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PHYLOGENETIC ANALYSIS OF LOCAL MAIZE COLLECTIONS IN BANGSAMORO REGION

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Abstract

Great diversity in local maize exists in the farmer's field of Bangsamoro region. A total of 140 accessions were collected throughout the region. These collections were initially screened for glyphosate resistance to separate local and genetically modified maize accessions. A total of 24 native accessions were selected and used in the experiment including the check variety (USM Var 10) for characterization and assessment of the genetic diversity of local maize selections. The entries were laid out in 5x5 triple lattice design evaluating twenty-one (21) quantitative traits and 12 qualitative traits.

High genetic diversity was observed in the phylogenetic analysis. Accessions were clustered into five groups based on quantitative traits using Euclidean distance, while based on qualitative traits Unweighted Pair Group Method with Arithmetic mean (UPGMA) clustered accessions into four groups. High genetic diversity was observed in the phylogenetic analysis. The results show a wide range of variation in maize germplasm across the Bangsamoro region. The identified most divergent entries are found in Brgy. Campo 1, Municipality of Matanog, and Brgy. Pigalgan, Municipality of Sultan Kudarat.

Keywords

Accessions, Collections, Diversity, Germplasm, Maize, Quantitative traits, Qualitative traits

Introduction

Crop diversity is the primary factor in achieving sustainable food security in a particular place. The local native varieties are sources of novel genes for biotic, abiotic, stress tolerance and good quality traits. There are collections of local native maize in the Bangsamoro Region, but no information was available with regards to their morphological and agronomic characteristics. These local selections were evaluated to provide benchmark information for their conservation and possibly their utilization in corn improvement programs towards sustainable food security.

Characterization of plant genetic resources and exchange of breeding materials and information can lead to the identification of very useful germplasm. The traits of the native varieties can be used to further develop good quality maize seeds for farmers and protect novel local maize genetic resources, which are crucial in ensuring food security.

Objectives of the Study

This study was conducted to characterize the morphological traits of local native selections of white maize germplasm in Bangsamoro Region.

Specifically, this study aimed to

1. assess the diversity of local native selections of maize in the region.

Materials

The study used accessions of white maize germplasm collected at Bangsamoro region composed of landraces, native, traditional and indigenous varieties, USM Var 10 as check variety, fertilizers, pesticides insecticides/herbicides), knapsack sprayer, measuring tools (meter sticks, ruler) bamboo sticks, pencil, and record book.

Methods

Germplasm Collection

One hundred forty (140) accessions of white maize germplasm were gathered from the corn producing areas of Bangsamoro region within one year time. Only eighty four of the 140 of the accessions were left viable after storing and were screened for use in the study.

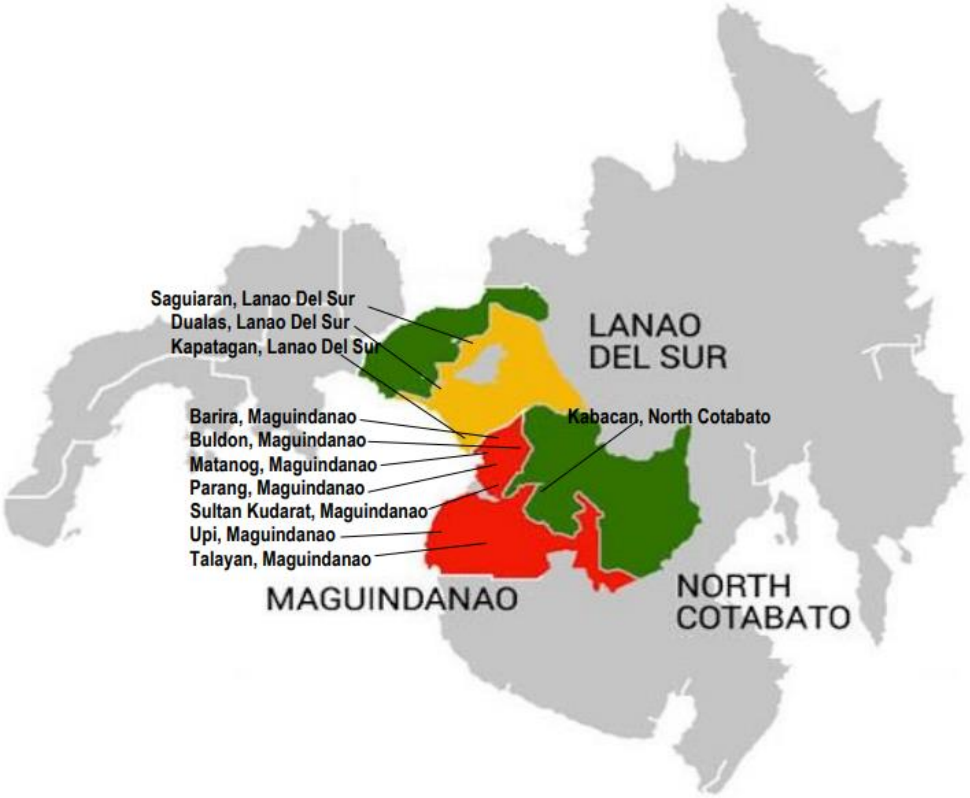

Figure 1. Mindanao map showing the sources of germplasm in the Bangsamoro Region.

Germplasm Screening

To ensure that the 84 accessions were native maize, they were subjected to herbicide resistant screening. The procedure discovered the transgenic varieties. Seedlings were grown in nursery garden and sprayed with glyphosate herbicide at the rate of 7.5 ml/liter of water. Severely affected plants indicate have not acquired glyphosate resistance and are true native varieties and they are used as entries in study (Table. 1).

Table 1. Local selections which passed the glyphosate screening confirming their non GMO.

Entry No.	Location of Germplasm
1	Saguiaran, Pamacutan, Lanao del Sur
2	Saguiaran, Pagalamatan, Lanao del Sur
3	Saguiaran, Bobong, Lanao del Sur
4	Pagalamatan, Saguiaran, Lanao del Sur
5	Pendulungan Saguiaran, Lanao del Sur
6	Pob. Saguiaran, Saguiaran, Lanao del Sur
7	Dinganin, Buldon, Maguindanao
8	Pigalgan, Sultan Kudarat, Maguindanao
9	Mapayag, Talayan, Maguindanao
10	Mirab, Upi, Maguindanao
11	Danguan, Kapatagan, Lanao del Sur
12	Poblacion, Matanog, Maguindanao
13	Bugasan Sur, Matanog, Maguindanao
14	Sapad, Matanog, Maguindanao
15	Tuga-ig, Barira, Maguindanao
16	Langkong, Matanog, Maguindanao
17	Matanog, Langkong Maguindanao
18	Basak, Matanog, Maguindanao
19	Bayanga, Matanog, Maguindanao
20	Campo 1, Matanog, Maguindanao
21	Campo 1, Matanog, Maguindanao
22	Poblacion, Parang, Maguindanao
23	Tumapongpong, Dualas, Lanao del Sur
24	Pigalgan, Sultan Kudarat, Maguindanao
25	USM, Kabacan, North Cotabato

Experimental Design

This study carried out in 5x5 triple lattice design replicated three times. Each replication had five blocks and each block was composed of five plots with a measurement of 15m². Twenty five (25) entries of white corn were used in the experiment. Each entry was planted in four rows with a plot size dimension of 3x5 meters.

Data Gathered

21 Quantitative traits includes days to tasseling, days to silking, plant height (cm), number of tillers, total number of leaves per plant, leaf length (cm), leaf width (cm), ear height of placement (cm), number of leaves above the uppermost ear including ear leaf, days to ear leaf senescence, root lodging (%), stalk lodging (%), tassel length (cm), ear length (mm), ear diameter (cm), number of kernel per row Number of rows per ear, kernel length (mm), kernel width (mm), thousand seed weight and Yield data (t/ha).

12 Qualitative traits includes leaf orientation, Stem color at flowering, Sheath pubescence, Tassel type at milk stage, Ear cob color, Ear husk cover, Shape of uppermost ear, Ear damage (rots/insects), Kernel row arrangement (uppermost ear), Shape of upper surface kernel, Kernel color, Kernel type,

Cluster Analysis

Using quantitative traits, the accessions were subjected to a hierarchical cluster algorithm base on Euclidean Distance between and among the accessions.

Using qualitative traits, the accessions were grouped by cluster analysis using Unweighted Pair Group Method with Arithmetic Mean (UPGMA).

Results and Discussions

Phylogenetic Analysis

Knowledge of genetic diversity among accessions is indispensable in maize research and breeding programs, which provides scientific proof for the evaluation of qualitative and quantitative traits. First priority strategy is to set descriptors to use in assessing and utilize maize genetic resource for the use of local and global accession in gaining level of information.

A dendogram provide explanations about the genetic relationship of 24 collected white maize accessions in Bangsamoro region. For the quantitative traits (Fig. 4) hierarchical clustering using Euclidean resemblance coefficients was used in clustering the 24 genotypes into groups. Maize varieties were grouped into five different clusters. Cluster 1 contain the maximum number of 15 genotypes, followed by cluster III with five genotypes, and clusters II and IV with two genotypes each, variety 22 and 14, 25 and 3, respectively. Cluster five consists of the most divergent genotype, entry 20.

Similarity coefficients ranged from 21.82 to 468.1, and are used for knowing the similarities between and among the entry varieties. Two maize cultivars, variety entry 6 and 11, had the closest relationship with coefficients value of 21.82, which means they come from the same production environment and possess little difference in their measurable traits.

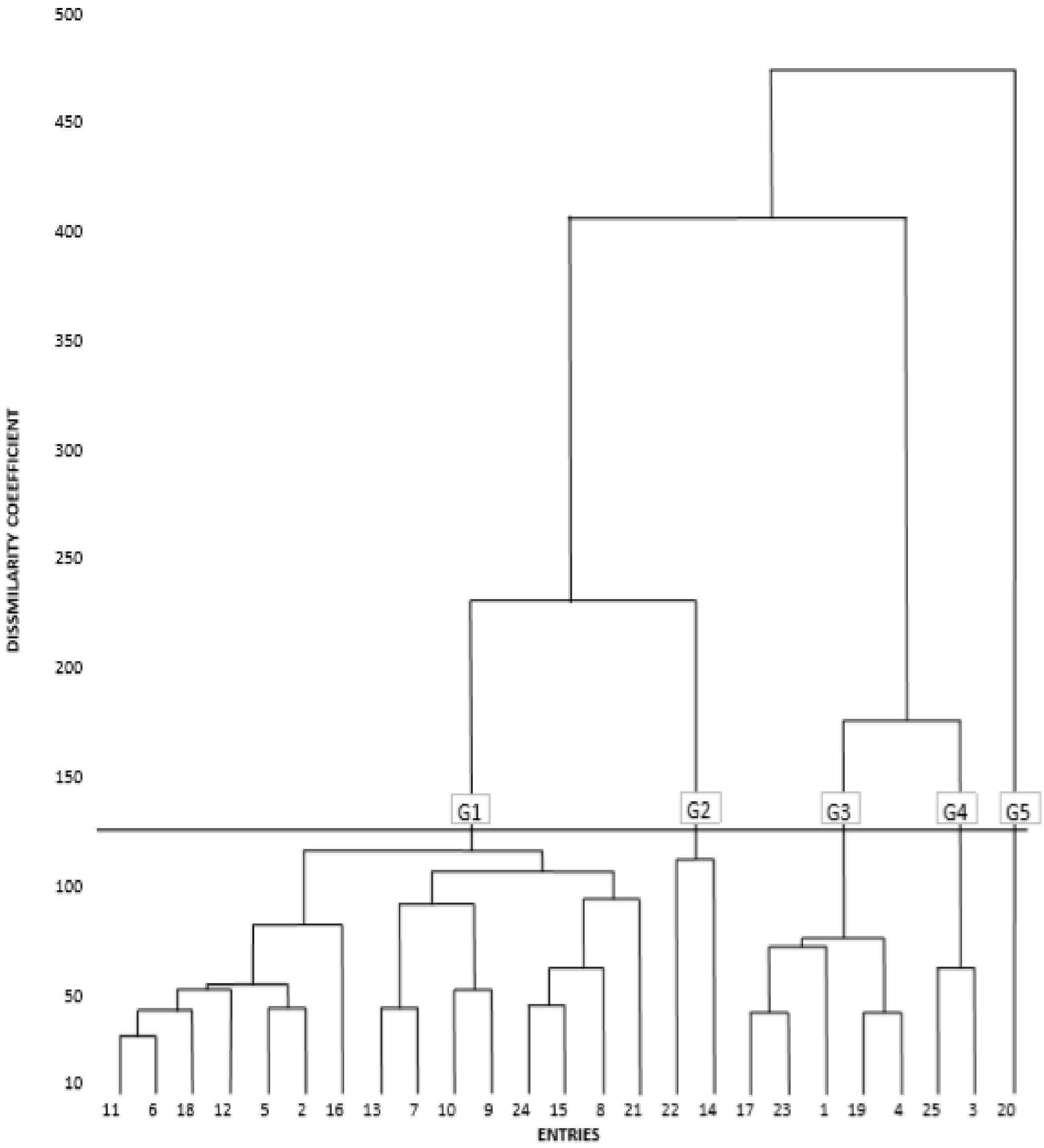

Figure 2. Dendogram showing the relationship of maize accessions from Bangsamoro region based on quantitative traits using Euclidean distance resemblance.

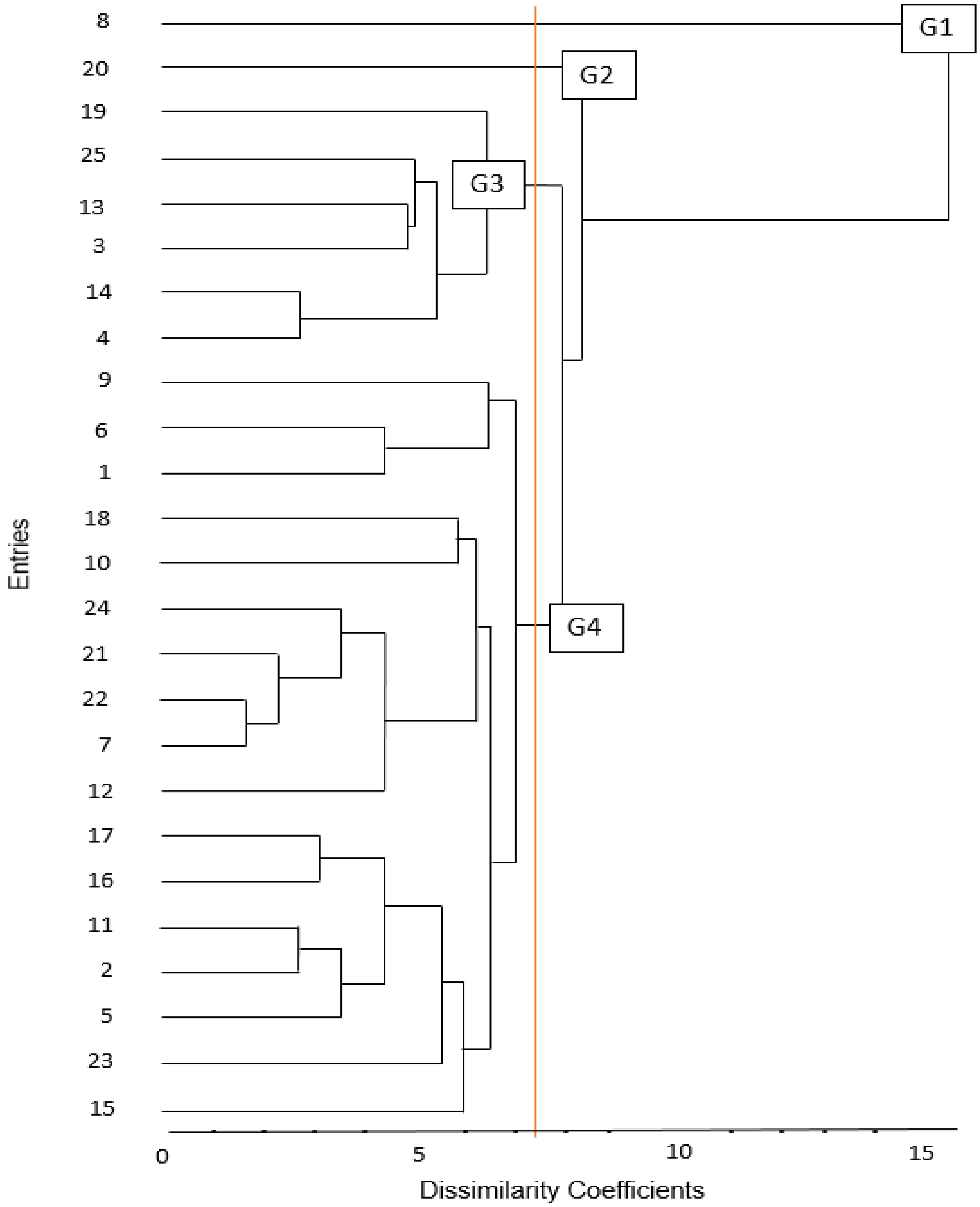

Figure 3. Dendogram showing the relationship of maize accessions from Bangsamoro region based on qualitative traits using Unweighted Pair Group Method with Arithmetic mean (UPGMA). .

For qualitative traits (Figure 5), twelve qualitative genotypes were used to group accessions into clusters using Unweighted Pair Group Method with Arithmetic mean (UPGMA). Accessions were grouped into four different clusters. Group 1 and II contain a single genotype each accession, entry 8 and 20. Group 3 was able to cluster six accessions, while all other entries cluster into group 4. Estimation of relative kinship is shown in the dendogram.

Paired relative kinship ranged from 1.66 to 15. The closest paired relative kinship was entries 22 and 7 with equal value of 11.06%. The furthest by relative kinship were accessions found in G4 x G3 x entries 20 and 8 with a value of 46.66%. The result of the analysis indicated divergent relative kinship existing among the collected white maize germplasm in the Bangsamoro region. Phylogenetic analysis based on visual evaluation of results was used in taking the complexity of traits of the entry cultivars. It showed that closely related varieties were similarly raised for 15 years in the upland plain under the same climate, soil type and management. Whereas, the most divergent entry 20 was collected alone in the rolling areas of the Bangsamoro region.

The implications are that representatives from certain groups are identified for testing as parent to improve traits of interest, specifically in the improvement of yield traits. It was also observed that closely related accessions were from the same geographical origin. For the improvement of quantitative traits, accessions will be identified by representative from each group. To generate heterosis, selection of breeding lines should start from the most divergent entry 20 and group three (entry 19) and group 4 (entry 3) that have higher yield performance. For the qualitative traits, entry numbers 8 and 20 are distantly related in the region. They were found to have poor ear traits and likely to be discarded in the accessions. Therefore, to maintain perfect qualitative genotypes of white maize in the Bangsamoro Region, appropriate selections should be made from cluster three and four.

Summary

Twenty four varieties out of 85 accessions of local maize germplasm in the Bangsamoro region were qualified for use in the study after glyphosate herbicide screening. The experiment was conducted at the University of Southern Mindanao Agriculture Research Center (USMARC) from January to May 2019. Laid out in incomplete block (triple lattice) design replicated three times, USM Var10 was used as local check. There were 21 quantitative traits and 12 qualitative traits.

Phylogenetic analysis showed high genetic diversity among entry varieties. Five hierarchical clusters were created out of the entry varieties using the Euclidean distance for quantitative traits and four cluster groups for qualitative traits using the Unweighted Pair Group method with arithmetic mean (UPGMA). The maximum number of genotypes clustered was 15 and 20 for quantitative and qualitative traits, respectively. The divergent selections are entry 20 and 8.

Conclusion

Discovering the relationship among plant morphological and quantitative features is very important in maize breeding and production. The study concluded that the use of descriptors in evaluating maize has provided exact information in accepting or discriminating the traits present in a cultivar. Based on the study results, the obviously excluded accessions are entry numbers 8 and 20. The results of the experiment also provided scientific evidences of the wide range of genetic diversity and variation of maize germplasm existing within the Bangsamoro region. The results provided scientific information which can serve as bases for the quantitative and qualitative assessment of the morphological and agronomical genotypes, not only for the characterization but more importantly to facilitate the maize breeding program in the region by having the information of the genetic architecture of the germplasm of the studied variety entries.

Recommendations

For future improvement of corn in the Bangsamoro region, it is highly recommended to use the identified accessions from different groups in order to generate higher heterosis. Entries 3, 4 and 19 are the potential breeding lines to generate heterosis, mainly on improving yield traits. These accessions can be used for further field testing and purification for use in future maize breeding program. The study recommends further investigation of the other collected materials to discover genes in stress tolerance, like drought and water lodging, resistance to insect and disease, which are of common occurrence in the origin of germplasm.

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Appendix 1. The eighty-four (84) accessions of white maize germplasm

Appendix 2. Field layout, basal fertilization and seed sowing

Appendix 3. Application of water thru surface irrigation

Appendix 4. Drought phenomenon during vegetative stage

Appendix 5. Plant standing during data gathering