

Genomic analysis of Vavilov's historic chickpea landraces using GWAS, AMMI and GGE biplot analyses



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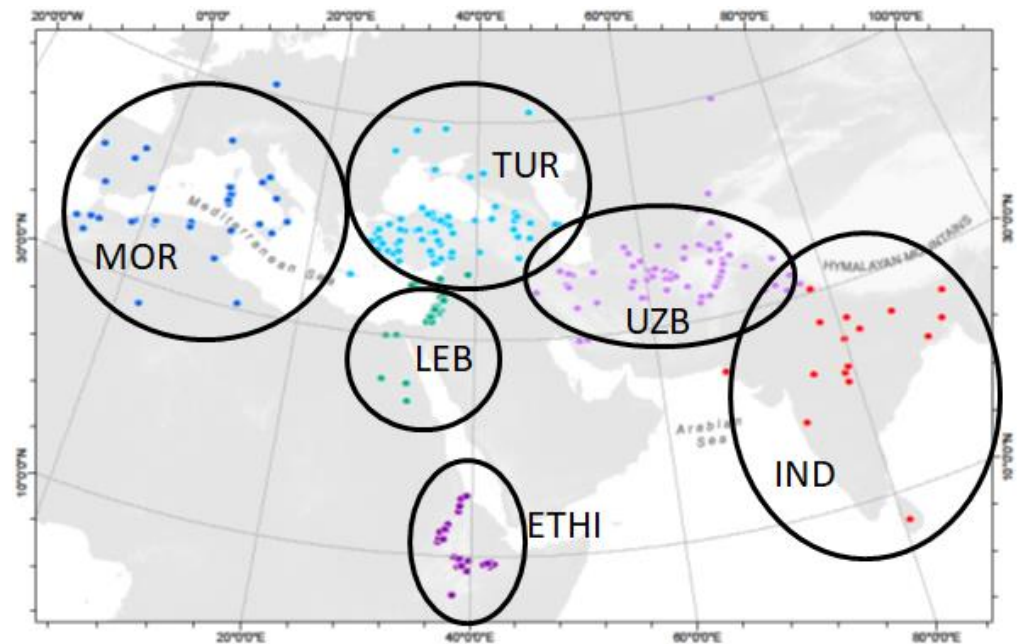
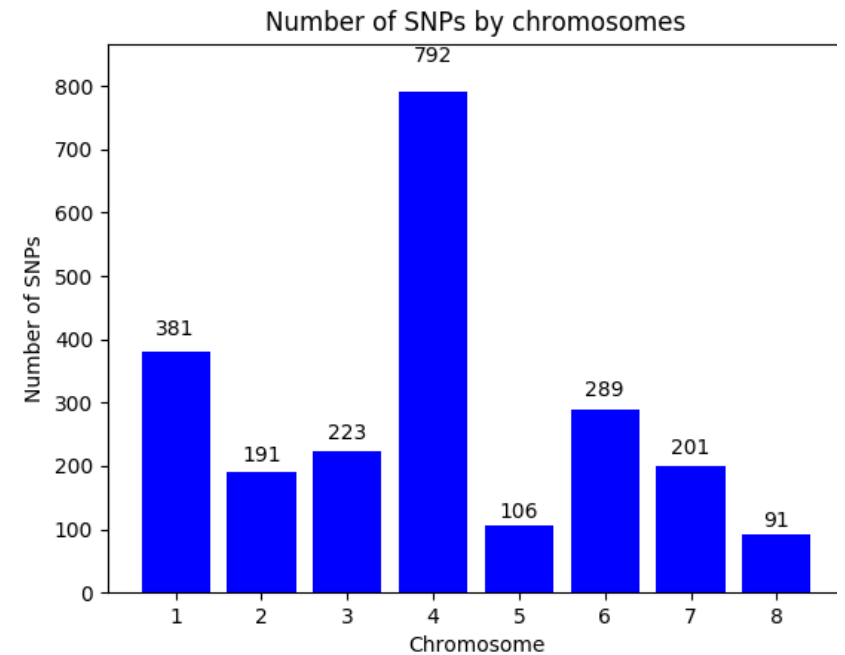
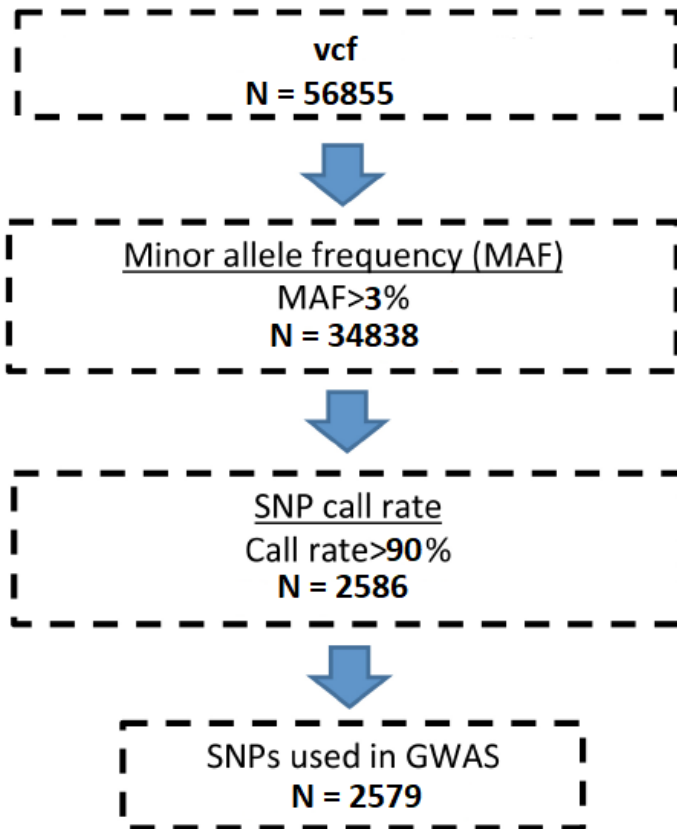
1. Introduction

The Vavilov seed bank contains numerous landraces collected nearly hundred years ago, before intensive breeding of most crops, and thus is a potential reservoir of historic crop adaptations. Here we analyze the genomes of 407 of Vavilov's original landraces, sampled from major historic centers of chickpea cultivation and secondary diversification. We performed GWAS to find associations between VIR's chickpea accessions and phenotypic data obtained in Kuban experimental station of VIR in 2016 and in 2017 under infectious conditions.

2. Materials and Methods

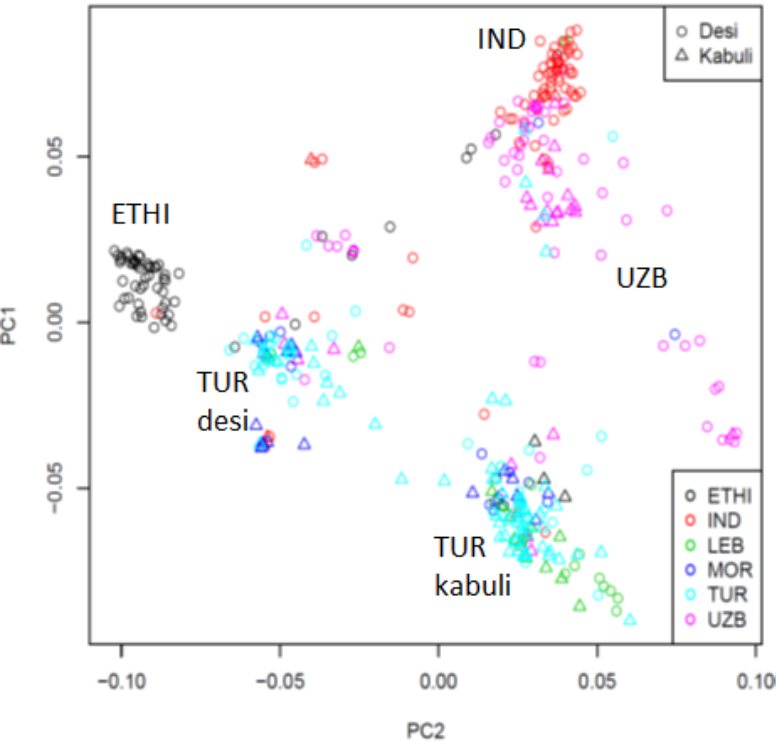
The dataset:

- 407 chickpea accessions from 6 regions
- 56,855 segregating SNPs



3. Results

GWAS analysis identified three SNPs on chromosomes 2, 7 and 8, respectively, significantly associated with days from beginning to end of flowering under infectious conditions. SNP on chromosome 8 was also detected in previous GWAS analysis performed with phenotypic traits obtained in 2016 [1] and with specific climatic variables at collection sites [2]. This SNP is a strong candidate marker for future selection.



SNP Position	Chromosome	Variable	Is in genic region
17161867	2	PlantWeightWithoutPods2016	Ca_16015
17161884		BegFloEndFlo2017	
30930779	7	NumberOfSeedsPerPlant2016	-
		PlantWeightWithoutPods2016	
		BegFloEndFlo2017	
		SeedsWeightPerPlant2016	
		BiologicalYield2016	
10314452	8	PodsWeight2016	-
		PlantWeightWithoutPods2016	
		BegFloEndFlo2017	
		BiologicalYield2016	
		PC1_group1 (Temperatures)	
		PC1_group3 (T of warmest periods)	

4. References:

1. Sokolkova A. et al. (2020) Genomic Analysis of Vavilov’s Historic Chickpea Landraces Reveals Footprints of Environmental and Human Selection. *Int. J. Mol. Sci.* **2020**, *21*, 3952.
2. Sokolkova A.B. et al. (2020) Signatures of ecological adaptation in genomes of chickpea landraces. *Biofizika.* 65(2): 1-4.

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