Genetic and Morphological Characterization of Maize Landraces for Tolerance to Heat Stress

by

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Outline of Presentation

- Introduction
- Materials and Methods
    - ✓ Germplasm
    - ✓ Phenotyping under optimal and heat stress
    - ✓ Genotyping of germplasm
- Discussion of preliminary results
- Conclusions and perspectives

Background

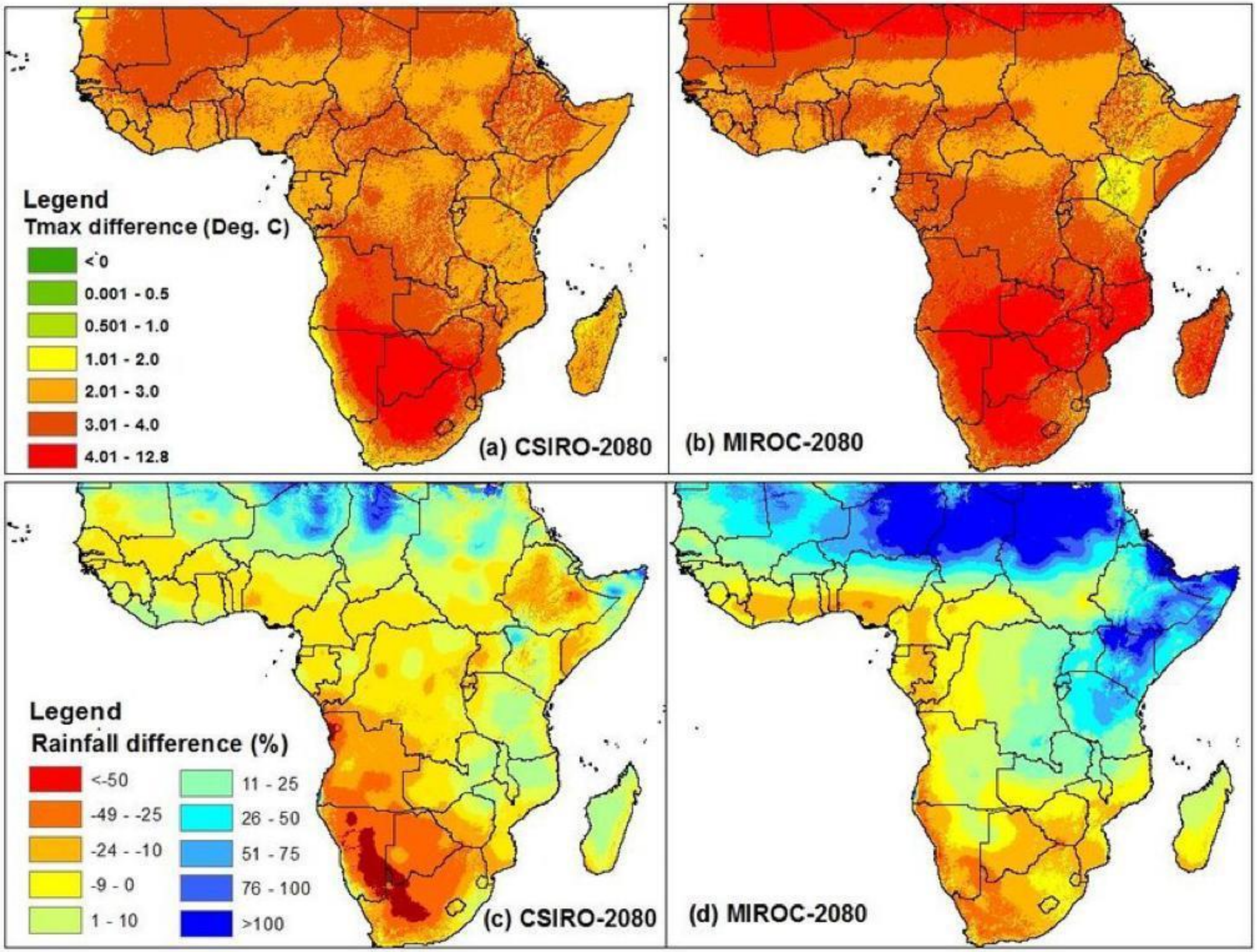


Fig. 1: Projected changes in mean annual temperature (up) and rainfall (down) in sub-Saharan Africa by 2080. Adapted from Cairns *et al*. (2012).

Background

- Maize is key to food and income security in Africa (Edmeades, 2021)
- Drought and heat at the reproductive stages causes >40% to 100% yield loss in maize (Meseka *et al*., 2018)
- +2°C would result in a greater reduction in maize yields than a decrease in precipitation by 20% (Lobell and Burke, 2010)
- Landraces harbor alleles/genes useful for resilience breeding (Garcia-Oliveira *et al*., 2013; Djalovic *et al*., 2023)
- Systematic characterization of landraces is crucial for genetic improvement of maize (Wurschum *et al*., 2022).

Objectives

- **Goal:** Contribute to discovery, characterization and deployment of novel gene variations conferring resilience to climate-related stresses in maize.

Specific Objectives:

1. Identify accessions with high value for climate-adaptive breeding of varieties needed by farmers.

2. Decipher the genetic architecture of drought and heat adaptive traits- *to identify favorable alleles/genes for use in genomics-assisted breeding.*

Materials and Methods

Genetic materials

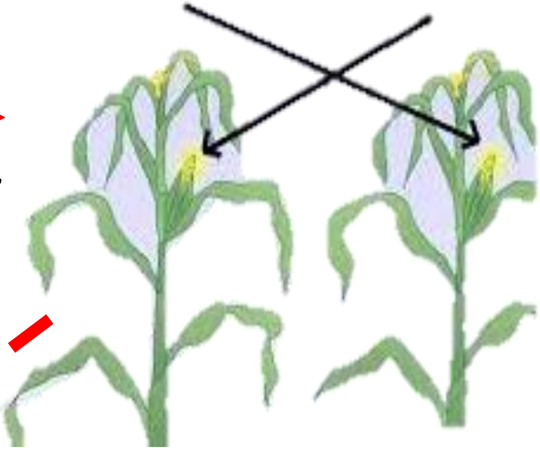
250 landraces

- ✓145– GRC, IITA
- ✓100 - CSIR-PGRRI
- ✓5 - CIMMYT

Breeding nursery

CSIR-SARI, August 2021.

Seed Multiplication



A panel of 210 accessions

Phenotyping & Genotyping of Germplasm

- **Optimal Conditions**
  - ✓ Nyankpala & Damongo
  - ✓ Growing season, 2022
- **Heat Stress**
  - ✓ Bontanga
  - ✓ Guinea Savanna
  - ✓ 31- 45°C
  - ✓ Mid-February, 2023
  - ✓ Furrow irrigation

- **Experimental Procedure**
  - ✓ 15*16 lattice design
  - ✓ Replicated twice
  - ✓ Plots 3 m long
  - ✓ 0.40 × 0.75 m
  - ✓ 66,666 plants/ha
  - ✓ Weed control, Fertilizer
  - ✓ Data - weather & maize crop

Bulked Leaf Samples → EIB → Intertek, Australia

2wks old → Bulked Leaf Samples

Intertek, Australia → 3,305 DArTag Markers

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Phenotypic Data Analyses

- Analyses of Variance
  - ✓ Heritability
  - ✓ Blups

- Phylogenetic /Cluster analysis

- Identification of promising accessions

  ✓ $BI = [(2 \times GY_S) + EPP - ASI - PASP - EASP - SG]$

  + values indicated tolerance and – values, susceptibility (Badu-Apraku *et al.*, 2015).

Genotypic Data Analysis

- **Data Filtering (in Tassel)**
  - ✓MAF (<5%)
  - ✓Missing rates (>20%)
  - ✓Accessions with missing rate (>20%)

- **Diversity parameters**
  - ✓Observed heterozygosity
  - ✓Expected heterozygosity
  - ✓PIC (PowerMarker)

- **Cluster analysis**
  - ✓Population structure (Structure 2.3.4).
  - ✓PCoA (GenAlEx)
  - ✓Neighbor joining tree (Figtree Software)
  - ✓DAPC

Results and Discussion

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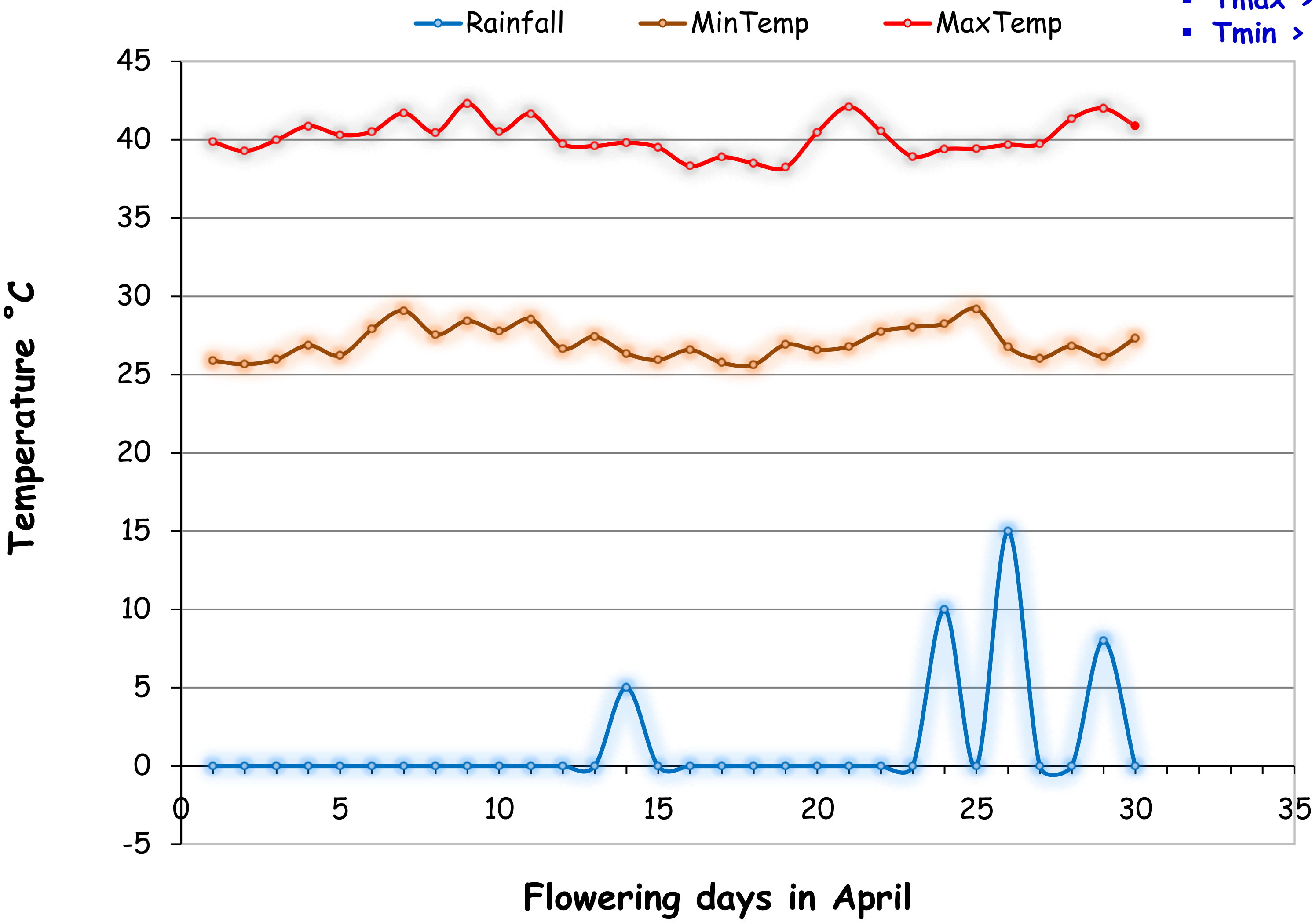
Results and discussion



- Tmax > 35 °C
- Tmin > 25 °C

Fig 1. **Weather conditions (day and night temperatures and rainfall) at Botanga during the flowering period in April, 2023.**

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Results and discussion

Table 1. Grain yield and other traits of the best ten and worse five accessions evaluated under heat stress condition at Botanga.

Entry	GY tons/ha NS	GY tons/ha HS	YR %	ASI days	PASP 1-9	EPP	EASP 1-9	TB %	LF %	BI
41	3.32	2.88	13.25	1.73	5.29	1.04	4.72	0.0	0.0	13.61
best check	3.30	2.58	21.82	1.22	5.19	0.86	5.03	0.0	0.0	11.82
42	3.40	2.95	13.24	2.88	5.13	0.97	5.05	0.0	0.0	11.53
177	3.17	2.73	13.88	2.47	5.05	0.91	5.07	0.0	0.0	10.88
205	3.82	3.07	19.63	3.58	5.05	0.83	4.55	0.0	0.0	10.80
123	3.98	3.06	23.12	3.27	5.19	0.87	5.03	0.0	0.0	10.67
12	3.96	3.12	21.21	3.18	5.23	0.87	5.14	0.0	0.0	10.22
32	3.21	2.51	21.81	2.72	5.10	0.91	4.63	2.45	2.70	9.98
117	3.28	2.60	20.73	3.23	5.24	1.03	4.89	6.69	13.01	9.48
111	2.79	2.64	5.37	3.27	5.29	0.87	5.00	3.79	5.89	8.47
202	3.26	2.35	27.91	3.17	5.25	0.90	5.25	3.79	3.71	7.42
Worse Five										
20	2.85	1.04	63.51	6.08	6.01	0.49	7.07	63.05	48.04	-12.46
46	2.14	0.89	58.41	-	6.38	0.33	7.60	45.13	41.86	-12.92
54	2.12	0.00	100	-	7.00	0.00	8.00	100.00	100.00	-21.64
27	2.40	0.00	100	-	8.00	0.00	9.00	100.00	100.00	-22.61
95	1.52	0.00	100		8.00	0.00	9.00	100.00	98.00	-31.59
Mean	2.86	1.69	40.91	3.42	5.60	0.74	5.98	7.87	7.34	
P	***	***		***	***	***	***	**	**	
Heritability	0.74	0.49	0.89	0.40	0.32	0.57	0.55	0.60	0.56	

NS=non-stress, HS=heat stress; GY=grain yield; YR=yield reduction; AD=days to anthesis; SD=days to silking; ASI=anthesis-silking interval; PASP=Plant aspect; EPP=ears per plant; EASP=Ear aspect; TB=Tassel blast; LF=Leaf firing; BI=Base index. *;**;***=significance at 0.5; 0.1 and 0.001 probability levels, respectively.

Results and discussion

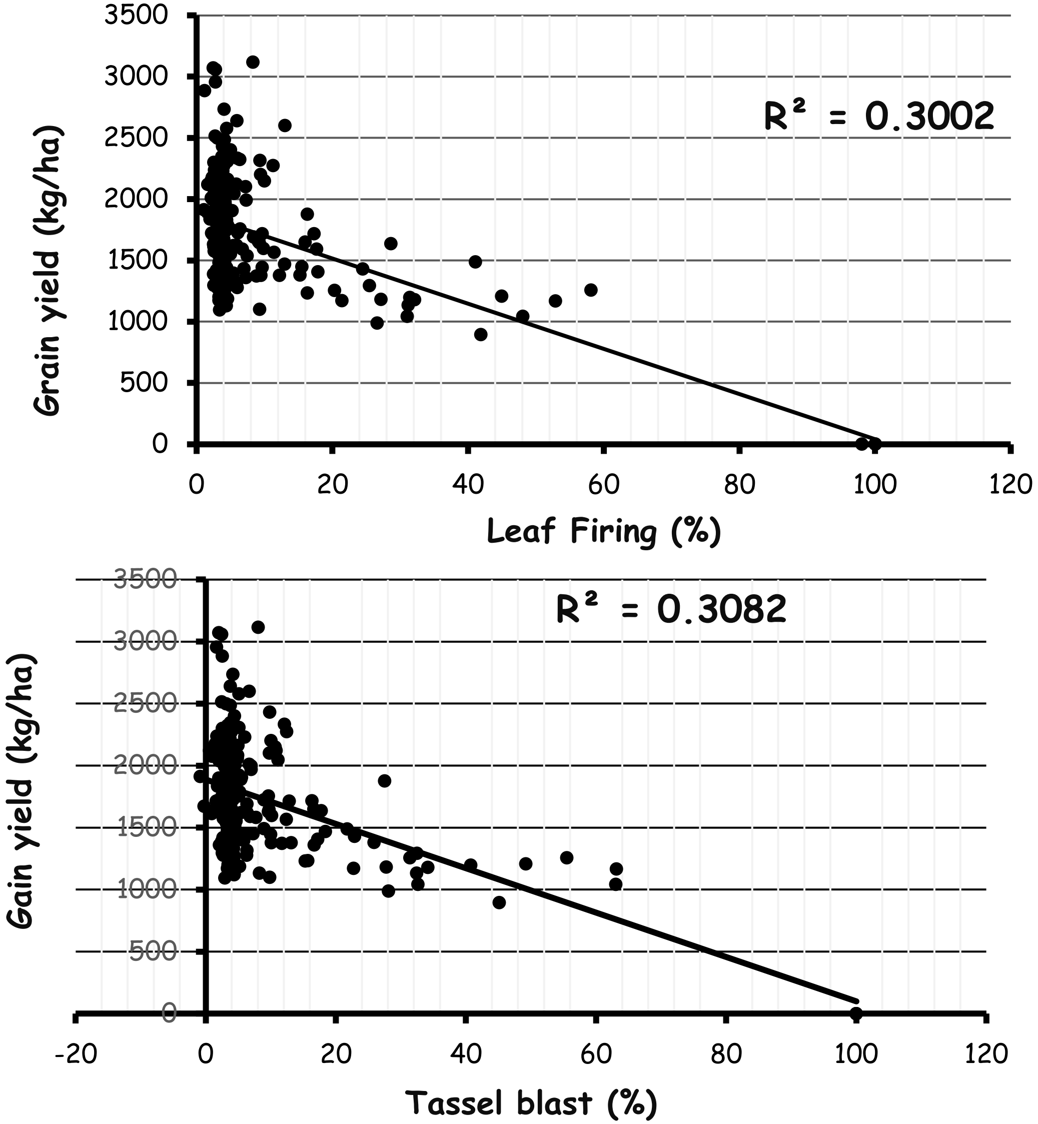
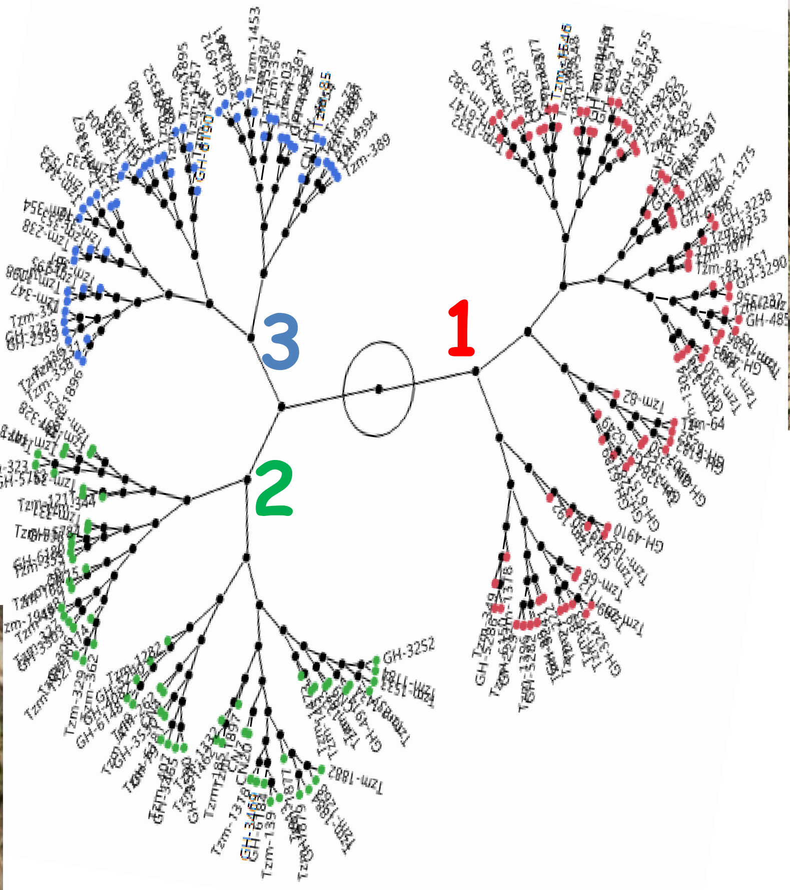


Fig 2. Relationship between grain yield and leaf firing(up) and tassel blast (down).

Results and discussion



Meseka *et al.* (2018) Tandzi *et al.* (2018)

Fig 3. Phylogenetic tree of the 210 maize accessions based on phenotypic data under heat stress conditions at Botanga.

Results and discussion

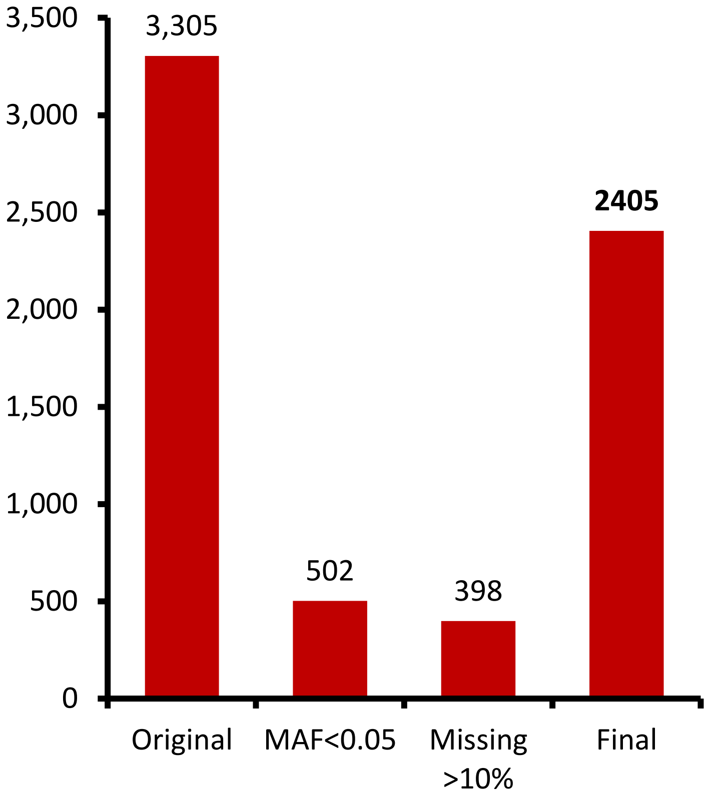


Fig. 4: Quality processing of genotypic data

Table 2: Diversity statistics based on 2,405 DArTag markers across 203 maize accessions.

	MAF	GD	H	PIC
Min	0.50	0.09	0.01	0.08
Max	0.95	0.50	1.00	0.38
Mean	**0.72**	**0.37**	**0.51**	**0.29**

MAF: Minor allele frequency, GD: Gene diversity; Ho: heterozygosity; PIC: Polymorphic information content;

Nelimor *et al.* (2020); Badu-Apraku *et al.* (2021)

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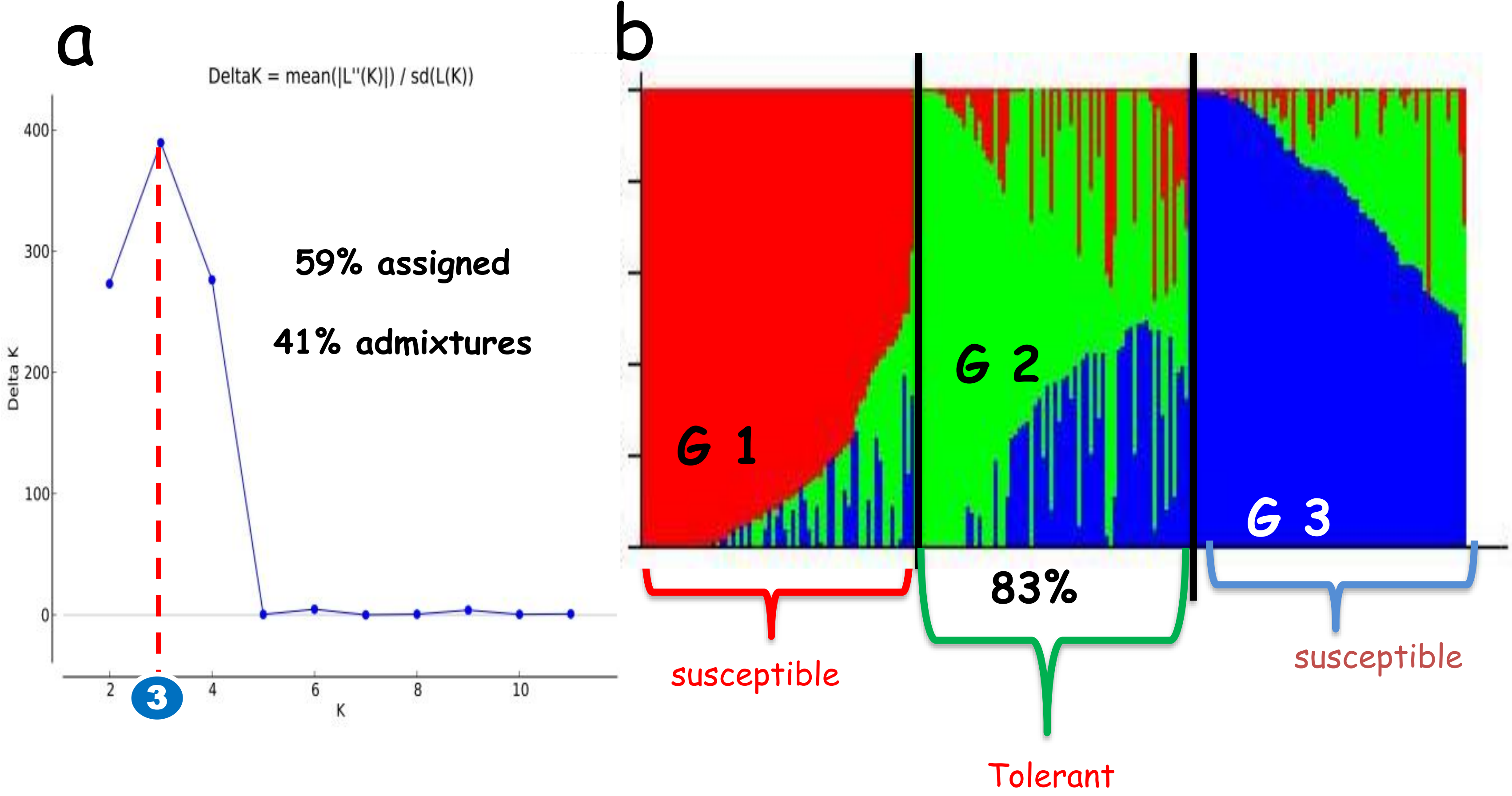
Results and discussion



59% assigned

41% admixtures

Fig. 5: Structure analysis of the 203 maize accessions based on 2,405 DArTag markers showing the best delta K (**a**) estimated by Evanno method and the estimated population structure (**b**).

Conclusions and Perspectives

1. The maize panel harboured ample genetic diversity
2. Fifty-five (55) promising accessions were identified for heat stress tolerance
3. Based on our results, tassel blast and leaf firing should be considered for inclusion in index selection for heat tolerance
4. Next steps: identification of molecular markers associated with important traits via GWAS and applying it through KASP technology for easy screening

Acknowledgments

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Thank you