

Comparative analyses of 32 complete plastomes of *Tef* (*Eragrostis tef*) accessions from Ethiopia: phylogenetic relationships and mutational hotspots

BACKGROUND

Eragrostis tef is an important cereal crop in Ethiopia with excellent storage properties, high-quality food, and the unique ability to thrive in extreme environmental conditions. However, the **application of advanced molecular tools for breeding and conservation of these species is extremely limited**. Therefore, developing chloroplast genome resources and high-resolution molecular markers are valuable to *E. tef* population and biogeographic studies.

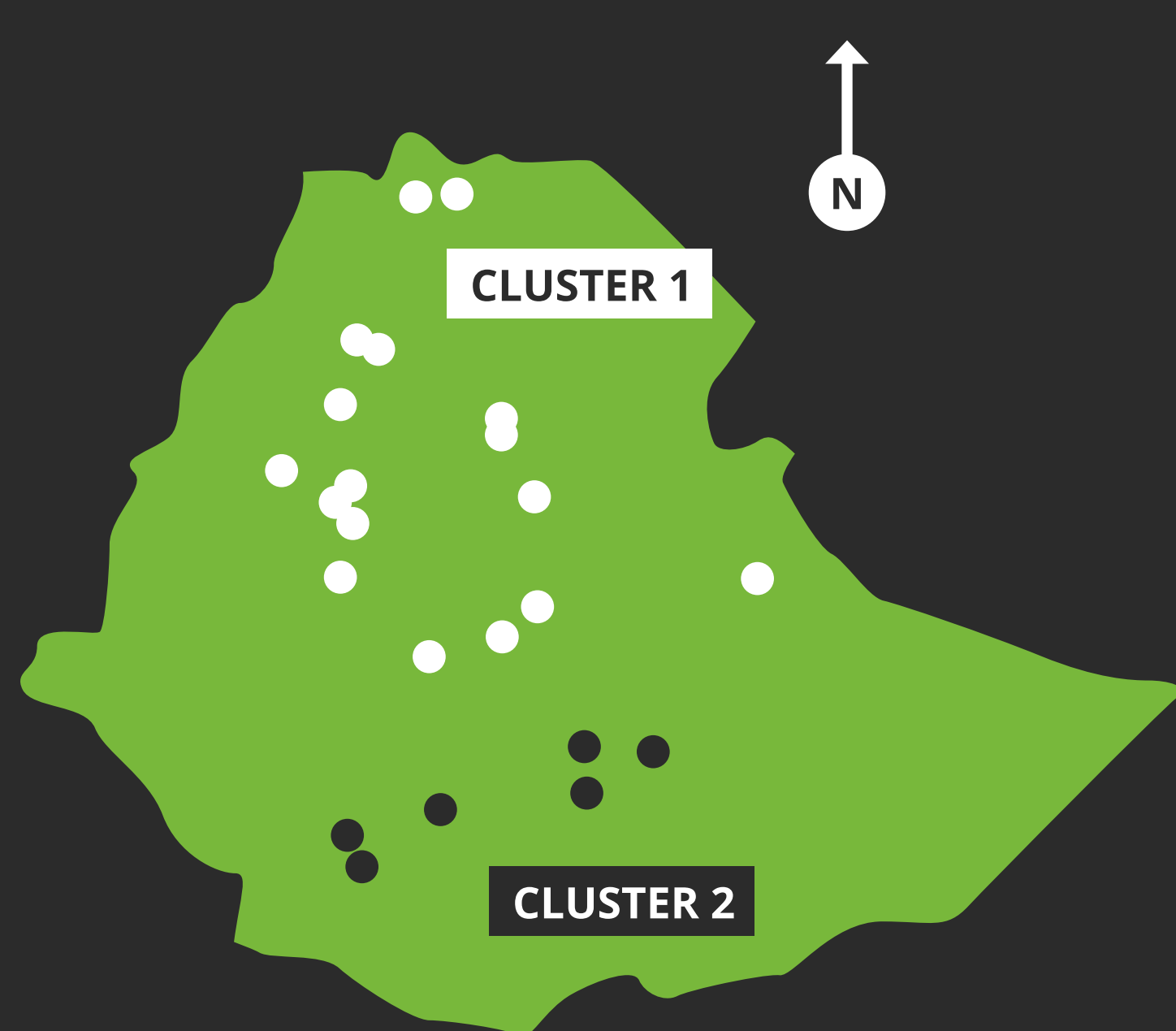


ERAGROSTIS TEF

METHODS

In the current study, **we assembled and compared the complete plastomes of 32 *E. tef* accessions**. These accessions were sampled from Amhara, Benishanguz Gumuz, Tigray, Oromia, and Southern regions, representing the geographic distribution of the species in Ethiopia.

The size of the plastomes ranged from 134,349 to 134,437 bp with similar GC content (~ 38.3%).



RESULTS

Annotated genomes revealed 112 individual genes, including 77 protein-coding, 31 tRNA, and 4 rRNA genes. Comparison of *E. tef* plastomes revealed a low degree of intraspecific sequence variations and no structural differentiations. Furthermore, we found 34 polymorphic sites (13 cpSSRs, 12 InDels, and 9 SNPs) that can be used as valuable DNA barcodes. Among them, the majority (88%) of the polymorphic sites were identified in the noncoding genomic regions. Nonsynonymous (k_a) and synonymous (k_s) substitution analysis showed that all PCGs were under purifying selection ($k_a/k_s < 1$).



The phylogenetic analyses of the whole plastomes and polymorphic region sequences were able to distinguish the accession from the southern population, indicating that they can be used as a super-barcode.



Phylogenetic relationships among *E. tef* accessions were inferred from Bayesian (BI) (A, B) and maximum likelihood (ML) methods (C, D) using complete plastome sequences and twenty variable loci, respectively.



CONCLUSIONS

The newly generated plastomic and polymorphic markers developed here can be a useful genomic resource in molecular breeding, population genetics, and the biogeographical study of *E. tef*.