ASSESSING CASSAVA BREEDING CLONES IN TWO AGROECOLOGIES IN THE DEMOCRATIC REPUBLIC OF CONGO

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ABSTRACT

Breeding is the most economical approach for controlling production constraints in cassava (*Manihot esculenta* Crantz) smallholder farms. This study aims at assessing the performances of elite cassava clones in the province of Kwilu, Democratic Republic of Congo (DRC). Three sets of trials were established using an alpha lattice and a randomized complete block designs in two contrasting locations, upland savanna and valley forest agroecologies. Eleven traits were used in phenotyping the cassava clones along with two checks varieties (local cultivar Biele and improved variety OBAMA). High heritability was recorded for the traits and it ranged from 0.52 to 0.75 except for yield (0.45). They are significant differences between the tested clones and the improved variety OBAMA. Overall, the Best Linear Unbiased Estimates (BLUEs) used for weighing in the selection index led to two candidate clones, KYK2016-048 and KYK2015-04 that outperformed both checks, Obama and Biele in this study and they could be potential candidates for variety replacement.

RÉSUMÉ

Évaluation des clones issus de la sélection du manioc dans deux agroécologies en République Démocratique du Congo

La sélection reste l'approche la plus économique pour la gestion des contraintes dans la production agricole notamment avec les petits exploitants de manioc (*Manihot esculenta Crantz*). Cette étude vise à évaluer les performances des clones de manioc dans la province de Kwilu, en République démocratique du Congo (RDC). Trois types d'essais ont été installés uniforme suivant le schéma de sélection du manioc avec un dispositif alpha lattice en essai préliminaire et le bloc aléatoire complet pour les essais avancé et uniforme. Les essais ont été installés dans deux sites différents dont les agroécologies de la savane et de la forêt de la vallée. Onze paramètres ont été reportés pour le phénotypage des clones de manioc y compris les deux variétés témoins (cv. local Biélé et la variété améliorée OBAMA). Une héritabilité élevée a été enregistrée pour l'ensemble des paramètres mesurés et elle varie de 0,52 à 0,75 sauf pour le rendement en racine (0,45). Il existe des différences significatives entre les clones testés et les témoins. Dans l'ensemble, les meilleures estimations linéaires non biaisées (BLUEs) utilisées pour mesurer l'indice de sélection ont montré que deux clones KYK2016-048 et KYK2015-04 présentent une meilleure performance comparativement aux témoins Biélé et Obama dans cette étude et ils pourraient être des candidats potentiels pour le remplacement de la variété.

Mots-clés : *sélection, RDC, Manihot esculenta, savane, forêt de la vallée, rendement.*

I - INTRODUCTION

Tropical starchy root, cassava (Manihot esculenta Crantz), originally from South America, has self-spread almost worldwide. It constitutes the staple food crop for more than 800 million people in sub-Saharan Africa [1, 2]. Across the globe, the Democratic Republic of Congo (DRC) is among the top 10 producers and the first producer in the Central and East Africa regions [3, 4]. In sub-Saharan Africa, particularly in DRC, cassava is served as a doughy ball called fufu that accompanies stews and greens like cassava leaves and spinach. Besides its high contribution to food security, it also contributes to farmers' income generation [4 - 7]. According to FAO [8], the highest peak of cassava production in DRC was recorded from 2000 to 2011, from which the yield was above 15 million tons per year. Since then, the production has decreased despite the population growth and the

high demand for cassava as the major staple food. This decline is due to several biotic and abiotic constraints. In DRC, as well as in Africa, major diseases and pests with a substantial threat to cassava production cassava mosaic geminiviruses (CMGs), cassava mosaic disease (CMD), cassava brown streak viruses (CBSVs), whitefly vector, CBSD-like symptoms, Cassava green mite (CGM), cassava mealybug (CMB), anthracnose (CAD), cassava bacterial blight (CBB), cassava root necrosis disease (CRND) and variegated grasshopper [9 - 14]. At the same time, abiotic stress, including floods, drought, poor soil fertility (pH, nutrient contents and ratios) are the most contributors to flow cassava yields in DRC [15 - 19]. Farmers in the province of Kwilu face the above challenges which lead to low cassava productivity and low-income generation [3, 18]. Hopelessly optimistic, forests are destroyed by farmers to establish agricultural fields as a solution of high yield production and poor soil. Previous studies have shown that one of the main causes of deforestation in the worldwide are the extension of agricultural areas that involves the clearing of land by shifting cultivation [20 - 23]. Researchers have reported similar information in DRC which holds the second largest forest in the world after the Amazon [24]. In 2018, an average annual of 1 million hectares of forest reduction were recorded in DRC [25] and the pressure might increase regarding the population growth and country development to overcome food and other resources needed. In most cases, the best approach and most affordable to face the multi stresses in crop production, particularly for smallholders, is the adoption of improved varieties, with high and stable yields, resistant/tolerant to stress with high dry matter. Here, I will present the challenges related to cassava production in the forest as well as in the savanna (lack of improved varieties) and justify the need of evaluating cassava clones to identify top performing cassava varieties. Therefore, this study aimed to evaluate the performances of cassava clones in different trials across valley and upland ecologies to identify the new candidates for release and the improvement of cassava breeding scheme in Kiyaka program.

II - MATERIAL AND METHODS

II-1. Experimental Sites

Two agroecologies, upland savanna and valley forest, at the "Institut National des Etude et Recherche Agraonomiques (INERA)" station of Kiyaka in the province of Kwilu in DRC were used to establish the trials. The savanna dry land and valley forest are located at 5°33'S, 19°47E, 723 m above sea level (masl) and 5°32'S, 18°96'E, 455 masl, respectively. The

Kiyaka's valley is characterized by the dense moist or semi-deciduous young forest fallows and palm groves while the upland is dominated by wooded savanna, most of which belong to the Guinean-Congolese transition zone. The experiments were conducted over two cropping seasons 2017 to 2019 across two agroecologies *(Figure 1)*.
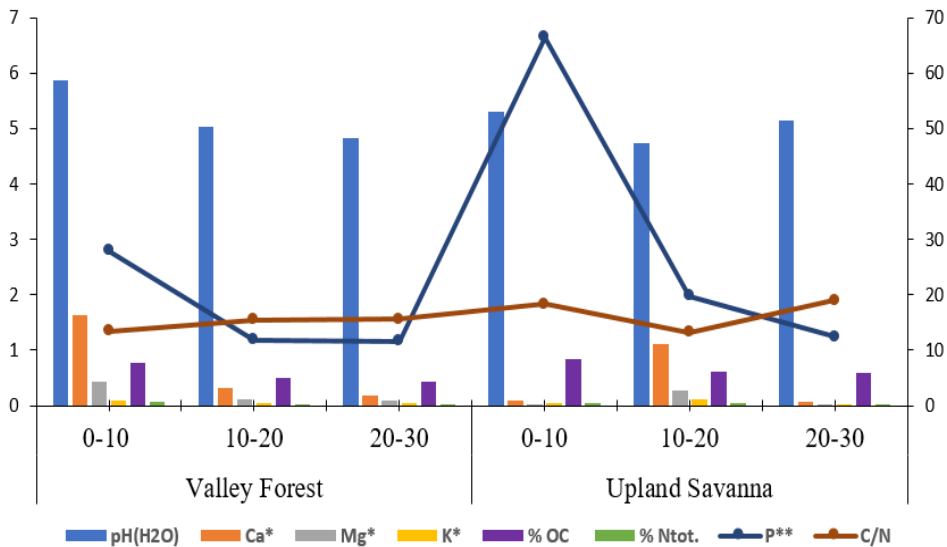

Figure 1 : *Characteristics of the soils of the valley and upland sites>*
*cmol $^{[+]}$kg^{-1} and **mg kg^{-1}

II-2. Planting Material

Half-sib (HS) cassava varieties are the dominant popular varieties grown currently in Central, East and West Africa. The planting materials evaluated at Kiyaka in this study were generated through half-sib progenies obtained from the elite's parents introduced from the INERA, Mvuazi research center, in the province of Kongo Central in DRC. Eighteen parents were used in this breeding program. Across the trials, TME 419 (also known as OBAMA/improved variety) and Biele (local variety) were used as checks. Biele and OBAMA are highly susceptible and resistant to CMD, respectively [26]. *Table 1* shows the pedigree and clones evaluated in this study with respective flesh root color.

Table 1 : *Pedigree of cassava genotypes evaluated in this study across valley and upland agroecologies in 2017 - 2019*

N	PEDIGREE	Clones	Color of Flesh	N	PEDIGREE	Clones	Color of Flesh
1	MM 97-2015	KYK2016-048	White	28	ZIZILA	KYK2017-08	White
2	BIELE	KYK2016-041	White	29	BIELE	KYK2016-042	White
3	OBAMA	OBAMA	White	30	MVZ 99-038	KYK2016-016	White
4	MVZ 99-150	KYK2015-015	White	31	MM 97-2015	KYK2016-046	White
5	KINTUNTU	KYK2016-061	White	32	MVZ 99-038	KYK2016-010	White
6	MVZ 85-297	KYK2016-037	White	33	RAV	KYK2017-035	White
7	KINTUNTU	KYK2016-057	White	34	OBAMA	KYK2016-017	White
8	KINTUNTU	KYK2016-060	White	35	KINTUNTU	KYK2017-059	White
9	MVZ 99-038	KYK2016-08	White	36	KINTUNTU	KYK2016-059	White
10	KINDISA	KYK2014-073	Yellow	37	KYK 2012-028	KYK2017-031	White
11	MM 97-2015	KYK2016-049	White	38	MVZ 99-038	KYK2015-062	White
12	KINTUNTU	KYK2016-056	White	39	MVZ 99-038	KYK2016-02	White
13	OBAMA	KYK2017-020	White	40	ZIZILA	KYK2017-014	White
14	MUBULU	KYK2014-060	White	41	MVZ 99-038	KYK2016-03	White
15	MVZ 99-038	KYK2016-025	White	42	Mabungi	KYK2015-054	White
16	MVZ 85-297	KYK2016-035	White	43	ZIZILA	KYK2017-06	White
17	OBAMA	KYK2017-018	White	44	MVZ 99-0395	KYK2016-038	Yellow
18	NSANSI	KYK2017-022	White	45	MUGOLI	KYK2017-050	White
19	M'VUAMA	KYK2016-052	White	46	MVZ 99-038	KYK2016-024	White
20	BIELE	KYK2017-047	White	47	OBAMA	KYK2017-019	White
21	MVZ 99-038	KYK2016-09	White	48	MVZ 99-038	KYK2016-04	White
22	MVZ 99-038	KYK2016-014	White	49	BUTAMU	KYK2017-038	White
23	BIELE	KYK2017-045	White	50	ZIZILA	KYK2017-07	White
24	BIELE	BIELE	White	51	MVZ 99-038	KYK2016-07	White
25	BUTAMU	KYK2017-039	Yellow	52	RAV	KYK2017-037	White
26	ZIZILA	KYK2017-03	White	53	OBAMA	KYK2017-015	White
27	KYK 2012-028	KYK2017-033	White				

II-3. Clones evaluation across trials

A total of twelve trials in three sets were conducted for this study following the cassava breeding scheme comprising preliminary yield trial (PYT), advanced yield trial (AYT) and uniform yield trial (UYT). The three trials were evaluated at Kiyaka, upland savanna and valley forest during the cropping seasons 2017-2018 and 2018-2019. For 2018-2019 cropping season, 22 clones were evaluated as PYT and the selected clones from subsequent trials PYT and AYT of 2017-2018 trials were advanced to AYT and UYT of 2018-2019 trials. An alpha lattice design was used to establish the PYT while AYT and UYT was settled in randomized complete block design. PYT was established with two replications and AYT and UYT four replicates, at 1 m x 1 m spacing between and within rows.

II-4. Data collection

Eleven traits were collected at appropriate growth stage following the morphological and agronomical descriptors for the characterization of cassava [27] and the methods for diagnosing plant virus diseases laboratory manual [28]. Disease and pest infestations were recorded while conducting the trials. Among these traits, the *Table 2* shows qualitative traits collected six months after planting (MAP) and the cassava root necrosis disease at 12MAP.

Table 2 : *Traits collected from 2017 to 2019 during the experiments*

N°	Type of traits	Traits	Abbreviations	Description
1		Cassava Anthracnose Disease	CAD	
2		Cassava Bacterial Blight	CBB	Disease and pest infestations
3	Qualitative	Cassava Mosaic Disease	CMD	
4		Cassava root necrosis	CRND	
5		Helopeltis	HEL	
6		Biomass	Biomass	
7		Plant height	Plant height	
8	Quantitative	Diameter at root collar	DRCo	Agronomic traits
9		Dry Matter Content	DMatter	
10		Starch	Starch	
11		Yield	Yield	

Helopeltis is a pest commonly occurring in cacao and known as cassava disease in Kiyaka. Its typical symptoms are a discolored, necrotic area. Lesion appears around the point of entry of the labial stylets in the leaf. In response to salivary secretion by the insect, the affected leaves often curl and deformed, and dieback of young shoots [29]. All the diseases and pests' infestations recorded in this study were scored on a scale of 1-5, where 1 = healthy, no visible symptoms, and 5 = most severe symptoms in all the trials. However, mean disease severity was computed as the average between severity scores 2 to 5 and the incidence disease was estimated as the percentage of plants with severity scores between 2 to 5. Remaining data were collected at harvest (12 MAP).

II-5. Statistical Analysis

Data curation was done to identify outliners among individual clones before estimating genotypic means used in downstream analysis. We estimated quantitative genetic parameters following a single trait linear mixed model analysis that was fitted as :

$$y = X\beta + Zd + Wa + \varepsilon \qquad (1)$$

Where; y is the vector of phenotypic values (BLUEs), β is the vector of fixed effects attributed to the clonal genotypes, d is a vector random factors related to the design effects, where replications are nested within environments that were independent and identically distributed, is the vector of random additive genetic effects, and ε is the vector of random residual effects that followed a normal distribution. The broad-sense heritability (H) was estimated from variance components as :

$$H^2 = \frac{\sigma_G^2}{\sigma_G^2 + \frac{\sigma_{Ge}^2}{e} + \frac{\sigma_E^2}{er}} \qquad (2)$$

where $\sigma^2 G$, $\sigma^2 Ge$, $\sigma^2 e$ and r are the genetic variance from the clones, variance from clone x ecology, error variance and number of replications, respectively. In this paper, a multi-trait selection index was used to rank and select the most superior cassava genotypes in our breeding program. A range of different index weights were assigned to the different traits based on their significance relative to the end-user preferences. Different index weights were used and these included; a weight of 20 for fresh root yield, 10 for plant height, 15 for dry matter content, 10 for starch content, 15 for biomass and -10 for CMD resistance. The developed selection index ranking was then developed as summative product of the phenotypic BLUEs (Scaled) and the index weights as shown below :

SI = 20xYield + 10xHeight + 15xDMatter + 10xStarch + 15xBiomass – 10xCMD   (3)

The phenotypic correlation estimates between the evaluated traits was assessed in R using the '*cor*' function in the *"stats"* package [30].

III - RESULTS

III-1. Descriptive summary of eleven traits used for cassava clone's discriminant across twelve trials

This study evaluated cassava clones in twelve trials of different stage in cassava breeding scheme over two agro-ecologies. The topsoil (0-10 cm) chemical properties in valley forest ecology offered high nutrients of calcium, magnesium and potassium in addition to phosphorus, carbon and azote that favour the good establishment of the cassava growth from the early stage compared to the upland savanna *(Figure 1)*. High Kurtosis was

reported for CRND as well as for yield. At the same time, negative or positive low to moderate Kurtosis were recorded for the remaining traits *(Table 3)*.

Table 3 : *Summary descriptive of the 11 traits used for cassava clone's discriminant over the two ecologies of savanna and forest in the twelve trials at Kiyaka, DRC, 2017 - 2019*

Traits	Mean	Median	Min	Max	Kurtosis	SE	SD
CMD	1.33	1.00	1.00	4.00	3.64	0.05	0.83
CAD	2.01	2.00	1.00	4.00	-0.84	0.04	0.71
CBB	1.91	2.00	1.00	4.00	-0.62	0.04	0.68
CRND	1.11	1.00	1.00	3.00	12.61	0.02	0.37
Biomass	11.69	6.06	0.26	47.63	0.46	0.72	11.81
HEL	1.59	1.50	1.00	3.00	-0.61	0.04	0.65
Yield	29.32	21.38	0.95	101.64	8.22	1.62	26.36
DMatter	37.82	37.81	19.71	71.93	3.85	0.41	6.68
Starch	20.94	20.93	8.11	45.09	3.85	0.29	4.73
Height	2.31	2.10	0.40	4.75	-0.72	0.06	0.91
DRCo	2.43	2.30	1.10	4.10	-0.41	0.04	0.68

SD : Standard deviation; SE : Standard Error; CMD : Cassava Mosaic Disease; CAD : Cassava Anthracnose Disease; CBB : Cassava Bacterial Blight; CRND : Cassava Root Necrosis; HEL : Score Helopeltis damage; DMatter : Dry Matter content; DRCo : Height : Plant Height; Diameter at Root Collar.

III-2. Performance of clones under different agro-ecologies

Distribution of raw phenotypic values are showed in Fig. 2. Biomass, CAD, CBB, Dry Matter, starch, height, yield showed meaningful variation with normal distribution of phenotypic values. Significant (P < 0.05) to very highly significant (P < 0.001) differences were recorded for disease and pests as well as agronomic traits. A total of 5 pest and diseases (CMD, CAD, CBB, CRND, HEL) were recorded in different trials at forest and savanna ecologies across seasons. At 6 MAP, the most susceptible clones have recorded the maximum of 4 for disease as score, with leaves displayed general distortion. However, score of 3 was recorded for CRND at harvesting (12 MAP) indicating pronounced necrotic lesions (11–25 %) in the root irrespective of the ecologies over the year. In this study, yield varied between 0.95 to 101.64 T/ha, averaging 29.32 T/ha. High yield was recorded in the PYT with decreasing while size of the experimental plot

increases to access the root yield with less influence on the estimation. Also, 20.94 to 37.82 % were recorded for starch and for Dry Matter content respectively. The same trend was recorded for Biomass, DRCo and plant height *(Table 3)*.
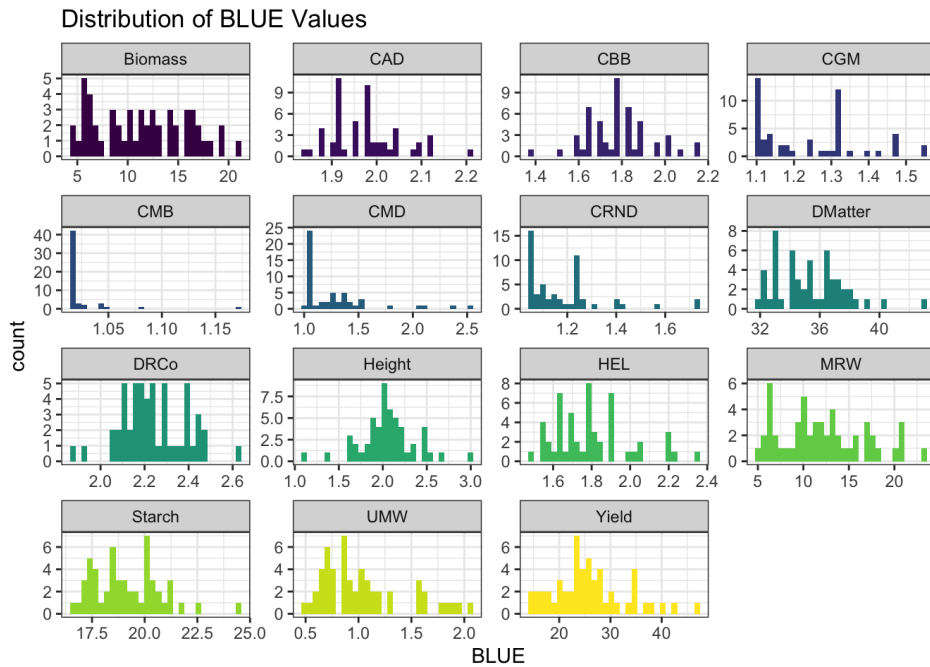

Figure 2 : *Distribution of phenotypic BLUEs of breeding clones across the agroecologies*

CAD : Cassava Anthracnose Disease; CBB : Cassava Bacterial Blight; CMD : Cassava Mosaic Disease; CRND : Cassava Root Necrosis; DRCo : Diameter at Root Collar; Height: Plant Height; HEL : Score Helopeltis damage; DMatter : Dry Matter Content.

Figure 3 highlights the relative performance of 53 cassava clones, evaluated across agro-ecologies over the years per trait relative to a weighted selection index (SI). Phenotypic data spanning key production traits was used in the selection index to rank those clones with outstanding performance. In our breeding program, we usually focus on six traits that represent our product profiles that fit the end user preferences of our target clients. Two checks were used to compare the performance of the promising candidate clones across agro-ecologies. Obama is known for its excellent tolerance to CMD, good plant architecture and Dry Matter

content while Biele was used as the most CMD susceptible check variety. In this study, we could see a couple of promising clones that outperformed Obama our best check variety. Therefore, two candidate clones KYK2016-048 and KYK2015-041 had consistently better performance than Obama for all the traits and high selection index. These clones are more resistant to CMD, higher Dry Matter content, higher plant height, higher starch content and fresh root yields than the best check, Obama. These promising clones show potential for broad and specific adaptation and must be closely monitored as they progress into the advanced testing stages and it comes up as potential clones be released to replace Obama.
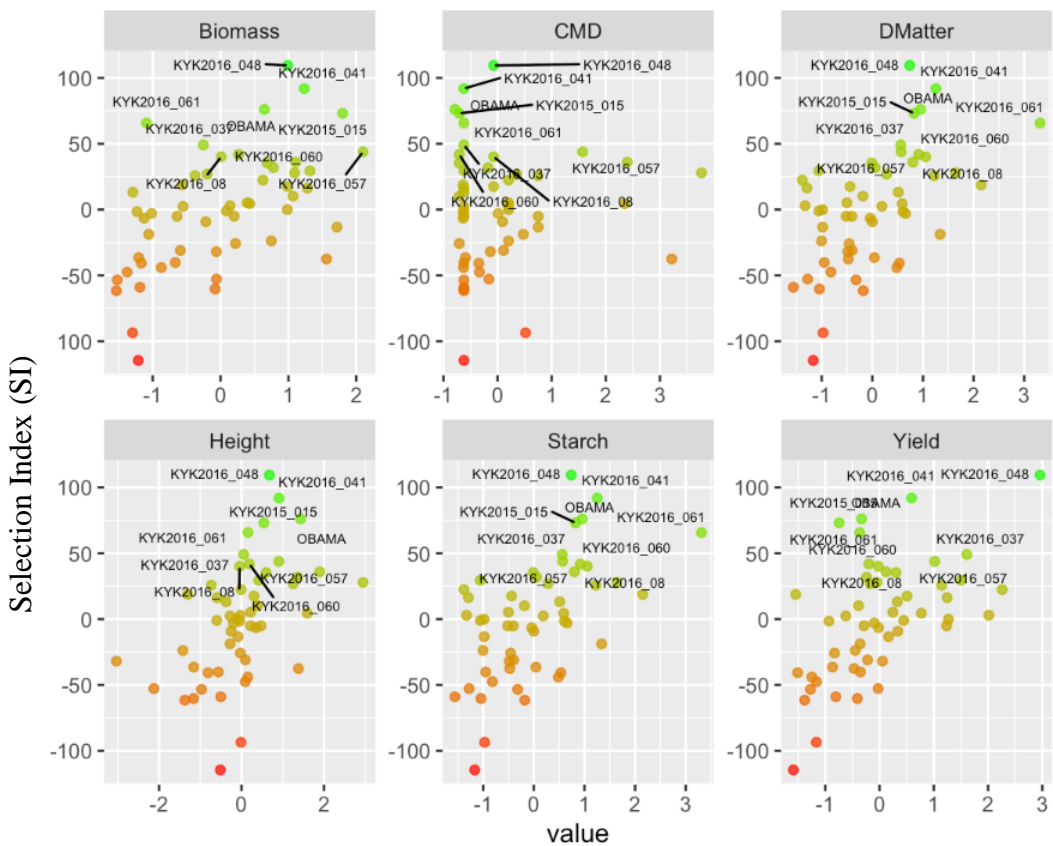
Figure 3 : *A graph of scaled phenotypic BLUEs against the selection index ranking of showing clonal performance across the different breeding trials during 2018-2020 cropping season*

CMD : Cassava Mosaic Disease; DMatter : Dry Matter Content, Height : Plant Height.

Relative high heritability (0.45 to 0.75) was recorded for the traits except for CAD (0.24) and Biomass (0.21) for the overall trials over the two years in different agro-ecologies *(Figure 4)*.
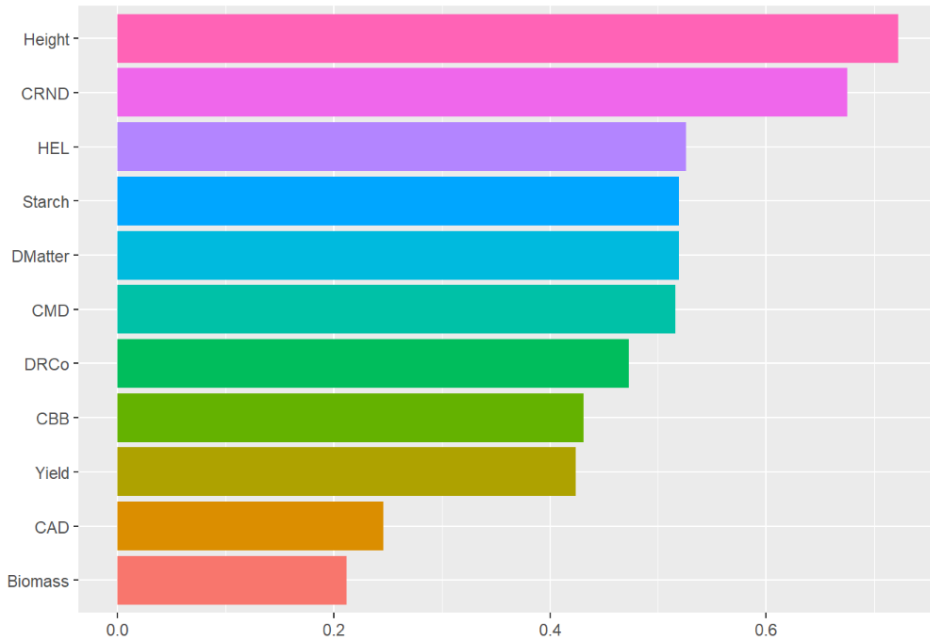

Figure 4 : *Traits heritability across the trials over the year in savanna upland and valley forest agro-ecologies in the province of Kwilu*

CAD : Cassava Anthracnose Disease; CBB : Cassava Bacterial Blight; CMD : Cassava Mosaic Disease; CRND : Cassava Root Necrosis; DRCo : Diameter at Root Collar; Height : Plant Height; HEL : Score Helopeltis damage; DMatter : Dry Matter Content. [#]Selection Index Weight

The expected selection gain is presented based on BLUE values average across different environments in DR Congo *(Figure 5)*. Overall, the proportion of selected clones compared to the unselected clones across traits was way above the mean performance values. For Biomass, almost 80 % of the selected clones had scores better than the population mean (0) and were skewed towards the highest biomass clones with a maximum BLUE score of 2. The same trend could be seen for resistance to CMD where a skewed distribution of clones towards the most resistant clones (above population mean of 1) were selected. Other key traits like starch content, fresh root yield, Plant height and Dry Matter content also followed more less a similar trend.
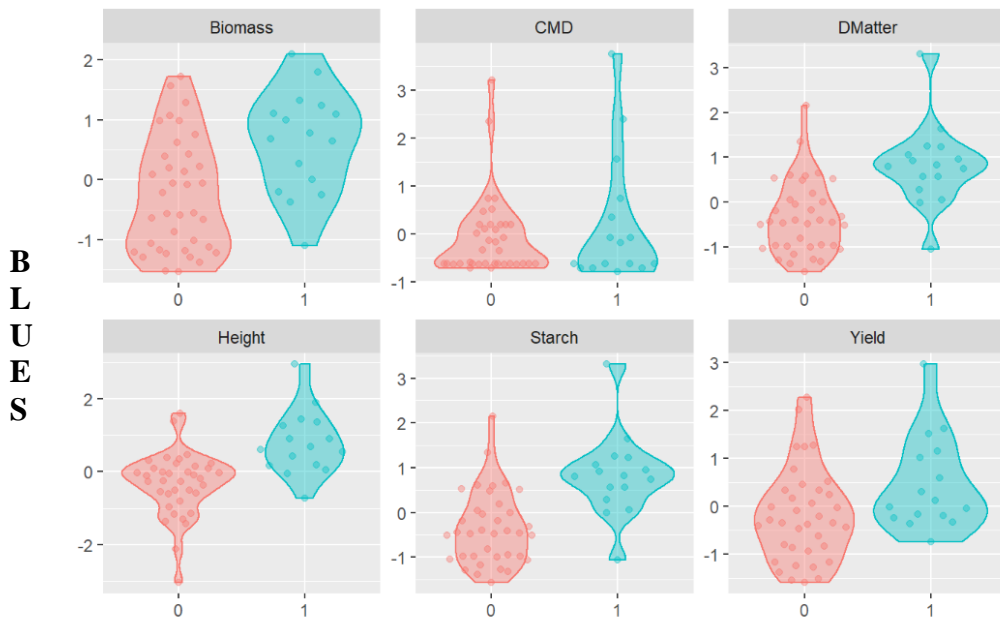
Figure 5 : *Best Linear Unbiased Estimates (BLUEs) of clones with expected selection gain in breeding the program across ecologies. (BLUEs of unselected (0) against selected (1))*

CMD : Cassava Mosaic Disease; DMatter : Dry Matter Content, Height : Plant Height

III-3. Relationship between traits across upland and forest ecologies

The contribution of each trait and the most discriminating ones across the ecologies were assessed *(Figure 6)*. Significant correlations were recorded between traits in this study. Positive and significant relationship was recorded between agronomic traits two by two; ie Dry Matter and starch, yield and Biomass, and between DRCo and height. Also, this study recorded positive correlation for disease symptoms except between HEL and CMD and CBB. However, yield and agronomic traits have significantly and negatively correlated to CRND and HEL. The positive correlation between CRND in one hand and negative between HEL on other hand respectively with CMD and CBB might hidden the effect of CMD on yield and leads to positive correlation between both traits.
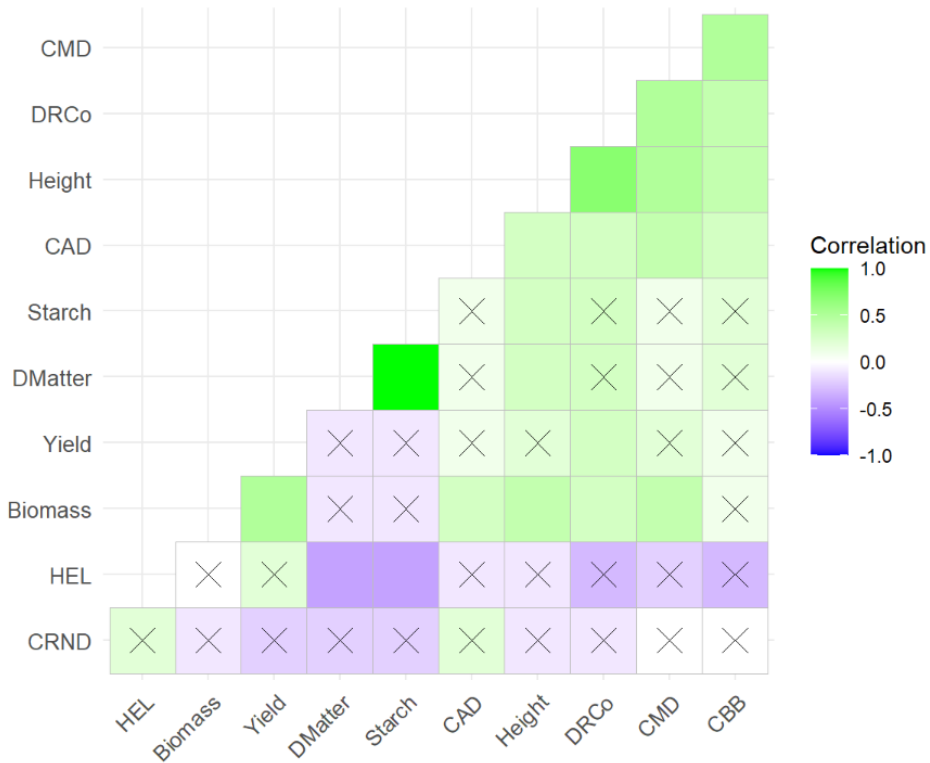
Figure 6 : *Corrplot displaying correlation among traits in upland savanna and valley forest. White cells indicate a non-significant correlation (p > 0.05)*

Circles below and above the blue round line correspond to the correlations obtained for trials under Savanna and Forest ecologies respectively. CAD : Cassava Anthracnose Disease; CBB: Cassava Bacterial Blight; CMD : Cassava Mosaic Disease; CRND: Cassava Root Necrosis; DRCo : Diameter at Root Collar; Height : Plant Height; HEL : Score Helopeltis damage; DMatter : Dry Matter Content. [#]Selection Index Weight.

IV - DISCUSSION

IV-1. Traits responses in the clone's phenotyping

Cassava is one of the most promising multi-purpose food crops in DR Congo mainly for its root and leaf products. Therefore, our breeding efforts respond to two major important market segments: fresh roots (including the processing of fufu and chikwangue) and the cassava leaves as vegetables.

Evaluation of the fifty-three clonal genotypes identified a significant level of variability that is comparable with the process selection and advancement process. The key output from this study was the identification of the top genotypes for the different product profiles that would serve the entire region. So, this study evaluated the performances of cassava clones through twelve trials across different breeding stages in the province of Kwilu in upland savanna and valley forest ecologies. The genetic and environmental parameters as well as the phenotypic correlation estimates among the studied traits are important in guiding the selection process in cassava. These parameters are vital in informing breeders about how well the observed phenotypic variation is explained by either genetic or non-genetic factors. Hence, breeders are able to dispose off the clones with undesirable trait combinations against those that have a combination of desired traits and are often advanced to later stages of selection. The clones used in this study are half sib (HS, Table 2). HS has the capability of polycross which expresses high heterosis in the progenies. Similar research was published in Uganda while assessing the breeding scheme for local adoption of cassava with farmers preferences [31]. In addition, HS seems the low-cost effective option in the cassava breeding program particularly in African national program where the research funds are limited (Sikirou, pers. Comm.). The evaluated cassava genotypes used in this study had high mean BLUE estimates for Dry matter content of 37.8 %, fresh root yield of 29.32, starch of 20.94 % and lowest CMD resistance score compared to the two common checks : Biele and Obama. Across the different traits, the observed range, minimum and maximum values are given a fair indication of that we had significant genetic variation from which to select and advance the most outstanding clones that could meet the end-user trait preference. Also, the magnitude of the heritability estimates for the various traits is a very important metric useful in obtaining satisfactory genetic gains with several series of selection.

IV-2. Relationship between traits and heritability

In this study plant height, CRND, HEL, Starch, Dry matter content, and CMD could be classified as being high to moderately heritable traits. The rest of the traits had low to moderate trait heritability estimates. Knowledge of trait relationships allows cassava breeders to select the main traits of interest characterized by low heritability and hard to evaluate faster and at lower cost. Trait correlations between disease related traits that are characterized by lowering the yield components of cassava formed that were strongly negative correlated to each other and to yield related traits.

In addition, a significant and positive correlation was recorded between Dry Matter content and starch, indicating that this study can generate repeatable results and could be used to target the cassava market. Also, the performances of the selected clones compared to the unselected clones across traits using BLUEs was way above the mean performance values. Bernado [32] has highlighted that BLUE is an effective approach to assess the phenotypic data in breeding program while advising the reinventing of quantitative genetics. About five diseases and pest were recorded in this study but only CRND and HEL showed significant and negative correlations on yield, dry matter and starch content respectively. Several researchers have reported similar results while stating that cassava is vulnerable to more than 20 virus diseases and pests [33] leading to important yield losses. CMD is endemic to cassava production in DRC. However, this study showed no significant negative impact on CMD and agronomic traits. CRND might hide the effect on yield, knows to negatively impact the fresh root and like cassava brown streak disease which causes annually economic losses of about 100 million USD [34, 35]. High heritability for the main traits like Dry Matter, yield, Biomass, starch, Height and CMD which resulting the preferences of the end users. This confirmed that the traits selected are representative of the product profile in this breeding program.

IV-3. Performances of clones evaluated

Multi-trait selection index is important in maximizing selection gains in cassava with yield related traits being the most efficient contributors to direct selection hence providing greater genetic gains among all evaluated traits across environments. Since selection of cassava involves the simultaneous evaluation of the different traits at the different evaluation stages, the yield related traits must be associated with a single numeric value to enhance advancement and selection decisions [36 - 39]. Through this selection process, cassava genotypes that combine desirable traits are simultaneously selected and advanced. Therefore, two clones, KYK2016-048 and KYK2015-041 outperformed significantly both improved (OBAMA) and local (BIELE) checks varieties, based selection and BLUEs in this study. The two clones could be recycling at the late stage and new released will be targeted to improve the Kiyaka breeding program and new varietal released to increase cassava production in DR Congo with add value to the incomes of producers and households' farmers.

V - CONCLUSION

In this study, the clones with agronomic traits like high dry matter content and starch preferred by end users were identified with high heritability. Among the clones evaluated against the checks, KYK2016-048 and KYK2015-041 has outperformed consistently using multi-trait selection index with the key traits of the breeding program like high fresh yield roots, dry matter, biomass, starch, height and CMD resistant. These clones could be released for cassava production in the province of Kwilu, DRC could be used for the improvement of the breeding program, and the two clones will be submitted to sensory evaluation by the end-users.

RÉFÉRENCES

[1] - IFAD, FAO, The world cassava economy : Facts, trends and outlook, in, Rome, (2000)

[2] - R. HOWELER, N. LUTALADIO, G. THOMAS, Save and grow : Cassava - a guide to sustainable production intensification, in : R. Howeler, Ed., Rome, (2013)

[3] - FaoStat, Statistical Database of the Food and Agriculture Organization of the United Nations, (2015) 1 - 10, http://faostat.fao.org (19 Fevier, 2022)

[4] - S. DUNSTAN, C. SPENCER, C. EZEDINMA, Cassava cultivation in sub-Saharan Africa, in ''Achieving sustainable cultivation of cassava'', Ed. *Burleigh Dodds Science Publishing*, London, (2017)

[5] - J. LEGG, E. A. SOMADO, I. BARKER, L. BEACH, H. CEBALLOS, W. CUELLAR, W. ELKHOURY, D. GERLING, J. HELSEN, C. HERSHEY, et al., A global alliance declaring war on cassava viruses in Africa, *Food Security*, 6 (2014) 231 - 248

[6] - N. THANDAR, Improving agronomic efficiency in cassava- based farming systems in the democratic republic of congo using organic and inorganic inputs, in, Kenyatta University, School of Environmental Studies, (2014) 172 p.

[7] - A. I. MALIK, P. KONGSIL, V. A. NGUYỄN, W. OU, SHOLIHIN, P. SREAN, M. N. SHEELA, L. A. BECERRA LÓPEZ-LAVALLE, Y.

UTSUMI, C. LU et al., Cassava breeding and agronomy in Asia : 50 years of history and future directions, *Breeding science*, 70 (2020) 145 - 166

[8] - FAO, Crop production statistic, (2020), http://faostat.fao.org (08 Septembre 2020)

[9] - C. M. FAUQUET, D. M. BISARO, R. W. BRIDDON, J. K. BROWN, B. D. HARRISON, E. P. RYBICKI, D. C. STENGER, J. STANLEY, Revision of taxonomic criteria for species demarcation in the family Geminiviridae, and an updated list of begomovirus species, *Archives of Virology*, 148 (2003) 405 - 421

[10] - B. V. H. CAMPO, G. HYMAN, A. BELLOTTI, Threats to cassava production: Known and potential geographic distribution of four key biotic constraints, *Food Security*, 3 (2011) 329 - 345

[11] - C. M. CASINGA, G. MONDE, R. R. SHIRIMA, J. P. LEGG, First Report of Mixed Infection of Cassava Brown Streak Virus and Ugandan Cassava Brown Streak Virus on Cassava in North-eastern Democratic Republic of Congo, *Plant Disease*, 103 (2019)

[12] - Z. BAKELANA, M. L. BOYKIN, M. KEHOE, J. PITA, G. MONDE, N. MAHUNGU, M. LEMA, K. TSHILENGE, M. KALONJI, Cassava Root Necrosis Disease (CRND) : A New Crop Disease Spreading in Western Democratic Republic of Congo and in Some Central African Countries, *Journal of Agricultural Science*, 12 (2020) 105 - 116

[13] - T. ALICAI, C. A. OMONGO, M. N. MARUTHI, R. J. HILLOCKS, Y. BAGUMA, R. KAWUKI, A. BUA, G. W. OTIM-NAPE, J. COLVIN, Re-emergence of Cassava Brown Streak Disease in Uganda, Plant Disease, 91 (2007) 24 - 29

[14] - J. P. LEGG, S. JEREMIAH, H. OBIERO, M. MARUTHI, I. NDYETABULA, G. OKAO-OKUJA, Comparing the regional epidemiology of the cassava mosaic and cassava brown streak virus pandemics in Africa, *Virus Research*, 159 (2011) 161 - 170

[15] - M. A. EL-SHARKAWY, Physiological characteristics of cassava tolerance to prolonged drought in the tropics : implications for breeding cultivars adapted to seasonally dry and semiarid environments, *Brazilian Journal of Plant Physiology*, 19 (2007) 257 - 286

[16] - E. OKOGBENIN, T. SETTER, M. FERGUSON, R. MUTEGI, H. CEBALLOS, B. OLASANMI, M. FREGENE, Phenotypic approaches to drought in cassava : *review, Frontiers in Physiology*, 4 (93) (2013) 1 - 15

[17] - E. J. D. OLIVEIRA, S. D. T. AIDAR, C. V. MORGANTE, A. R. D. M. CHAVES, J. L. CRUZ, M. A. COELHO FILHO, Genetic parameters for drought-tolerance in cassava, *Pesquisa Agropecuária Brasileira*, 50 (2015) 233 - 241

[18] - K. KINTCHÉ, S. HAUSER, N. M. MAHUNGU, A. NDONDA, S. LUKOMBO, N. NHAMO, V. N. E. UZOKWE, M. YOMENI, J. NGAMITSHARA, B. EKOKO et al., Cassava yield loss in farmer fields was mainly caused by low soil fertility and suboptimal management practices in two provinces of the Democratic Republic of Congo, *European Journal of Agronomy*, 89 (2017) 107 - 123

[19] - UNDP, The magic of cassava: Adapting to climate change in the Democratic Republic of the Congo, (2020), https://reliefweb.int/report/democratic-republic-congo/magic-cassava-adapting-climate-change-democratic-republic-congo (15 Novembre 2022)

[20] - L. A. THRUPP, S. HECHT, J. BROWDER, The diversity and dynamics of shifting cultivation: Myths, realities, and policy implications, in ''World Resources Institute'', Ed. J. L. OWEN, M. NABIHA, O. B. WILLIAM, Washington, (1997) 42 p.

[21] - B. FINEGAN, R. NASI, The biodiversity and conservation potential of shifting cultivation landscapes, in "Agroforestry and biodiversity conservation in tropical landscapes", Ed. G. SCHROTH, G. A. B. DA FONSECA, C. A. HARVEY, C. GASCON, H.L. VASCANCELOS, A.-M. N. IZAC, Island Press, Washington and London, (2004) 153 - 197

[22] - R. A. HOUGHTON, Tropical Deforestation as a Source of Greenhouse Gas Emissions, in Tropical Deforestation and Climate Change, Ed. P. MOUTINHO, Ed. S. *Schwartzman Scientific Research*, Belém, Brazil, (2005) 13 - 21

[23] - J. R. MAKANA, S. C. THOMAS, Impacts of selective logging and agricultural clearing on forest structure, floristic composition and diversity, and timber tree regeneration in the Ituri forest, Democratic Republic of Congo, *Biodiversity and Conservation*, 15 (2006) 1375 - 1397

[24] - R. NOGHEROTTO, E. COPPOLA, F. GIORGI, L. MARIOTTI, Impact of Congo Basin deforestation on the African monsoon, *Atmospheric Science Letters*, 14 (2013) 45 - 51

[25] - A. TYUKAVINA, M. C. HANSEN, P. POTAPOV, D. PARKER, C. OKPA, S. V. STEHMAN, I. KOMMAREDDY, S. TURUBANOVA, Congo Basin forest loss dominated by increasing smallholder clearing, *Science advances*, 4 (2018) 1 - 12

[26] - SENASEM, Catalogue variétal des cultures vivrières en République Démocratique du Congo, Service National de Semences (SENASEM), Democratic Republic of Congo, (2020) 111 p.

[27] - W. M. G. FUKUDA, C. L. GUEVARA, R. KAWUKI, M. E. FERGUSON, Selected morphological and agronomic descriptors for the characterization of cassava, in, International Institute of Tropical Agriculture (IITA), Nigeria, (2010) 19 p.

[28] - K. LAVA, P. L. JAMES, Laboratory manual for the diagnosis of cassava virus diseases, in, International Institute of Tropical Agriculture, Nigeria, (2009) 111 p.

[29] - G. M. STONEDAHL, The Oriental species of Helopeltis (*Heteroptera Miridae*): A review of economic literature and guide to identification, *Bulletin of Entomological Research*, 81 (1991) 465 - 490

[30] - R. C. TEAM, R : A Language and Environment for Statistical Computing., in "R Foundation for Statistical Computing'', Ed. A. Vienna, (2016)

[31] - R. S. KAWUKI, A. PARIYO, T. AMUGE, E. NUWAMANYA, G. SSEMAKULA, S. TUMWESIGYE, A. BUA, Y. BAGUMA, C. OMONGO, T. ALICAI et al., A breeding scheme for local adoption of cassava (Manihot esculenta Crantz), *African Journal of Crop Science*, 6 (2018) 001 - 011

[32] - R. BERNARDO, Reinventing quantitative genetics for plant breeding: something old, something new, something borrowed, something BLUE, Heredity, (2020)

[33] - O. J. ALABI, P. L. KUMAR, R. A. NAIDU, Cassava Mosaic Disease : A curse to food security in sub-Saharan Africa, APSnet Features, (2011)

[34] - J. NDUNGURU, P. SSERUWAGI, F. TAIRO, F. STOMEO, S. MAINA, A. DJINKENG, M. KEHOE, L. M. BOYKIN, Analyses of Twelve New Whole Genome Sequences of Cassava Brown Streak Viruses and Ugandan Cassava Brown Streak Viruses from East Africa : Diversity, Supercomputing and Evidence for Further Speciation, PLoS ONE, 10 (2015)

[35] - Z. BAKELANA, M. L. BOYKIN, M. KEHOE, J. PITA, G. MONDE, N. MAHUNGU, M. LEMA, K. TSHILENGE, M. KALONJI, Cassava Root Necrosis Disease (CRND) : A New Crop Disease Spreading in Western Democratic Republic of Congo and in Some Central African Countries, *Journal of Agricultural Science*, 12 (2020) 105 - 116

[36] - L. L. BHERING, B. G. LAVIOLA, C. C. SALGADO, C. F. B. SANCHEZ, T. B. ROSADO, A. A. ALVES, Genetic gains in physic nut using selection indexes, *Pesquisa Agropecuária Brasileira*, 47 (2012) 402 - 408

[37] - A. A. C. DE AZEREDO, L. L. BHERING, B. P. BRASILEIRO, C. D. CRUZ, L. C. I. SILVEIRA, R. A. OLIVEIRA, J. C. BESPALHOK FILHO, E. DAROS, Comparison between different selection indices in energy cane breeding, *Genetics and molecular research*, 16 (2017) 1 - 13

[38] - M. LOPEZ-CRUZ, G. DE LOS CAMPOS, Optimal breeding-value prediction using a sparse selection index, Genetics, 218 (2021) 1 - 36

[39] - L. D. S. ROSADO, C. E. M. SANTOS, B. DOS, C. H., E. S. NUNES, C. D. CRUZ, Simultaneous selection in progenies of yellow passion fruit using selection indices, *Revista Ceres*, 59 (2012) 95 - 101