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Analysis for the genetic polymorphism of Korean Ginseng (*Panax ginseng* C. A. Meyer) varieties in GBS(Genotyping-by-sequencing)

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INTRODUCTION

Currently, Whole Genome Sequencing (WGS) technology is being effectively utilized in various crops. The several studies on the characteristics of Korean Ginseng cultivars and breeding lines have already been carried out the level of molecular Classification analysis in Korea. In spite of where Geumsan is a representative place of Korean Ginseng, Geumsan native species(breeding lines) have not yet been carry out analysis of morphological, genetic characteristics and relationship. This study was conducted to develop an SNP set that can be useful for marker-assisted breeding (MAB) in Korean ginseng (*Panax ginseng* C. A. Meyer) using Genotyping-by-sequencing (GBS) analysis of 96 Ginseng breeding lines. The several studies on the characteristics of Korean Ginseng cultivars and breeding lines have already been carried out the level of molecular Classification analysis in Korea. Using the developed SNP set, We could be used diverse genetic resources for Ginseng breeding.

MATERIALS AND RESULT

We collected 15 Ginseng breeding variety from Korea, 1 American ginseng and 6 breeding line. GBS analysis of the collection were conducted for extraction gDNA using sprout. Each DNA sample was quantified at the final DNA concentration of 5ng/mL using sterilized distilled water. We selected total 10,100 SNP through SNP filtering and clustered for the selection to develop markers for variety identification using SNPs.

Table 1. GBS library-22 varieties list.

No.	Name	Classification	No.	Name	Classification	No.	Name	Classification
1	Geumseon	Korean variety	9	K-1	Korean variety	17	CN7	Breeding line
2	Geumjin	Korean variety	10	Gopoong	Korean variety	18	CN8	Breeding line
3	Geumwon	Korean variety	11	Sunpoong	Korean variety	19	CN9	Breeding line
4	Yunpoong	Korean variety	12	Sunun	Korean variety	20	CN10	Breeding line
5	Chunpoong	Korean variety	13	Sunwon	Korean variety	21	GS00-58	Breeding line
6	Keumpoong	Korean variety	14	Chonsun	Korean variety	22	GS98-1-5	Breeding line
7	Cheonryang	Korean variety	15	Sunhyang	Korean variety			
8	Kowon	Korean variety	16	American ginseng	Wild type			

Table 2. Statistics of GBS sequencing raw data.

Analysis of contents	Mapping Statistics
No. of clean reads	6,835,097
No. of mapped reads	6,803,427
Mapping rate(%)	99.42%
No. of mapped region	96,846
Avg. depth of mapped region	23.28
Reference genome coverage (%)	0.66820%

The result of GBS showed that 99.42% of approximately 6,835,097 clean reads were mapped on the ginseng genome with an average mapping region of about 96,846 bp, which indicated genome coverage of 0.67%. After the filtering process, We selected a total of 10,100 SNPs through SNP filtering. For the understanding genetic relationship of total 22 variety and elite breeding lines, Population genetic structure analysis was carried out with 10,100 SNPs, which resulted in the classification of inbreds, thus causing differentiation between the varieties.

Table 3. Statistics of SNP filter processes.

Filtering Process	No. of SNPs
Total SNP	629,213
Missing < 40%	346,139
Missing < 30%	296,793
MAP >5%	107,118
Missing < 40% and MAF 5%	14,801
Missing < 30% and MAF 5%	**10,100**

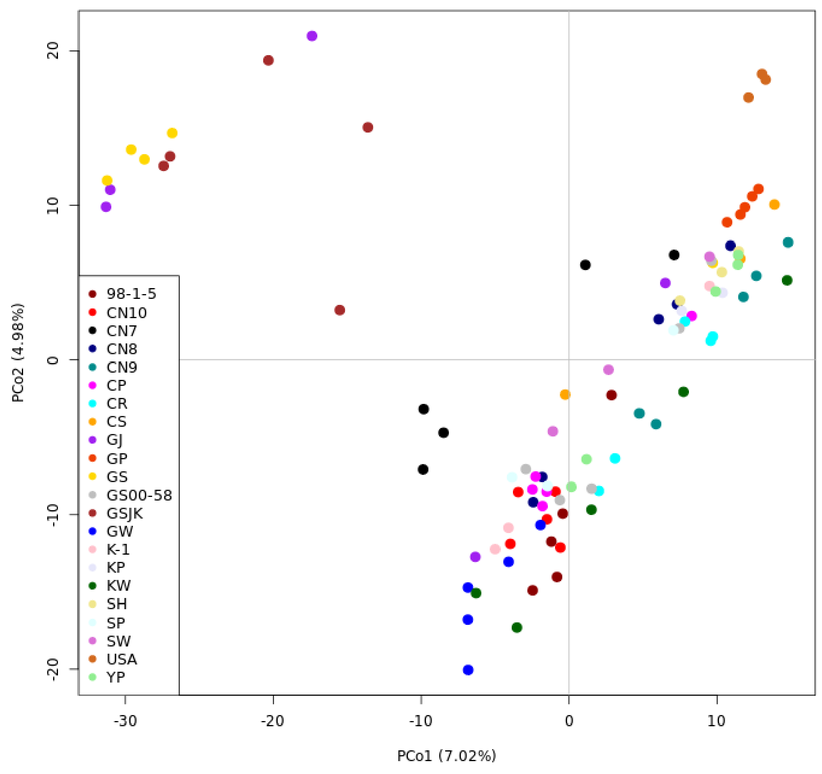

Fig. 1. PCoA(Principal Coordinates Analysis) using 10,100 SNPs of 23 ginseng varieties.

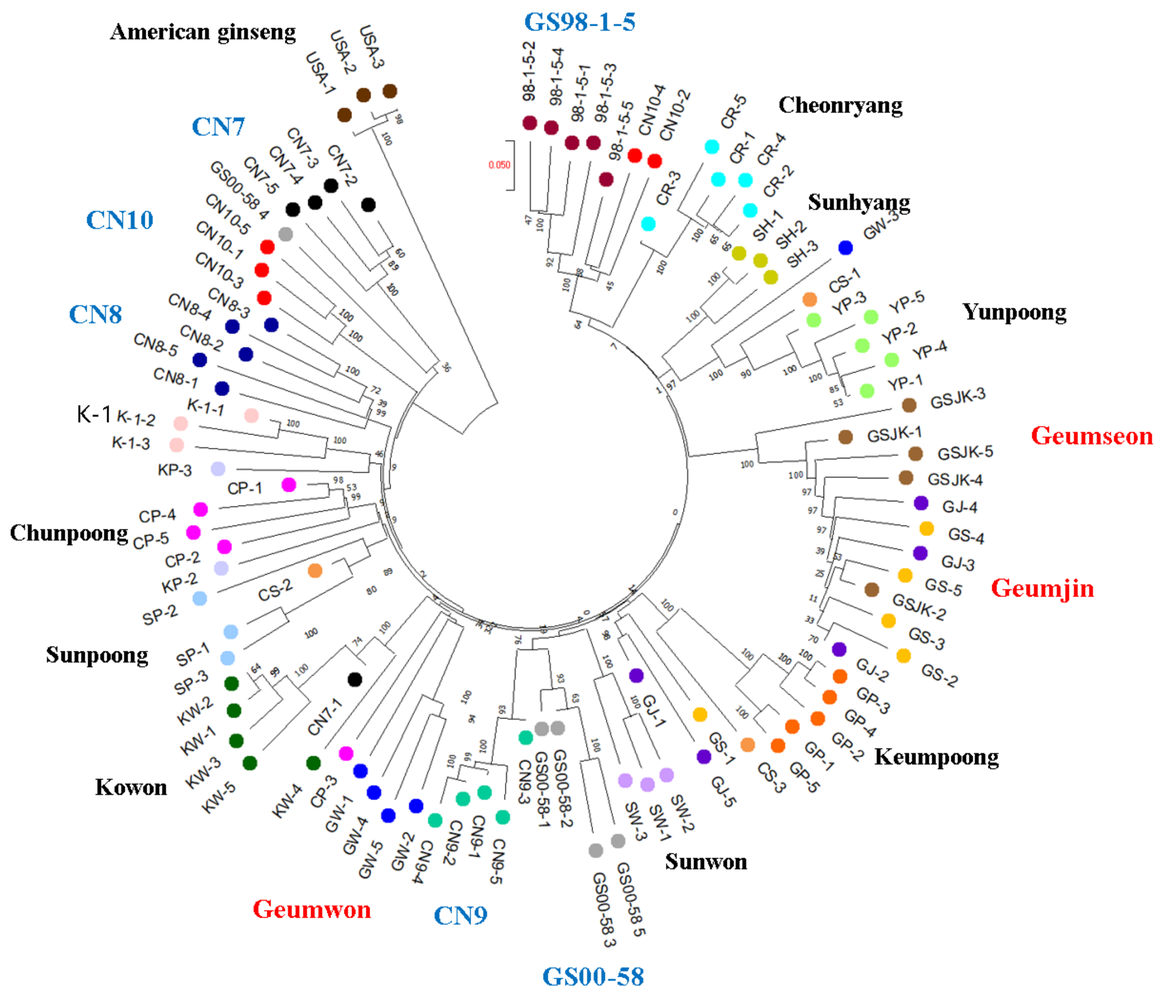

Fig. 2. Phylogenetic tree using 10,100 SNPs of 23 ginseng varieties.

CONCLUSION

There was no significant difference in the growth characteristics of the arerial part of ginseng in 1-year-old according to the specific gravity of seeds. This result was different from the increase in the arerial part growth due to the increase in the seed specific gravity of foxtail millet studies (Jung et al. 2019), and further investigation is needed through underground growth and component analysis.

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