Screening of Maize (Zea mays L.) Genotypes for Adaptation on Contrasted Acid Soils in the Humid Forest Zone of Cameroon

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Authors’ contributions

This work was carried out in collaboration between all authors. Authors ELM, NLT, ZA and OB designed the study. Authors WN and ELMN reviewed the experimental design, enabled the practical realization of this work, performed physical and chemical soil analysis. Authors JMB, HT and DM performed the statistical analysis. Authors CLP, NLT, HM and ELMN wrote the protocol and the first draft of the manuscript. Authors CLP and NLT managed the analyses of the study. Authors CLP and WN managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

Soil acidity is a major limiting factor for maize productivity in the humid forest zone of Cameroon. A yield loss of up to 60% has been reported in acid tolerant population. The objective of this study was to determine the level of tolerance of some selected inbred lines under Aluminum and Manganese toxicities on chosen experimental site soils and to classify them into specific pools. The experiment was laid out in a Split-plot design and genotypes were completely randomized within the blocks. Three replications were used. An assessment of 52 inbred lines of maize which consisted of 25 IRAD Cameroon lines, 3 IITA lines and 24 lines from CIMMYT-Colombia was then carried out in a contrasted acidic soil with Al (Nkoemvone site) and Mn (Nkolbisson site) toxicities.

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1. INTRODUCTION

Acid soils cover approximately 3950 million ha, which is about 30% of the total ice free land area on the earth [1,2]. In the tropics, more than 8 million ha of acid soils are planted with maize, and 17% of tropical Africa is covered by acid soil [1]. In Cameroon, acid soil covers up to 75% of the soil, and this is mainly in the humid forest zones (HFZ). Acid soils in these zones are characterized by low pH, deficiency in Ca, Mg, P, K and Mo contents and toxic levels of Al and Mn [3]. These characteristics limit the fertility of the soil and inhibit root development, thus leading to low water and nutrient uptake and low maize yields [4]. [5] reported the average yield of maize production ranged from 0.8 – 1 t/ha. However, this production is not sufficient to meet the demand of the population. In 2008, the quantity of maize flour imported was estimated to 24,815 tons [6] and this continue to increase until to date. Moreover, over the past decades, farmers’ interest in maize production has increased, and maize has become a cash crop like coffee and cocoa, and is now an important source of income [7,8]. There is an increasing demand for the crop because of its use as feed in animal production and in the brewing industry. The annual demand of maize for human consumption and animal feed in Cameroon was estimated to 870,000 and 320,000 tons, respectively [9]. Maize production in Cameroon has been increasing steadily from 2004 to 2013 [10]. These increases have mainly been due to increases in area harvested (832,400 ha) rather than yield increase per unit area (0.8 – 1 t/ha). The HFZ which covers an area of 21.7 million hectares, by virtue of its bimodal rainfall pattern holds promise for increasing the output for maize if the main fertility constraint of low soil pH can be solved. Soil amendment with lime, phosphorus and organic matter has been suggested to bring unproductive acid soil under acceptable agricultural production. However, such solutions are temporary and expensive for the resource-poor farmers [12]. To correct acid soil in one ha area, 2 to 4 tons of dolomitic lime are required and should be applied 2-3 years for better plant growth [13]. Significant genetic variation for tolerance to soil acidity has been reported. Early studies demonstrated qualitative inheritance [14]. Quantitative inheritance to Al resistance was later demonstrated [15,2,16]. Considerable progress has been made in breeding maize for acid soil tolerance through recurrent selection [3,17]. Developing acid-tolerant maize genotypes is an effective and sustainable way of alleviating the impact of Al toxicity in maize production areas. Studies have shown that Al-tolerant maize genotypes outperformed the adapted local and susceptible genotypes by 13% and 61%, respectively [18]. These results suggest that growing Al-tolerant maize genotypes will ensure a high sustained maize productivity. Five maize open pollinated varieties (OPVs) from Cameroon were reported to have some level of tolerance to soil acidity [19]. Three of these (ATP-SR-Y, ATP-S4 SYN Y and ATP SYN I-W) have been found to give 13% increase in grain yield over local varieties in the humid forest area of Cameroon [19]. However, most of the materials used exhibited significant non-additive genetic variance x environment interaction, suggesting that the

Keywords: Aluminum toxicity; manganese toxicity; phytotoxicity; soil correction; Acid-soil tolerant maize; lime.
materials had specific adaptation [15]. Only ATP SR Y out of these three acid tolerant population is the open-pollinated variety released and commercialized in Cameroon [20]. However, the impacts of climate change Associates to acid soils with aluminum and manganese toxicities increase yield losses in maize [21]. Yield losses of 60% have been reported in this acid tolerant population (ATP SR Y) [19]. There is a need of reducing yield loss due to soil acidity especially Al toxicity and increasing yield productivity per unit area. Thus it is necessary to develop other varieties adapted in many areas that will consider these constraints in order to provide farmers with maize cultivars which offer ecological, economical and a permanent solution, contributing to sustainable crop production in acid soils [22]. To identify and improve varieties that would perform well under acid soil, selections would have to be based on performance across a range of environments. This would lead to germplasm with broader adaptation. One way to obtain such germplasm is by introgression of exotic germplasm to locally adapted cultivars. The objective of this study is to evaluate the genetic potential of introduced inbred lines and identify high yielding and perform one under acid soil conditions and enables the breeder to choose appropriate combination for hybrid production or cultivar development programs.

2. MATERIALS AND METHODS

2.1 Study Area

Two experimental sites were used for this study and were situated in a humid forest area of Cameroon, with bimodal rain fall. The first site is located at Nkolbisson (Yaounde) and the second at Nkoemvone (Ebolowa) and they are both separated by a distance of 180 km (Fig. 1.).

At Nkolbisson (11°36'E; 3°44'N), the mean annual temperature is 23.5°C, with an annual mean rain fall of 1560 mm, the vegetation is caducifoliated semi-deciduous forest. The soil has a sandy-clay texture with a strong hydromorphic tendency and with Manganese toxicity of (90.6 c mol (+) kg), a saturation rate of 39.02%, a pH of 5.12, an efficient Cation exchange capacity (ECEC) of 4.20 C mol (+) kg and a C/N ratio of 13.86 c mol (+) kg.

Fig. 1. Geographical location of study sites
At Ebolowa (2°40'N 12°24'E), the site was located at the heart of humid forest zone at 615 m altitude above sea level and with a semi-deciduous vegetation. Its climate is of the Guinean type with an average rain fall of 1875 mm/year and a mean temperature of 24°C. The soil has a clay texture with Aluminium toxicity (2,326 c mol (+) kg), a saturation rate of 32.74%, pH$_{H_2O}$ of 4.33, an ECEC of 3.5 C mol (+) kg and a C/N ratio of 9.28 c mol (+) kg (Table 1).

### 2.2 Germplasm

The germplasm used was made up of 52 maize inbred lines genotypes consisted of 25 IRAD Cameroon lines, 3 IITA (Nigeria) lines and 24 lines from CIMMYT-Colombia. The characteristics of these maize inbred lines genotypes are presented in Table 2.

#### Table 1. Soil characteristics of the fields trials

| Sites               | pH$_{H_2O}$ | H$_{(+)}$(cmol(+))kg | C/N ratio (cmol(+))kg | Al (cmol(+))kg | Mn (ug/g) | SR (%) |
|---------------------|-------------|-----------------------|-----------------------|----------------|-----------|--------|
| Nkoemvone (Al toxicity) | 4.33        | 4.67.10$^{-3}$        | 9.28                  | 2.32           | 6.49      | 32.74  |
| Nkolbisson (Mn toxicity) | 5.12        | 7,58.10$^{-4}$        | 13.86                 | 0.52           | 90.6      | 39.02  |

SR: saturation rate; C/N: Carbon is to nitrogen ratio

#### Table 2. Characteristics of 52 maize inbred lines genotypes

| Entry | Genotypes | Genetic base | Origin | PTL | Color | Vegetative cycle (day) |
|-------|-----------|--------------|--------|-----|-------|-------------------------|
| 1     | ATP S5 20Y-2 | ATP         | IRAD   | T   | Yellow | 115                     |
| 2     | ATP S5 26Y-2 | ATP         | IRAD   | T   | Yellow | 115                     |
| 3     | ATP S5 31Y-2 | ATP         | IRAD   | T   | Yellow | 115                     |
| 4     | ATP S6 20Y-1 | ATP         | IRAD   | T   | White  | 115                     |
| 5     | ATP S6 21Y-2 | ATP         | IRAD   | T   | Yellow | 115                     |
| 6     | ATP S6 32Y-2 | ATP         | IRAD   | T   | White  | 115                     |
| 7     | ATP S6 33Y-1 | ATP         | IRAD   | T   | Yellow | 115                     |
| 8     | ATP S6 31Y-BB | ATP        | IRAD   | T   | Orange | 115                     |
| 9     | ATP S8 26Y-2 | ATP         | IRAD   | T   | Orange | 115                     |
| 10    | ATP S8 30Y-3 | ATP         | IRAD   | T   | Orange | 115                     |
| 11    | ATP S9 17Y-4 | ATP         | IRAD   | T   | White  | 115                     |
| 12    | ATP S9 30Y-1 | ATP         | IRAD   | T   | Yellow | 115                     |
| 13    | ATP S9 35Y-4 | ATP         | IRAD   | T   | Orange | 115                     |
| 14    | ATP S9 36Y-BB | ATP     | IRAD   | T   | Orange | 115                     |
| 15    | ATP-49     | ATP         | IRAD   | T   | White  | 115                     |
| 16    | ATP-50     | ATP         | IRAD   | T   | Yellow | 115                     |
| 17    | ATP-53     | ATP         | IRAD   | T   | Yellow | 115                     |
| 18    | CML 304    | /           | CIMMYT | T   | Orange | 115                     |
| 19    | Clgp1-17   | Suwanl-SR   | IRAD   | T   | White  | 115                     |
| 20    | 88069      | /           | IRAD   | AT  | Yellow | 115                     |
| 21    | ATP 14     | ATP         | IRAD   | T   | Orange | 115                     |
| 22    | ATP 43     | ATP         | IRAD   | T   | Yellow | 115                     |
| 23    | ATP 46     | ATP         | IRAD   | T   | Yellow | 115                     |
| 24    | ATP- Last  | ATP         | IRAD   | T   | Yellow | 115                     |
| 25    | 87036      | Crossing between TMZ$_{SR}$ and Pop$_{43}$ | IRAD | AT | White | 115                     |
| 26    | Cam-Inb gp117(F) | Suwanl-SR | IRAD | T   | Yellow | 115                     |
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| Entry | Genotypes   | Genetic base | Origin | PTL | Color | Vegetative cycle (day) |
|-------|-------------|--------------|--------|-----|-------|------------------------|
| 27    | 4001        | /            | IITA   | AT  | Yellow| 105                    |
| 28    | 9450        | B73          | IITA   | AT  | Yellow| 105                    |
| 29    | D 506-2     | /            | CIMMYT | AT  | White | 105                    |
| 30    | CML 358     | Pop SA3      | CIMMYT | T   | Yellow| 105                    |
| 31    | CLA 154     | /            | CIMMYT | S   | Orange| 105                    |
| 32    | CLA 106     | /            | CIMMYT | T   | Yellow| 105                    |
| 33    | CLA 18      | /            | CIMMYT | T   | Yellow| 105                    |
| 34    | D 506-3     | /            | CIMMYT | AT  | Yellow| 105                    |
| 35    | D 504-4     | /            | CIMMYT | AT  | Orange| 105                    |
| 36    | Ku 1414     | /            | IITA   | AT  | Yellow| 105                    |

| Entry | Genotypes   | Genetic base | Origin | PTL | Color | Vegetative cycle (day) |
|-------|-------------|--------------|--------|-----|-------|------------------------|
| 37    | CML 357     | /            | CIMMYT | T   | Orange| 90                     |
| 38    | CML 435     | /            | CIMMYT | T   | Yellow| 90                     |
| 39    | CML 436     | /            | CIMMYT | T   | Orange| 90                     |
| 40    | CML 437     | /            | CIMMYT | T   | Yellow| 90                     |
| 41    | CML 438     | /            | CIMMYT | T   | Orange| 90                     |
| 42    | CML 439     | /            | CIMMYT | T   | Orange| 90                     |
| 43    | CML 533     | /            | CIMMYT | T   | Orange| 90                     |
| 44    | CML 534     | /            | CIMMYT | T   | Orange| 90                     |
| 45    | CML 535     | /            | CIMMYT | T   | Orange| 90                     |
| 46    | CML 322     | /            | CIMMYT | T   | White | 90                     |
| 47    | CML 332     | /            | CIMMYT | T   | White | 90                     |
| 48    | CML 486     | /            | CIMMYT | T   | Yellow| 90                     |
| 49    | CML 479     | /            | CIMMYT | T   | Yellow| 90                     |
| 50    | CLA 183     | /            | CIMMYT | AT  | White | 90                     |
| 51    | CML 434     | /            | CIMMYT | T   | Orange| 90                     |
| 52    | D 300-17    | /            | IITA   | AT  | White | 90                     |

Reference sources: [23] and [21]

T: Tolerant, AT: Averagely Tolerant, S: Susceptible, PTL: Presumed Tolerance Level, CML: CIMMYT Maize Line, CLA: CIMMYT Line Acid, ATP: Acid Tolerant Population, ATP SRY: Acid Tolerant Population Streak Resistant Yellow; Pop: Population; Suwanl-SR: Thailand Research Station; CIMMYT: Centro Internacional de Mejoramiento de Maíz y Trigo (Centre international pour l’amélioration du maïs et du blé); IRAD: Institute of Agricultural Research for Development; IITA: International Institute of Tropical Agriculture.

2.3 Seed Sowing and Fertilizer Application

On each experimental site, land was ploughed and divided into two major parts with an alley of 2m. On one part of the field, the acidity of the soil was corrected with the incorporation of 2t/ha of dolomite. As soon as the rain started during the first rainy season, maize inbred lines were sown on rows of 4 m long with 9 hills. The distance between two consecutive rows was 75 cm and 50 cm between two consecutive hills in a row. Two maize seeds were planted per hill with no thinning. Plant density at planting was approximately 53,333 plants/ha. Weeds and insects were chemically controlled.

Mineral fertilizers were applied twice [22]: the basal application was done 15 days after sowing and was composed of a bag of 100 kg NPK 14-24-14 + 5(S) + 3.5 (MgO) with a bag of 50 kg/ha of urea. The second application was done 32 days later, at a dose of 50 kg/ha of urea.

2.4 Experimental Design

The trials were carried out in each experimental site on an area of 1326.8 m². The experiment setup was a split plot; where the main plot was the soil type made of the native acid soil with Aluminum or Manganese toxicity known as treatment “O” and the corrected acid soil known as treatment ‘T’. The subplots were made of genotypes. The genotypes were arranged into a complete randomized block design with three replications.

2.5 Data Collection

The following phenotypic parameters were measured: plant height (HP) and ear insertion
height (HIE), the ears weight (WE) and grain moisture content (MC) measured in the field during harvest. Grain yield (Y in kg/ha) of the genotypes were obtained using the formula below:

\[
Y = \frac{EFW \times SP (100 - MC) \times 10000}{DMP}
\]

- Percentage yield loss PYL due to the acidity of the soil was calculated following the formula:

\[
PYL(\%) = \frac{YC - YA}{YC} \times 100
\]

2.6 Data Analysis

Data were subjected to the analysis of variance using the SAS 9.0 software package. The SPSS 16.0 software package was used for the construction of a dendrogram for each site. The Student Newmann Keul’s test enabled the comparison of means at 1% and 5% probability levels. The mathematical model used was:

\[
Y_{ij} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij}
\]

3. RESULTS AND DISCUSSION

3.1 Results

3.1.1 Genotypes identification adapted in acidic soil with Al and Mn toxicity

At Nkolbisson, grain yield of inbred lines on acidic soil varied from 0.11 t/ha (CLA 154) to 4.11 t/ha (CLA 183), making a deviation of about 4 t/ha between the most productive and the least productive. 17 genotypes produced a yield greater than 2t/ha and were grouped into three classes [2-3], [3-5] and [5-6] (Fig. 2). Genotypes CLA 183 (4.11 t/ha), ATP-14 (4.08 t/ha), 9450 (4.07 t/ha) and CML 535 (4.07 t/ha) were revealed as the best varieties.

Grain yield on corrected acid soil (control) varied from 0.37 t/ha (ATP S5 20Y) to 5.57 t/ha (CML 358), making a difference of about 5.2 t/ha. In the control, 22 genotypes produced a yield greater than 2 t/ha and are grouped into three classes [2-3], [3-5] and [5-6] (Fig. 2). Genotypes CML 358 (5.57 t/ha), ATP-14 (5.00 t/ha) and ATP-46 (4.42 t/ha) were revealed as the best varieties.
Inbred lines responding well on acid and corrected acid soil presenting regressive losses less than -50% were: CML 535 (4.07 t/ha), CML 437 (3.28 t/ha), CML 486 (2.17 t/ha). These inbred lines were said to be efficient on acid soils with Manganese toxicity. For 17 genotypes that produced yields greater than 2 t/ha, five of them showed less than 54% yield loss and were considered as tolerant strains to acidic soils with Manganese toxicity. These were ATP-14 (18.40 %), ATP S5 31Y-2 (34.11%), ATP S9 30Y-1(29.79%), ATP-43 (29.39%) and Camlnbgp1 17 (F) (45.80%). 37 parents (69.81%) had low yields (less than 1 t/ha) and yield losses greater than 50%. They were grouped as susceptible genotypes while 8 genotypes (15.09%) showed very regressive losses beyond -50% and high yields on acid soil; they were considered as negative control genotypes at Nkolbisson (Table 3).

At Nkoemvone, grain yield of lines on acidic soil vary from 0.22 t/ha (ATP S6 33Y-1) to 3.9 t/ha (Clgp1 17), making a yield deviation of about 3.68 t/ha between the most productive and the less productive lines. On the same acidic soil, only 5 genotypes gave in a yield greater than 2 t/ha and were grouped into two classes [3-4] while 10 genotypes were in the less class [1-2] and had yield greater than 1 t/ha (Fig. 3.). Clgp1 17 (3.9 t/ha), CML 322 (2.24 t/ha), CML 479 (2.24 t/ha) and CML 533 (2.05 t/ha) were the best under acid soils at Nkoemvone.

Table 3. Grouping of screened progeny on acidic soil at Nkolbisson

| Efficient genotypes | Tolerant genotypes | Susceptible genotypes | Negative control genotypes |
|---------------------|--------------------|-----------------------|---------------------------|
| CML 535             | ATP-14             | ATP S6 20Y-1          | CLA 183                   |
| CML 486             | ATP-43             | CML 357               | 9450                      |
| CML 437             | ATP S9 30Y-1       | CML 439               | 88069                     |
|                     | ATP S5 31Y-2       | CML 436               | ATP S9 35Y-4              |
|                     | Camlnbgp1 17 (F)   | ATP S9 36Y-BB         | CML 479                   |
|                     |                    | CML 322               | CML 438                   |
|                     |                    | Clbg1 17              | CML 534                   |
|                     |                    | CLA 18                | CML 332                   |
|                     |                    | ATP-53                |                           |
|                     |                    | CML 358               |                           |
|                     |                    | ATP S8 26Y-2          |                           |
|                     |                    | D 300-17              |                           |
|                     |                    | ATP-32                |                           |
|                     |                    | ATP S8 30Y-3          |                           |
|                     |                    | ATP-46                |                           |
|                     |                    | CML 304               |                           |
|                     |                    | ATP-50                |                           |
|                     |                    | Ku 1414               |                           |
|                     |                    | CML 435               |                           |
|                     |                    | D 506-3               |                           |
|                     |                    | CLA 135               |                           |
|                     |                    | ATP S6 31Y-BB         |                           |
|                     |                    | 87036                 |                           |
|                     |                    | 9848                  |                           |
|                     |                    | ATP S5 20Y-2          |                           |
|                     |                    | D 506-2               |                           |
|                     |                    | D 506-4               |                           |
|                     |                    | ATP S5 20Y-3          |                           |
|                     |                    | CLA 106               |                           |
|                     |                    | CLA 154               |                           |
|                     |                    | ATP S6 21 Y-2         |                           |
|                     |                    | ATP 49                |                           |
|                     |                    | CML 486               |                           |
|                     |                    | 4001                  |                           |
were said to be susceptible genotypes to the soil and percentage yield losses greater than 50%. 40 parents which expressed yield less than 1 t/ha characterized as negative control genotypes on yields on control treatments: they were 535 (31.84%) and CML 439 (16.79%). 6 lines tolerant on acid soil of Aluminum toxicity (CML 2 genotypes out of the 43 left were retained as grouped as efficient and tolerant genotypes.

At Nkoemvone, four lines responding on both acidic and corrected acid soils gave yield losses between -14.70% and 0%. These lines were grouped as efficient and tolerant genotypes. They are Clgp1 17 (3.9 t/ha), CML 479 (2.24 t/ha), CML 533 (2.05 t/ha) and ATP S9 30Y (1.04 t/ha). The yield and yield loss percentages varied from 0.21 t/ha (D 300-17, ATP S8 26Y-2, CML 438, 87036, CLA 135) to 8.20 t/ha (ATP S6 535 (31.84%), CML 437 (16.34%), CML 358 (14.70%) and 0%. These lines were

A comparative study of screened genotypes on the two sites revealed that ATP S5 30Y-1 and CML 535 were the best among all, both at Nkoemvone and at Nkolbisson. Hence they are considered as ubiquitous strains, while 15 genotypes perfectly expressed themselves as susceptible on both experimental sites and were equally most susceptible of all tested genotypes. They are: ATP S6 21Y-1, ATP 53, CLA 106, CLA 154, ATP-32, Ku 1414, D 506-4, 87036, ATP S6 31Y-BB, ATP-46, CLA 135, ATP-50, ATP S8 30Y-3, D 506-3 and CML 304.

3.1.2 Classification of genotypes into specific pools

The dendrogram obtained after analysis by grouping genotypes based on yield at Nkolbisson (Fig. 4.) showed that, it was made up of three large groups. Group I consisted of 31 averagely tolerant genotypes, group II had 3 tolerant genotypes and group III had 18 susceptible genotypes. The distance between group I and II and that between group II and III was 77.42 and 86.66 respectively. Each group encloses parents which look alike phenotypically.

Group I contains varieties that were efficient (CML 535, CML 486, CML 437) and tolerant (ATP-14, ATP-43, ATP S9 30Y-1, ATP S5 31Y-2, Camlnbg1) 17 (F). Observations within studied parameters in each group revealed that group II appears to be the best with good ears, Y (4.33 t/ha), HP (1.59 m), HIE (0.73 m) and GR (64.81%) higher than group I and III.

Fig. 3. Yield and yield loss of the best inbred lines on acidic and corrected soil at Nkoemvone
Same letters indicates: non-significant, different letters indicates: significant

| Rank of yield of genotypes | Acid soil | Corrected acid soil | % Yield loss |
|---------------------------|----------|---------------------|-------------|
| [8-9]                      |          |                     |             |
| [4-8]                      |          |                     |             |
| [4-4]                      |          |                     |             |
| [2-3]                      |          |                     |             |
| [2-2]                      |          |                     |             |
| [0-1]                      |          |                     |             |

The yield of inbred lines on corrected acid soil varied from 0.21 t/ha (D 300-17, ATP S8 26Y-2, CML 438, 87036, CLA 135) to 8.20 t/ha (ATP S6 32Y-2), making a deviation of about 7.99 t/ha. O...
Table 4. Grouping of screened progeny on acid soil at Nkoemvone

| Efficient genotypes | Tolerant genotypes | Susceptible genotypes | Negative control genotypes |
|---------------------|--------------------|-----------------------|---------------------------|
| Clgp1 17            | CML 535            | ATP S6 21Y-1          | CML 322                   |
| CML 479             | CML 435            | ATP 53                | ATP S8 26Y-2              |
| CML 533             |                    | CLA 183               | D 300-17                  |
| ATP S9 30Y-1        |                    | ATP-43                | ATP SR Y                  |
|                     |                    | CML 436               | CML 358                   |
|                     |                    | CLA 18                | ATP-49                    |
|                     |                    | 88069                 | CML 437                   |
|                     |                    | CML 438               |                           |
|                     |                    | CLA 106               |                           |
|                     |                    | CLA 154               |                           |
|                     |                    | ATP S5 26Y-2          |                           |
|                     |                    | CML 486               |                           |
|                     |                    | ATP-32                |                           |
|                     |                    | Ku 1414               |                           |
|                     |                    | D 506-4               |                           |
|                     |                    | 9450                  |                           |
|                     |                    | CML 534               |                           |
|                     |                    | ATP S6 20Y-1          |                           |
|                     |                    | 87036                 |                           |
|                     |                    | ATP S6 32Y-2          |                           |
|                     |                    | CML 434               |                           |
|                     |                    | ATP-14                |                           |
|                     |                    | ATP S6 31Y-BB         |                           |
|                     |                    | 4001                  |                           |
|                     |                    | CML 332               |                           |
|                     |                    | ATP-46                |                           |
|                     |                    | Camlnbgp1 17(F)       |                           |
|                     |                    | CLA 135               |                           |
|                     |                    | ATP S9 36Y-BB         |                           |
|                     |                    | ATP-Last              |                           |
|                     |                    | CML 439               |                           |
|                     |                    | ATP-50                |                           |
|                     |                    | ATP S8 30Y-3          |                           |
|                     |                    | ATP S9 35Y-4          |                           |
|                     |                    | ATP S5 31Y-2          |                           |
|                     |                    | D 506-3               |                           |
|                     |                    | CML 357               |                           |
|                     |                    | ATP S6 33Y-1          |                           |
|                     |                    | ATP S9 17Y-4          |                           |
|                     |                    | CML 304               |                           |

The dendrogram obtained after analysis by grouping genotypes based on yield at Nkoemvone showed that, it was made up of four large groups (Fig. 5.). Group I was made up of 17 averagely tolerant genotypes; group II had 8 tolerant genotypes. Group III had five averagely susceptible parents and group IV had 21 susceptible genotypes. The distance between groups I and II was 20.19, that between groups II and III is 23.60 and that between groups III and IV is 40.38. Hence, each group encloses parents that look alike phenotypically.

In group I, some efficient varieties (CML 479, ATP S9 30Y-1) and tolerant (CML 435) were obtained after screening. Group II was the best with good ears (1.6), Y (1.68 t/ha), HP (1.28 m), HIE (0.57 m), GR (40.27%) and these data were higher than those in groups I, III and IV.
Fig. 4. Dendrogram obtained by linkage between groups and by the non-hierarchical classification process of endogamous genotypes at Nkolbisson
Fig. 5. Dendrogram obtained by linkage between groups and by the non-hierarchical classification process of endogamous genotypes at Nkoemvone
3.2 Discussion

3.2.1 Genotypes identification adapted in acidic soil with Al and Mn toxicity

At Nkolbisson; the following genotypes CML 535, CML 437, CML 486 representing a proportion of 5.76% revealed efficient and tolerant genotypes on acid soil more than on corrected soil. Also, four inbred lines (ATP S5 31Y-2, ATP S9 30Y-1, ATP-43, and Cam Inb gp1 17 (F)) presumed as tolerant from origin, confirmed their level of tolerance on acid soil especially under Manganese toxicity at Nkolbisson. This result was a proof that these genotypes could possess major tolerance genes as compared to other susceptible genotypes and this result are in line with those obtained by previous authors [24,25,23,26] who identified four inbred lines (ATP-46, 87036, and Cam Inb gp117, C4SRRA7) with high general combining ability (GCA) and were retained as good progenitors. Both the GCA and SCA (specific combination ability) effects showed that the tolerance to Aluminum toxicity was controlled by additive effects of genes while on acid soil with manganese toxicity, the contribution of non-additive effects of genes was dominant. The serious regressive yield losses obtained within negative control genotypes were a consequence of environmental effects such as flooding which washed soil elements from upstream, to the benefit of the lines downstream. Similar results were obtained by [27] in the course of evaluating hazards caused by flooding in Tandjille, mayo kebbi East, mayo kebbi West, which proved that the impact of flooding on harvest were very significant and losses predicted with regards to a normal year move up to 91% for maize.

Besides that, in Aluminum toxicity at Nkoemvone, Clgp1 17, CML 479, CML 533, and ATP S9 30Y-1 were more performant on acid soil than on control soil and were ranged as efficient genotypes (7.54%). Among these lines, Clgp1 17 which was specified from the origin as tolerant actually revealed to be the best. This result is in agreement with that of [13], who identified specific groups for maize (Zea mays L) tolerance to acid soils in the tropics. Only two genotypes: CML 535 and CML 439 out of the 49 remaining revealed themselves as tolerant. This result suggests that, the environment favors a better expression of their genes as compared to susceptible genotypes. Moreover, the low yields and yield losses obtained among varieties CLA 18 (0.87 t/ha), D 506-4 (0.65t/ha), Ku 1414 (0.65 t/ha) and D 506-3 (0.22 t/ha) were mainly due to floral abnormalities. This phenomenon, observed within varieties for which the male and female inflorescence are found on the same stalk gives reason to affirm that acid soils have a considerable impact on the entire maize plant. Actually, this floral abnormality named ‘mantled’ with reference to the ‘mantled’ appearance of the gentle fruit had been observed in regenerated oil palm plants (Elaeis guineensis Jacq.) (6%) which is a monoecious plant like maize, by [28].

On corrected acid soil at Nkolbisson, quick lime had a significant effect on genotypes from germination to maturity. This result is similar to the one with the results obtained by [29] for where Calcium improvement compensates the acidification produced by biological activity, increasing the lowering of the soil pH and therefore favoring the assimilation of soil nutrients.

On corrected acid soil at Nkoemvone, dolomitic lime equally had a significant effect on the evaluated genotypes in the course of maturity comparatively to the results of [23]. In addition, low yield and high yield losses obtained in this corrected plot are due to repercussions of stems borer and hedgehog. These results confirm those conducted by [30]. This author had proved on cereals pathology study in Cameroon that yields losses due to these crops pests vary from 15 to 50% compared to total annual production.

A similar study of screened genotypes on the two sites showed that ATP S5 30Y-1 and CML 535 manifested as the best in terms of yield. These genotypes tolerance ability, retained on contrasting soil are considered as ubiquitous lines. The following genotypes: ATP S6 21Y-1, ATP 53, CLA 106, CLA 154, ATP-32, Ku 1414, D 506-4, 87036, ATP S6 31Y-BB, ATP-46, CLA 135, ATP-50, ATP S8 30Y-3, D 506-3 and CML 304 revealed to be susceptible on acid soils in both sites. These genotypes are very sensitive to acid soil. On the contrary, CML 304 showed itself as the most susceptible variety among all with relatively very low germination rate and poor yield. The inferiority of the number of tolerant and efficient genotypes obtained at Nkoemvone as compared to those obtained at Nkolbisson was one of the demonstrative proofs that Aluminum toxicity had more significant impact on maize development than Manganese toxicity. This observation was explained by the fact that Aluminum is more polynuclear than Manganese, thus provoking a more drastic phytotoxicity)
4. CONCLUSION

The evaluation of 52 inbred lines under Aluminum and Manganese toxicities soils showed a great variability on the level of tolerance of genotypes to the different types of soil acidity studied. Some numbers of efficient, tolerant and susceptible lines were identified. Also, common groups of progeny for acidity tolerance were known: 3 groups at Nkolbisson and 4 groups at Nkoemvone. The best progeny of Nkolbisson were: ATP-14 (4.08 t/ha), Camlnb1 17 F (3.93 t/ha), ATP S9 30Y-1 (3.86 t/ha), CML 437 (2.72 t/ha) and CML 535 (2.54 t/ha). The best genotypes at Nkoemvone were: Clgp1 17 (3.9 t/ha), CML 322 (2.24 t/ha), CML 479 (2.24 t/ha) and CML 533 (2.05 t/ha). The results of this study showed that maize cultivation on acid soils could lead to grain yield reduction of 60% or more in tropical environments. Grain yield loss due to soil acidity could be minimized by the development of hybrids from crosses between locally adapted inbred lines and those introduced from CIMMYT Colombia and soil program. Farmers of Center, South and East regions of Cameroon would benefit if they adopt hybrids developed with these inbred lines identified to be efficient and tolerant genotypes.

COMPEting INTERESTS

Authors have declared that no competing interests exist.

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