



The first in-depth insight into the genetic diversity of a buffelgrass (*Cenchrus ciliaris* L.) collection using genotyping-by-sequencing analysis

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Introduction

Buffelgrass (*Cenchrus ciliaris* L.) is an important drought tolerant, warm season, perennial forage grass widely grown in the tropics and subtropics, and is native to different parts of Africa, the Middle East and Asia (Heuzé et al., 2006). A large collection of buffelgrass obtained from different parts of Africa is maintained in the genebank at the International Livestock Research Institute (ILRI) in Ethiopia. So far, most of the diversity information on the collection is based on agro-morphological characterization, where plenty of variation has been identified (Sánchez Gutiérrez et al., 2017 and Jorge et al., 2008). Thus, there is an opportunity to complement this with molecular data to advance and accelerate selection of climate resilient superior genotypes. In this study, we report on the genetic diversity of a buffelgrass collection based on a genotyping-by-sequencing (GBS) approach using the DArTseq platform.

Materials and Methods

Buffelgrass accessions collected from different parts of Africa (Figure 1) were selected. DNA was extracted from freeze dried leaf samples collected from actively growing plants in the field genebank in Zwai, Ethiopia. Data analyses were done using different R packages (<https://www.R-project.org/>) and structure software (Evanno et al., 2005).

Genotyping-by-sequencing

Genotyping data of 111,917 Silico DArT and 93,501 SNP markers were obtained for 185 buffelgrass accessions. Figure 2 shows the polymorphism information content (PIC) values of both types of markers.

Mapping of markers on the reference genome

The markers were mapped on the reference genome of a closely related species, *Setaria italica*, with the aim of selecting representative markers covering the whole genome for in-depth diversity analysis and other related studies. Accordingly, 8,053 (7 %) Silico DArT and 15,465 (16 %) SNP markers were mapped on the reference genome (Figure 3 a and b). One thousand from both silico DArT and SNP markers, distributed across the reference genome, were selected for in-depth diversity assessment of the collection and further genome-wide association studies (GWAS) (Figure 4 a and b).

Genetic diversity of the collection

Population structure analysis using the 1,000 selected markers revealed the presence of two main groups with further sub-groups in the collection based on structure analysis (Figure 5 a and b), phylogenetic tree (Figure 5 c) and PCA (Figure 5 d).

Conclusions

Molecular information of a buffelgrass collection has been generated using GBS and the results revealed the genetic richness of the collection. This information will be useful for different purposes including core collection development, trait-marker association analysis and impact assessment of the use of genetic resources from the genebank.

Reference

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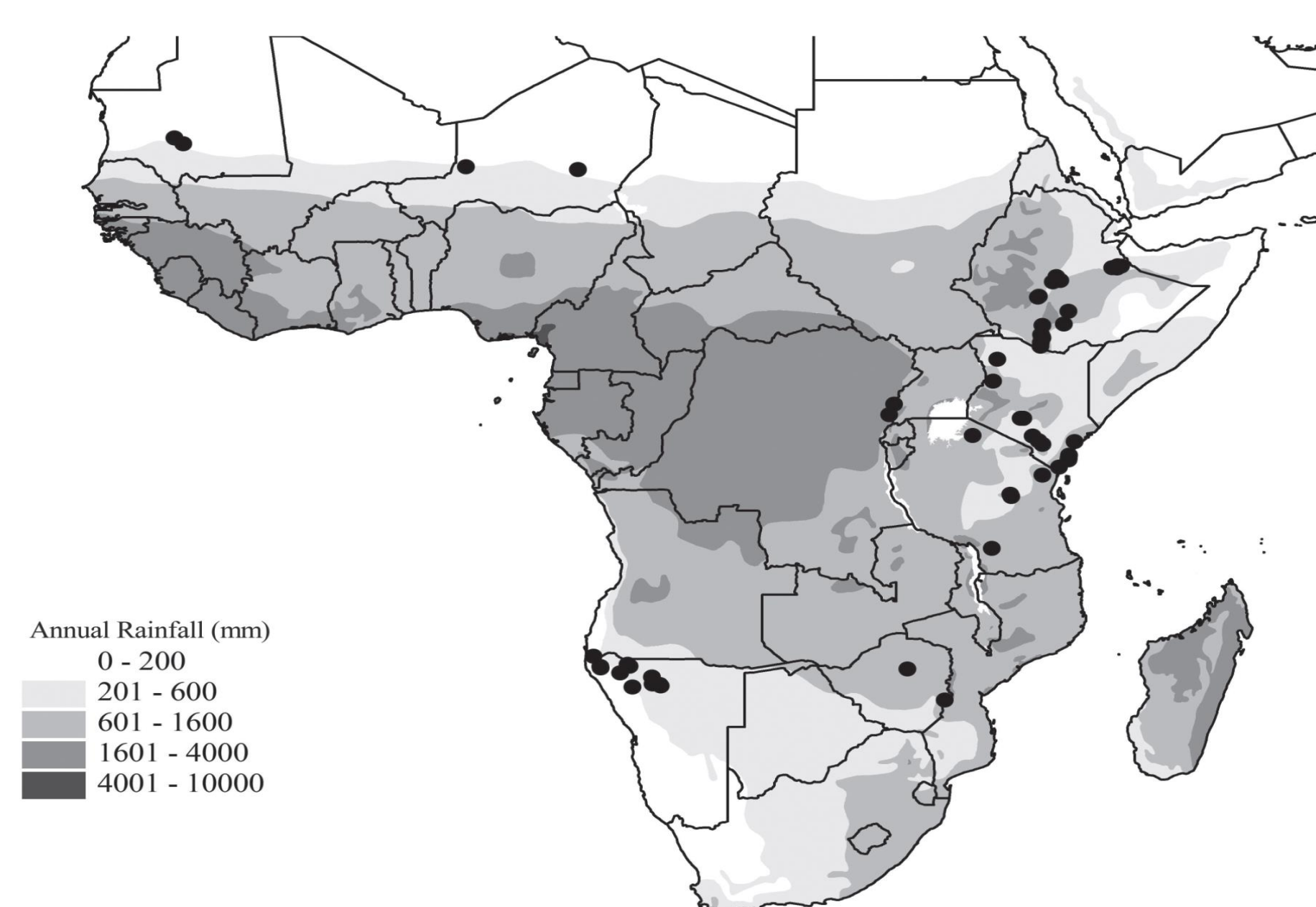


Figure 1. Map showing countries where the buffelgrass accessions were collected in Africa (adapted from Jorge et al., 2008)

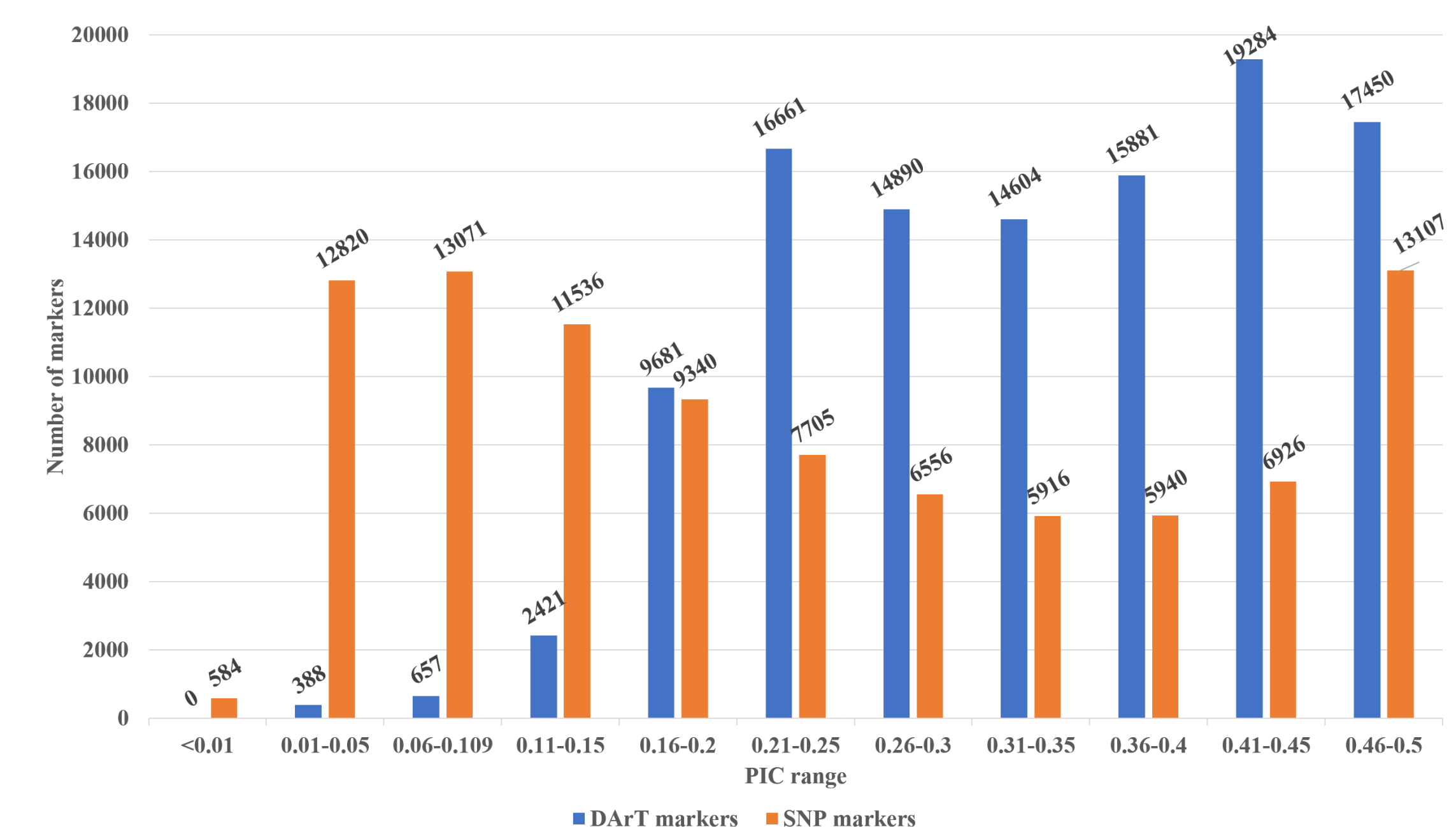


Figure 2. PIC values of Silico DArT and SNP markers

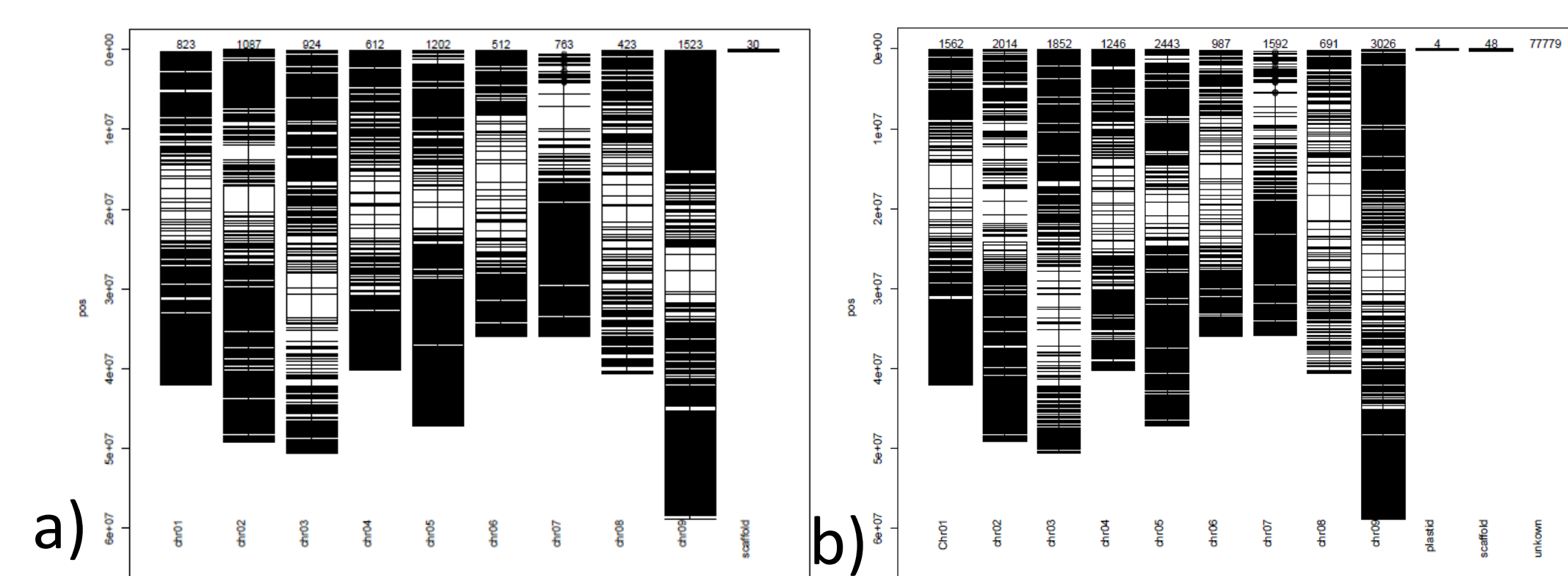


Figure 3. Distribution of Silico DArT (a) and SNP (b) markers across the *Setaria italica* reference genome

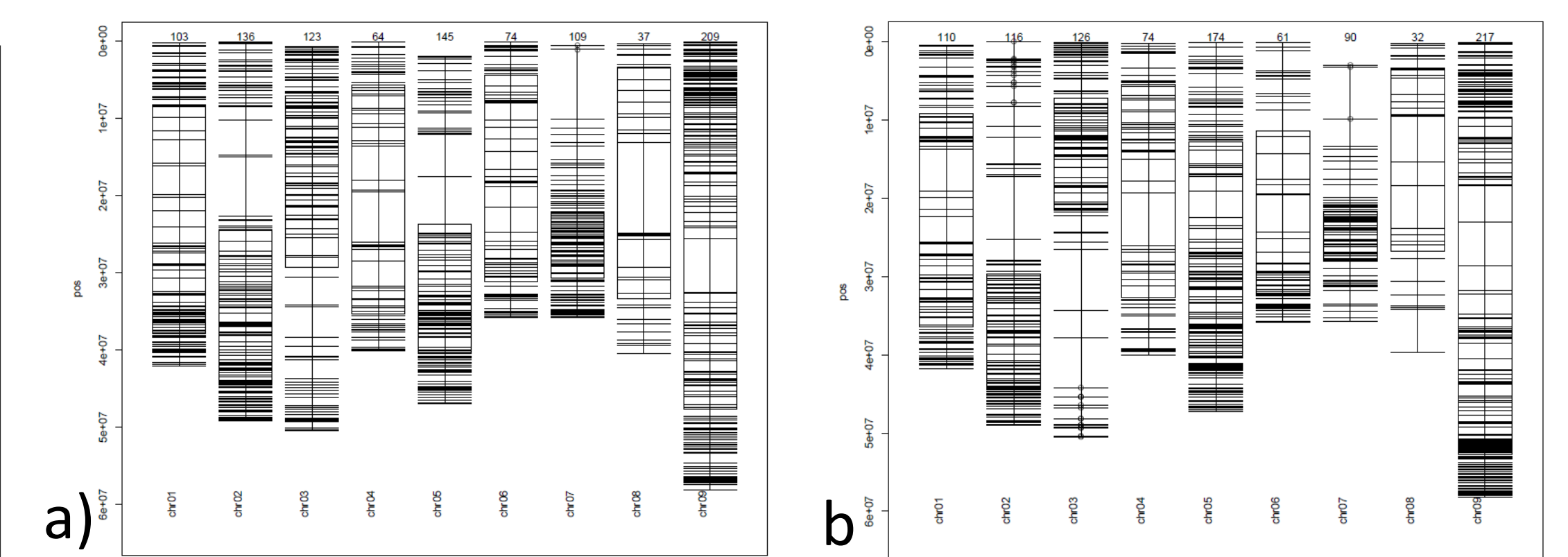
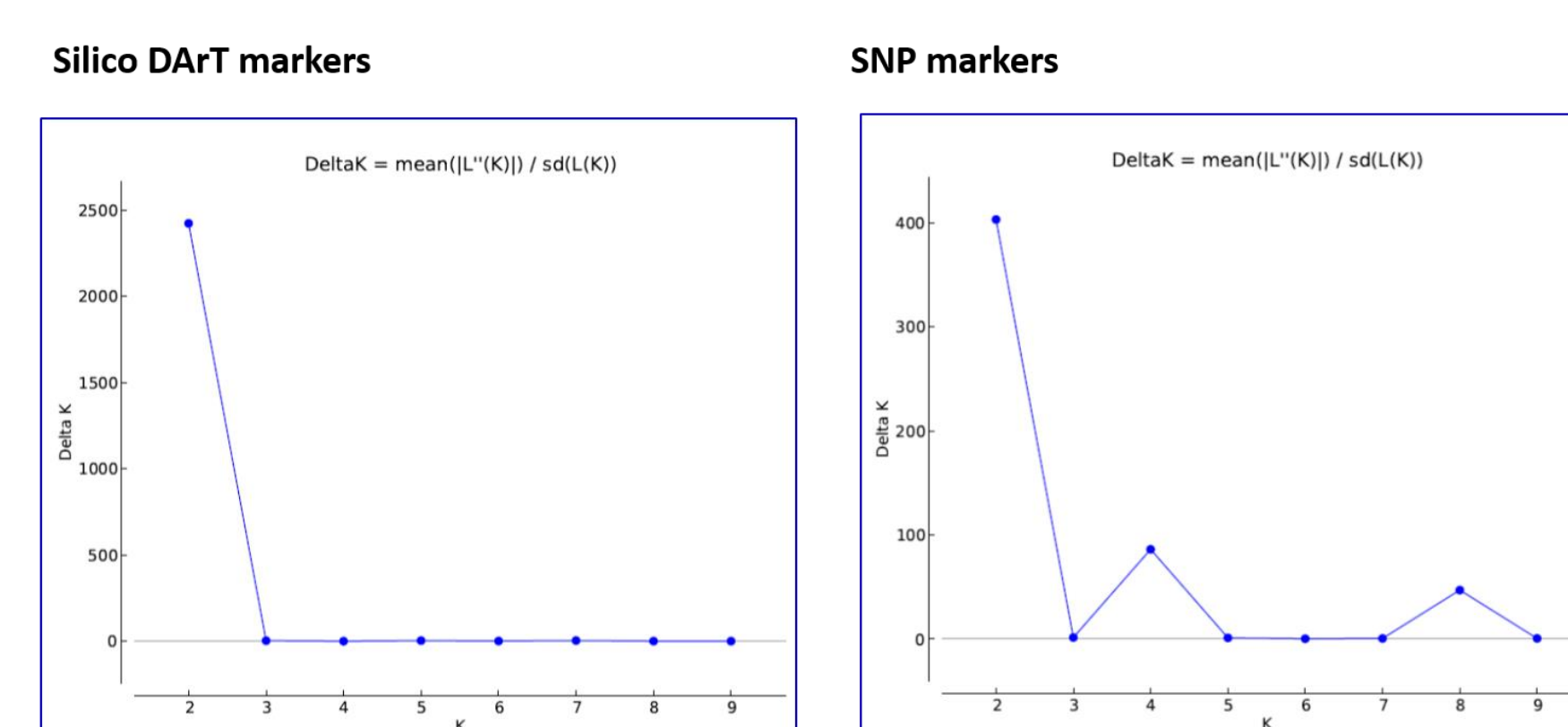
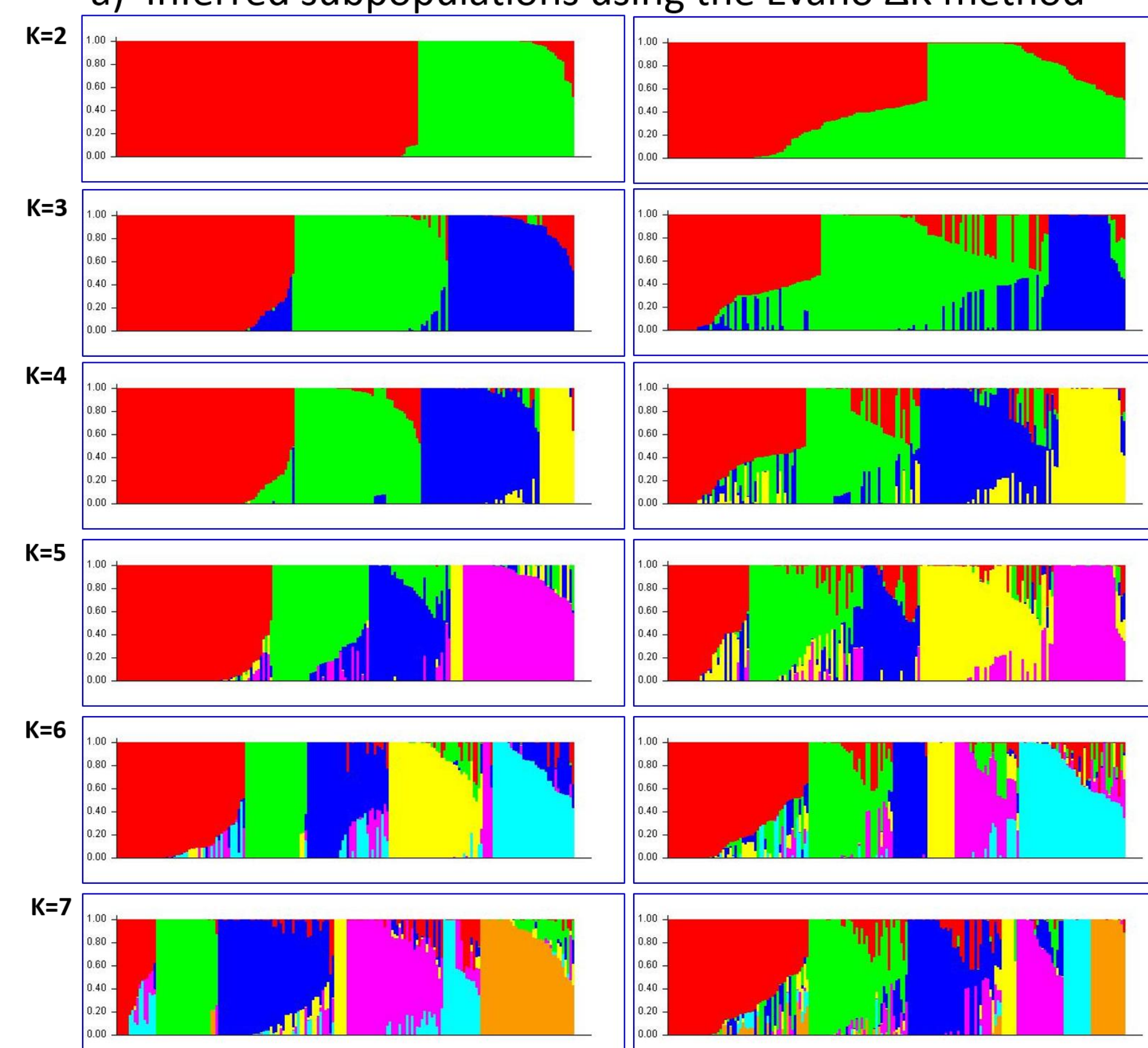


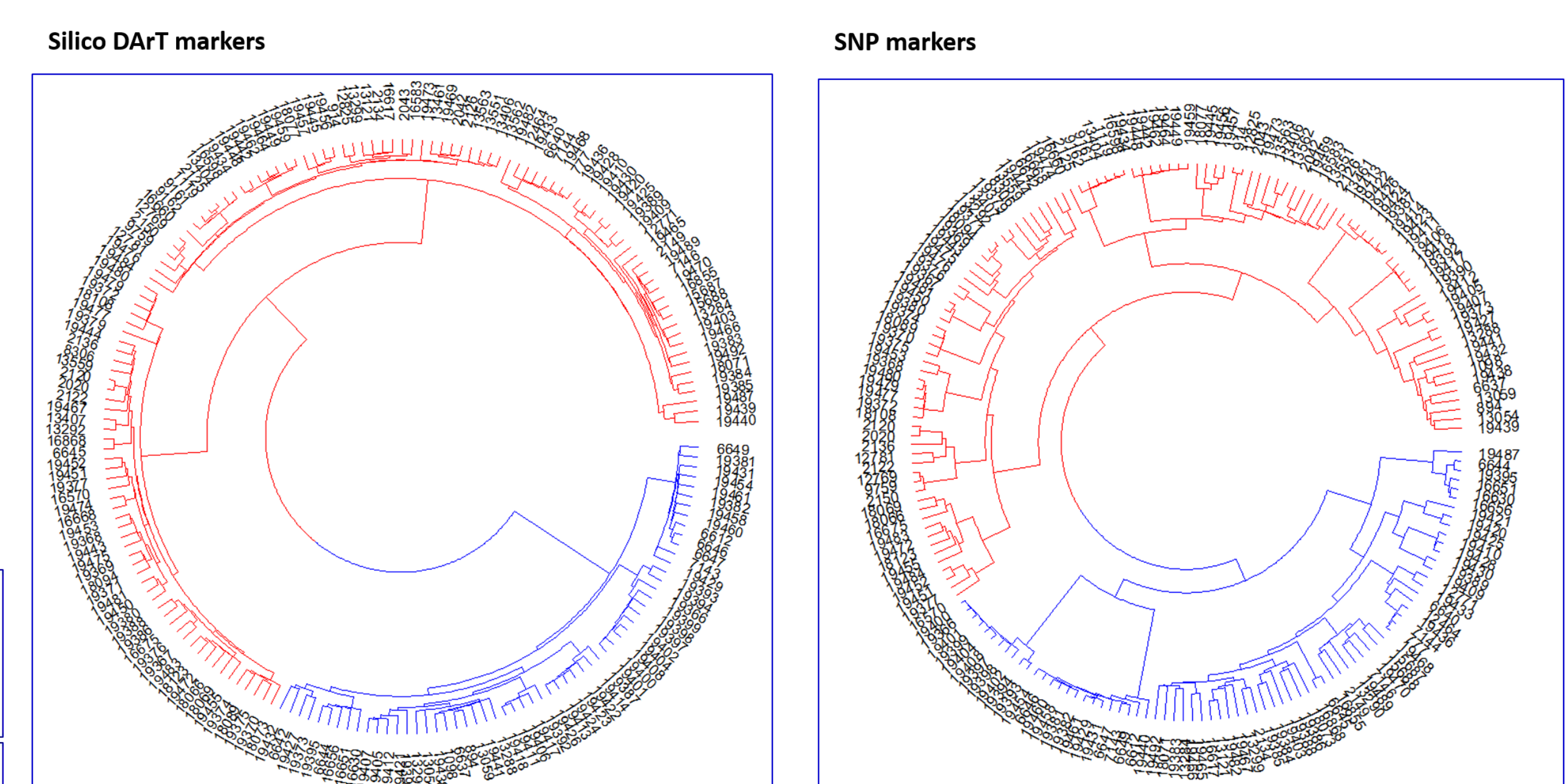
Figure 4. Genome distribution of the selected 1,000 Silico DArT (a) and SNP (b) markers for in-depth diversity studies



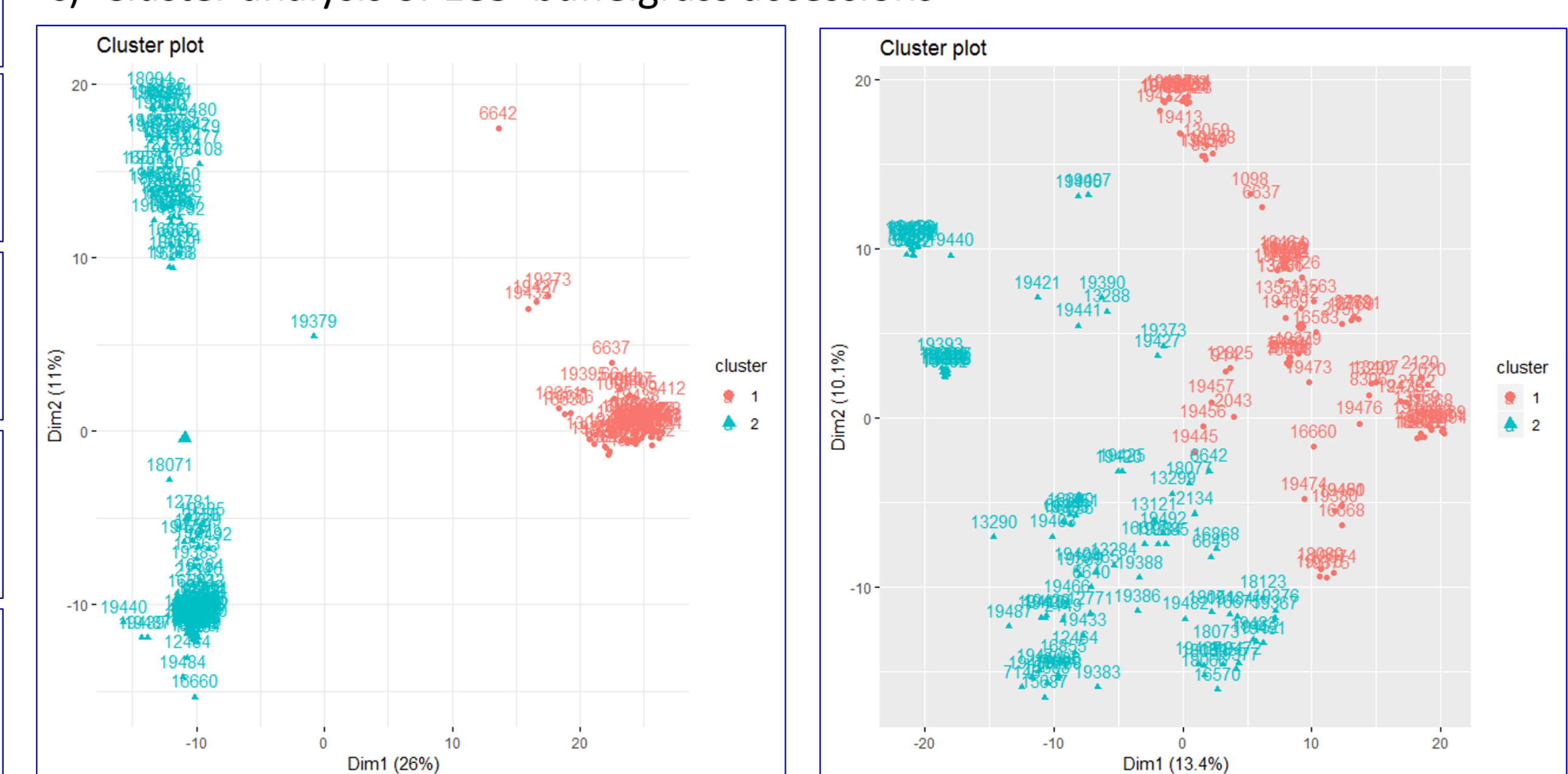
a) Inferred subpopulations using the Evanno ΔK method



a) Bar plots showing the suggested subpopulations



c) Cluster analysis of 185 buffelgrass accessions



d) PCA showing the grouping of the 185 buffelgrass accessions

Figure 5. Population structure and diversity of the buffelgrass collection

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