January 14-18, 2017
Town & Country Hotel
San Diego, CA

PLANT & ANIMAL GENOME XXV

THE INTERNATIONAL CONFERENCE ON THE STATUS OF PLANT & ANIMAL GENOME RESEARCH

FINAL PROGRAM & EXHIBIT GUIDE

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Plant & Animal Genome XXV
Registration & Meeting Schedule

Registration - ATLAS FOYER

Friday	January 13	12:00pm - 9:00pm
Saturday - Sunday	January 14-15	7:00am - 8:00pm
Monday	January 16	7:00am - 5:00pm
Tuesday	January 17	7:00am - 3:00pm
Wednesday	January 18	7:00am - 12:00pm

Plenary Session - ATLAS BALLROOM

Sunday	January 15	6:15pm - 7:00pm
Monday	January 16	8:00am - 10:00am
Tuesday-Wednesday	January 17-18	8:00am - 9:30am

Poster Access Hours – GRAND EXHIBIT HALL & LOWER LEVEL

Saturday	January 14	7:00am - 9:00pm
Sunday	January 15	7:00am - 9:00pm
Monday	January 16	7:00am - 9:00pm
Tuesday	January 17	7:00am - 3:00pm
Wednesday	January 18	7:00am - 12:00pm

ALL POSTERS MUST BE REMOVED BY 12:00PM WEDNESDAY, JANUARY 18.

Speaker Ready Room – TERRACE SALON 2

Friday	January 13	12:00pm - 8:00pm
Saturday - Tuesday	January 14-17	7:00am - 8:00pm
Wednesday	January 18	7:00am - 12:00pm

Poster Sessions - GRAND EXHIBIT HALL & LOWER LEVEL

Monday (Even Numbers)	January 16	10:00am - 11:30am
Monday (Odd Numbers)	January 16	3:00pm - 4:30pm

Exhibit Hours - GRAND EXHIBIT HALL

Sunday	January 15 **(Reception: 7:00-8:30)**	3:00pm - 8:30pm
Monday	January 16	9:30am - 5:00pm
Tuesday	January 17	9:30am - 3:00pm

Computer Room - CALIFORNIA

Friday	January 13	12:00pm - 10:00pm
Saturday - Tuesday	January 14-17	6:00am - 10:00pm
Wednesday	January 18	6:00am - 3:00pm

Computer Demonstrations: Computer system demonstrations will be conducted Sunday - Wednesday in the "computer room", located in the California Room, see Computer Demo schedule for times.

Welcome Reception - GRAND EXHIBIT HALL & LOWER LEVEL

Sunday	January 15	7:00pm - 8:30pm

Closing Banquet Dinner – GRAND EXHIBIT HALL

Wednesday	January 18	7:00pm - 12:00am

Genome wide association studies (GWAS) in *Capsicum* core collection

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ABSTRACT

Genome-wide association study (GWAS) is an effective approach for identifying genetic variants associated to useful agronomic traits. As we are performing GWAS for various agronomic traits in pepper, a genotyping-by-sequencing (GBS) approach was used to provide dense genome-wide marker coverage (>33,000 SNPs) for a 350 pepper core collection. Using GBS platform, a high density haplotype map was constructed and various stratification methods, including principal component analysis (PCA), and bayesian phylogenetic methods (STRUCTURE) were performed to show the genetic diversity and population stratification. Based on the STRUCTURE, four subgroups were identified and each of Q values was estimated. Through these results, MLM using Q values combined with kinship matrix were performed to identify quantitative trait loci controlling the variation of 12 agronomic traits. A set of 37 SNP locus distributed over 12 *Capsicum* chromosomes was identified for associations. For a validation, the associations were compared with the location of known QTLs which were surveyed from bi-parental population. It showed that, at least two QTLs were matched well with previous study. These results will help to understand associations between phenotype and genotype and also will give more power to validate the candidate genes or quantitative trait loci.

OBJECTIVES

- **Detection of genome-wide SNPs among pepper GWAS population using genotyping-by-sequencing (GBS) approach**
- **Construction of high density haplotype map**
- **Population structure analysis using various stratification methods**
- **Detection of candidate QTLs associated with interested phenotypes**

MATERIALS & METHODS

- **Plant material**

A pepper GWAS population including 9 species, consisting of 351 accessions was constructed by combining three different collections. *Capsicum* species included in this population are shown in figure 1.

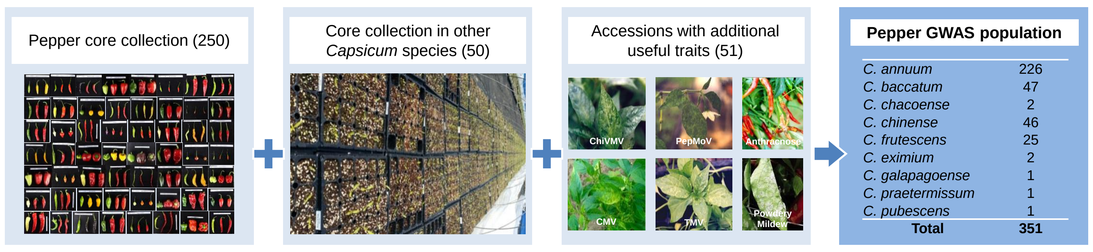

Figure 1. Pepper GWAS population using in this study. A total of 351 accessions were placed in this population constructed by combining three different pepper collections.

- **Genotyping-by-sequencing (GBS)**

DNA of germplasm was extracted by CTAB method. Two restriction enzymes (*PstI*-*MseI*), and a compatible set of 96 barcode were used to prepare the GBS library. Single end sequencing was performed on four lanes of an Illumina HiSeq 2000 at the Macrogen Inc (Seoul, Korea).

- **SNP observation and haplotype map construction**

The CLC Genomics Workbench was used to check sequencing quality (QC) and trim the sequence reads. Two software tools, BWA and GATK were used for the processing of Illumina sequence read trimmed data. Haplotype map was constructed using FILLIN in TASSEL 5 (Figure 2).

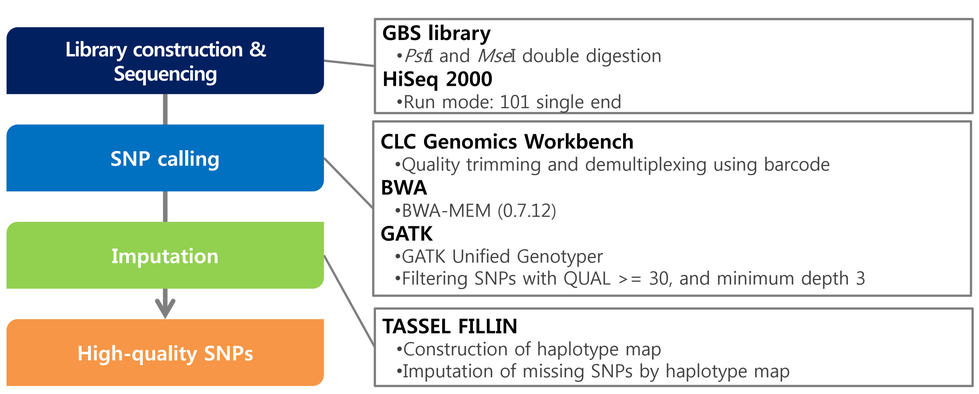

Figure 2. Workflow of SNP calling and haplotype map construction.

- **Population structure and genetic diversity analysis**

To better understand the genetic diversity of germplasm, phylogenetic analysis and PCA were performed by DARwin 6.0.9 (Perrier and Jacquemoud-Collet, 2006). Population structure was identified using STRUCUTRE 2.3.4 software.

REFERENCE

1. Elshire RJ, Glaubitz JC, Sun Q, Poland JA, Kawamoto K, Buckler ES, et al. A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. PLoS One. 2011;6(5):1–10.
2. Liu L, Zhang D, Liu H, Arendt C. Robust methods for population stratification in genome wide association studies. BMC Bioinformatics. 2013;14(1):132.
3. Pritchard JK, Stephens M, Donnelly P. Inference of population structure using multilocus genotype data. Genetics. 2000;155(2):945–59.
4. Han K, Jeong H-J, Yang H-B, Kang S-M, Kwon J-K, Kim S, et al. An ultra-high-density bin map facilitates high-throughput QTL mapping of horticultural traits in pepper (Capsicum annuum). DNA Res. 2016;23(2):81–91.

ACKNOWLEDGEMENT

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RESULTS

- **SNP observation in high density haplotype map**

Overall 3,000,000 SNPs were detected among pepper 351 Capsicum GWAS population using PstI-MseI double digest enzyme set (average SNP depth: 86). SNPs with > 50% missing data and monomorphic SNPs were dropped from the data set. After strong SNP filtering, 33,843 SNPs were remained with call rates > 0.5 (Figure 3).

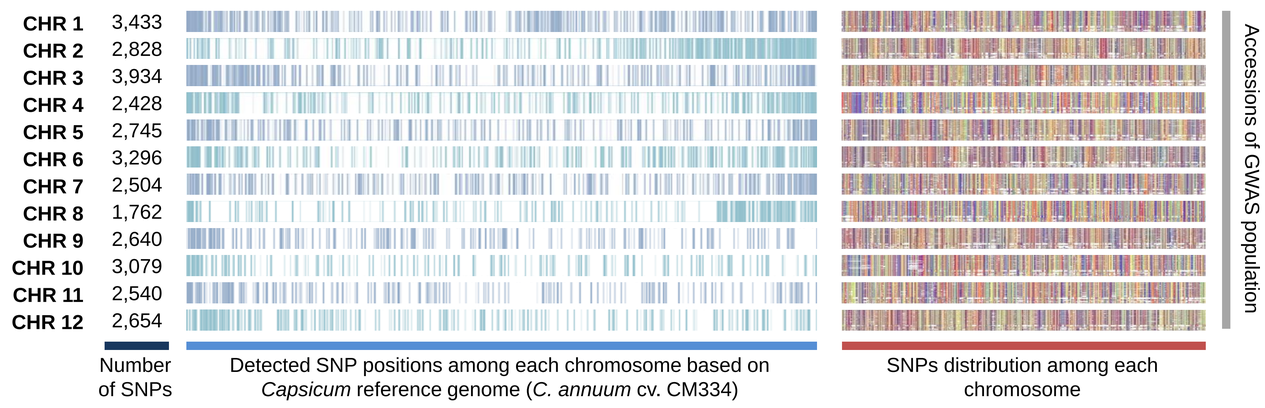

Figure 3. SNP distribution among 12 pepper chromosomes. Over 33,843 SNPs were used for construct the high density haplotype map.

- **Genomic structure of pepper GWAS population**

Based on the Bayesian phylogenetic methods, whole population showed two subpopulations as *C. annuum* and the other species. The first subpopulation which contains the other species was also divided in two subgroups as *C. baccatum* and the other species. The second subpopulation which contains all the *C. annuum* was tend to separate by fruit shape as hot pepper type and bell pepper type (Figure 4).

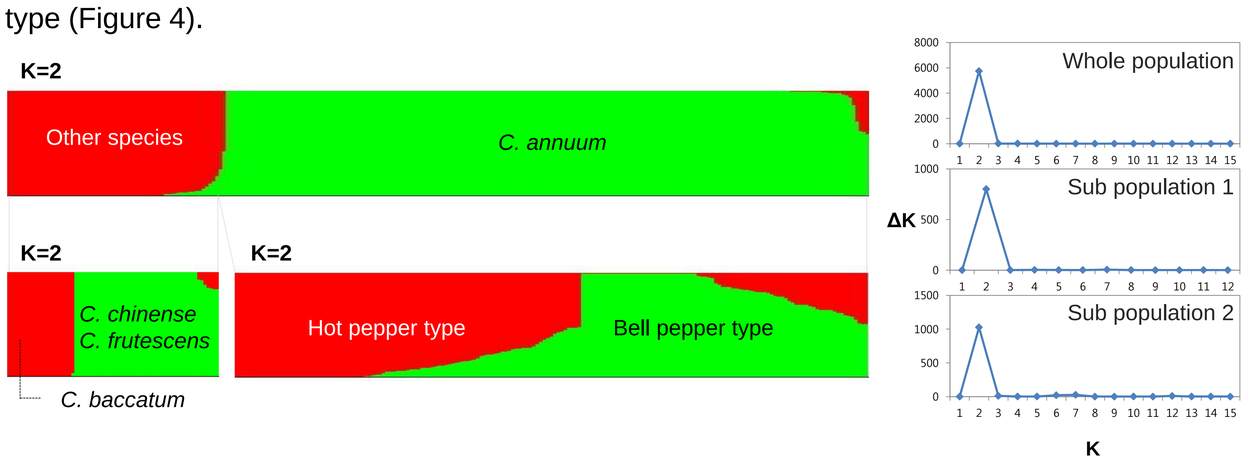

Figure 4. Population structure of the *Capsicum* core collection (CC250) using GBS data. ΔK reached its maximum value when K=2 following the *ed-hoc* method. Subpopulations were grouping by Q. Each subpopulation was separated in to two subgroups.

- **GWAS on Capsicum GWAS population of various interested agronomic traits**

Using MLM (K+Q), a total of 56 candidate QTLs associated with 12 various agronomic traits was detected among 12 *Capsicum* chromosome.

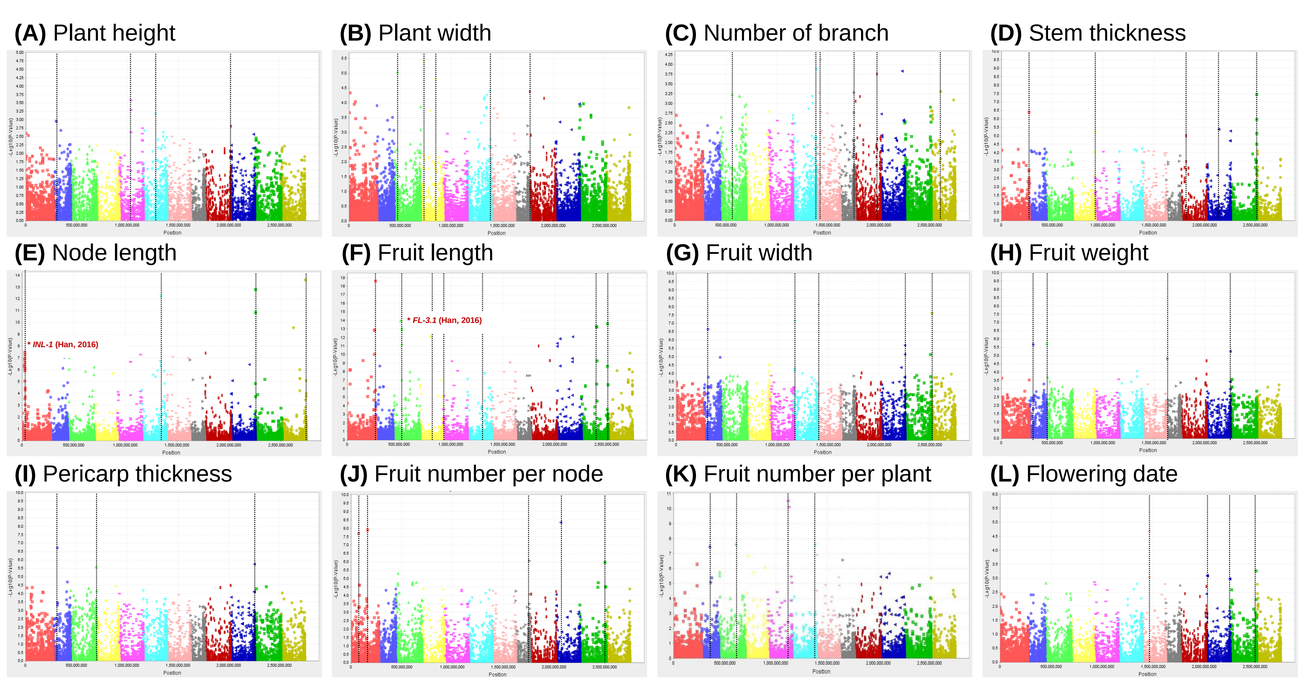

Figure 5. Manhattan plots of association p-values over the 12 pepper chromosome. MLM (K+Q) model was used to screen for association between genotype and (A) Plant height, (B) Plant width, (C) Number of branch, (D) Stem thickness, (E) Node length, (F) Fruit length, (G) Fruit width, (H) Fruit weight, (I) Pericarp thickness, (J) Fruit number per node, (K) Fruit number per plant, and (L) Flowering date.