

Genome-wide association mapping of agronomically important traits in quinoa

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Plant Breeding
Institute



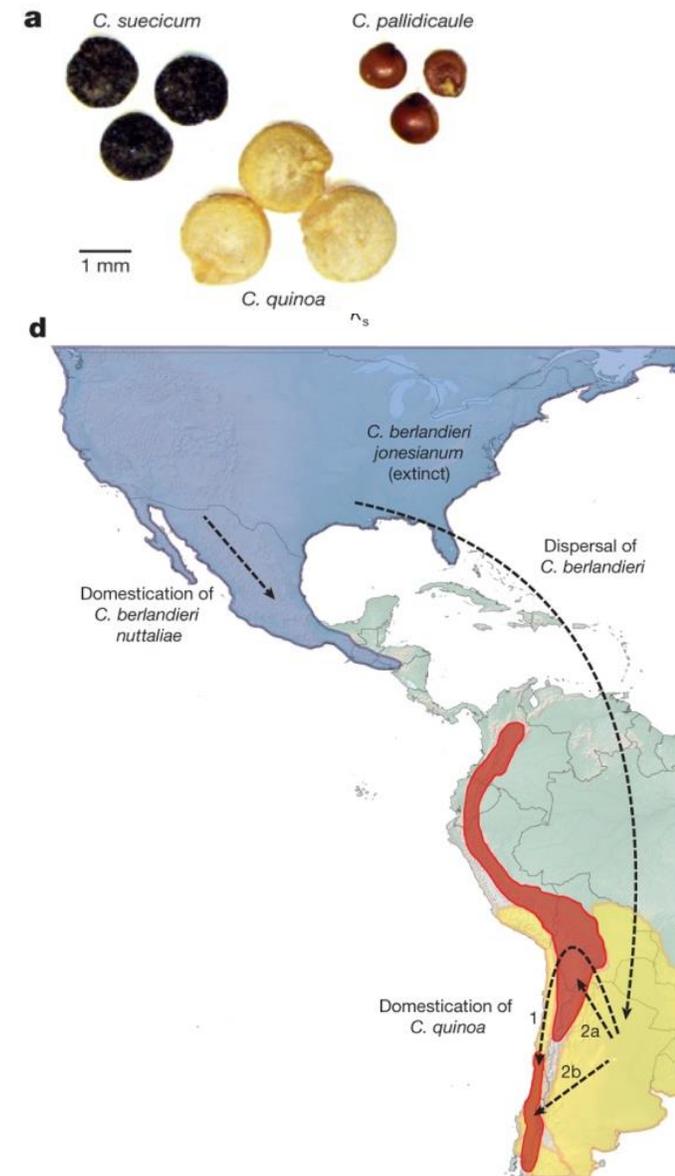
Introduction

- Quinoa (*Chenopodium quinoa*), $2n=4x=36$, genome size: 1.45 Gb
- Sub-genome A (*C. pallidicaule*) and B (*C. suecicum*)
- Native to South America, first domesticated 5,000-7,000 years ago
- Higher protein, dietary fiber, B vitamins, and dietary minerals compared to wheat, corn, rice, and oats
- Perfect balance of all the essential amino acids
- Gluten free
- Frost, drought and salinity tolerance

Scientific Problem:

Quinoa cultivation in Central and Northern Europe requires adaptation to long day conditions

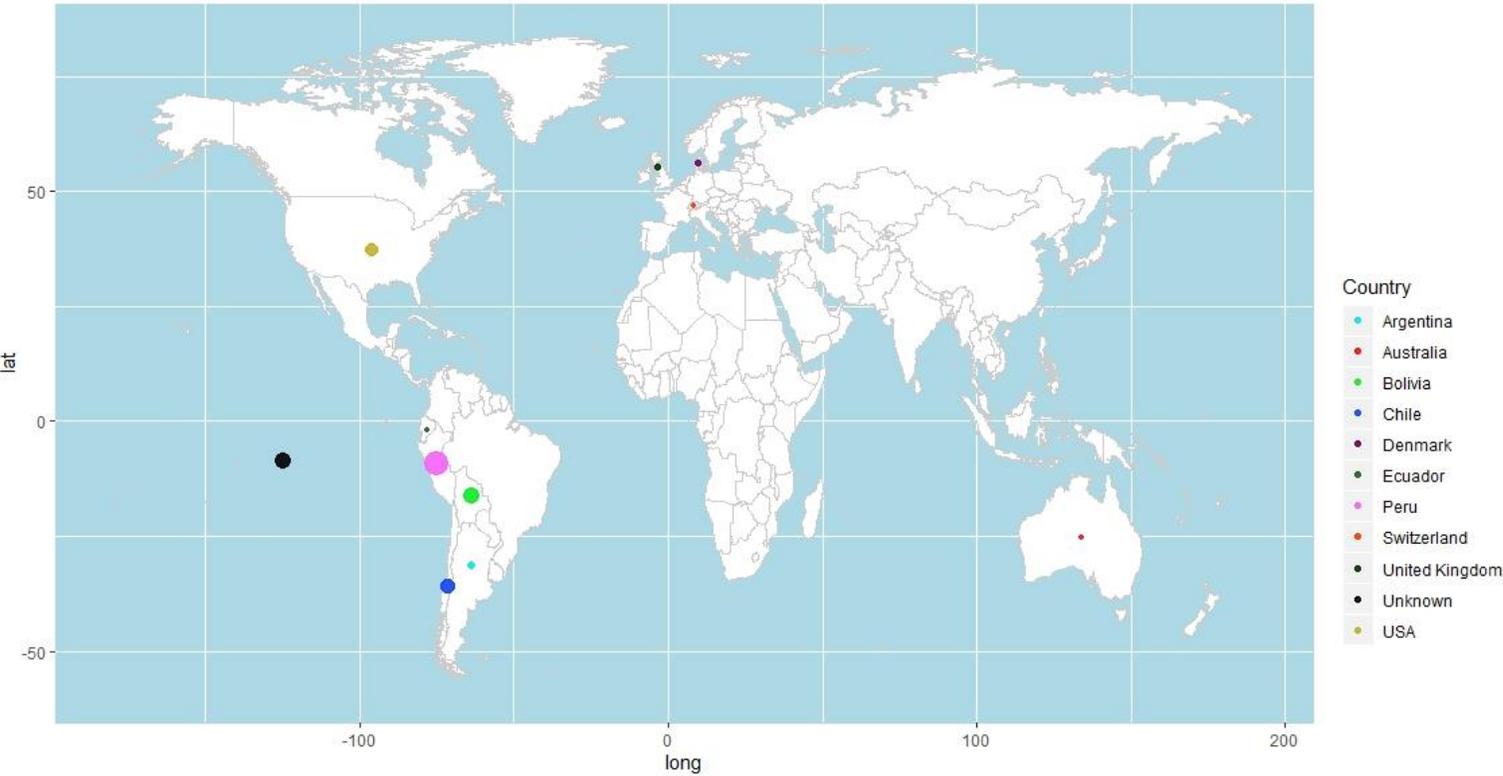
Evolutionary history of quinoa



Aims of the study

- Evaluating genetic diversity
 - Assessing phenotypic diversity in the field
- To identify the genetic basis of flowering time regulation and other agronomically important traits
 - Genome-wide association study in quinoa

Phenotyping of a world wide collection of quinoa



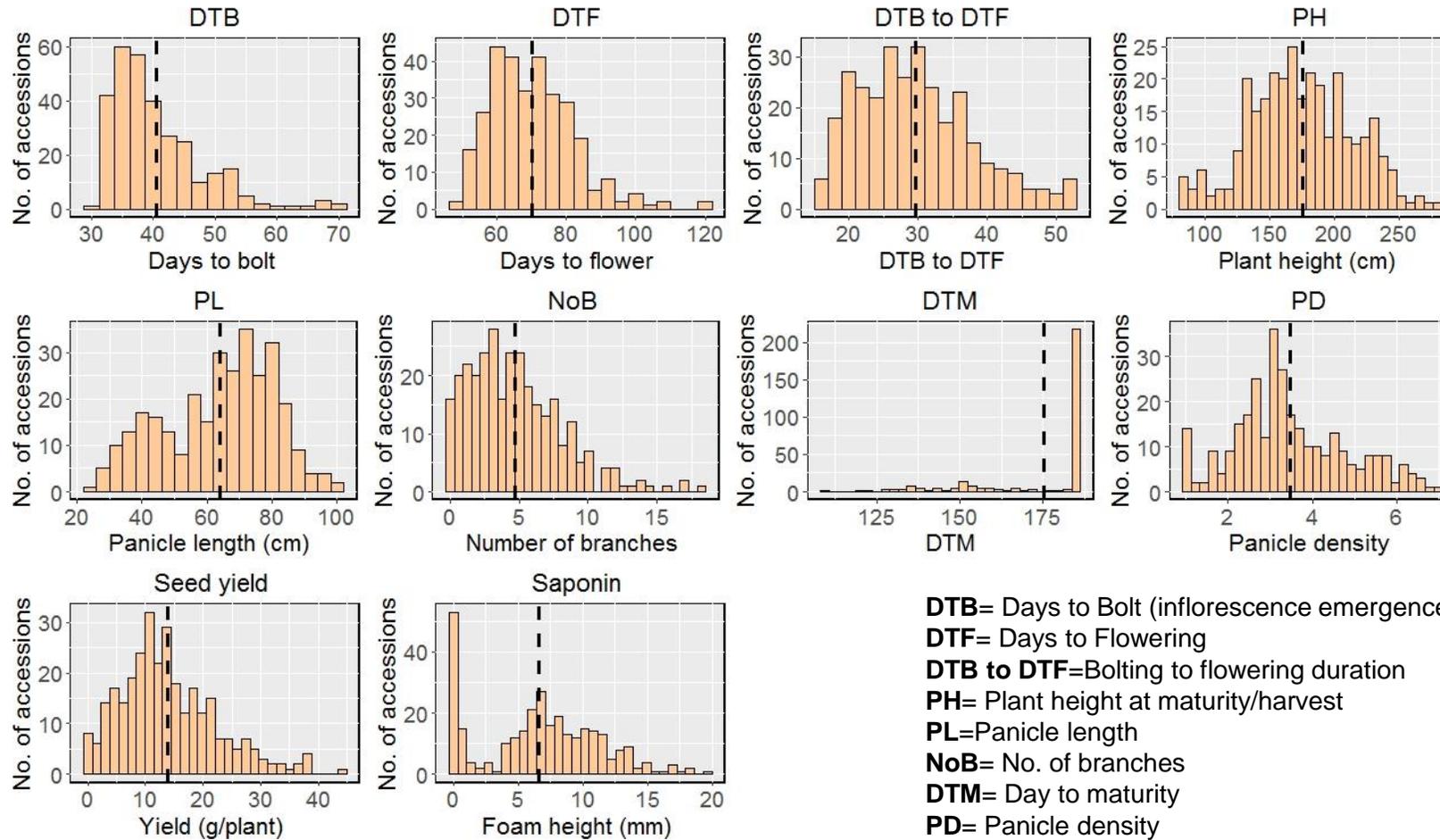
Composition of the quinoa diversity panel

Origin	No. accessions
Peru	165
Bolivia	57
Chile	42
USA	34
Argentina	7
United Kingdom	2
Denmark	2
Australia	1
Ecuador	1
Switzerland	1
Unknown	38
Total	350

Year	2018	2019
No. of accessions	350	350
Number of blocks	3	3
Plot information	Single row plot (7 plants/plot)	Single row plot (7 plants/plot)
Spacing	20cm between plants 60cm between rows	20cm between plants 60cm between rows



Phenotyping of a world wide collection of quinoa



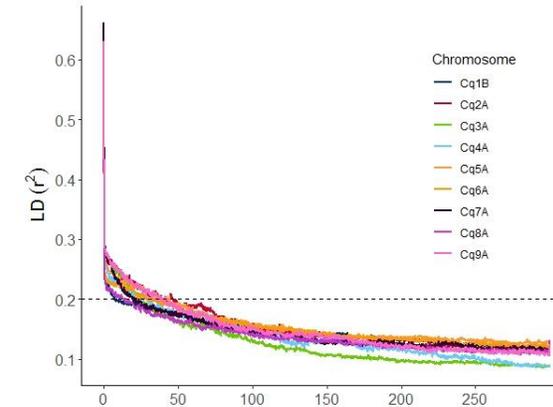
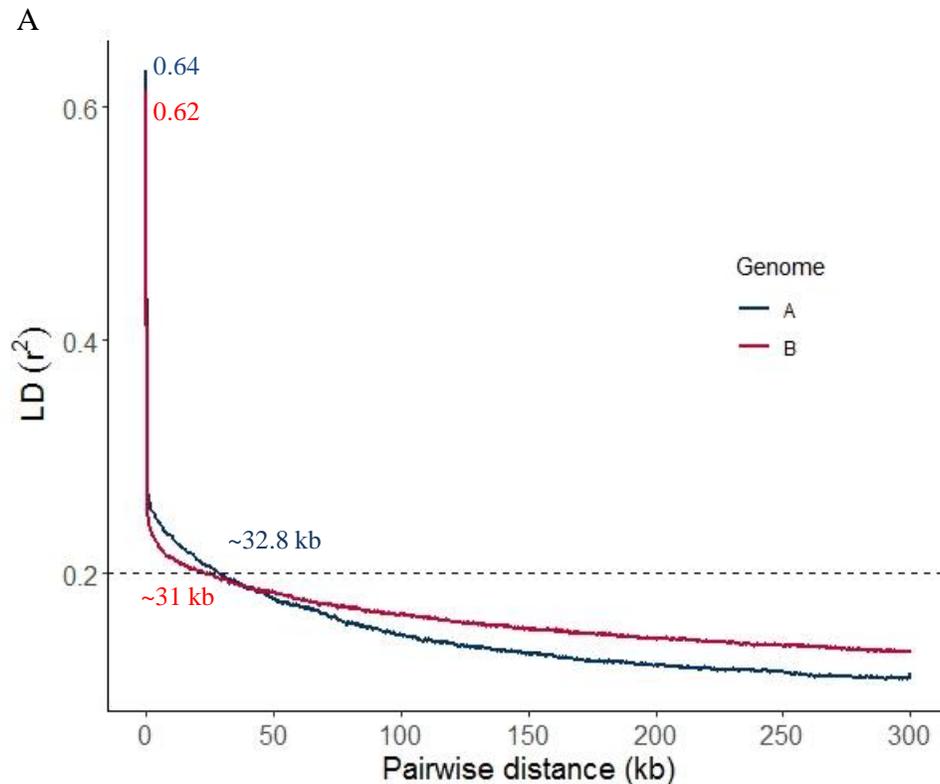
Trait	DTB (days)	DTF (days)	DTB to DTF (days)	PH (cm)	PL (cm)	NoB	DTM (days)	PD	Yield (g/plant)	Saponin* (cm)
Min	31.06	48.88	15.13	83.17	24.14	0	110	0.9919	0	0
Mean	40.41	70.13	29.7	175.15	63.94	4.71	175.2	3.47	13.93	6.69
Max	70.38	120.76	52.63	279.35	101.06	18.21	185.5	6.95	43.94	19.67
Heritability	0.87	0.90	0.84	0.84	0.70	0.38	0.92	0.65	0.47	0.62

Whole genome re-sequencing and Genome wide association analysis

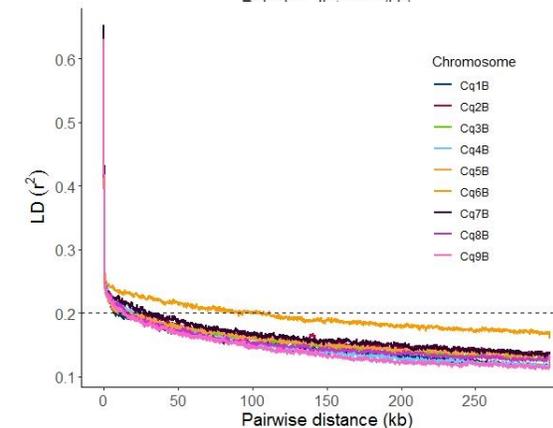
- 328 accessions of the quinoa diversity panel were re-sequenced using NovaSeq S4 flowcell. (Coverage 0.68X to 16.8X)
- Reads were mapped to the quinoa reference genome V2 with bwa-mem and variant calling was done using GATK 3.8
- ~3M high quality SNPs were obtained after filtering (min-read depth 5, MAF = 0.05, and max -missing 50%).
- GWAS was performed using the Efficient Mixed-Model Association eXpedited (EMMAX) software. Population stratification and hidden relatedness were controlled with PCA and a kinship (k) matrix.
- Phenotype data from 6 traits were obtained from field trials in Kiel

Genome wide LD decay

- Rapid LD decay was observed in the diversity panel indicating a weak genome-wide footprint of the short history of quinoa breeding and selection
- The magnitude of LD decay did not drastically vary among two subgenomes and different chromosomes



Subgenome A

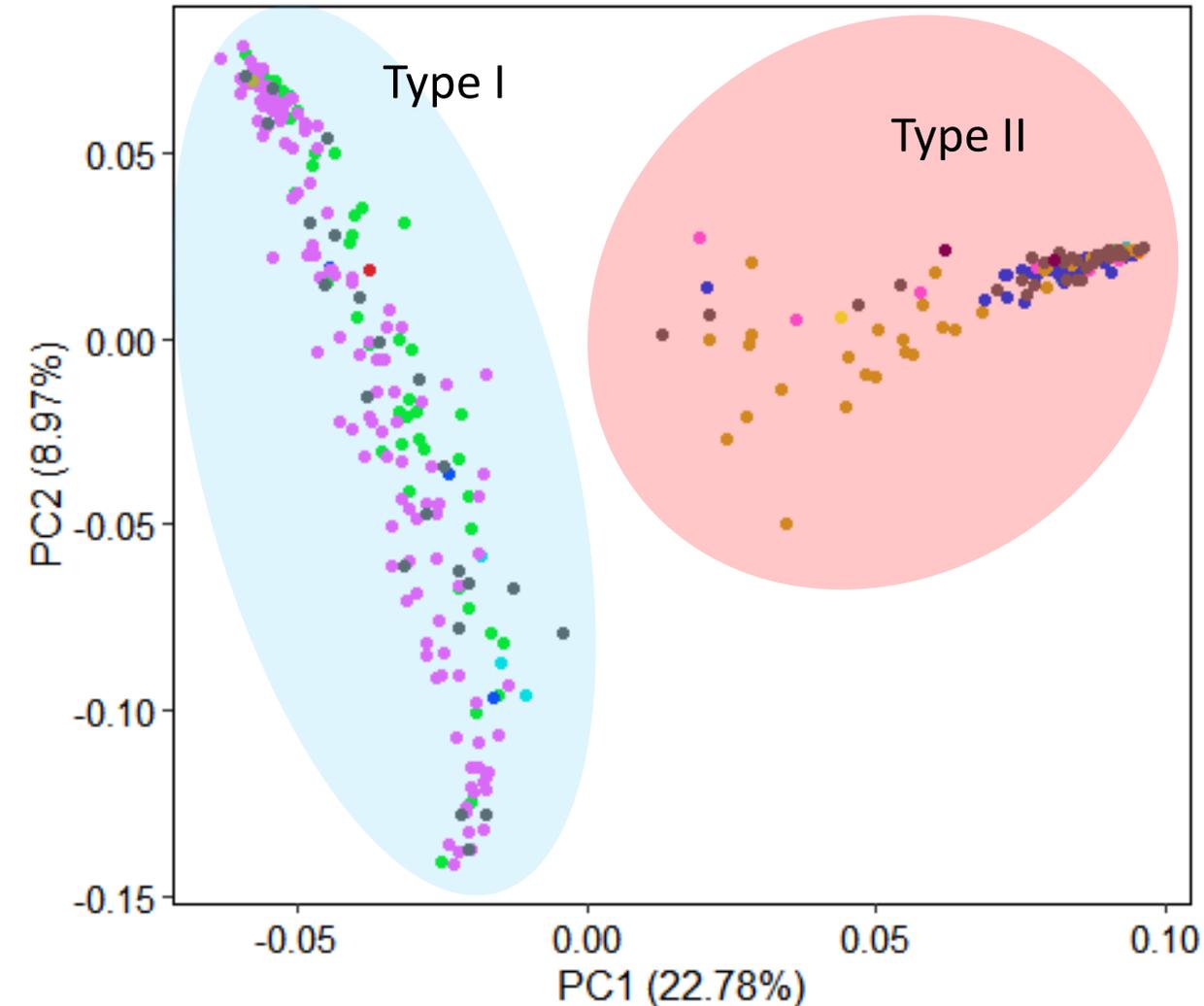


Subgenome B

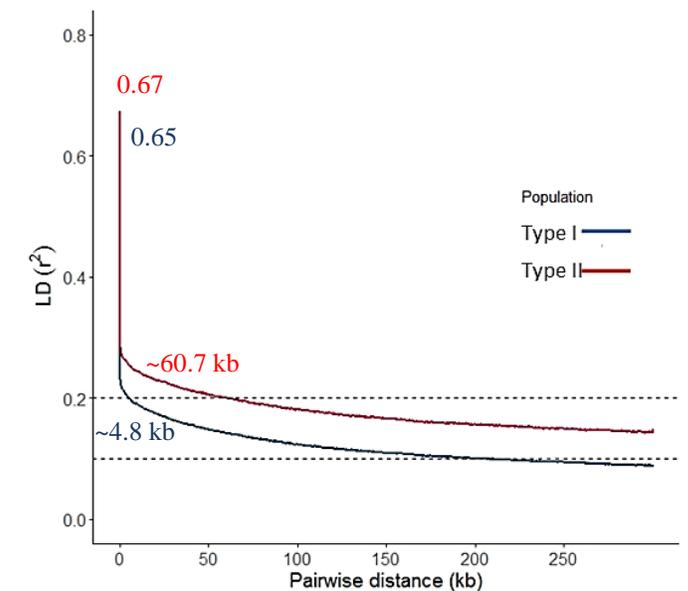
- The correlation coefficient (r^2) between SNPs up to 300kb was calculated using the PopLDdecay (Zhang et al. 2018) software

Genetic structure of the quinoa diversity panel

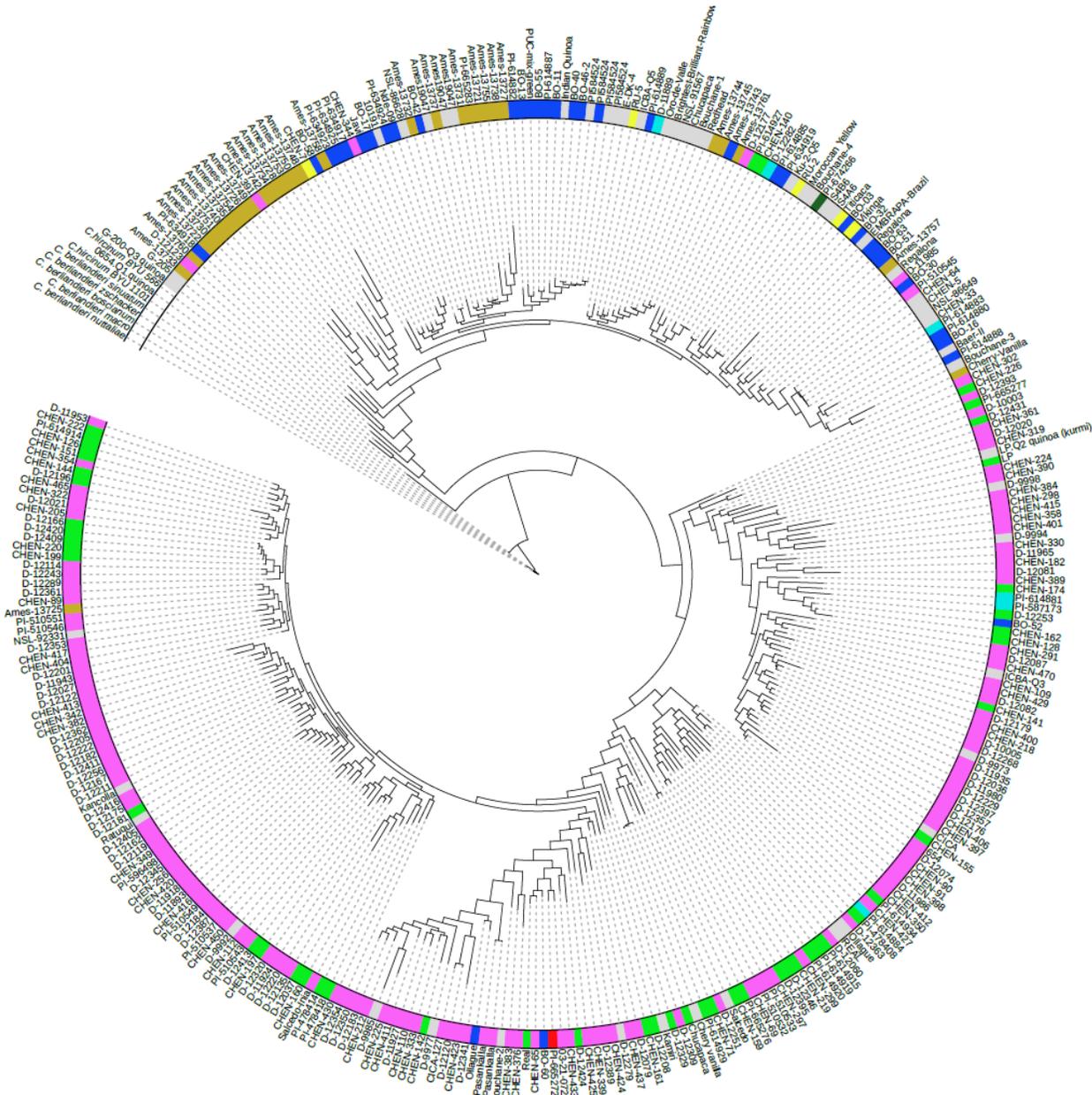
Principal components of the diversity panel



- 325 quinoa accession
- ~3 M high confident SNPs
- PC1 separates “Highland” (Type I) and “Lowland” (Type II) Quinoa



Phylogenetic relationship of 332 different *Chenopodium* genotypes

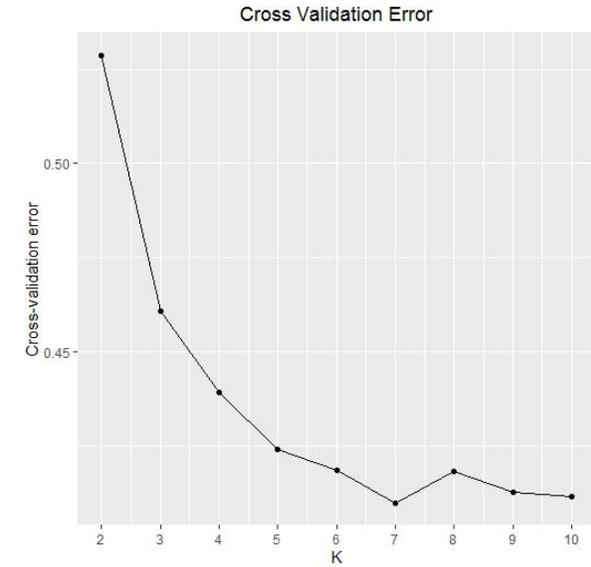
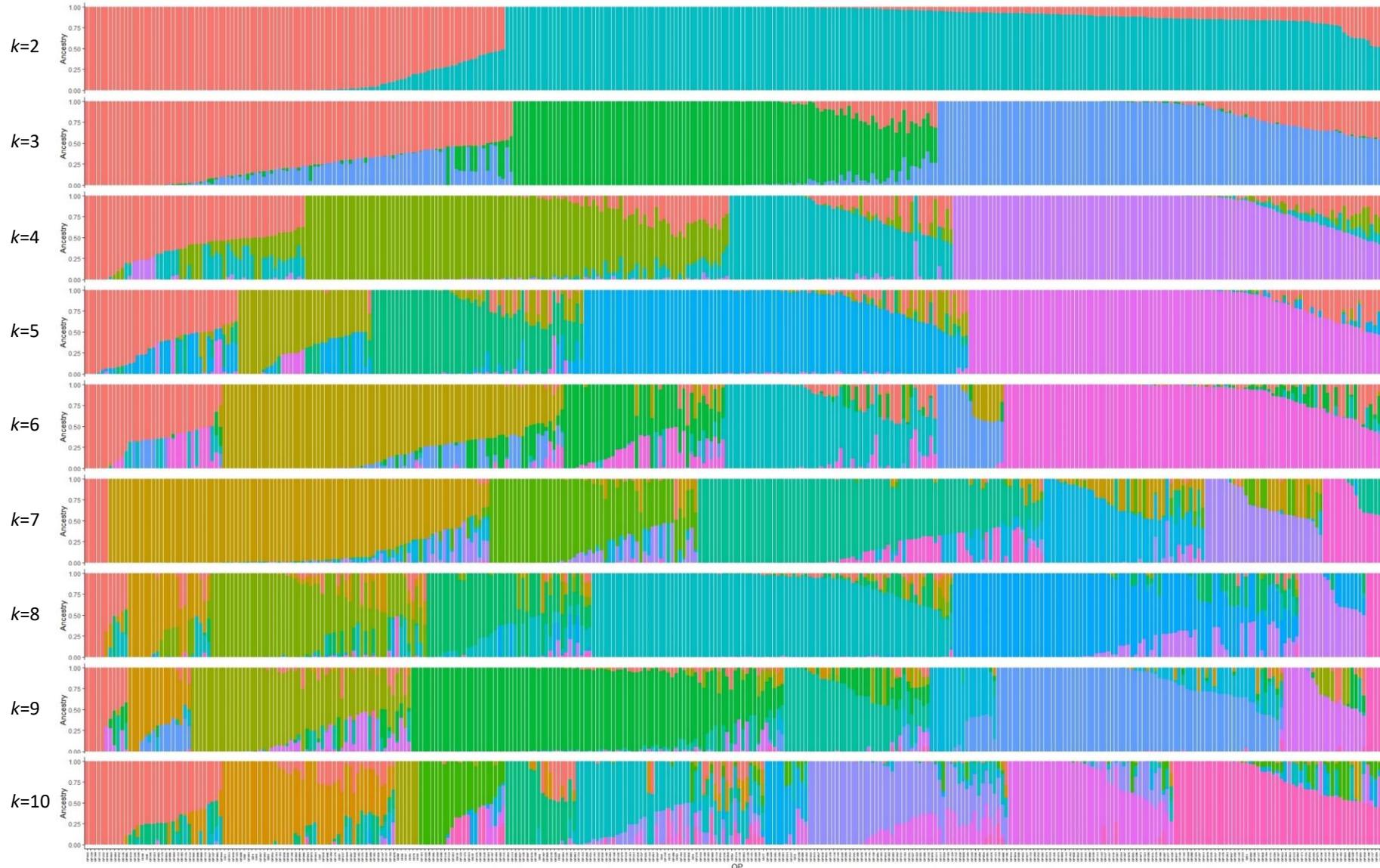


- We used a subset of 229,017 SNPs
- 7 wild *Chenopodium* species and 325 quinoa accessions
- European accessions are related to the Chilean and US accessions

Phylogenetic tree was constructed using IQ-TREE v1.6.619 software (Nguyen et al. 2014) with the model finder (GTR+F+R8) (Kalyaanamoorthy et al. 2017) with 1000 bootstraps.

Genetic structure of the quinoa diversity panel

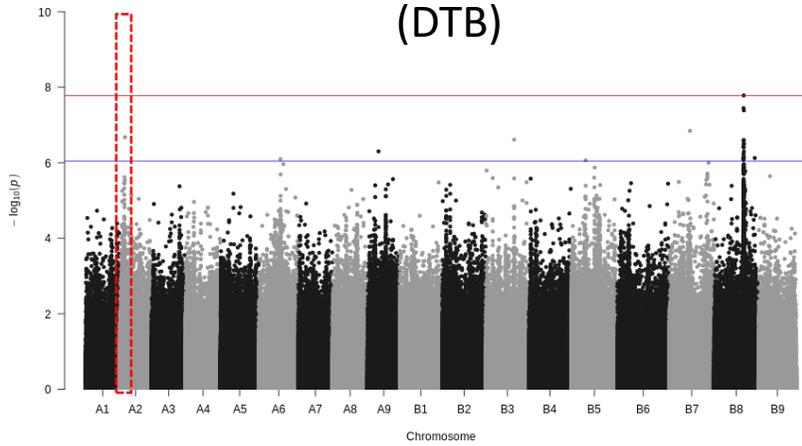
ADMIXTURE ancestry coefficients ($k = 2, 10$) for 332 *Chenopodium* genotypes



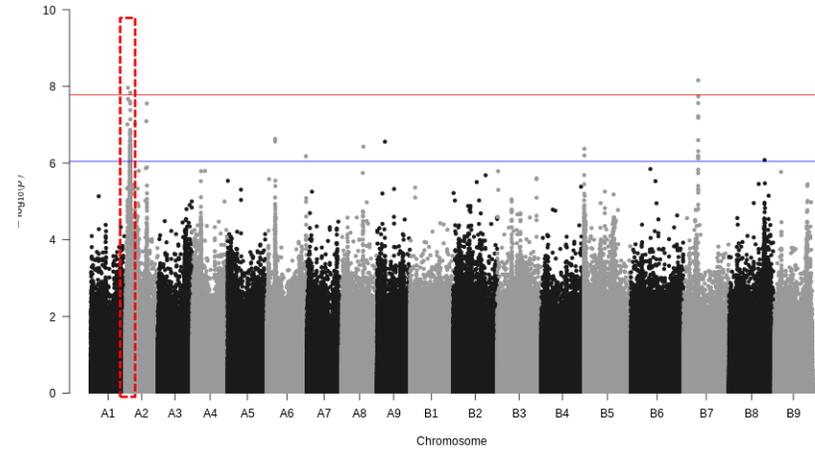
- The ADMIXTURE (Alexander et al. 2009) (Version: 1.3)
- Subset of 889,452 high quality SNPs were used
- Predefined the number of genetic clusters k from 2 to 10
- The best k value was determined by the ADMIXTURE cross-validation procedure

GWA to map QTL for agronomically important traits

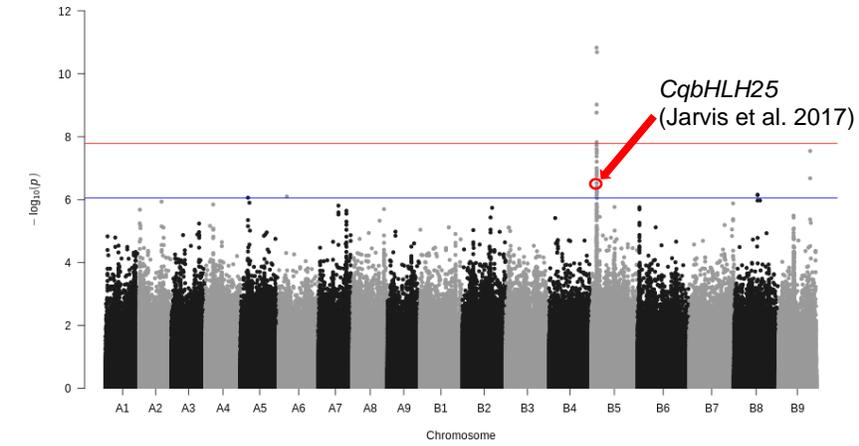
Day to inflorescence emergence
(DTB)



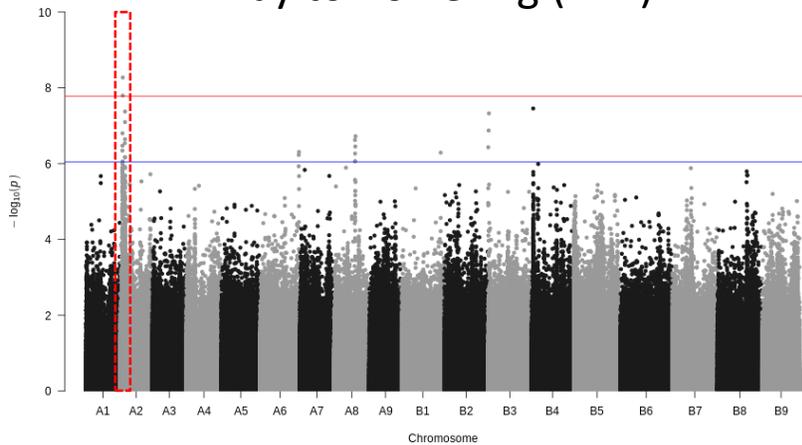
Plant height



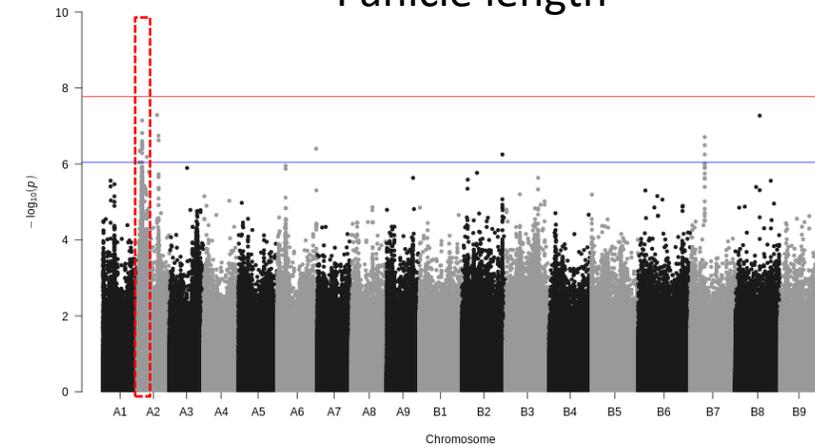
Saponin content



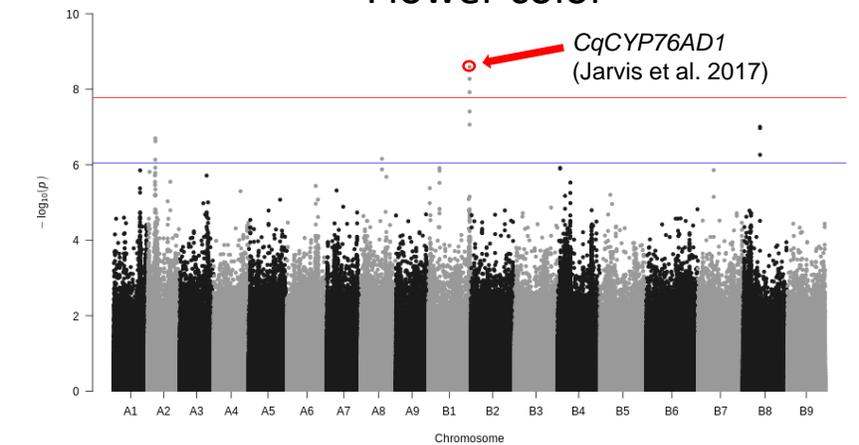
Day to flowering (DTF)



Panicle length



Flower color



- Red line : Bonferroni thresholds ($0.5/n$) Blue line : suggestive p-value ($1/n$) using the Genetic Type I error calculator (GEC) software (Li et al. 2012).
- Manhattan plots using qqman R package (Turner 2014).

Conclusions

- Quinoa diversity panel shows a substantial variation for many agronomically important traits which can be used in future breeding programs
- Rapid LD decay in the diversity panel indicates a weak genome-wide footprint of breeding and selection in the history of quinoa
- Sequence variations in the associated regions can be used to develop markers for selection of promising accessions as crossing partners to breed new varieties well adapted to European climate conditions
- We provide tools for fast-track genetic improvement of the underutilized pseudocereal quinoa
- Similar approaches can be used to improve other orphan crops

Outlook

- Identification of candidate genes that are in LD with significantly associated SNPs

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Thank you very much!

