	48	-0.111	41	0.16	0.10	44
No. 39	-0.0154	53	-0.710	48	-1.270	52	-0.110	40	0.25	0.04	50
No. 67	-0.0227	54	-1.347	54	-2.057	54	-0.133	43	0.05	0.08	36
No. 79	-0.0257	55	-1.561	55	-2.669	55	-0.153	45	0.00	0.00	9

*: The breeding value, presented as the deviation from average. **: The rate of fruits bearing or fungal infected tree to the total investigated trees across 4 main-sites. ***: investigated number of trees for growth traits across 4 main-sites.

Table 4: Plus Tree traits table for each site

clone	Across Sites**		Kasigau***						Kibwezi***					
	V (m^3)*	rank	H (m)*	rank	DBH (cm)*	rank	V (m3)*	rank	H (m)*	rank	DBH (cm)*	rank	V (m^3)*	rank
No. 6	0.0246	1	0.639	9	0.250	22	0.0036	18	0.559	7	0.537	10	0.0050	7
No. 9	0.0210	2	0.498	12	1.262	5	0.0079	7	0.707	3	1.237	2	0.0113	1
No. 7	0.0199	3	0.118	25	0.731	12	0.0037	16	0.863	1	0.758	5	0.0066	5
No. 43	0.0173	4	-0.354	40	-0.482	39	-0.0043	39	0.607	5	0.596	8	0.0050	6
No. 49	0.0172	5	0.501	11	0.866	11	0.0068	9	0.283	13	0.470	13	0.0035	13
No. 51	0.0153	6	1.007	2	1.071	6	0.0098	4	0.172	23	-0.037	30	0.0004	21
No. 48	0.0130	7	1.200	1	2.196	1	0.0173	1	0.277	15	-0.133	34	-0.0002	24
No. 53	0.0124	8	0.106	27	0.273	21	0.0027	20	0.658	4	0.481	12	0.0047	9
No. 29	0.0109	9	0.219	21	0.867	10	0.0061	11	0.241	18	0.620	7	0.0039	12
No. 11	0.0108	10	0.735	7	1.926	3	0.0137	3	0.249	17	0.705	6	0.0045	11
No. 3	0.0100	11	0.423	14	0.040	26	0.0009	22	0.713	2	0.919	4	0.0086	3
No. 46	0.0094	12	-0.885	50	-0.682	42	-0.0062	47	0.095	25	0.110	22	0.0008	20
No. 40	0.0082	13	0.731	8	0.645	13	0.0071	8	0.002	30	-0.720	48	-0.0049	50
No. 57	0.0080	14	0.519	10	2.151	2	0.0139	2	0.200	20	-0.155	35	-0.0009	27
No. 4	0.0063	15	0.150	22	0.897	9	0.0049	14	0.587	6	1.259	1	0.0095	2
No. 8	0.0061	16	0.385	15	0.570	15	0.0037	17	0.203	19	1.129	3	0.0075	4
No. 60	0.0054	17	0.011	31	-0.120	30	-0.0012	32	0.055	28	0.353	16	0.0022	15
No. 19	0.0043	18	0.768	6	0.454	18	0.0050	13	0.280	14	0.578	9	0.0046	10
No. 58	0.0039	19	0.085	28	0.018	28	-0.0001	28	-0.283	39	-0.233	38	-0.0025	39
No. 20	0.0029	20	-0.173	37	-0.286	34	-0.0019	33	-0.594	52	0.047	25	-0.0012	32
No. 22	0.0028	21	0.824	4	0.987	8	0.0083	5	0.527	8	-0.433	40	-0.0014	34
No. 14	0.0026	22	0.337	17	0.085	24	0.0016	21	0.298	11	0.089	24	0.0009	19
No. 65	0.0022	23	0.774	5	0.631	14	0.0054	12	0.480	10	0.513	11	0.0047	8
No. 33	0.0018	24	0.006	32	-0.370	35	-0.0035	36	-0.293	40	-0.038	31	-0.0010	31
No. 70	0.0011	25	-0.223	38	0.546	16	0.0006	23	0.023	29	-0.526	44	-0.0024	37
No. 74	0.0008	26	0.112	26	0.154	23	0.0001	26	-0.263	38	0.264	18	0.0001	23

clone	Across Sites**		Kasigau***						Kibwezi***					
	V (m^3)*	rank	H (m)*	rank	DBH (cm)*	rank	V (m3)*	rank	H (m)*	rank	DBH (cm)*	rank	V (m^3)*	rank
No. 16	0.0008	27	0.430	13	-0.161	32	-0.0011	31	-0.173	36	0.011	27	-0.0009	30
No. 61	0.0005	28	0.219	20	-1.260	52	-0.0052	43	0.493	9	0.097	23	0.0019	16
No. 5	0.0004	29	-0.060	34	-0.123	31	0.0004	25	0.177	22	-0.439	41	-0.0009	28
No. 2	0.0002	30	0.342	16	1.030	7	0.0067	10	-0.356	43	-0.736	51	-0.0041	46
No. 100	-0.0010	31	0.140	23	1.602	4	0.0081	6	-0.201	37	-0.296	39	-0.0024	38
No. 31	-0.0031	32	0.063	30	0.482	17	0.0029	19	-0.161	35	-0.182	36	-0.0016	35
No. 34	-0.0033	33	-0.612	46	-0.377	36	-0.0038	37	-0.037	31	0.440	15	0.0014	18
No. 10	-0.0034	34	-0.531	44	-1.251	51	-0.0077	51	-0.439	47	-0.008	28	-0.0021	36
No. 13	-0.0034	35	0.870	3	0.330	19	0.0046	15	-0.386	44	-0.933	53	-0.0054	52
No. 1	-0.0043	36	0.063	29	-0.234	33	-0.0005	29	-0.155	34	-0.034	29	-0.0008	26
No. 27	-0.0045	37	-0.386	41	-1.105	48	-0.0068	49	-0.547	49	0.306	17	-0.0012	33
No. 17	-0.0049	38	0.285	19	0.273	20	0.0006	24	0.113	24	0.134	20	0.0002	22
No. 37	-0.0062	39	-0.167	36	-1.149	49	-0.0049	41	0.250	16	0.232	19	0.0019	17
No. 55	-0.0071	40	-0.560	45	-0.443	37	-0.0032	34	-0.493	48	-0.725	49	-0.0043	48
No. 76	-0.0079	41	-0.659	47	-0.481	38	-0.0058	45	-0.415	46	-1.048	55	-0.0066	53
No. 23	-0.0088	42	-1.074	53	-0.848	45	-0.0081	52	-0.345	42	0.133	21	-0.0004	25
No. 32	-0.0090	43	-0.916	51	-1.245	50	-0.0057	44	0.079	27	-0.494	42	-0.0029	42
No. 12	-0.0097	44	-0.024	33	0.036	27	-0.0007	30	-0.584	51	-0.539	45	-0.0052	51
No. 21	-0.0104	45	0.289	18	0.061	25	0.0000	27	0.193	21	-0.499	43	-0.0031	43
No. 30	-0.0104	46	-0.414	42	-0.563	40	-0.0039	38	-0.843	54	-0.098	33	-0.0040	45
No. 91	-0.0117	47	-0.132	35	-0.821	44	-0.0059	46	0.293	12	-0.690	47	-0.0026	40
No. 97	-0.0123	48	-0.685	48	-0.051	29	-0.0033	35	-0.584	50	-0.233	37	-0.0032	44
No. 59	-0.0130	49	-0.309	39	-0.869	46	-0.0051	42	0.083	26	0.449	14	0.0033	14
No. 41	-0.0130	50	0.125	24	-0.927	47	-0.0063	48	-1.058	55	-0.961	54	-0.0069	54
No. 36	-0.0144	51	-1.117	54	-1.413	53	-0.0124	53	-0.344	41	-0.579	46	-0.0048	49
No. 24	-0.0148	52	-0.952	52	-1.709	54	-0.0125	54	-0.408	45	-0.077	32	-0.0026	41
No. 39	-0.0154	53	-0.870	49	-0.667	41	-0.0073	50	-0.113	33	0.025	26	-0.0009	29
No. 67	-0.0227	54	-1.352	55	-1.976	55	-0.0143	55	-0.606	53	-0.909	52	-0.0069	55
No. 79	-0.0257	55	-0.520	43	-0.820	43	-0.0047	40	-0.081	32	-0.736	50	-0.0042	47

clone	Across Sites**		Marimanti***						Tiva***					
	V (m^3)*	rank	H (m)*	rank	DBH (cm)*	rank	V (m3)*	rank	H (m)*	rank	DBH (cm)*	rank	V (m^3)*	rank
No. 6	0.0246	1	0.869	2	0.696	7	0.0110	4	1.794	1	3.961	1	0.0512	1
No. 9	0.0210	2	0.399	12	0.595	11	0.0062	12	0.993	6	3.825	2	0.0425	2
No. 7	0.0199	3	0.247	15	0.961	5	0.0100	6	0.720	12	3.763	3	0.0373	3
No. 43	0.0173	4	0.334	13	0.601	9	0.0075	8	0.923	8	2.992	4	0.0323	4
No. 49	0.0172	5	0.602	6	0.974	4	0.0121	2	0.740	11	1.331	8	0.0159	7
No. 51	0.0153	6	0.853	3	0.442	14	0.0070	9	1.101	5	1.308	9	0.0195	6
No. 48	0.0130	7	0.565	7	0.027	24	0.0024	20	0.236	18	-1.180	44	-0.0059	36
No. 53	0.0124	8	0.230	16	0.561	12	0.0069	10	1.157	4	-0.618	37	0.0005	25
No. 29	0.0109	9	0.409	11	1.048	3	0.0114	3	0.089	25	0.291	26	0.0014	23
No. 11	0.0108	10	0.106	20	0.597	10	0.0042	15	-0.001	29	1.274	10	0.0081	14
No. 3	0.0100	11	0.229	17	0.666	8	0.0069	11	0.903	9	0.888	14	0.0121	10
No. 46	0.0094	12	0.410	10	0.399	15	0.0049	14	1.671	2	1.153	12	0.0212	5
No. 40	0.0082	13	1.125	1	1.318	1	0.0181	1	-0.171	33	-0.386	31	-0.0059	35

clone	Across Sites**		Marimanti***						Tiva***					
	V (m^3)*	rank	H (m)*	rank	DBH (cm)*	rank	V (m3)*	rank	H (m)*	rank	DBH (cm)*	rank	V (m^3)*	rank
No. 57	0.0080	14	0.100	22	0.136	19	0.0009	25	0.142	22	0.751	16	0.0053	18
No. 4	0.0063	15	0.108	19	0.116	20	0.0011	23	0.035	27	0.336	24	0.0004	27
No. 8	0.0061	16	-0.584	52	-0.539	48	-0.0053	43	-0.231	36	2.026	5	0.0143	9
No. 60	0.0054	17	0.460	9	0.138	18	0.0029	18	0.888	10	-0.412	33	0.0032	22
No. 19	0.0043	18	-0.308	42	0.220	17	0.0021	21	-0.224	35	0.174	27	-0.0021	29
No. 58	0.0039	19	0.217	18	0.083	21	0.0010	24	0.157	20	1.220	11	0.0113	11
No. 20	0.0029	20	0.105	21	1.152	2	0.0107	5	-0.123	31	-0.033	28	-0.0024	31
No. 22	0.0028	21	-0.036	27	-0.477	44	-0.0025	30	0.927	7	0.439	22	0.0080	15
No. 14	0.0026	22	-0.256	38	-0.360	38	-0.0030	33	0.241	17	1.582	6	0.0147	8
No. 65	0.0022	23	-0.106	33	-0.248	35	-0.0030	32	-0.454	42	-1.072	43	-0.0119	44
No. 33	0.0018	24	-0.013	25	0.751	6	0.0077	7	-0.365	38	0.479	21	0.0004	26
No. 70	0.0011	25	0.752	4	-0.059	28	0.0058	13	0.285	16	-1.220	45	-0.0100	41
No. 74	0.0008	26	-0.088	32	-0.414	41	-0.0054	44	0.077	26	1.000	13	0.0084	13
No. 16	0.0008	27	0.052	24	0.031	23	0.0011	22	0.364	14	0.574	18	0.0071	16
No. 61	0.0005	28	0.603	5	-0.137	30	0.0001	26	1.398	3	-0.640	38	0.0013	24
No. 5	0.0004	29	0.541	8	-0.033	26	0.0033	17	0.434	13	-0.642	39	-0.0029	32
No. 2	0.0002	30	-0.025	26	-0.507	46	-0.0044	41	0.360	15	0.397	23	0.0054	17
No. 100	-0.0010	31	-0.311	43	-0.035	27	-0.0024	29	-1.475	54	-0.088	29	-0.0122	45
No. 31	-0.0031	32	-0.079	31	0.296	16	0.0026	19	-0.932	51	-1.358	46	-0.0160	47
No. 34	-0.0033	33	-0.296	41	-0.432	42	-0.0057	45	-0.441	41	0.294	25	-0.0021	30
No. 10	-0.0034	34	-0.481	49	0.063	22	-0.0031	34	-0.092	30	1.445	7	0.0088	12
No. 13	-0.0034	35	0.279	14	-0.298	36	-0.0019	27	0.115	23	-0.388	32	-0.0029	33
No. 1	-0.0043	36	-0.391	47	-0.696	51	-0.0079	51	0.150	21	0.546	19	0.0048	20
No. 27	-0.0045	37	-0.359	44	-0.351	37	-0.0044	39	-0.362	37	0.887	15	0.0035	21
No. 17	-0.0049	38	-0.569	51	-0.231	34	-0.0062	46	0.207	19	-0.594	36	-0.0047	34
No. 37	-0.0062	39	-0.077	30	-0.180	32	-0.0020	28	-0.525	43	-0.728	40	-0.0072	39
No. 55	-0.0071	40	-0.761	54	-0.648	49	-0.0098	54	0.106	24	0.660	17	0.0049	19
No. 76	-0.0079	41	-0.139	34	-0.832	54	-0.0066	47	-0.186	34	0.516	20	0.0002	28
No. 23	-0.0088	42	-0.283	40	0.001	25	-0.0032	35	-0.393	39	-0.476	34	-0.0065	37
No. 32	-0.0090	43	-0.044	28	0.517	13	0.0035	16	-0.633	45	-2.480	52	-0.0247	52
No. 12	-0.0097	44	-0.755	53	-0.726	52	-0.0097	53	-0.417	40	-0.560	35	-0.0079	40
No. 21	-0.0104	45	0.076	23	-0.395	40	-0.0038	37	-0.800	50	-2.588	53	-0.0227	51
No. 30	-0.0104	46	-0.499	50	-0.437	43	-0.0070	50	-0.790	49	-1.570	47	-0.0176	49
No. 91	-0.0117	47	-0.061	29	-0.812	53	-0.0069	49	0.002	28	-1.659	49	-0.0153	46
No. 97	-0.0123	48	-0.248	37	-0.107	29	-0.0026	31	-1.218	52	-2.313	50	-0.0223	50
No. 59	-0.0130	49	-0.181	36	-0.366	39	-0.0042	38	-0.137	32	-1.011	42	-0.0106	43
No. 41	-0.0130	50	-0.282	39	-0.218	33	-0.0044	40	-0.672	47	-0.809	41	-0.0104	42
No. 36	-0.0144	51	-0.385	46	-0.535	47	-0.0067	48	-0.575	44	-1.599	48	-0.0173	48
No. 24	-0.0148	52	-1.109	55	-0.976	55	-0.0124	55	-0.661	46	-0.150	30	-0.0068	38
No. 39	-0.0154	53	-0.155	35	-0.160	31	-0.0037	36	-0.786	48	-3.412	54	-0.0329	54
No. 67	-0.0227	54	-0.427	48	-0.680	50	-0.0083	52	-1.440	53	-2.383	51	-0.0278	53
No. 79	-0.0257	55	-0.362	45	-0.501	45	-0.0052	42	-2.111	55	-3.742	55	-0.0347	55

*The breeding value, presented as the deviation from average. **Breeding values and rank across 4 sites. The values are same as in table 3. ***Breeding values and rank at each site.

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