

Association Mapping of Aphid Resistance in USDA Cowpea

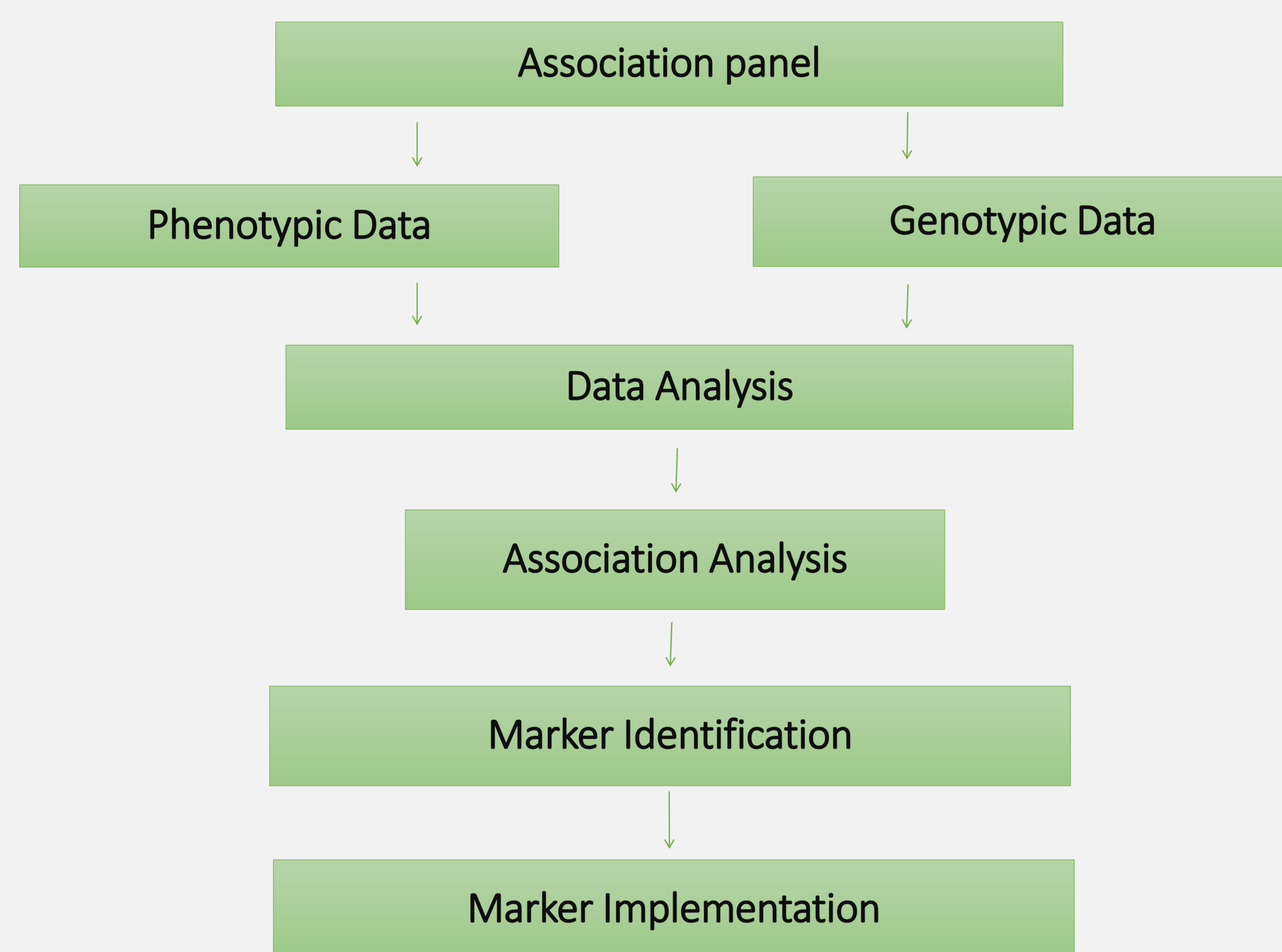
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Abstract

Cowpea aphid (CPA; *Aphis craccivora*) is a destructive insect pest of cowpea, and also causes significant yield losses in other legume crops including alfalfa, beans, chickpea, lentils, lupins and peanuts. The utilization of aphid resistance in cowpea breeding is one of most efficiency and environmental friendly methods and using marker-assisted selection will expedite cowpea breeding procedure, but it is limited by the lack of information on marker associations of the aphid resistance. The objective of this study was to identify single nucleotide polymorphism (SNP) markers associated with aphid resistance in cowpea. In this study, 338 cowpea accessions from the cowpea core collection in USDA-GRIN, originally collected from 40 countries, were evaluated for their aphid resistance and 1047 SNPs identified from genotyping by sequencing (GBS) as the genotypic data. Single marker regression (SMR), general linear model (GLM), and mixed linear model (MLM) in TASSEL were used for association analysis between the SNPs and the phenotypic data. Three clusters were inferred by STRUCTURE analysis, in good agreement with the phylogenetic tree drawn by MEGA 6 based on the maximum likelihood model with neighbor joining method. A genome-wide association study revealed two SNP markers, C35011941_894 and Scaffold30061_3363 were strongly associated with aphid resistance across three models with the log of odds (LOD) value greater than 2.5. The results will provide useful information for selecting. aphid resistance in cowpea molecular breeding.

Method



Plant material

A panel of 338 cowpea accessions, obtained from the United States Department of Agriculture Germplasm Resources Information Network (USDA-GRIN) was used for association analysis. The accessions collections were from 40 different countries/regions.

Results

Fig 1. The infection of cowpea plants by Aphid.



Fig.2 Model-based populations in the cowpea association panel of 369 cowpea accessions of core collection: The distribution of the accessions to different populations is indicated by the color code (Q1: red, Q2: green, Q3: blue), consistent in the figure A, B and C.

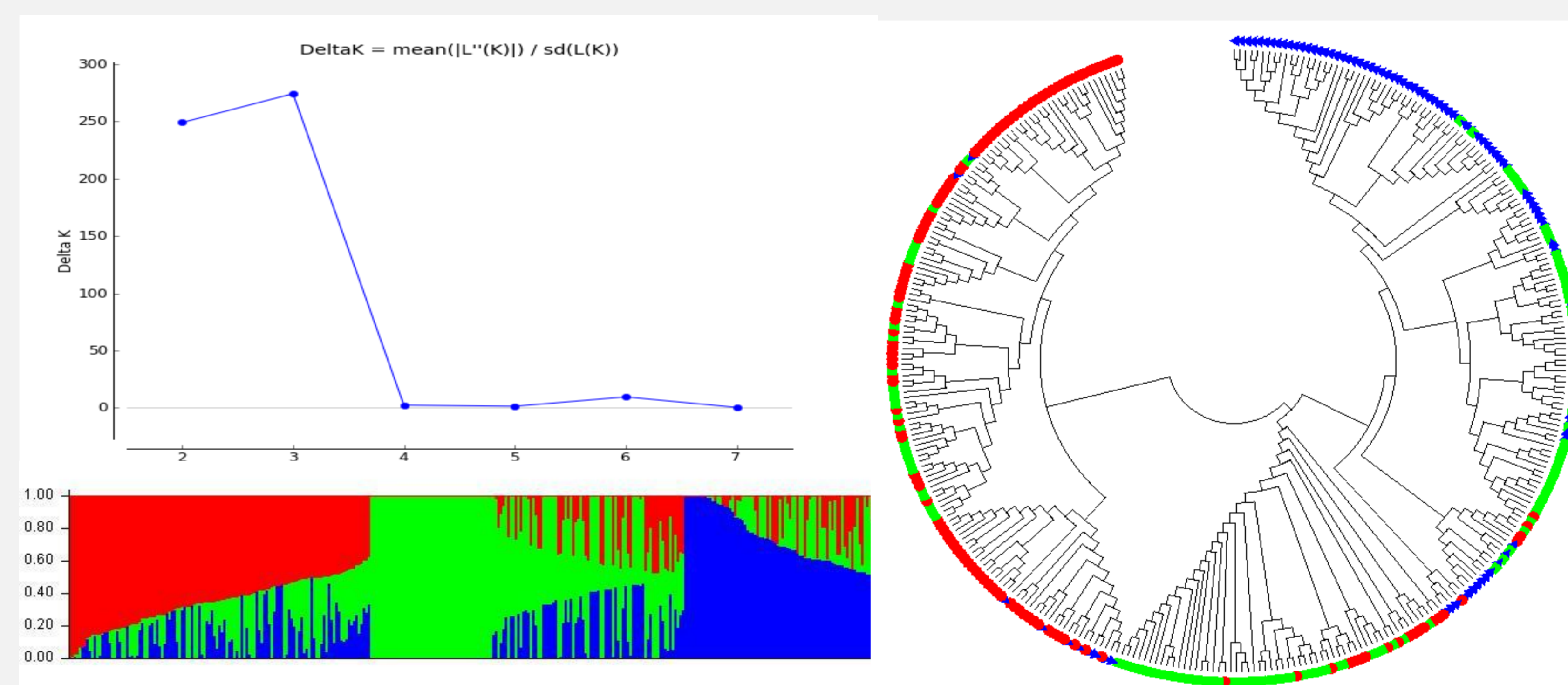


Table 1 SNP markers associated with aphid using three statistical models.

SNP marker	SMR (LOD)	GLM (LOD)	MLM (LOD)
C35011941_894	5.3	3.80	3.0
Scaffold8849_21404	3.3	2.97	2.0
Scaffold30061_3363	3.1	2.63	2.6
Scaffold9649_62	2.8	2.69	2.4
C34993906_711	1.2	2.61	1.5
C35052141_508	2.7	2.31	1.8
C35067730_818	2.5	2.39	2.1
Scaffold48811_2524	5.2	3.30	1.7
Scaffold50992_9329	1.1	2.55	1.6
Scaffold96701_5969	3.0	1.99	1.9