Phenotypic diversity of barley (*Hordeum vulgare* L.) accessions in Ethiopia on the basis of qualitative traits

Gebremedhin Welu Teklu * 1, Gebremedhin Bahre Gebregergis 1, Mehari Geberemicheal Gebru 2, Ameteyesus Berhe Muruts3, Haftay Gebreyesus Gebreziher 2, Yohannes Gerezihier Gebremedhin3, Araya Kasay Gerezgiher 3, Gebremariam Gebrezgabher Gebremedhin 4

[1] Department of Plant Sciences, College of Agriculture and Environmental Science, Adigrat University, Adigrat, Ethiopia
[2] Department of Horticulture, College of Agriculture and Environmental Science, Adigrat University, Adigrat, Ethiopia
[3] Department of Natural Resource Management, College of Agriculture and Environmental Science, Adigrat University, Adigrat, Ethiopia
[4] Department of Environmental Science, College of Agriculture and Environmental Science, Adigrat University, Adigrat, Ethiopia

INTRODUCTION & AIM: Barley is used in numerous traditional foods, including injera, kinche, dabo, roasted grain (kolo), tihlo, basso, and porridge, and it is also used in making local drinks, including tela, borde, and areki (Fig 1) (Mohammed et al., 2016). Ethiopia is the second-largest barley-producing country in Africa behind Morocco (FAOSTAT., 2019) and contributes approximately 25% of the overall barley production on the continent. Identifying genetic diversity is essential for conserving and utilizing the genetic resources of staple crops such as barley (Temesgen, 2021). Currently, approximately 17000 barley accessions collected from barley-growing regions of the country are stored in the Ethiopian Institute of Biodiversity gene bank (Angassa and Mohammed, 2021). However, not enough known about Ethiopian barley's genetic diversity. To determine the utilization and conservation of available barley genetic resources, studies on genetic diversity are paramount (Nyiraguhirwa et al., 2022) Therefore, this study was conducted to ascertain the morphological diversity of barley accessions in Ethiopia.

Fig. 1 Different traditional foods from barley

MATERIALS AND METHODS: One hundred barley accessions were obtained from the Biodiversity Institute, Addis Ababa, Ethiopia, for this research (Fig 2). In addition, two local landraces were included in the experiment as local controls. The experiment was laid out in an alpha lattice design by using two replications having two rows of one meter in length and one meter in spacing between blocks. All the qualitative data were subjected to statistical analysis via Minitab 17th Edition, Microsoft Excel and SPSS software. Principal component (PC) analysis, cluster analysis, the chi-square test (X^2), the Shannon–Weaver diversity index (H'), and distribution frequency were used for the qualitative traits. Analysis of variance (ANOVA) was carried out. The means were separated via the Tukey test at the 5% and 1% significance levels.

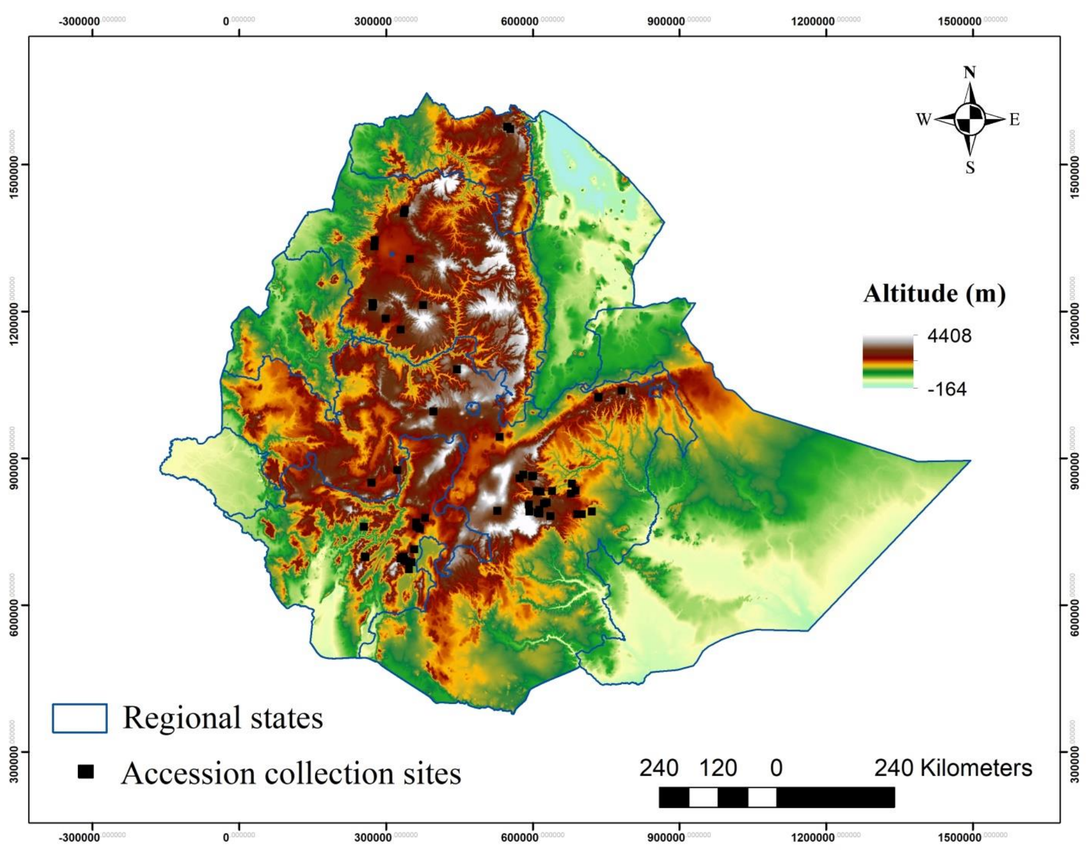
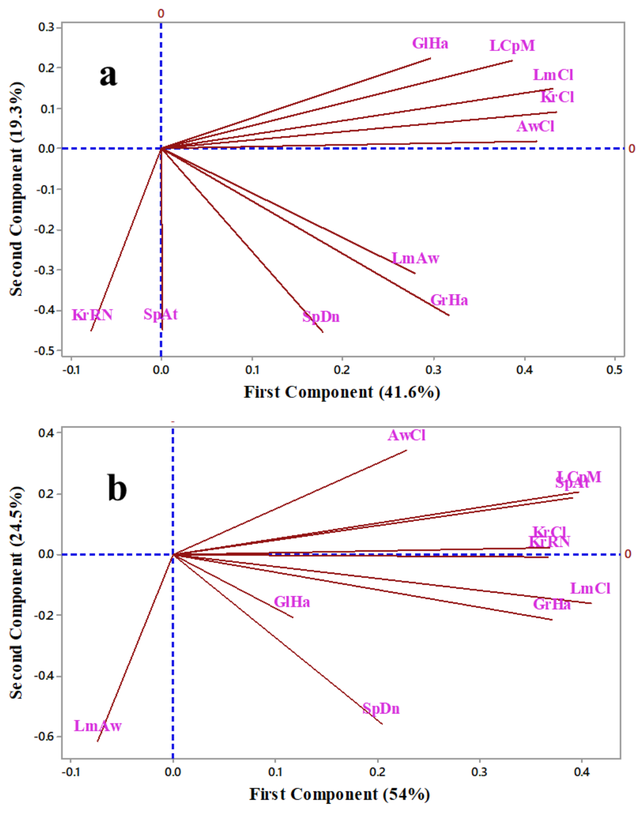


Fig. 2 Map of Ethiopia showing the collection sites of accessions

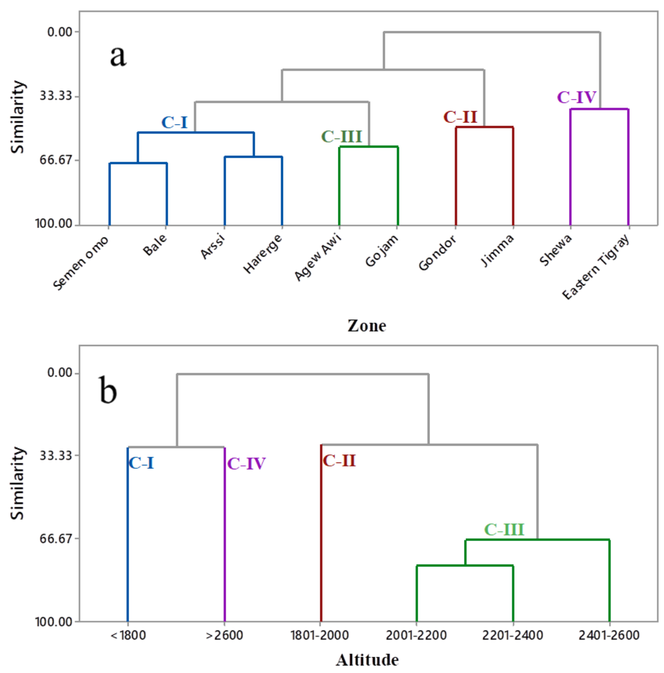
RESULTS & DISCUSSION: The frequency distribution of the phenotypic traits revealed a considerable degree of genetic variability among the accessions. The estimate of H' ranged from 0.83 (glume hairiness) to 0.99 (lemma awn). The highest value of H' in the zones of origin was (H'=1.00) for the kernel row number in Shewa, growth habit and spike attitude in Gojam, glume hairiness in Harerge, and lemma awn in Semen omo. For the altitude classes, the trait lemma awn had the highest value of H' (H'=1.00) in accessions collected at an altitude of ≥2600 m.a.s.l. Among the total variation among the populations, 71% was found within the zones of origin, and 75% was found within the altitude classes. The ANOVA for H' values on the basis of the altitude class and zones of origin showed very highly significant ($p \leq 0.001$) variation to significant ($p \leq 0.05$) variation. On the basis of eigenvalues greater than 1, the first 3 PCs had cumulative contribution rates of 70.6%, 77.4%, and 95.7% of the total variation among accessions, zones of origin, and altitude classes, respectively. Cluster analysis revealed four distinct groups among the zones of origin and altitudinal classes (Fig 4).



From the loading plot, traits like the KrCl, LmCl, and GrHa were the most significant once, as they were found far from the center of the origin (Fig 3a).

Due to their distance from the center of origin, traits such as LmCl, LCpM, SpAt, and LmAw had the highest loading values on the total variation in the altitude class (Fig 3b).

Fig. 3 PC of loading plots showing the associations (a. zone of origin and b. altitudinal classes) of 10 qualitative traits of barley accessions



The patterns of cluster I in our study indicate that genetic material interchange among farmers in neighboring zones is highly likely.

These results suggested that the genetic diversity among accessions was highly impacted by altitudinal variation.

Fig. 4 Dendrogram showing the relationships among ten groups of zones of origin (a) and six altitudinal classes (b) on the basis of qualitative traits of 102 barley accessions

CONCLUSION: In general, traits such as kernel color, lemma color, and growth habit in the zone of origin and traits such as lemma color, lemma awn, and lemma color at physiological maturity in altitude classes (Fig 3) were the most determinant traits among the barley accessions and could be used as selection criteria for crop improvement.

FUTURE WORK / REFERENCES

Angassa D, Mohammed J. Genetic Diversity Assessment of Ethiopian Landrace Barley (<i>Hordeum Vulgare </i>(L.)) Genotypes Through Multivariate Analysis. Am J Biol Environ Stat. 2021;7(3):67.

FAOSTAT. Food and Agriculture Organization of the United Nations. Rome, Italy; 2019.

Mohammed J, Seleshi S, Nega F, Lee M. Revisit to Ethiopian traditional barley-based food. J Ethn Foods [Internet]. 2016;3(2):135–41. Available from: http://dx.doi.org/10.1016/j.jef.2016.06.001

Nyiraguhirwa S, Grana Z, Henkrar F, Ouabbou H, Mohammed I, Udupa SM. Genetic diversity and structure of a barley collection predominatly from North African region. Cereal Res Commun [Internet]. 2022;50(4):647–54. Available from: https://doi.org/10.1007/s42976-021-00209-2

Temesgen B. Role and economic importance of crop genetic diversity in food security. Int J Agric Sci Food Technol. 2021;7:164–9.