



Exploiting cowpea genetic resources to improve tolerance to high temperatures

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Food Insecurity & Climate Change

Future Scenarios

Emissions

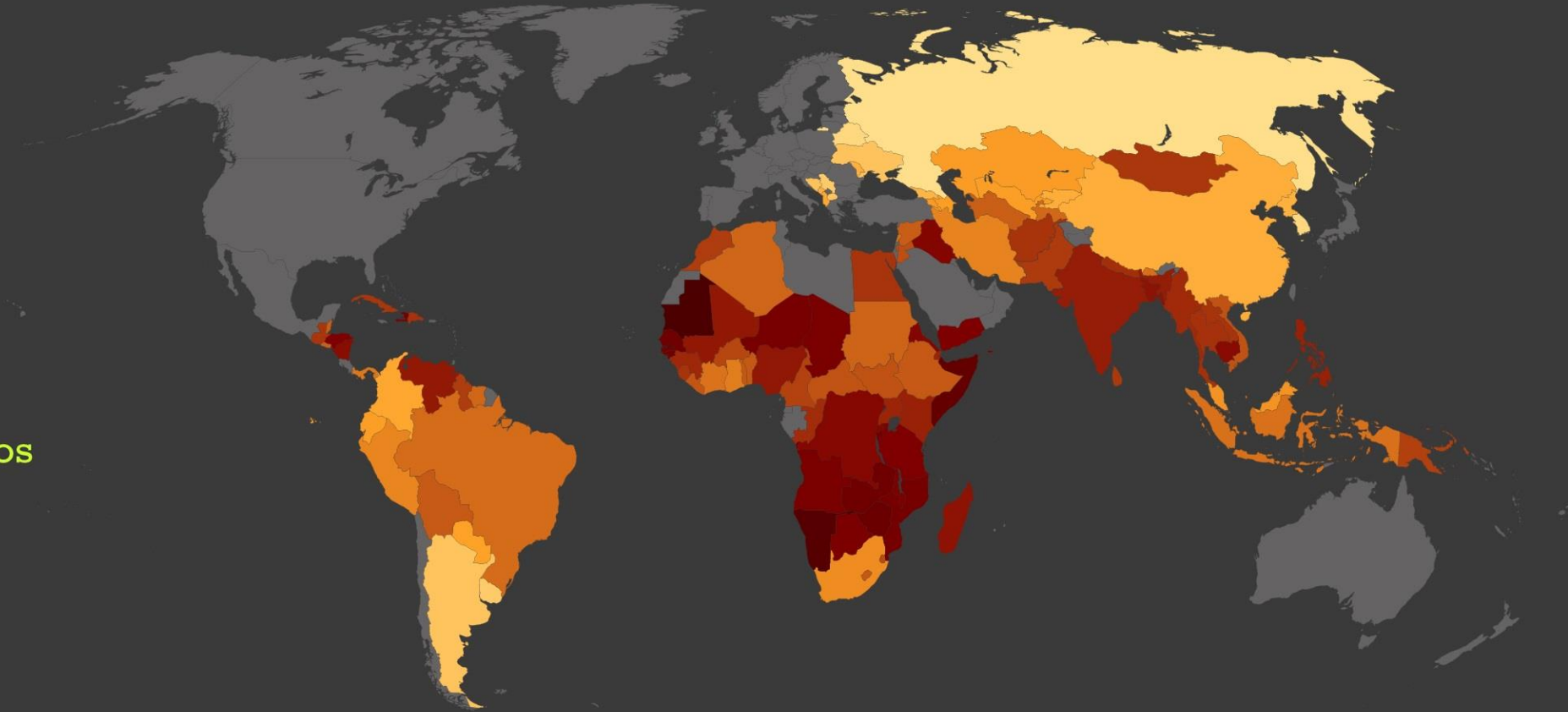
● HIGH

Adaptation

● NONE

Key

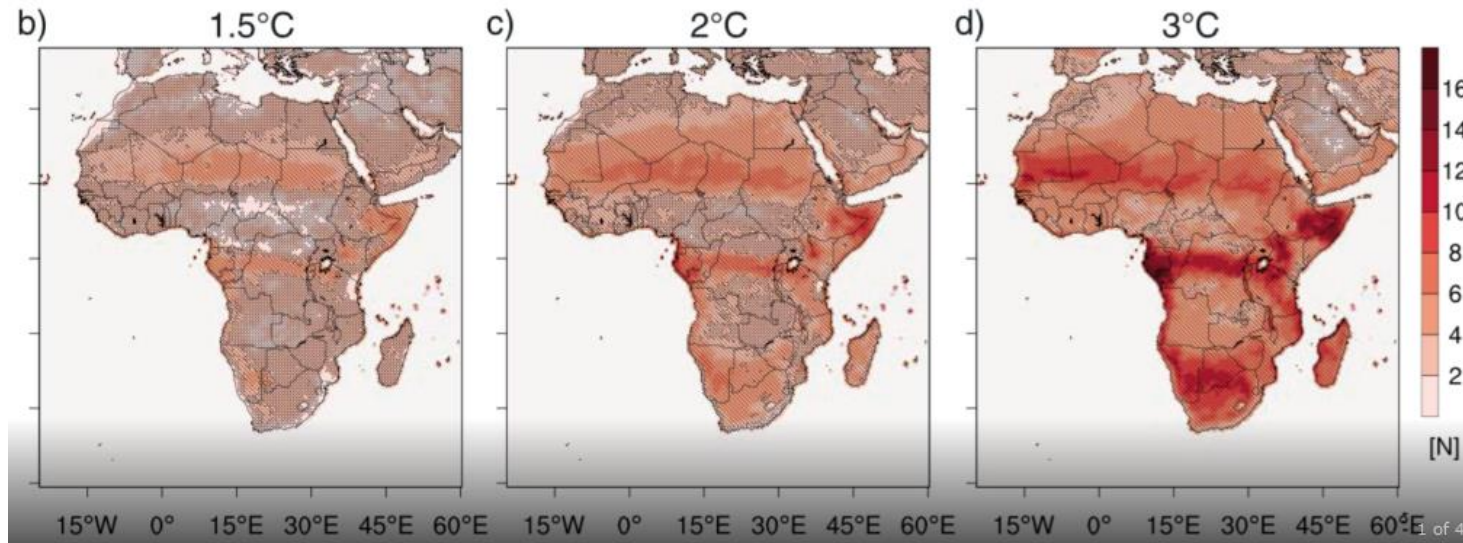
Vulnerability to food insecurity



2050s

The problem of high temperatures

- Daily maximum and minimum temperatures are increasing... and so **heat waves!**



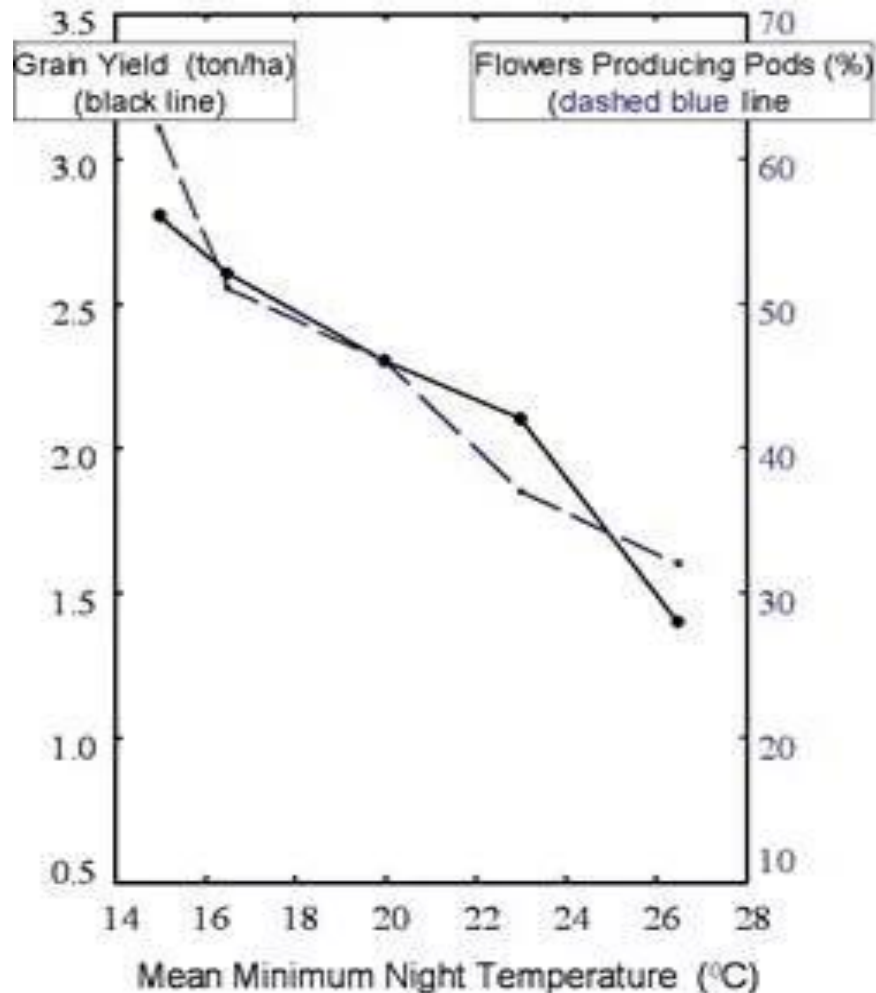
Weber et al. (2018)

- High temperatures have damaging effects on plant function and/or development, and can increase the rate of reproductive development, reducing yield

Cowpea is one of the legume crops most tolerant to high temperatures during germination, vegetative growth and reproductive development, making it a good system to understand the genetics of adaptation to heat stress

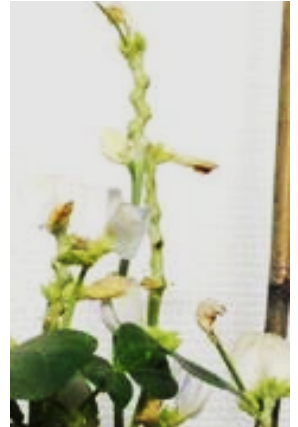
The problem of high temperatures

➤ However, **high night temperatures** can have damaging effects on cowpea reproductive processes



- High night temperatures **reduce pod set** (i.e., the proportion of flowers producing pods)

- ✓ A **4.4% decrease in grain yield per 1°C increase in min. night temperature** above a threshold of 15°C has been observed (50% yield reduction at a minimum temperature of 26°C)



- Increased night temperatures **accelerate reproductive development**, which shortens the time for resource capture during pod-filing, also reducing yields

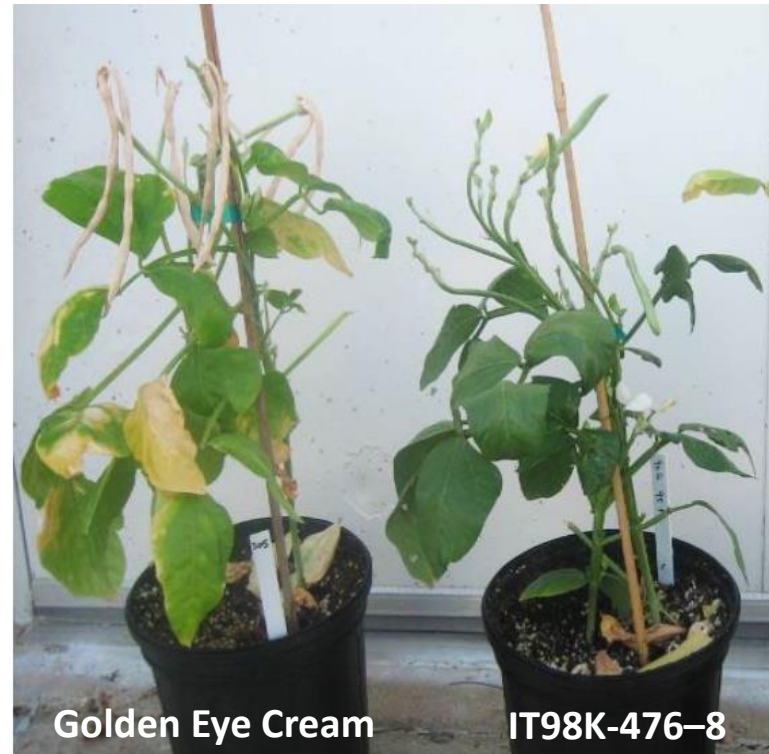
- ✓ **Increases of min. night temperature from 16°C to 26°C** can cause a **7-day reduction** of pod development period

Cowpea germplasm

- Cowpea germplasm is **very diverse** (available from genebanks)!!!
And **variation** for **heat stress tolerance** has been observed in cowpea
- The number of accessions with superior heat tolerance identified to date is low
- Not so much progress has been made in breeding cultivars with high heat tolerance (e.g. CB27)



Lucas et al. (2013)



Angira et al. (2022)

- Two cowpea studies have mapped QTLs for heat tolerance using RIL populations

Mining diverse germplasm

- We need to survey a **larger set of diverse germplasm!**
- We need to **expand the work** to the **short-day conditions** of the major tropical production regions!
 - Photoperiod-sensitive germplasm could be a reservoir of beneficial alleles for heat stress tolerance

Cowpea collection

IITA



Description: IITA Cowpea collection
Prefixes: TVu
Collection size: 16460 accessions



IITA Core

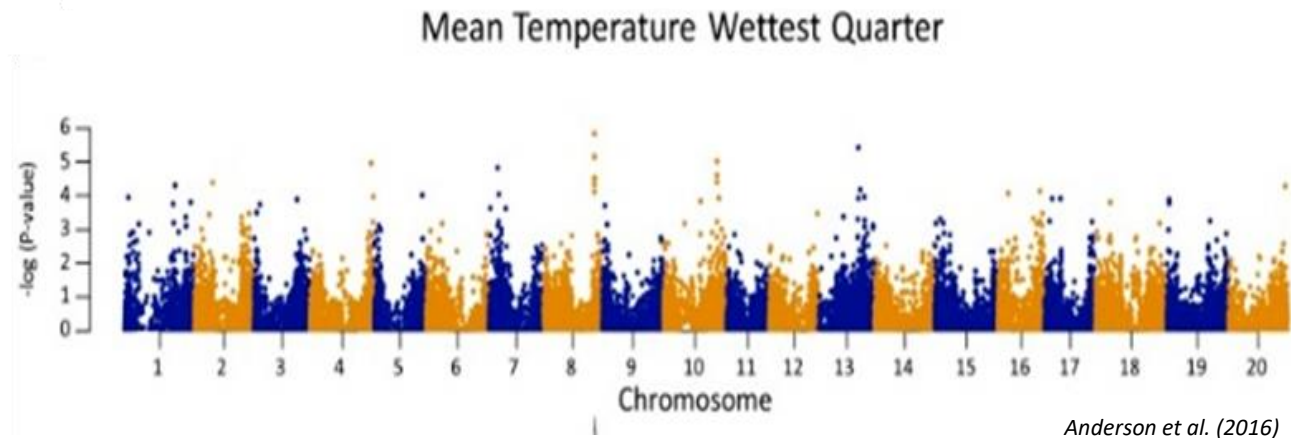
- **2,021 accessions** genotyped with Illumina iSelect Array (51,128 SNPs):
 - 209 breeding/research material
 - 1612 traditional cultivar/landrace
 - 38 weedy
 - 20 wild
 - 142 unknown biological status

How do we mine this large collection to identify beneficial alleles for heat tolerance???

Mining genebank collections through envGWAS

The approach: environmental GWAS (envGWAS) or genome-environment association

- **Associates** genome-wide **SNPs** with **climatic variables** based on the sampling location of the accession (latitude/longitude) to identify loci involved in adaptation to specific growing environments
- Uses **landraces** and **crop wild relatives** adapted to different environments (including severe environments) to understand the genetic basis of natural adaptation to abiotic stresses



What's needed: landraces/wild accessions with high-density SNP data and geographic information + global climatic data

IITA Core passport data

Accession name	Country of origin	Location	Latitude	Longitude	Elevation	Biological status of accession
TVu-11952	Nigeria					Traditional cultivar / Landrace
TVu-11953	Nigeria					Traditional cultivar / Landrace
TVu-11954	Sudan	AYLAFON VILLAGE ,53KM EAST KHARROUN ,KHARROUN PROVINCE	15.8333	32.833302		Traditional cultivar / Landrace
TVu-11955	Sudan	KHARROUN MARKET,KHARROUN PROVINCE	15.6667	32.5		Traditional cultivar / Landrace
TVu-11959	Sudan	WAD-EL-NEIL ,63KM SOUTH ABU NAAMA BLUE NILE PROVINCE	12.7333	34.1333	433	Traditional cultivar / Landrace
TVu-11960	Sudan	WADMEDANI,GEUIRA PROVINCE	14.0833	32.450001	412	Traditional cultivar / Landrace
TVu-11963	Sudan	63KM SOUTH ABU NAAMA BENE NILE PROVINCE	12.7333	34.1333	433	Traditional cultivar / Landrace
TVu-11971	Sudan	100KM SOUTH ,ABU NAAMA BENE NILE PROVINCE	12.7333	34.1333	433	Traditional cultivar / Landrace
TVu-11977	Sudan	ABU NAANA RESEARCH STATION ,ABU NAANA ,BENE NILE PROVINCE	12.7333	34.1333	433	Traditional cultivar / Landrace
TVu-11990	Sudan					Traditional cultivar / Landrace
TVu-1207	Guyana					Traditional cultivar / Landrace
TVu-1208	Guyana					Traditional cultivar / Landrace
TVu-12139	India					Traditional cultivar / Landrace
TVu-123	Botswana					Traditional cultivar / Landrace
TVu-12340	Mozambique					Traditional cultivar / Landrace
TVu-12351	Mozambique					Traditional cultivar / Landrace
TVu-12354	Mozambique					Traditional cultivar / Landrace
TVu-12357	Mozambique					Traditional cultivar / Landrace
TVu-12415	Zambia					Traditional cultivar / Landrace
TVu-12430	Zambia					Traditional cultivar / Landrace
TVu-12431	Zambia					Traditional cultivar / Landrace
TVu-12432	Zambia					Traditional cultivar / Landrace
TVu-12449	Zambia					Traditional cultivar / Landrace
TVu-12470	Zambia					Traditional cultivar / Landrace
TVu-12526	Yemen	9KM NORTH OF HAJJAGH	15.695	43.5975	1791	Traditional cultivar / Landrace

- Not all landrace/wild accessions had location information
- Some accessions had been collected at a “market”
- For many countries, we had no access to reliable cropping season information

The dataset:

- ✓ 681 accessions (mostly landraces) from Africa whose collecting site was not a market
- ✓ 45,763 polymorphic SNPs
- ✓ 19 climatic variables (BIO1-BIO19) extracted from WorldClim 2.1 (historic 30-year period climate data)

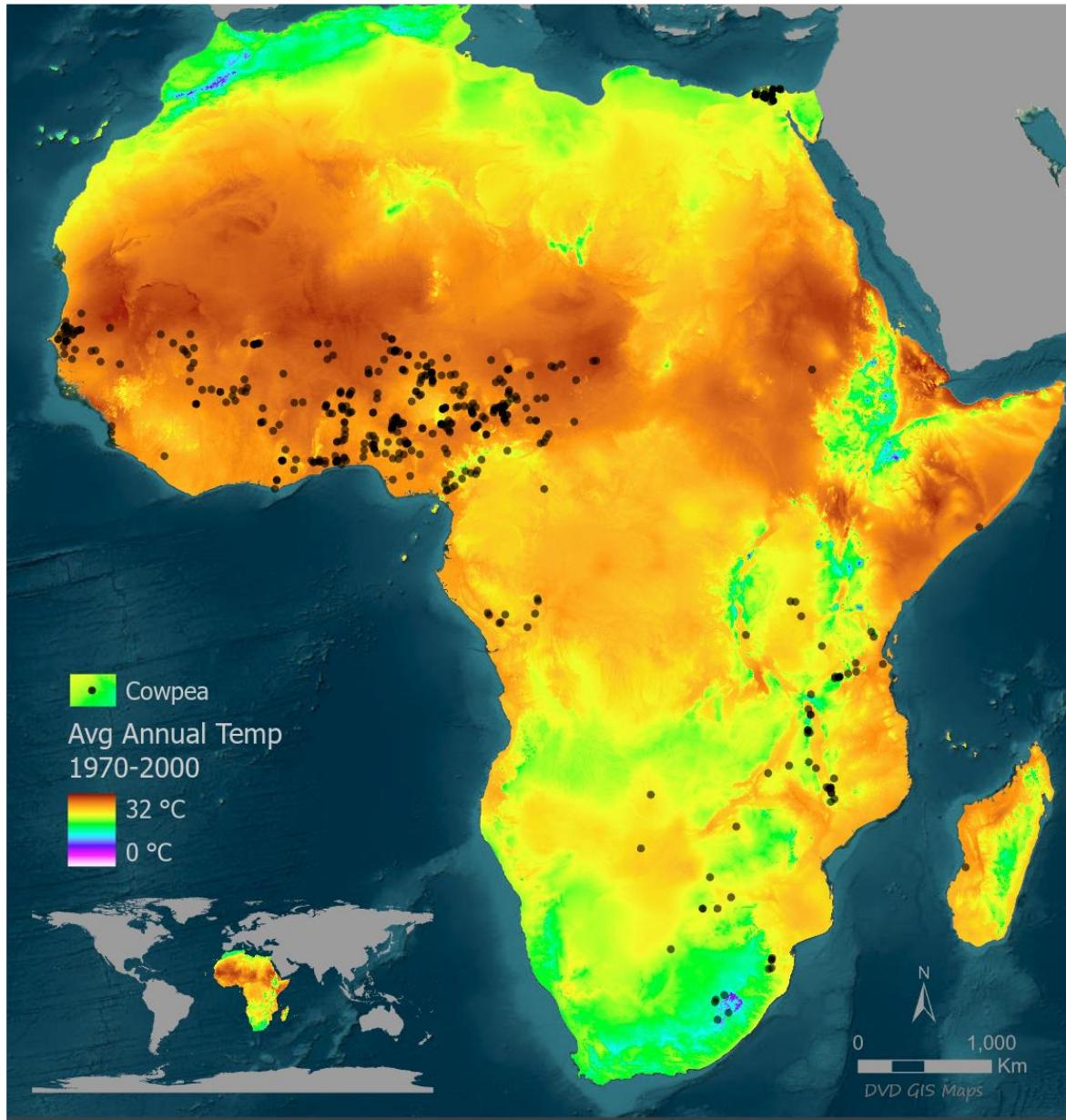
IITA Core passport data

Is all passport data reliable?

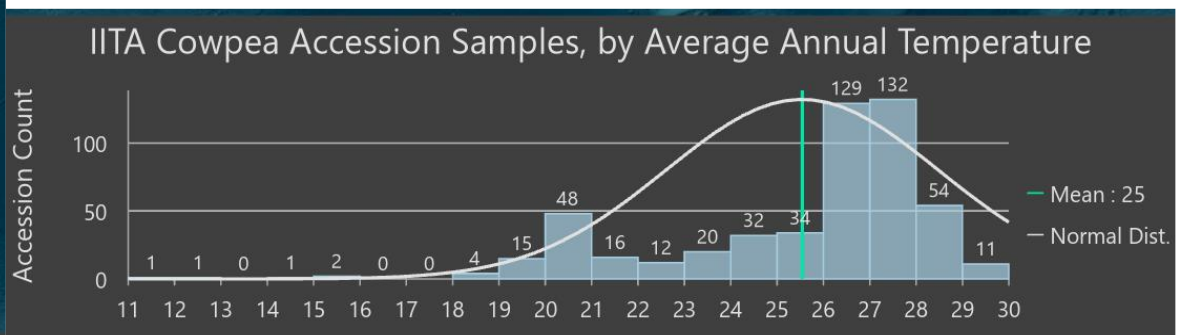
Accession	Country	State/Prov	Location	Latitude	Longitude	Elevation	
TVu-14395	Senegal		50KM MEKHE TO DARON	15.3167	-16.133301	40	
TVu-14396	Senegal		43KM DAGANA TO MATAM	16.4667	-15.2	11	
TVu-14401	Senegal		MATAM AREA	15.5	-13.2667	15	
TVu-14402	Senegal		16KM MATAM TO BAKEL	15.4833	-15.25	15	Lat/Lon completely wrong 300 KM from M
TVu-14932	Niger	DOSSO	3KM S OF TARA	3.25	3.25	252	Lat/Lon in the middle of the ocean. There
TVu-4669	Niger			13.033334	8.366667		Lat/lon not matching country. Could info b
TVu-4672	Niger			13.033334	8.366667		Lat/lon not matching country. Could info b
TVu-4676	Niger			13.033334	8.366667		Lat/lon not matching country. Could info b
TVu-4696	Niger			13.033334	8.366667		Lat/lon not matching country. Could info b
TVu-14405	Senegal		5KM LINGAERE TO DARA	15.3833	-15.2333	29	
TVu-14406	Senegal		5KM LINGAERE TO DARA	15.3833	-15.2333	29	

- ✓ All passport data has been manually checked
- ✓ **512 accessions** have GPS coordinates matching location information
- ✓ IITA genebank curators are checking all other accessions to update Lat/Lon information (whenever possible)

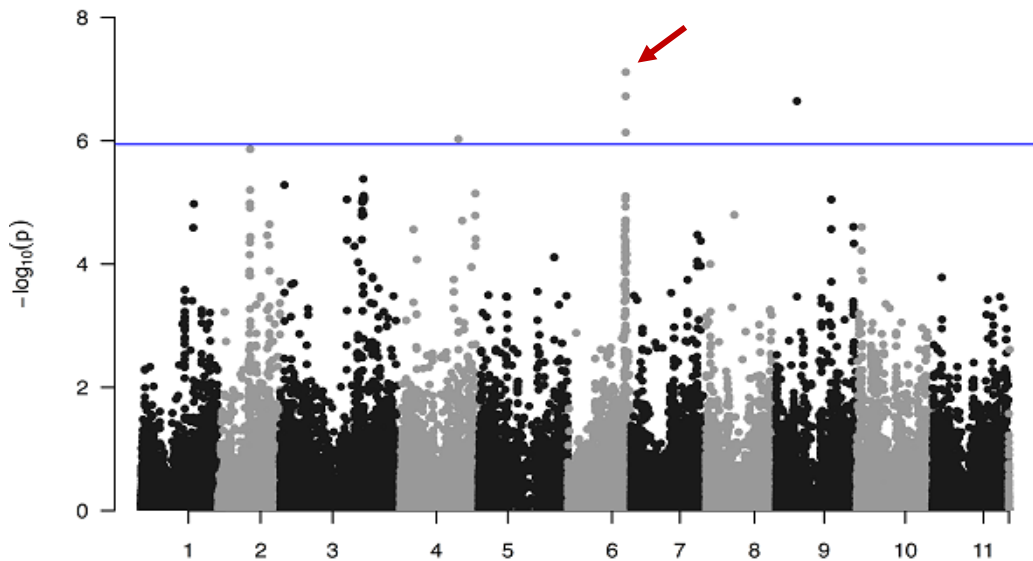
Geographic location of accessions



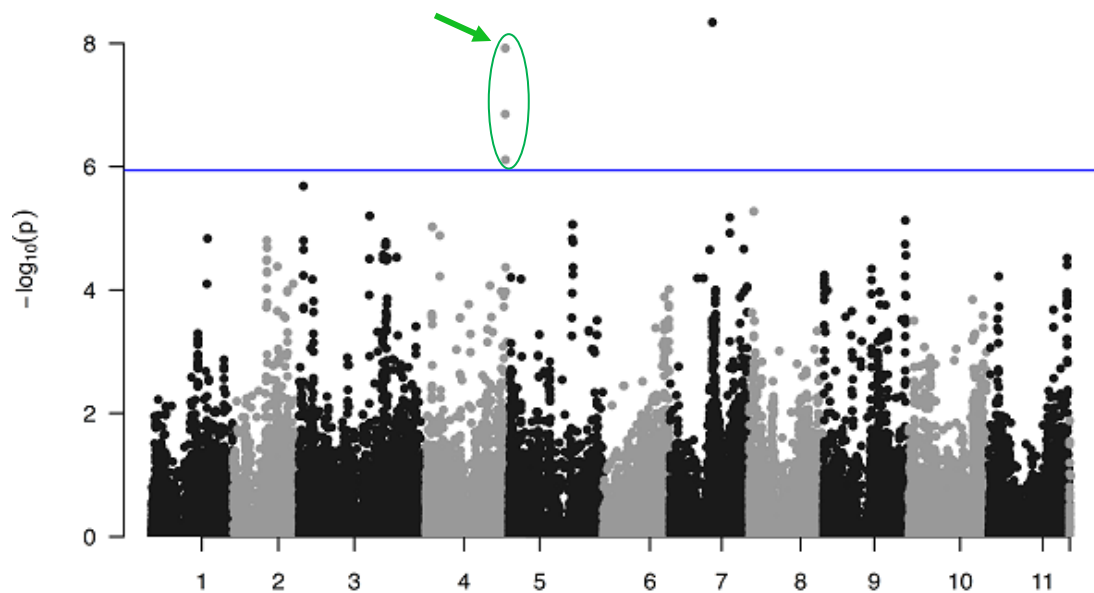
- 512 accessions from 28 countries in Africa
- Color gradient representing Annual Mean Temperature (BIO1) extracted from WorldClim 2.1
- Most accessions are from West Africa, where temperatures are higher



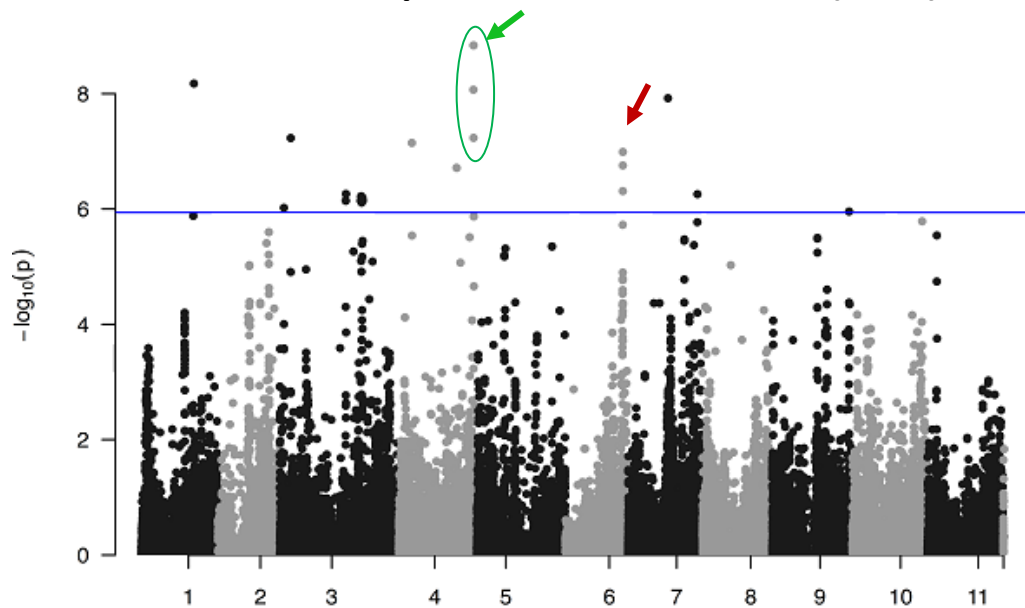
Annual Mean Temperature (BIO1)



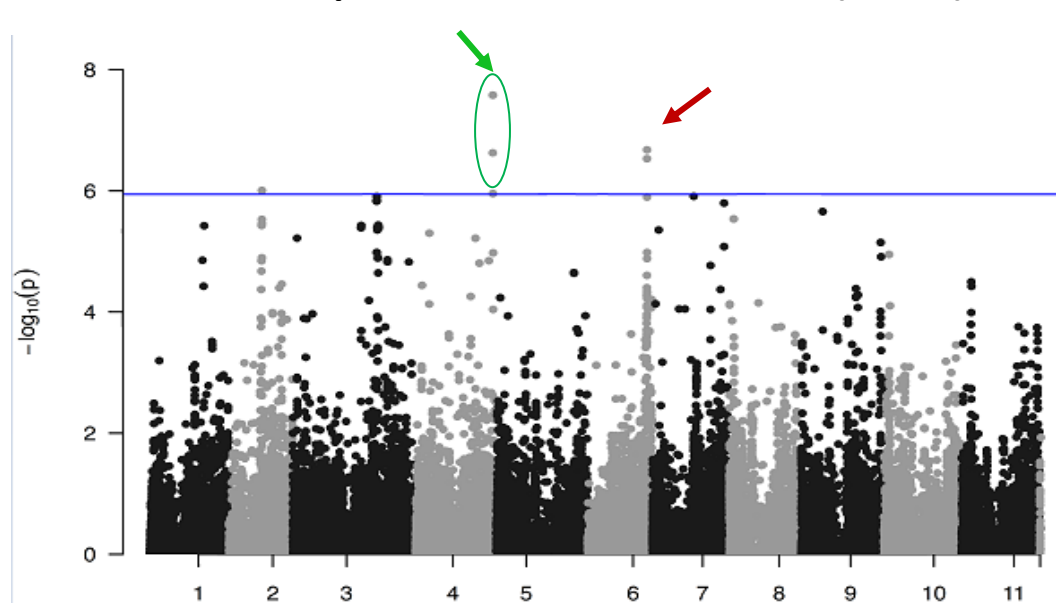
Min. Temperature of Coldest Month (BIO6)



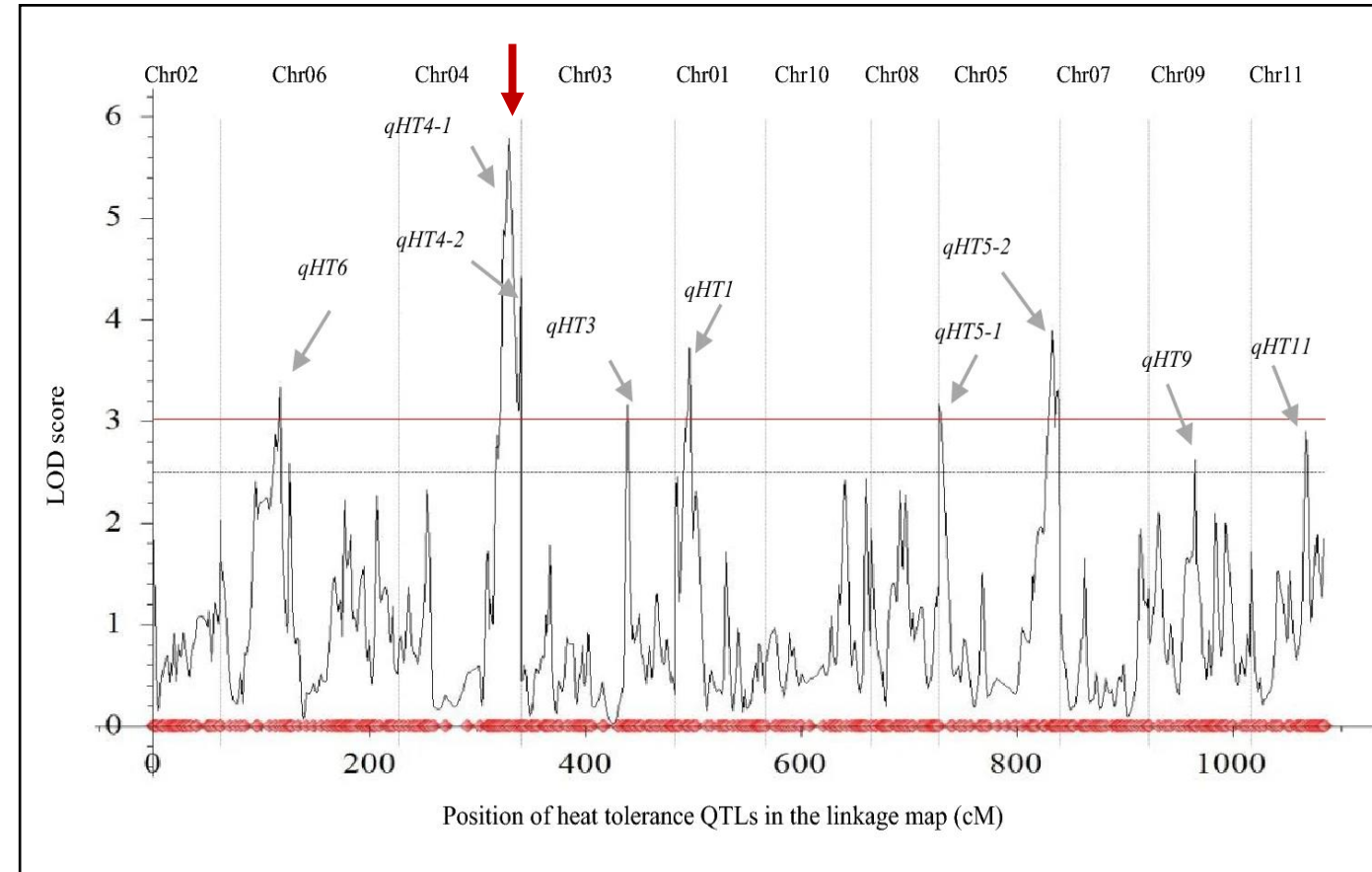
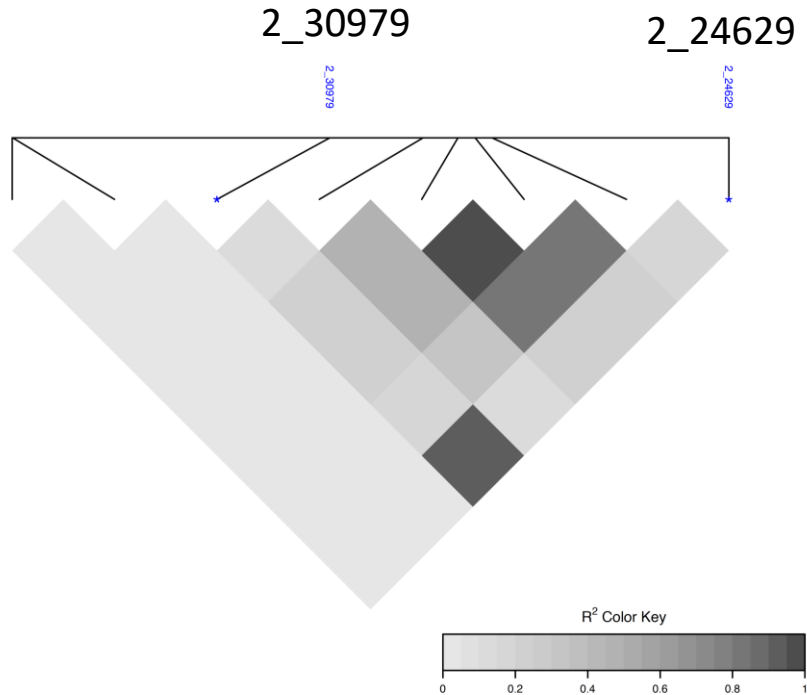
Mean Temperature Driest Quarter (BIO9)



Mean Temperature of Coldest Quarter (BIO11)



- The Vu04 locus coincides with the *qHT4-2* heat-tolerance QTL from Angira et al (2022)

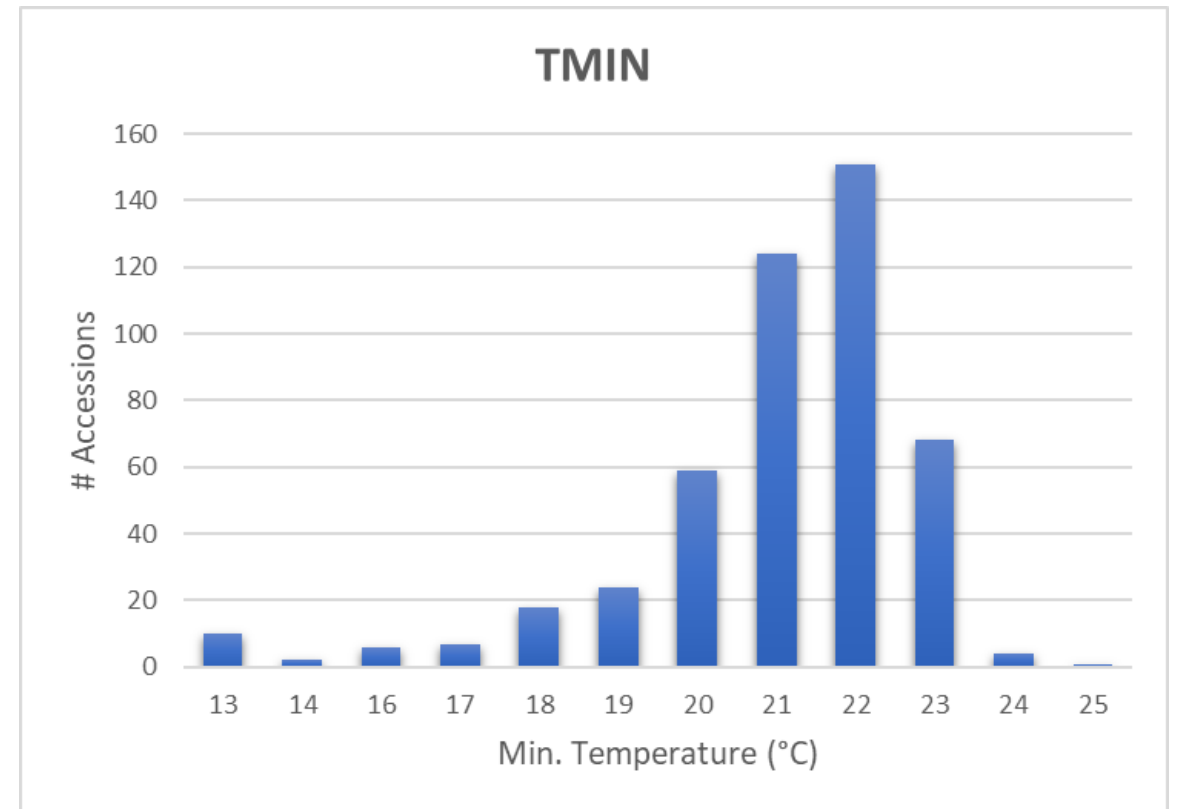
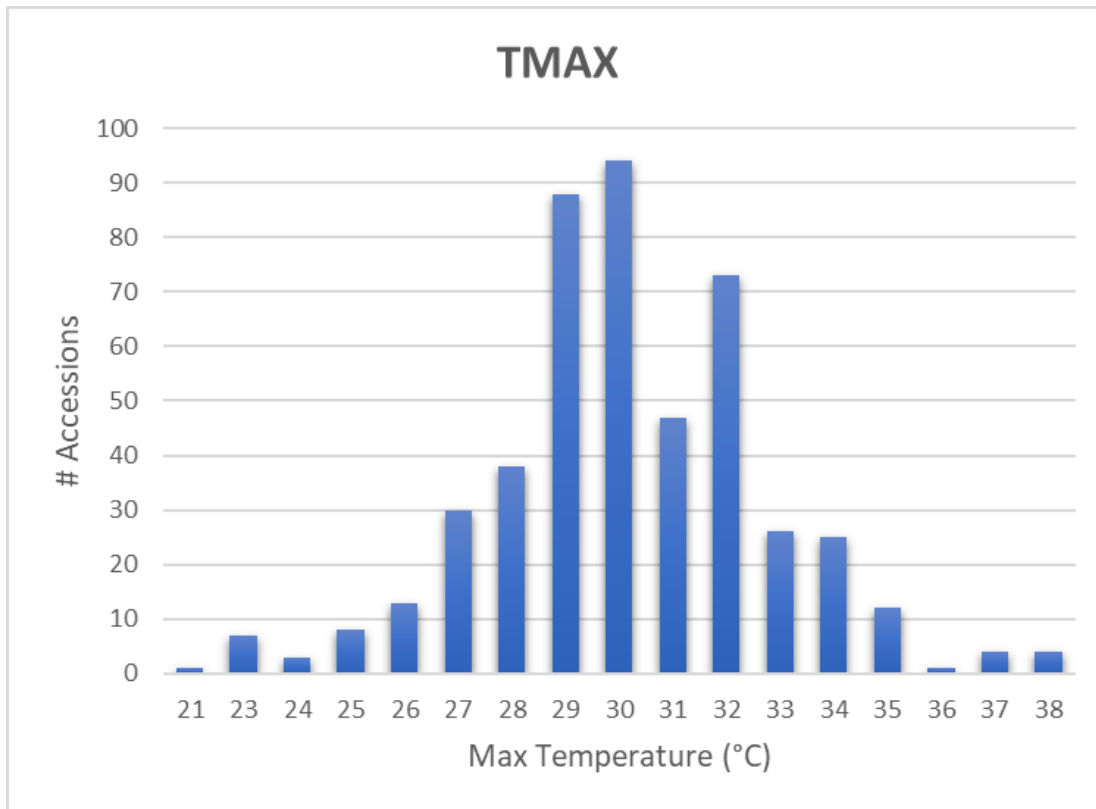


- MAF = 0.021
- Total size region = 90 kb
- # Gene models = 8 (including 2 genes encoding SWEET sugar transporters)

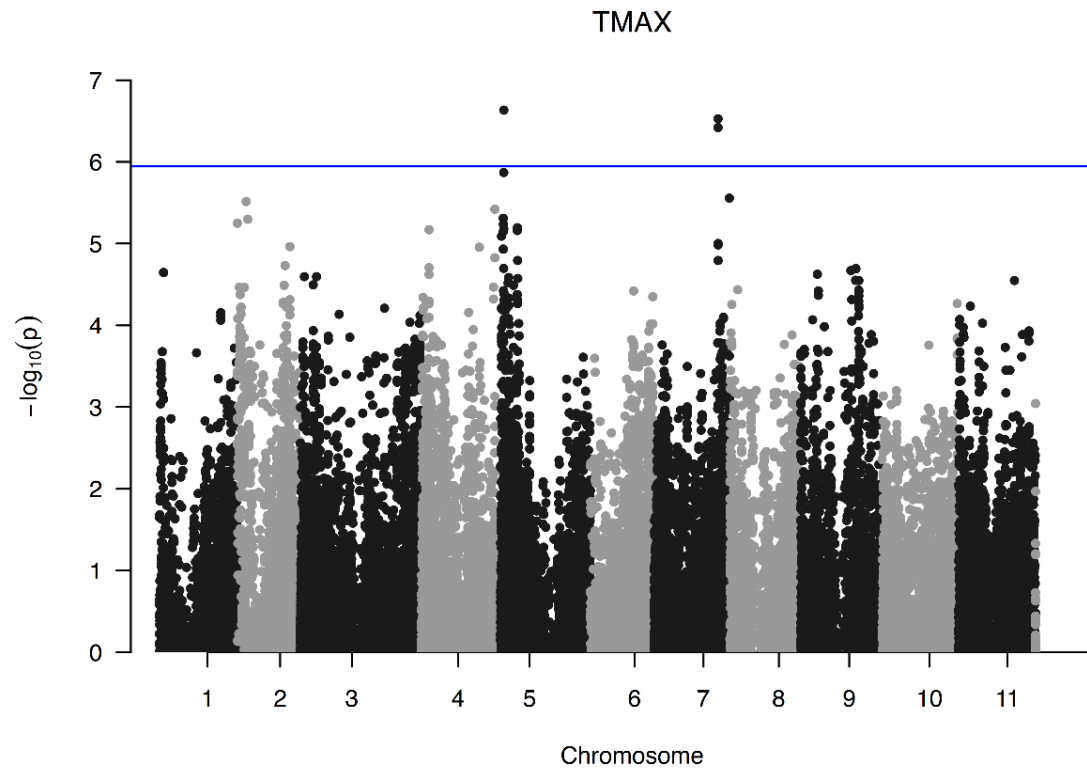
Angira et al. (2022)

Targeting the reproductive period of cowpea

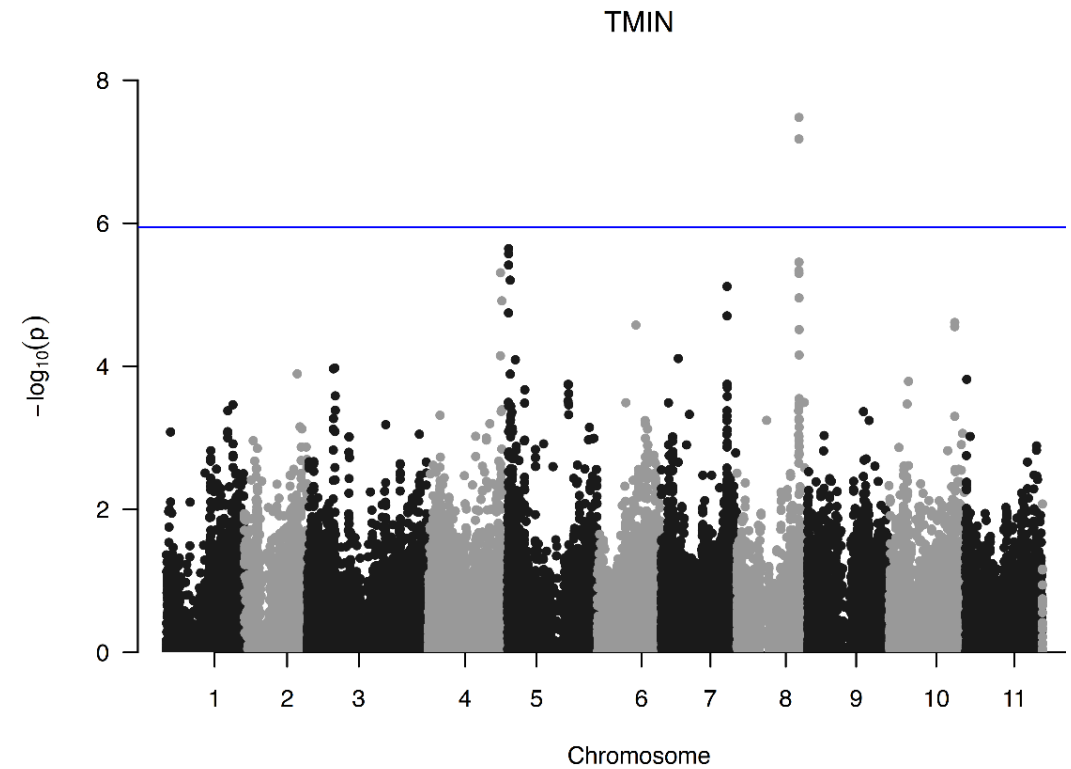
- Focusing on the **reproductive period** of cowpea (main cropping season)
- Average of Maximum Temperature (**TMAX**) and of Minimum Temperature (**TMIN**) during the reproductive phase for 474 accessions extracted from WorldClim 2.1



Targeting the reproductive period of cowpea



SNP	Chr.	Pos (bp)	-Log10(p)	Marker R ² (%)
2_14325	Vu05	2001697	6.6	6.2
2_50836	Vu07	34457522	6.4	5.9
2_29507	Vu07	34458523	6.5	6.1



SNP	Chr.	Pos (bp)	-log10(p)	Marker R ² (%)
2_29117	Vu08	33558254	7.2	7.4
2_28165	Vu08	33573057	7.5	7.6

Next steps

Near future

- Re-do analysis with updated geolocation of excluded samples
- Explore other signals for environmental association (i.e., F_{ST})
- Explore LD around the significant regions, and candidate gene identification

Subsequent years

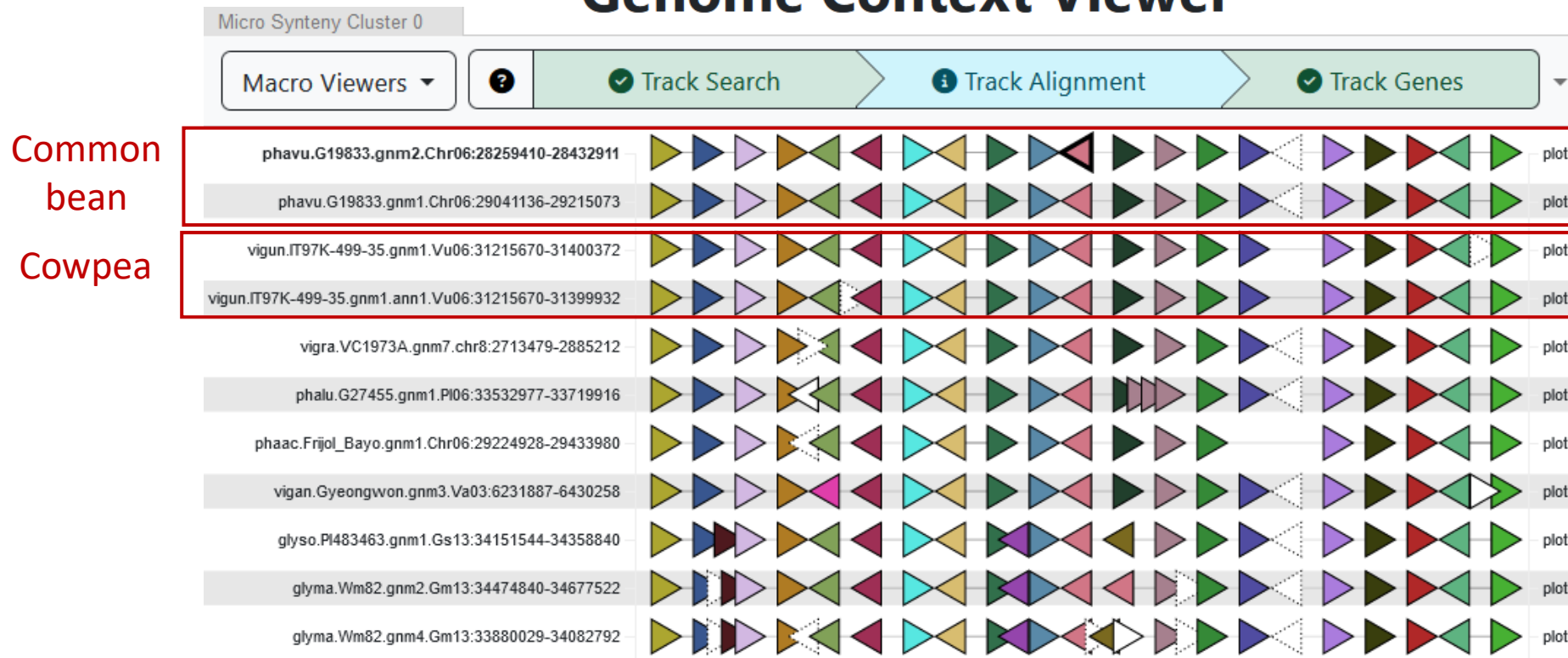
- Resequencing of candidate loci to identify alleles associated with thermotolerance
- Validation of heat tolerant germplasm (greenhouse and field) and development of breeder-friendly genetic markers
- Introgression of favorable alleles into elite West African germplasm using markers
- Identification of orthologous loci in common bean
- Optimization of the CROPGRO-Cowpea model with the phenotypic data generated

Reference genome of cv. IT97K-499-35

- PacBio sequencing (long reads) + 2 optical maps (Bionano) + 10 genetic maps
- Available from Phytozome (<https://phytozome-next.jgi.doe.gov>), NCBI, the Legume Information System (<https://www.legumeinfo.org/>)

LIS - Legume Information System

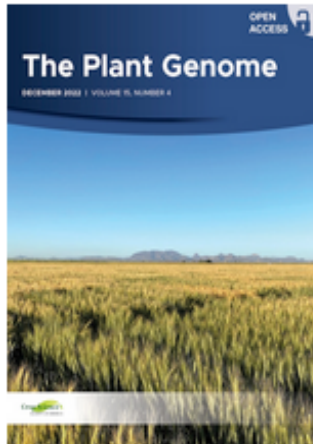
Genome Context Viewer



Genomic resources in cowpea

□ Development of a pan-genome

- The genome of **six additional accessions** has been sequenced and annotated
- They represent six different genetic subpopulations
- Available from Phytozome (CowpeaPan: <https://phytozome-next.jgi.doe.gov/cowpeapan>) and the Legume Information System



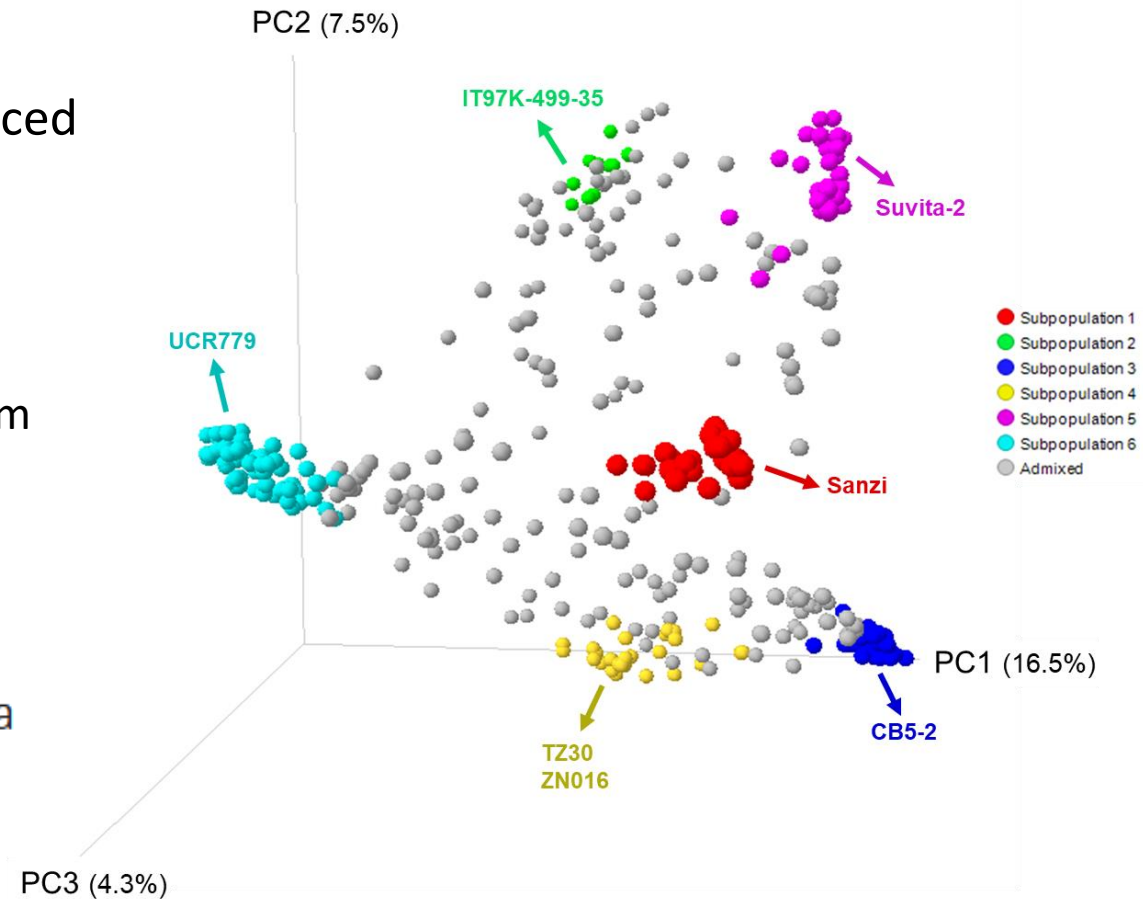
The Plant Genome

A View of the Pan-Genome of Domesticated Cowpea (*Vigna unguiculata* [L.] Walp.)

Open Access

DOI: 10.1002/tpg2.20319

Status: In Production



□ Two wild cowpeas have been sequenced

- TVNu-1145 (Botswana) and TVNu-1158 (Republic of the Congo)

Acknowledgments



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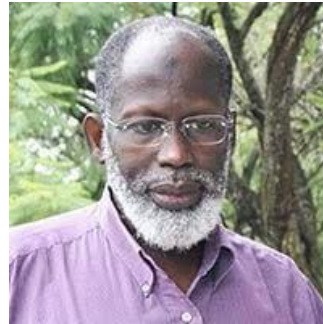
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THANK YOU!