Analysis of the Stability and Yield Performance of Biofortified Common Bean (Phaseolus vulgaris L.) Genotypes under Low Altitude Conditions

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Authors’ contributions

This work was done in collaboration among all the authors. Author AKM is the promoter of my doctoral thesis. In this article, he contributed in aspects related to plant diseases. Author PNN is a member of the supervising committee of my thesis. In this work, he contributed in the aspects of plant breeding. Author ALK is co-promoter of my PhD thesis and a specialist in biofortification. He carried out analyses of micronutrients in different varieties. Author MMM carried out the statistical analyses of this article. All the authors have read and approved the final manuscript.

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ABSTRACT

The supply of biofortified material to areas affected by malnutrition or micronutrient deficiency remains one of the major concerns of breeders. Nevertheless, this material must be efficient and stable. The evaluation of this performance and stability requires statistical indices. Biofortified genotypes are evaluated for the first time by these indices.

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The objective of this work is to analyze the performance and stability of biofortified common bean genotypes under low altitude conditions in the Democratic Republic of Congo. The present contribution uses the evaluation of twenty-six genotypes of biofortified common beans over six crop years using parametric ($W^2$, $s^2$, S(d), $\theta$, CVi, $\sigma^2$, $\theta_i$, $\theta$) and non-parametric ($S^{(1)}$, $S^{(2)}$, $S^{(3)}$, $S^{(4)}$, NP(1), NP(2), NP(3), NP(4), KR, AR) indices for the identification of successful and stable genotypes. The results indicate the presence of the genotype x year interaction. Principal Component Analysis (PCA) shows similarities between the indices. Mean sum rank (AR) identifies NYIRAMUHONDO, G59/1-2, CODMLV 086, MBC 23, NABE 4, and K 131 as performing and stable genotypes. In the end, the best genotypes are those that are both efficient and stable. However, where stability is much more desired in relation to performance, the use of ecovalence (Wi) is more appropriate in the stability calculation.

Keywords: Biofortified bean; stability; performance; low altitudes; parametric indices; genotype x environment interaction.

1. INTRODUCTION

Malnutrition is one of the world’s major public health problems. According to the latest studies conducted by the Ministry of Public Health in the Democratic Republic of Congo (DRC), malnutrition affects two out of three children, or more than 60% of children under five years of age. The same studies reveal that 47% of children and 38% of women suffer from anemia and a deficiency of essential micronutrients including iron and zinc. Among the most affected provinces is Kongo Central with a prevalence of over forty-five percent [1].

To fight against this malnutrition, several strategies such as diversification of the food ration, food fortification, biofortification and supplementation have been proposed. All these strategies have so far not been able to satisfactorily address the problem of malnutrition except bio fortification of food crops such as common beans, which has proven to be sustainable and effective for the DRC where the majority of communities have low income and cannot afford to buy diversified foods such as fruits and vegetables [2].

Indeed, agronomic research has developed in recent decades plant material characterized by a high content of micronutrients such as iron and zinc using conventional plant breeding techniques, these are the biofortified varieties [3]. These have the potential to disseminate iron, zinc and vitamin A to populations with limited access to commercial markets. They give higher yields and are resistant to diseases and pests than local varieties [4].

At Kongo Central, the introduction of the biofortified common bean started with the identification of promising lines by breeders, followed by testing the performance and stability of the identified varieties across different environments, to assess genotype x environment interactions [5]. The use of performance stability study is a means of identifying stable and performing material. Numerous stability analysis methods are proposed in the literature [6].

In DRC, little work has been done to study the stability of yield performance of recently introduced biofortified common bean varieties. In addition, to our knowledge, the use of parametric and non-parametric methods has not been studied before.

The objective of this study is to analyze the performance and stability of twenty-six genotypes of biofortified common bean under low altitude conditions (below 500 meters) using parametric and non-parametric methods.

2. MATERIALS AND METHODS

2.1 Study Framework

The study area is located in the Kongo Central province in the DRC. The agricultural sites of Kisantu, Kimpese and Luki were the sites of our trials. The geographical coordinates of the Kongo Central Province are 4° and 6° South latitude and 12° and 16° East longitude, and the altitude varies according to location [7].

Climate: The climate of Kongo-Central is tropical but of Sudanese type with a dry season of more than 4 months from May to September. There is a large rainy season accompanied by a small dry season in February. The climate of Kongo Central is a steppe climate characterized by high rainfall and the second type of climate is the AW4 type.
Temperature: The average annual temperature is around 25°C. The luminosity is particularly low (of the order of 50% between 7 and 17 hours), where it is around 20% during the dry season [7].

Precipitation: Rainfall is of short duration; it follows each other over about ten days during the month with an average monthly height of about 130 mm, and a maximum that can exceed 200 mm in January. Average annual rainfall varies from 900 mm to 1,500 mm.

The average climatic data of the test sites over six crop years are shown in Table 1.

Floors: There are different categories of soils in Kongo Central: (1) sandy soils of the arénoferral type, found in Kisantu (2) sandy-clay to clay soils, found in Kimpese and Luki (3) sandy-clay soils, and (4) sandy-clay soils with sandy-clay patches [7]. The average data in relation to organo-mineral fertility for the three sites tested are shown in Table 2.

Conduct of the experiment: Multi-year trials were set up in three agro-ecological zones of the Kongo Central during season C (dry season during which rainfall is almost non-existent) for a duration of six years (2014-2019) in the lowlands. The average geographical coordinates of the experimental sites are given in Table 3.

2.2 Plant Material

The plant material consists of twenty-six genotypes of common bean (P. vulgaris L.) pre-selected by the International Center for Tropical Agriculture, CIAT (Cali/Colombia), the Pan-African Bean Research Alliance, PABRA (Uganda, Kenya and Malawi) and the National Institute for Agricultural Research, INERA Mulungu; improved and pre-selected for their high iron (>50-94 mg/kg) and zinc (>25-40 mg/kg) content and pre-selected for their good agronomic performance (high yield, disease and insect resistance/tolerance, drought, low soil fertility, etc.).

These genotypes belonged to both bean gene pools, the Andean gene pool and the Mesoamerican gene pool, and were subdivided into two groups of trials according to their growth habit: the first trial included 15 dwarf bean genotypes and the second 11 voluble bean genotypes. The mean duration of sowing-flowering and sowing-maturity ranged from 36 to 41 days and 70 to 90 days for dwarf genotypes and 41 to 50 days and 91 to 120 days for broad bean genotypes, respectively. Note that for each trial we had a control genotype. In the three agro-ecological zones, the diseases frequently encountered are bean mosaic, rust and root rot. The biotic and abiotic constraints are about the same in the three trial sites and did not vary much within and between years during the six cropping seasons.

Seed samples of the 26 genotypes were analyzed at the Laboratory of the National Seed Service (SÉNASEM) for specific purity (to know the identity and degree of cleanliness of the seeds), germination test (to determine the viability of the seeds) and sanitary analysis (to check the presence or absence of pathogens in the seeds).

In each agro-ecological zone, the trial was conducted according to the randomized complete block design with 3 replicates in each experimental site. The plots each had 4 rows of 4 meters long sown at 0.40 m spacing between rows and 0.20 m spacing between plants with two seeds per poquet for dwarf genotypes and 0.50 m x 0.20 m with two seeds per poquet for voluble genotypes. The total number of plots for each trial corresponds to the number of genotypes. These trials were set up on soils with different cropping histories, however, precautions were taken to avoid soils that had carried the common bean crop for at least 2 previous years or seasons. No treatment or application of mineral or organic fertilizers or pesticides was used. Cultivation care had focused on void refilling, weeding and ridging. Ratings were based on vegetative parameters, phytosanitary evaluations and yield components according to the CIAT Bean Germplasm Standard Evaluation Standards [8].

Table 1. Average climatic data for the six crop years

| Month of the year | Precipitation (mm) | Wind speed (km/s) | Ground temperature (°C) | Air temperature (°C) | Humidity (%) |
|-------------------|---------------------|-------------------|-------------------------|----------------------|-------------|
| June              | 11,2                | 2,30              | 25,7                    | 24                   | 79,8        |
| July              | 0                   | 2,11              | 23,8                    | 22                   | 77,9        |
| August            | 0                   | 2,30              | 23,5                    | 22,9                 | 73,3        |
| September         | 16,0                | 2,97              | 27                      | 24,6                 | 70,6        |
Table 2. Soil chemical characteristics of test sites

| Agro-Ecological Zone | pH  | Exchange acidity (meq/100g) | CO (%) | Exchangeable bases (Meq/100g) | C.E.C. Meq/100g | P ppm  | N (%)  | Fe (%) |
|----------------------|-----|-----------------------------|--------|-------------------------------|-----------------|--------|--------|--------|
|                      |     | H₂O KCl Al³⁺⁺H⁺ Al³⁺ H⁺ Ca Mg K Na |        |                               |                 |        |        |        |
| Kisantu              | 5,01| 3,9 - 1,11 - 1,82 0,57 0,29 0,17 0,03 6,10 | 8      | 0,08 3,2                     |                 |        |        |        |
| Kimpese              | 6,74| 5,76 - - 2,46 3,41 2,19 0,18 0,08 13,6 | 24     | 0,34 7,4                     |                 |        |        |        |
| Luki                 | 4,93| 3,7 - 1,70 - 2,58 1,13 0,29 0,44 0,06 5,22 | 6      | 0,06 4,9                     |                 |        |        |        |

Table 3. Average geographical coordinates of the experimental sites

| Agro-ecological Zones | Altitude | Latitude | Longitude |
|-----------------------|----------|----------|-----------|
| Kisantu               | 496 m    | 04°55'69'' | 15°19'39'' |
| Kimpese               | 263 m    | 05°53'26'' | 14°43'78'' |
| Luki                  | 132 m    | 05°63'40'' | 13°05'45'' |
2.3 Data Analysis

The elite genotypes for each year were identified by an analysis of variance of common bean seed yield. The same is true for the identification of the performing genotypes and the genotype x environment interaction test [9].

Two statistical groups were used to interpret genotype x environment interactions for numerical analyses. These are the parametric statistics grouping the following indices:

Ecovalence of Wricke (Wi²): This is the contribution of each genotype to the sum of the squares of genotype x environment interactions. Thus genotypes with low values have smaller deviations from the mean between environments and are more stable [10].

Shukla stability variance (σ²i): This is the stability variance of genotype i as its variance between environments after the main effects of environmental averages have been removed. According to this statistic, genotypes with minimal values should be more stable [11].

Coefficient of variance (CVi): Francis and Kannenberg [12] suggest the coefficient of variance as a stability statistic by combining the coefficient of variation, average yield and environmental variance. Genotypes with low CVi, low environmental variance (EV) and high mean yield are considered most desirable.

Regression coefficient (bi): The slope regression bi is the response to the environmental index which is the derivative of the average performance of all genotypes in each environment [13]. If bi does not differ significantly from 1, then the genotype is adapted to all environments. A bi>1 indicates genotypes that are more sensitive to environmental change and greater specificity of adaptability to high-yield environments, while a bi<1 describes a measure of greater resistance to environmental change, thus increasing the specificity of adaptability to low-yield environments.

Deviation from regression (S²di): In addition to slope regression, the variance of deviation from regression has been suggested as one of the most widely used parameters for the selection of stable genotypes. Genotypes with S²di=0 would be the most stable, while S²di>0 would indicate lower stability in all environments. Therefore, genotypes with lower values are most desirable [14].

Mean variance component (θi): Plaisted and Peterson [15] proposed the variance component for genotype x environment interactions as a measure of stability. Genotypes with a lower θi value are considered more stable.

GE variance component θ(i): This statistic is a measure of the stability parameter. In this approach, the ith genotype is removed from the data set and the GxE variance of this subset is the stability index of the ith genotype. According to this index, varieties that show higher statistics for θ(i) are considered stable [14].

For the non-parametric statistics, the following indices were calculated:

Non-parametric statistics of Huhn and Nassar (S(1), S(2), S(3), S(6)): Huhn [16] and Nassar [17] proposed four nonparametric statistics: S(1) the mean of the absolute rank differences of a genotype in all tested environments, S(2), the variance between ranks in all tested environments, S(3), the sum of the absolute differences for each genotype from the mean of the ranks, and S(6), the sum of the squares of the ranks for each genotype. To calculate these statistics, the average yield data must be transformed into ranks for each genotype and environment, and genotypes are considered stable if their ranks are similar from one environment to another. Low values for each of these statistics indicate high stability for a certain genotype.

Thennarasu non-parametric statistics (NP(1) NP(2) NP(3) NP(4)): These four NP statistics (1-4) are a set of alternative nonparametric statistics defined by Thennarasu [18]. These parameters are based on the ranks of the adjusted means of the genotypes in each environment. The low values of these statistics reflect high stability.

Sum of Kang's rows (KR): The Sum of Kang's Rows [19] uses both yield and σ²i as selection criteria. This parameter gives weight to yield and stability statistics to identify high-yielding and stable genotypes. The genotype with the highest yield and lower σ²i compared to other genotypes is the most desirable.

Average of ranks (AR): This is the average of ranks or the average of the ranks of all parametric and non-parametric indices.

The stability analysis was performed using STABILITYSOFT software. The latter is a new
online program to calculate parametric and non-parametric stability statistics for the identification of performing and stable genotypes [14].

The data for the principal component analysis, Spearman's correlation matrix, which establishes the relationships between parametric and non-parametric statistics, were processed using SAS software (version 6.1).

3. RESULTS AND DISCUSSION

3.1 Presentation of Results

3.1.1 Genotypic variability of performance and performance analysis

There is significant intra- and inter-annual variation among dwarf beans. The average seed yield of all genotypes ranges from 682.17 to 1581.83 kg/ha. The analysis of variance of yield, by year, shows differences in performance between varieties. The classification of genotypes is done year by year according to the best yield of each genotype. Thus genotypes HM 21-7 and CODMLB 078 take the lead in the ranking respectively in the years 2014, 2015 and 2016. Genotype K 131 is ranked first successively in the years 2017, 2018 and 2019 (Table 4).

The yield of a cultivar varies from place to place and from year to year. Genotype analysis based on seed yield indicates that 2019 is the best year as it had the highest yield of all six crop years and 2015 is the bad year as it had the lowest yield of all six crop years (Table 4).

Analysis of the performance of dwarf genotypes: Performing genotypes are those whose average seed yields are higher than the general average of 1043.4 kg/ha. Thus the genotypes CODLMB 001, CODMLB 078, HM 21-7, K 131, NABE 4, RWR 2154 and RWR 2245 have proven to be performing genotypes.

Table 5 shows very significant differences (P<0.001) between genotypes and between years. NAMULENGA, MAC 44, NAIN DE KYONDO, NYIRAMUHONDO, and AFR 708 genotypes were superior in 2014, 2015, 2016, 2017, 2018, and 2019, respectively. Note the performance of the control genotype (2127 kg/ha) during 2019.

Analysis of the performance of voluble genotypes: The overall average performance of the voluble genotypes is 1235.6 kg/ha. The performing genotypes are G59/1-2, MAC 44, NAMULENGA, and NYIRAMUHONDO.

Table 4. Average yields (kg/ha) of sixteen dwarf bean genotypes in 6 crop years (2014-2019)

| Genotypes       | 2014 | 2015 BAY | 2016 | 2017 | 2018 | 2019 BY | OA  |
|-----------------|------|----------|------|------|------|---------|-----|
| A 445           | 863  | 897      | 1335 | 719  | 894  | 1021    | 954.83 |
| CODLMB 001      | 1160 | 692      | 842  | 1033 | 576  | 2144    | 1074.50 |
| CODMLB 078      | 921  | 2102     | 1887 | 1003 | 909  | 1043    | 1310.83 |
| HM 21-7         | 1714 | 920      | 780  | 1139 | 701  | 1495    | 1124.83 |
| K 131           | 1022 | 1665     | 1531 | 1740 | 2489 | 1581.83 |
| MARUNGI         | 1022 | 1665     | 1531 | 1740 | 2489 | 1581.83 |
| NABE 4          | 343  | 1101     | 1077 | 980  | 680  | 1099    | 987.67 |
| NUA 619         | 588  | 668      | 783  | 1435 | 411  | 1283    | 861.33 |
| NUA 709         | 502  | 654      | 776  | 923  | 569  | 1232    | 776.00 |
| NUA 8           | 473  | 976      | 1196 | 1152 | 618  | 1254    | 944.83 |
| NUA 99          | 1320 | 2062     | 1786 | 797  | 1512 | 1451    | 1488.00 |
| RWR 2245        | 1496 | 1256     | 1345 | 678  | 436  | 1440    | 1108.50 |
| RWR 2154        | 720  | 780      | 602  | 621  | 738  | 803     | 710.67 |
| T LOCAL         | 695  | 848      | 575  | 443  | 511  | 1788    | 810.00 |
| ZKA 98-6m/95    | 941.2| 1016.4   | 1086.6| 1042.3| 803.7| 1399.6| 1043.4 |
| Overall average | 603.8| 603.8    | 603.8| 603.8| 603.8| 603.8   | 603.8 |
| CV (%)          | 41   | 47       | 39   | 26   | 48   | 32      |     |
| P value         | <.0001| <.0001  | <.0001| <.0001| <.0001| <.0001  |     |

BY: Best year in all six crop years, BAY: Bad year in every six crop years, OA: overall average; T LOCAL: Control genotype
Table 5. Average yields (kg/ha) of 11 bean genotypes in 6 crop years (2014-2019)

| Genotypes          | 2014 BAY | 2015 | 2016BY | 2017 | 2018 | 2019 | OA         |
|--------------------|----------|------|--------|------|------|------|------------|
| AFR 708            | 1430     | 821  | 1853   | 770  | 112  | 2127 | 1185,50    |
| COD MLV 098        | 773      | 1201 | 1205   | 1174 | 894  | 1558 | 1134,17    |
| CODMLV 086         | 1139     | 1289 | 1282   | 1017 | 671  | 1984 | 1230,33    |
| CODMLV 095         | 1533     | 1203 | 1003   | 896  | 802  | 980  | 1069,50    |
| G59/1-2            | 1289     | 1626 | 1450   | 1250 | 1010 | 1430 | 1342,50    |
| KINURE             | 920      | 890  | 1200   | 1140 | 994  | 1350 | 1082,33    |
| MAC 44             | 1080     | 1650 | 946    | 1033 | 723  | 2013 | 1240,83    |
| MBC 23             | 1321     | 980  | 1240   | 1140 | 1005 | 1200 | 1147,67    |
| NAIN DE KYONDO     | 730      | 1174 | 2292   | 890  | 978  | 1002 | 1177,67    |
| NAMULENGA          | 1605     | 1140 | 2012   | 975  | 636  | 1233 | 1266,83    |
| NYIRAMUHONDO       | 1566     | 1633 | 1812   | 2078 | 1284 | 1913 | 1714,33    |
| Overall average    | 1219.4   | 1230.1 | 1466.3 | 1131.1 | 839.8 | 1524.9 | 1235.6    |
| CV (%)             | 25       | 23   | 29     | 30   | 35   | 26   |            |
| SDPP (5%)          | <.0001   | <.0001 | <.0001 | <.0001 | <.0001 | <.0001 |            |
| P value            | <.0001   | <.0001 | <.0001 | <.0001 | <.0001 | <.0001 |            |

BY: Best year in all six crop years, BAY: Bad year in every six crop years, OA: Overall average

Analysis of Tables 4 and 5 notes the change in genotype rankings from one year to the next, which is an indication of the interaction. This allows us to analyze yield stability in order to identify successful and stable genotypes.

3.1.2 Yield stability analysis

Stability based on conjoint regression analysis (bi): The regression coefficients range from 0.1 to 3.2 (Table 2).

The genotypes CODMLV 098, NUA 709, NUA 99, NAMULENGA, K 131, RWR 2154, MAC 44, ZKA 98-6m/95, CODMLV 086, CODMLB001 and AFR 708 have a regression coefficient greater than unity (b>1). On the other hand, T LOCAL, CODMLV 095, NABE 4, RWR 2245, MBC 23, A 445, NUA 619, KINURE, MARUNGI, CODMLB078, K 131, RWR 2245, CODLMB 001, NAMULENGA and NUA 619 (Table 6).

Stability based on ecovalence (Wi²): Ecovalence measures the contribution of each genotype to the genotype x environment interaction. Genotypes with low ecovalence values are considered stable. Those with high Wi² values are indicative of instability. The most stable genotypes according to this parameter are MARUNGI, KINURE, COD MLV 098, NUA 8, G59/1-2, MBC 23, A 445 and NYIRAMUHONDO, while unstable genotypes are AFR 708, NAIN DE KYONDO, CODMLB078, K 131, RWR 2245, CODLMB 001, NAMULENGA and NUA 619 (Table 6).

In breeding, farmers look for genotypes with small performance differences from one year to the next. Hence the use of ecovalence requires determining the weight to be given to stability in favor of yield potential by selecting genotypes that contribute moderately to the interaction. This is the case of genotype CODMLV 095 (Wi² = 530702.6) compared to unstable genotypes such as AFR 708 (Wi² = 1587830.9) and NAIN DE KYONDO (Wi² = 1432415.3) and genotypes considered stable such as MARUNGI (Wi² = 75119.6) and KINURE (Wi² = 107946.9) (Fig. 1).

Stability based on Shukla variance (σ²ᵢ): The stable genotypes according to this parameter are MARUNGI, KINURE, COD MLV 098, NUA 8, G59/1-2, MBC 23, A 445 and NYIRAMUHONDO. Unstable genotypes are AFR 708, NAIN DE KYONDO, CODMLB 078, K 131, RWR 2245, CODLMB 001, NAMULENGA, NUA 619, HM 21-7 (Table 6).

Stable or unstable genotypes identified by the Shukla stability variance parameter generally make it possible to better exploit the favorable year. All of these genotypes show higher yields in the best years (Fig. 2).
Table 6. Parameters of yield stability of genotypes from parametric statistics

| Genotypes         | Y     | Wᵢ²  | σᵢ² | s²dᵢ | bᵢ | CVᵢ | θᵢ | θᵢ |
|-------------------|-------|------|-----|------|----|-----|-----|-----|
| A 445             | 954.8 | 225842.8 | 43921.0 | 23623.5 | 0.5 | 22.0 | 123332.0 | 86132.3 |
| AFR 708           | 1185.5 | 1587830.9 | 339018.5 | 61595.0 | 3.2 | 63.7 | 111528.1 | 227779.1 |
| COD MLV 098       | 1134.2 | 122158.3 | 21456.1 | 17341.5 | 1.1 | 24.3 | 124230.6 | 75349.1 |
| CODMLB 001        | 1074.5 | 871820.0 | 183882.8 | 85766.4 | 2.1 | 52.7 | 117733.5 | 153313.9 |
| CODMLB 078        | 1310.8 | 1381446.2 | 294301.8 | 192667.2 | 0.6 | 40.9 | 113316.8 | 206315.1 |
| CODMLV 086        | 1230.3 | 276967.9 | 54998.1 | 10358.6 | 1.9 | 35.3 | 122889.9 | 91449.3 |
| CODMLV 095        | 1069.5 | 530702.6 | 109974.0 | 49204.8 | 0.1 | 24.6 | 120689.9 | 117837.7 |
| G59/1-2           | 1342.5 | 150642.0 | 27627.5 | 17588.0 | 0.7 | 15.7 | 123983.8 | 78311.4 |
| HM 21-7           | 1113.2 | 740991.2 | 155536.5 | 103857.3 | 0.8 | 37.2 | 118867.4 | 139707.7 |
| K 131             | 1581.8 | 1070593.4 | 226950.3 | 148994.3 | 1.3 | 34.2 | 116010.8 | 173986.4 |
| KINURE            | 1082.3 | 107946.9 | 18376.9 | 10499.3 | 0.6 | 16.5 | 124353.8 | 73871.1 |
| MAC 44            | 1240.8 | 630681.6 | 131636.1 | 73495.6 | 1.7 | 39.3 | 119823.4 | 128235.5 |
| MARUNGI           | 987.7  | 75119.6  | 11264.3 | 5973.1  | 0.6 | 16.3 | 124638.3 | 70457.1 |
| MBC 23            | 1147.7 | 189339.4 | 36012.0 | 10186.8 | 0.3 | 11.7 | 123648.4 | 82336.0 |
| NABE 4            | 1234.7 | 372490.4 | 75694.7  | 29721.2  | 0.2 | 16.7 | 122061.1 | 101383.7 |
| NAIN DE KYONDO    | 1177.7 | 1432415.3 | 305345.1 | 203936.8 | 0.9 | 48.0 | 112875.0 | 211615.8 |
| NAMULENGA         | 1266.8 | 841010.8 | 177207.4 | 118626.5 | 1.2 | 38.2 | 118000.6 | 150109.8 |
| NUA 619           | 682.2  | 821614.0 | 173004.8 | 111178.1 | 0.6 | 60.5 | 118168.7 | 148092.5 |
| NUA 709           | 861.3  | 552437.2 | 114683.1 | 78599.6  | 1.1 | 47.2 | 120501.5 | 120098.1 |
| NUA 8             | 776.0  | 142338.8 | 25828.5 | 20318.4  | 1.0 | 34.7 | 124055.7 | 77447.9 |
| NUA 99            | 944.8  | 256005.3 | 50456.2  | 36244.9  | 1.1 | 34.5 | 123070.6 | 89269.2 |
| NYIRAMUHONDO      | 1714.3 | 226545.8 | 44073.3  | 31775.4  | 0.9 | 16.4 | 123325.9 | 86205.4 |
| RWR 2245          | 1488.0 | 1026436.4 | 217383.0 | 129669.6 | 0.3 | 28.9 | 116393.5 | 169394.0 |
| RWR 2154          | 1108.5 | 509825.2 | 105450.6 | 64229.4  | 1.5 | 39.8 | 120870.8 | 115666.5 |
| T LOCAL           | 710.7  | 240477.6 | 47091.9  | 4772.7   | 0.1 | 11.6 | 123205.2 | 87654.3 |
| ZKA 98-6m/95      | 610.0  | 651038.2 | 136046.7 | 71829.9  | 1.8 | 61.7 | 119647.0 | 130352.6 |

Y: mean yield of a genotype, Wᵢ²: Ecovalence, σᵢ²: Shukla stability variance, s²dᵢ: regression deviation; bᵢ: regression coefficient, CVᵢ: coefficient of variation, θᵢ: GE variance component; θᵢ: mean variance component
Fig. 1. Variation in yield performance of genotypes contributing strongly (AFR 708, NAIN DE KYONDO,) moderately (CODMLV 095) and weakly (KINURE, MARUNGI) to genotype x environment interaction ($W^2$)

Fig. 2. Temporal stability and yield performance of genotypes with low (Marungi, Kinure, NUA 8) and high (AFR 708, K 131, CODMLV 098) $\sigma^2$ values
Stability based on the residual of the regression (S_{di}): According to this parameter, the ideal genotype is the one with the highest seed yield and a regression coefficient significantly close to unity and S_{di} values of zero or close to zero. From a selection point of view, the use of S_{di} is similar to that of evecovariance. Among the genotypes evaluated in this study T LOCAL, MARUNGI, MBC 23, CODMLV 086, KINURE, COD MLV 098 and G59/1-2 are stable (Table 6).

Stability based on the coefficient of variation (CVI): According to this index, the desirable genotype is the one that gives regular production, good performance and a low coefficient of variation in the region for which it is intended [20]. Based on this principle, T LOCAL, MBC 23, G59/1-2, MARUNGI, NYIRAMUHONDO, KINURE, NABE 4 and A 445 genotypes are considered stable (Table 6).

Stability based on Plaisted’s GXE variance components (θ_{i}) and Plaisted and Peterson’s mean variance (θ): The two associated indices give exactly the same types of stable and unstable genotypes. Stable genotypes for θ_{i} are the same for θ and vice versa. MARUNGI, KINURE, COD MLV 098, NUA 8, G59/1-2, MBC 23, A 445, and NYIRAMUHONDO are the stable genotypes for both indices. Unstable genotypes are AFR 708, NAIN DE KYONDO, COD MLV 098, and K 131 (Table 6).

Stability based on the sum of the Kang Ranks (KR): This parameter combines Shukla yield and stability variance to identify stable genotypes. KR class G59/1-2, NYIRAMUHONDO, COD MLV 098, KINURE, MBC 23, and MARUNGI as stable genotypes (Table 7).

Stability based on Huhn and Nassar nonparametric statistics (S_{1}^{(1)}, S_{2}^{(2)}, S_{3}^{(3)}, S_{4}^{(4)}): Huhn and Nassar consider as stable, any genotype whose ranks are similar from one environment to another. These statistics classify NYIRAMUHONDO, MARUNGI, G59/1-2, KINURE and COD MLV 098 as stable genotypes. AFR 708 and NAIN DE KYONDO are unstable genotypes according to these four indices (Table 7).

Table 7. Yield stability parameters of genotypes from non-parametric statistics

| Genotypes        | KR  | S_{1}^{(1)} | S_{2}^{(2)} | S_{3}^{(3)} | S_{4}^{(4)} | NP_{1}^{(1)} | NP_{2}^{(2)} | NP_{3}^{(3)} | NP_{4}^{(4)} | AR  |
|------------------|-----|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| A 445            | 27.0| 6.6         | 29.4        | 14.4        | 2.5         | 5.0         | 0.6         | 0.6         | 0.6         | 12  |
| AFR 708          | 36.0| 12.3        | 108.3       | 40.6        | 4.2         | 10.3        | 0.7         | 0.8         | 0.9         | 21  |
| COD MLV 098      | 16.0| 5.1         | 19.4        | 6.1         | 1.2         | 3.8         | 0.2         | 0.3         | 0.3         | 6   |
| CODMLV 001       | 38.0| 9.3         | 60.6        | 24.9        | 3.0         | 7.7         | 0.6         | 0.7         | 0.8         | 19  |
| CODMLV 078       | 29.0| 9.7         | 61.8        | 19.1        | 2.4         | 8.2         | 0.6         | 0.6         | 0.6         | 18  |
| CODMLV 086       | 20.0| 5.7         | 21.4        | 6.6         | 1.3         | 4.8         | 0.3         | 0.3         | 0.4         | 8   |
| CODMLV 095       | 32.0| 9.2         | 54.8        | 21.1        | 2.8         | 6.5         | 0.5         | 0.6         | 0.7         | 15  |
| G59/1-2          | 9.0 | 3.8         | 10.2        | 2.7         | 0.8         | 4.2         | 0.3         | 0.3         | 0.2         | 5   |
| HM 21-7          | 32.0| 9.3         | 57.0        | 20.1        | 2.5         | 7.7         | 0.4         | 0.6         | 0.7         | 17  |
| K 131            | 25.0| 7.1         | 35.9        | 8.7         | 1.5         | 8.0         | 0.3         | 0.5         | 0.3         | 13  |
| KINURE           | 18.0| 5.1         | 17.5        | 6.4         | 1.4         | 4.7         | 0.3         | 0.4         | 0.4         | 7   |
| MAC 44           | 23.0| 7.3         | 38.8        | 12.1        | 1.9         | 6.7         | 0.5         | 0.5         | 0.5         | 13  |
| MARUNGI          | 20.0| 2.9         | 6.6         | 2.9         | 0.8         | 2.8         | 0.4         | 0.3         | 0.3         | 5   |
| MBC 23           | 18.0| 5.9         | 22.7        | 7.4         | 1.4         | 4.5         | 0.2         | 0.4         | 0.4         | 7   |
| NABE 4           | 20.0| 6.8         | 31.1        | 9.0         | 1.5         | 7.3         | 0.3         | 0.5         | 0.4         | 10  |
| NAIN DE KYONDO   | 36.0| 10.4        | 74.7        | 28.0        | 3.3         | 7.7         | 0.6         | 0.6         | 0.8         | 21  |
| NAMULENGA        | 26.0| 8.7         | 56.6        | 17.9        | 2.3         | 7.3         | 0.6         | 0.6         | 0.6         | 15  |
| NUA 619          | 45.0| 7.9         | 66.3        | 58.5        | 5.8         | 7.0         | 3.7         | 1.4         | 1.4         | 22  |
| NUA 709          | 37.0| 9.3         | 70.3        | 41.4        | 4.5         | 5.0         | 1.2         | 0.8         | 1.1         | 19  |
| NUA 8            | 28.0| 3.7         | 9.1         | 8.3         | 2.7         | 5.0         | 1.7         | 1.0         | 0.7         | 12  |
| NUA 99           | 31.0| 6.5         | 30.7        | 14.6        | 2.1         | 4.8         | 0.5         | 0.6         | 0.6         | 13  |
| NYIRAMUHONDO     | 9.0 | 2.1         | 3.1         | 0.7         | 0.3         | 3.5         | 0.5         | 0.2         | 0.1         | 5   |
| RWR 2245         | 25.0| 8.3         | 50.7        | 13.7        | 1.7         | 9.3         | 0.3         | 0.5         | 0.5         | 14  |
| RWR 2154         | 28.0| 9.9         | 71.5        | 26.5        | 3.1         | 7.5         | 0.4         | 0.7         | 0.7         | 17  |
| T LOCAL          | 34.0| 5.3         | 23.2        | 23.2        | 4.0         | 5.7         | 3.0         | 1.3         | 1.1         | 15  |
| ZKA 98-6m/95     | 40.0| 7.6         | 50.3        | 39.7        | 4.5         | 5.7         | 2.1         | 1.1         | 1.2         | 20  |

KR: Sum of Kang rank; S_{1}^{(1)}, S_{2}^{(2)}, S_{3}^{(3)}, S_{4}^{(4)}: Huhn and Nassar nonparametric statistics; NP_{1}^{(1)}, NP_{2}^{(2)}, NP_{3}^{(3)}, NP_{4}^{(4)}: Thennarasu nonparametric statistics; AR: Average of Ranks or rank average of all statistical indices.
Table 8. Ranking of stable and unstable genotypes by the different stability indices used

| Indices | Stable genotypes | Unstable genotypes |
|---------|------------------|--------------------|
| Bi      | T LOCAL, CODMLV 095, RWR 2245, NABE 4, MBC 23, KINURE, A 445, CODMLB 078. | AFR 709, CODMLB 001, CODMLV 086, ZKA 98-6m/95, RWR 2154, NUA 709. |
| W²      | MARUNGI, KINURE, CODMLV 098, NUA 8, G59/1-2, MBC 23, A445, NYIRAMUHONDO. | AFR 709, NAIN DE KYONDO, CODMLB 078, K 131, RWR 2245, CODMLB 001, NAMULENGA, NUA 619. |
| σ²i     | MARUNGI, KINURE, CODMLV 098, NUA 8, G59/1-2, MBC 23, A445, NYIRAMUHONDO. | AFR 709, NAIN DE KYONDO, CODMLB 078, K 131, RWR 2245, CODMLB 001, NAMULENGA, NUA 619. |
| s²di    | T LOCAL, MARUNGI, MBC 23, CODMLV 086, KINURE, CODMLV 098, G59/1-2. | CODMLB 001, K131, RWR 2245, NAMULENGA, NAIN DE KYONDO, NUA 619. |
| CVi     | T LOCAL, MBC 23, G59/1-2, MARUNGI, KINURE, NYIRAMUHONDO, NABE 4. | AFR 709, ZKA 98-6m/95, NUA 619, CODMLB 001, NAIN DE KYONDO, NUA 709. |
| δ²R     | G59/1-2, NYIRAMUHONDO, COD98, KINURE, MBC 23, MARUNGI | NUA 619, ZKA 98-6m/95, CODMLB 001, AFR 709, NUA 709 |
| θi(0)   | MARUNGI, KINURE, CODMLV 098, NUA8, G59/1-2, MBC 23, A445, NYIRAMUHONDO. | AFR 709, NAIN DE KYONDO, CODMLB 078, K 131, RWR 2245, CODMLB 001, NAMULENGA, NUA 619. |
| θi      | AFR 709, NAIN DE KYONDO, COD78, K 131, RWR 2245, COD1, NAMULENGA, NUA 619 | MARUNGI, KIN, CODMLV 098, NUA8, G59, MBC 23, A445, NYIRAMUHONDO |
| NP Huhn and Nassar | NYIRAMUHONDO, MARUNGI, G59, KINURE, CODMLV 098 | AFR 709, NAIN DE KYONDO, NUA 98-6m/95. |
| NP      | NYIRAMUHONDO, G59/1-2, CODMLV | NUA 619, T LOCAL, ZKA 98-6m/95. |

**Stability based on Thennarasu's nonparametric statistics** (NP(1), NP(2), NP(3), NP(4)): These parameters place NYIRAMUHONDO, G59/1-2, COD MLV 098, and KINURE in the stable class and NUA 619, T LOCAL and ZKA 98-6m/95 in the unstable class (Table 7).

3.1.3 Similarity of indices

There are many similarities between different methods for the identification of stable and unstable genotypes. Each index specifically classifies the genotypes evaluated according to its definition. The same genotypes are found in almost all indices. There is a great deal of convergence in the choice of stable genotypes among the indices (Table 8).

Spearman’s correlation matrix indicates that ecovariance is negatively related to θi(0) and positively related to the indices and the average of all returns over the six years (Fig. 3).

The indices S(1), S(2), S(3), S(6) are positively correlated with the nonparametric statistics of Thennarasu NP(1), NP(2), NP(3), NP(4). All of these indices are negatively associated with the average of all six years’ returns (Y) with the exception of NP(1) (Fig. 3).

The average of all returns for the six years (Y) is positively correlated to NP(1), W², σ²i, s²di, bi, θi and negatively correlated to S(2), S(3), S(6), NP(2), NP(3), NP(4), KR, θi(0), and CVi (Fig. 3).

In order to establish the existing relationships between parametric and non-parametric statistics, a principal component analysis was performed (Fig. 4).

The first two main components account for 84.67% or 58.83% and 25.84% respectively for factors 1 and 2 of the total change.

Axis 1, which absorbed 58.83% of the variation, associated the indices, ecovariance (Wi², S(3),...
Shukla's stability variance ($\sigma_i^2$), regression residual ($S_{\text{di}}$), regression coefficient ($b_i$), Huhn and Nassar's nonparametric statistics ($S^{(1)}, S^{(2)}$) and a nonparametric statistic of Thennarasu (NP$^{(3)}$). The average yield for all six years ($Y$) was not positively related to Axis 1 (Fig. 4).

Axis 2, which explained 25.84% of the variation, combines Thennarasu's indices, nonparametric statistics (NP$^{(2)}, NP^{(3)}, NP^{(4)}$) Huhn and Nassar's nonparametric statistics ($S^{(3)}, S^{(6)}$) coefficient of variation (CVi) and the sum of Kangs ranks (KR). Indeed, the second axis was negatively correlated with the average yield for all six years ($Y$) (Fig. 4).

Generally speaking, axis 1 includes most of the parametric statistics, while axis 2 includes most of the non-parametric statistics. The similarity of classification of certain parameters such as evolence ($W_i^2$) and regression residual ($\sigma_i^2$) suggests that one can be substituted by the other.

3.2 Discussion

In plant breeding, the analysis of multi-year trials for variety identification and selection is a very crucial step. This analysis is often based on the performance and stability of genotypes. In breeding as well as in production, performing and stable genotypes are often sought [21].

The farmer, is interested in the variety which pays him the most, in his environment (temporal stability). The breeder, on the other hand, is mainly interested in selecting material that behaves satisfactorily, not only in a given environment but also when subjected to changes in the conditions of this environment (spatial stability or adaptability) [22,23,24].

The results of the present study indicate a change in the order of genotype ranking due to variations in the environment. They demonstrate the presence of genotype x year interaction, similarity between index grouping methods and positive as well as negative correlations between indices. Pearson's correlation coefficients show the interrelationships between stability statistics and performance performance [25].

Principal Component Analysis (PCA) groups the different indices into two sets, representing parametric and non-parametric statistics. The former are used to assess genotype stability by relating observed genotypic responses to a sample of environmental conditions, while the latter explain the different environments in which genotypes evolve in the face of biotic and abiotic factors [14].

Fig. 3. Rank (Pearson) correlation coefficients between stability metrics and six-year yields
Fig. 4. Similarity of the different stability measurement indices

The similarity in the grouping of stability indices such as ecovalence, regression residual and some non-parametric Huhn and Nassar statistics was noted. These results are similar to those of Sabaghia et al. [26] Benmahammed et al. [21] and Hannachi et al. [27].

With respect to differences in the classification of genotypes by different indices, Pearson's correlation was used to further investigate the relationships between the indices. As each method has its own merits and weaknesses, we integrated parametric and non-parametric methods for the selection of stable genotypes. Thus, the stability Soft software provides an estimate of the mean sum rank (MR) for all statistics in order to select successful and stable genotypes [14].

Consequently, a genotype with a low AR value can be selected as the superior stable genotype. Based on our results, the NYIRAMUHONDO, MARUNGI, G59/1-2, CODMLV 086, KINURE, MBC 23, NABE 4, NUA 8, K 131, and NUA 99 genotypes could be selected as stable for cultivation under low altitude conditions. Similar results have been found under high-altitude conditions with the same varieties [28,29,30].

In terms of yield performance, genotypes CODLMB001, CODMLB078, HM 21-7, K 131, NABE 4, RWR 2154 and RWR 2245 are the best performing dwarf genotypes with an average yield of all genotypes of 1043.4 kg/ha. This average yield is far higher than those recommended by Gepts et al. [31] who states that the average yield in neighboring countries is 638 kg/ha for Uganda, 671 kg/ha for Burundi and 918 kg/ha for Rwanda. Thus the use of biofortified bean genotypes can improve the current yield of 540 kg/ha and thus help to ensure food security by covering the deficit in the growing demand for beans [32]. For voluble genotypes, the most successful are G59/1-2,
MAC 44, NAMULENGA, and NYIRAMUHONDO with an average yield of all genotypes of 1235.6 kg/ha.

Almost all of the genotypes identified as stable and performing in this study are voluble (NYIRAMUHONDO, CODMLV 086, MBC 23). Indeed, the voluble varieties develop a lot with numerous ramifications and measure up to more than 2 m. These varieties are late and are harvested in several passes. The advantage of these varieties is that they show a higher productivity per plant and a certain tolerance to humidity and attacks compared to dwarf varieties [33].

4. CONCLUSION

This study was conducted to investigate the performance and yield stability of twenty-six genotypes of biofortified common beans over six crop years. In the presence of the GxE interaction, the study of the differential response of the genotypes to different environments over a period of six years was very important.

Several parametric and non-parametric statistics were used to quantify performance and yield stability. A comparative study of these methods identified CODLMB 001, CODMLB 078, HM 21-7, NABE 4, K 131, RWR 2154, RWR 2245, G59/1-2, MAC 44, NAMULENGA, and NYIRAMUHONDO as performing genotypes, then NYIRAMUHONDO, MARUNGI, G59/1-2, CODMLV 086, KINURE, MBC 23, NABE 4, NUA 8, K 131, and NUA 99 as stable genotypes. The use of the Rank Sum Average (RA) parameter, which integrates both stability and performance, allowed us to identify NYIRAMUHONDO, G59/1-2, CODMLV 086, MBC 23, NABE 4 and K 131 as stable and performing. Many similarities were noted between different parametric and non-parametric methods for the identification of stable and unstable genotypes.

In the case where stability takes precedence over performance, the ecovariance (\(W^2\)) is more useful as a stability parameter. \(W^2\) identifies MARUNGI, KINURE, CODMLV 098, NUA 8, G59/1-2, MBC 23, A 445 as stable genotypes. Future studies should extend the number of years and use other selection criteria such as the presence or absence of anti-nutritional factors, molecular analyses of biofortified genotypes before their use in a selection scheme.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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