

Analysis of agronomic traits of mungbean (*Vigna radiata*) accessions from the World Vegetable Gene Bank (Taiwan).



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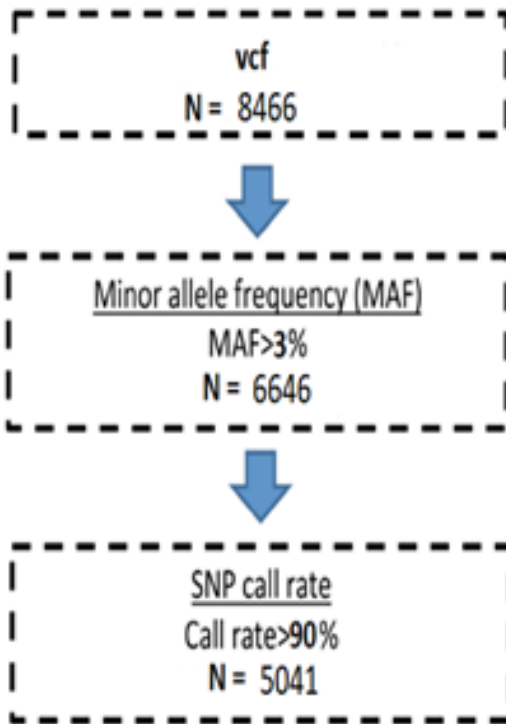
1. Introduction

The World Vegetable Gene Bank, in Taiwan, houses a unique genebank of mungbean [1]. Here we analyze the genomes of 293 accessions that represent the major market classes. GWAS analysis conducted on phenotypic data obtained in different locations and time periods (Taiwan 1984, Taiwan 2018, India 2016, Kuban 2018) identified a large number of genome intervals and potential gene candidates that may affect important agronomic traits. Phenotyping the mini-core collection of mungbean in different climatic locations can estimate phenology traits such as maturation. Uncovering SNPs for these traits will speed breeding efforts for production of mungbean suitable for cultivation in temperate regions.

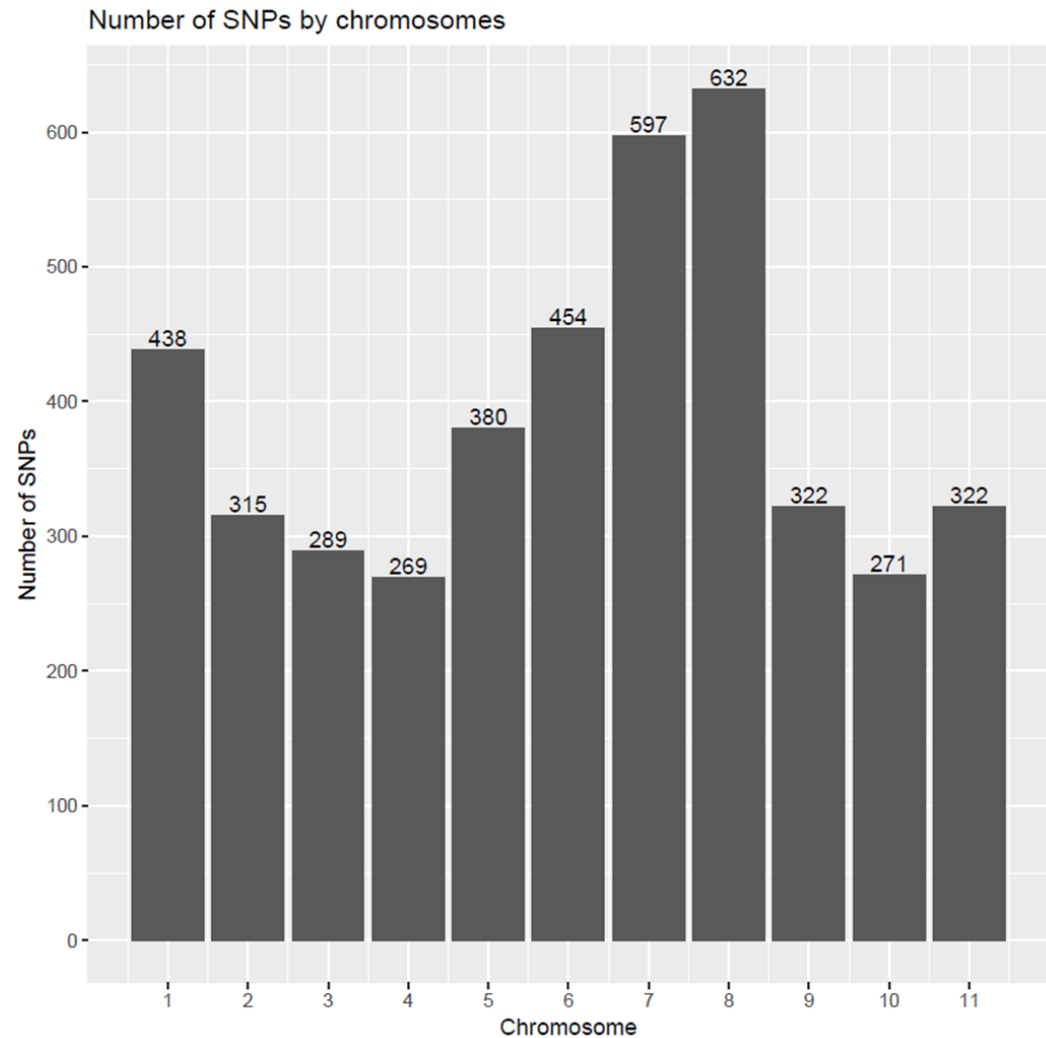
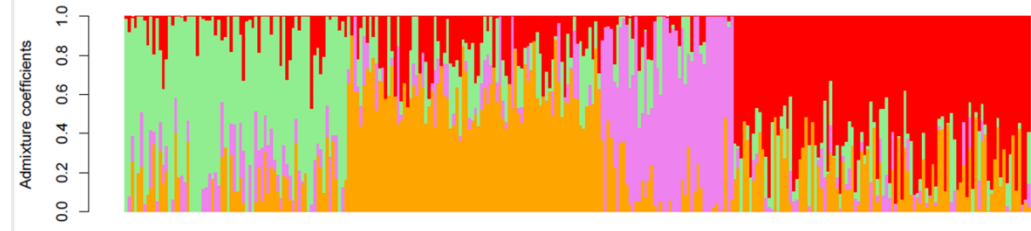
2. Materials and Methods

The dataset:

- 293 mungbean accessions from 17 countries
- 8,466 segregating SNPs

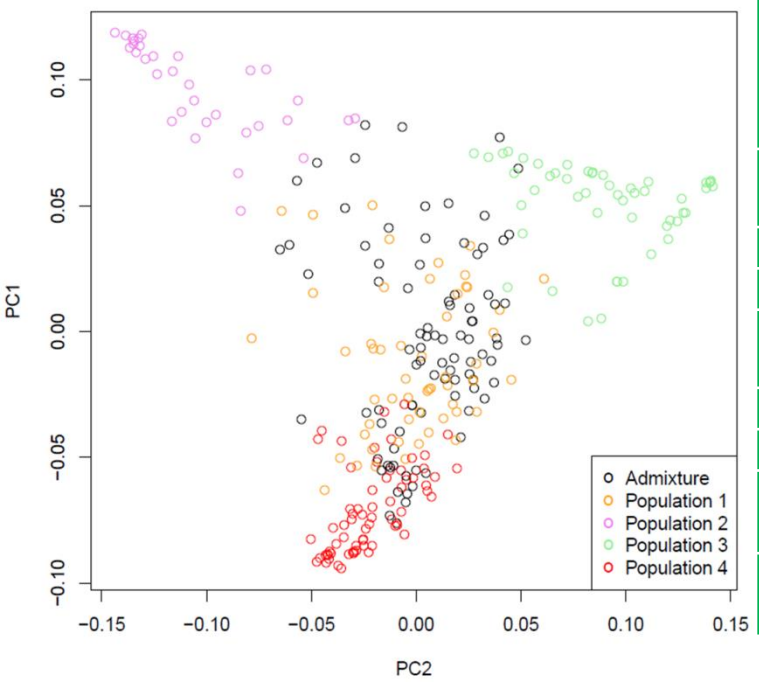


K = 4 populations



3. Results

GWAS analysis identified a block of four SNPs within the region of strong linkage associated with maturation in stress weather conditions (Kuban experimental station of VIR in 2018) in which genes encoding zinc finger A20 and AN1 domain stress-associated protein are located. SAPs are known to prevent the loss of yield caused by environmental stresses [2].



SNP Position	Chromosome	Phenotype	Is in the region of strong linkage	Is in genic region
4010542	2	PossibilityOfMaturationKuban2018	+	Vradi02g04250
4042537				-
4053368				-
4083513				Vradi02g04320
35724672	6	SeedWeightTaiwan1984	+	Vradi06g15580
35724738				580
496351	9	PrimaryLeafWidthTaiwan1984	+	-
		SeedWeightTaiwan1984		-
		PodLengthTaiwan1984	-	Vradi09g03630
4730927		SeedWeightTaiwan1984	-	630

4. References:

- Schafleitner R et al. (2015) The AVRDC – The World Vegetable Center mungbean (*Vigna radiata*) core and mini core collections. BMC Genomics. 16(1):344. doi: 10.1186/s12864-015-1556-7.
- Ben Saad R et al. (2019) Functional domain analysis of LmSAP protein reveals the crucial role of the zinc-finger A20 domain in abiotic stress tolerance. Protoplasma. 256(5):1333-1344. doi: 10.1007/s00709-019-01390-2.

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