



Analysis of Genetic Diversity and Population Structure of Wild-simulated Ginseng (*Panax ginseng*)

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ABSTRACT

Background : Wild-simulated ginseng (*Panax ginseng*), whose production have been steadily increasing in Korea since 2014, defines cultivated ginseng in the mountain areas without installing artificial facilities such as shading membranes. Since it is cultivated in a natural area, it is greatly affected by the cultivation environment and it is important to find suitable genetic resources for each cultivation area.

Methods and Results : In this study, we used 15 ginseng cultivars (60 plants), violet-stem variants (14 plants) and wild-simulation ginsengs collected from 22 regions of South Korea (271 plants) were used in this experiment. Population structure analysis after genotyping using Fluidigm SNP Chips (192 SNP markers) showed wild-simulated ginseng had a very high genetic diversity. In addition, the wild-simulated ginseng samples collected from each regions formed 2 to 5 populations.

Conclusion : Wild-simulated ginseng farms usually sow cultivated ginseng seeds without distinguishing cultivars. Therefore, by analyzing the genotypes of wild-simulated ginseng individuals from specific cultivation area, we can suppose which cultivar is suitable for the cultivation area. However, to establish suitable wild-simulated ginseng genotypes for each region, it is essential to collect more ginseng cultivars and wild-simulated ginseng samples. If we compare the genotypes of wild-simulated ginseng by regions, we can select suitable genotypes for each regions and it will help increase production and reduce cultivation costs.

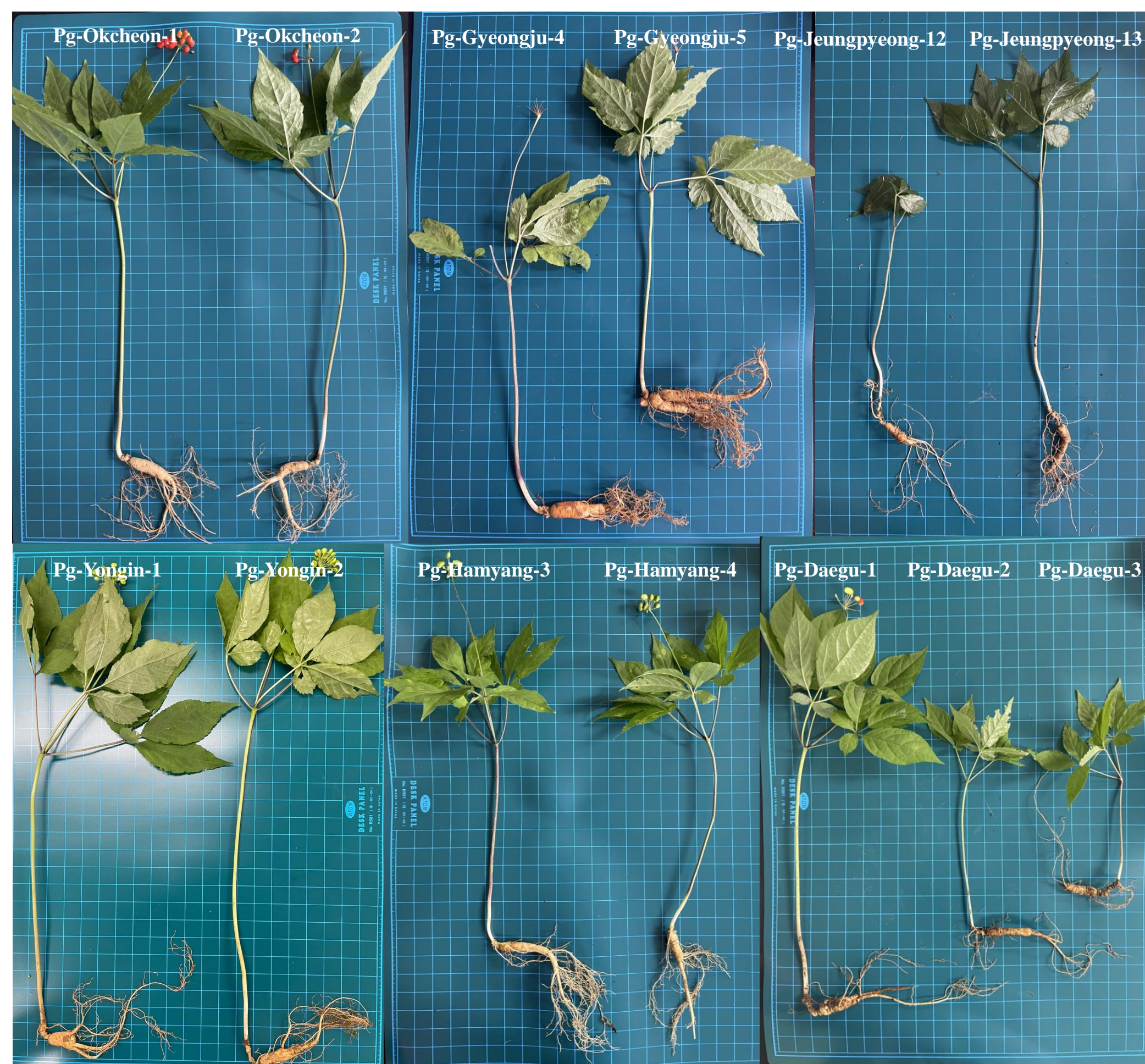


Figure 1. Photograph of the genetic resources used in this study.

Sample Collection Area of *P. ginseng*

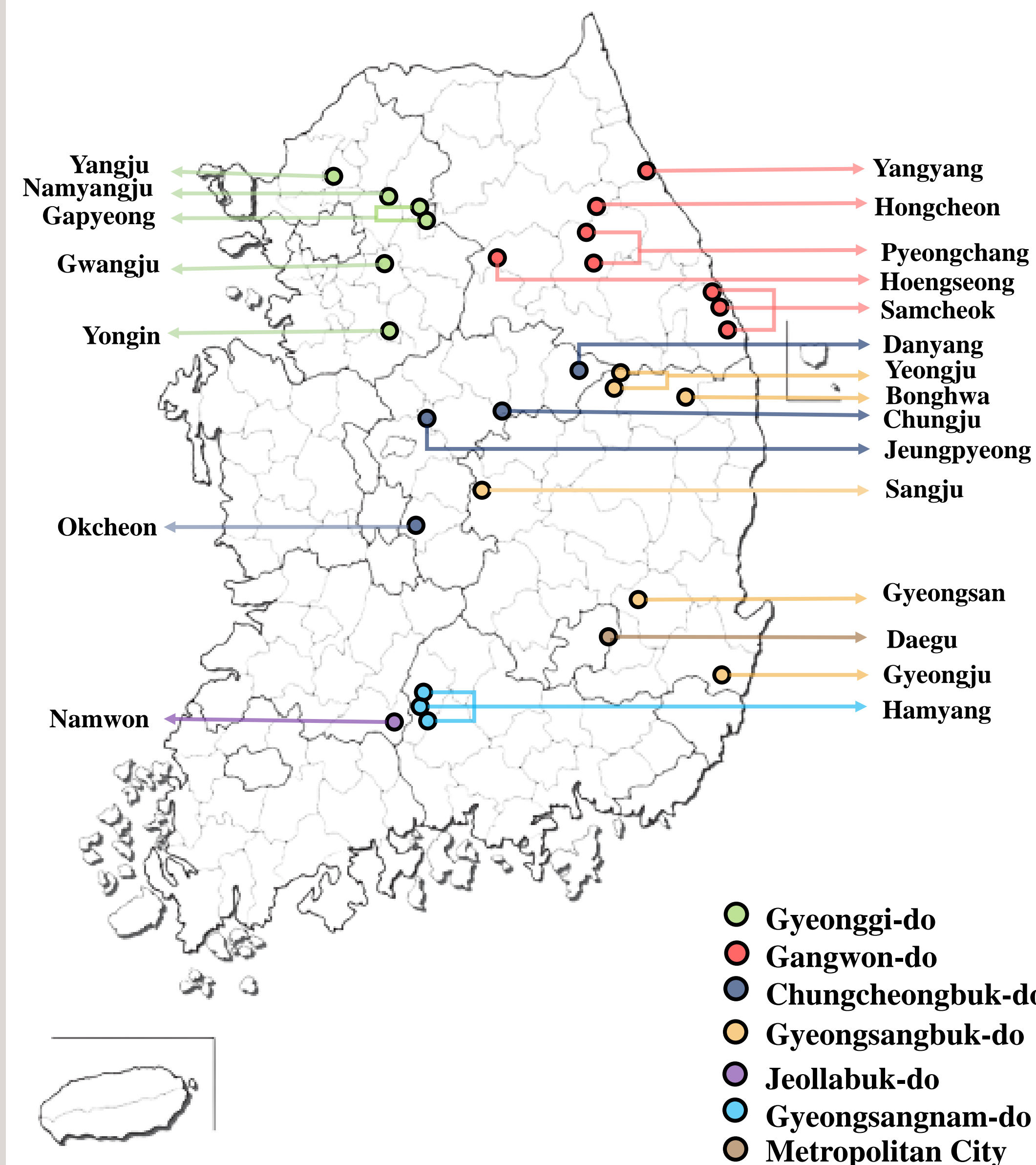
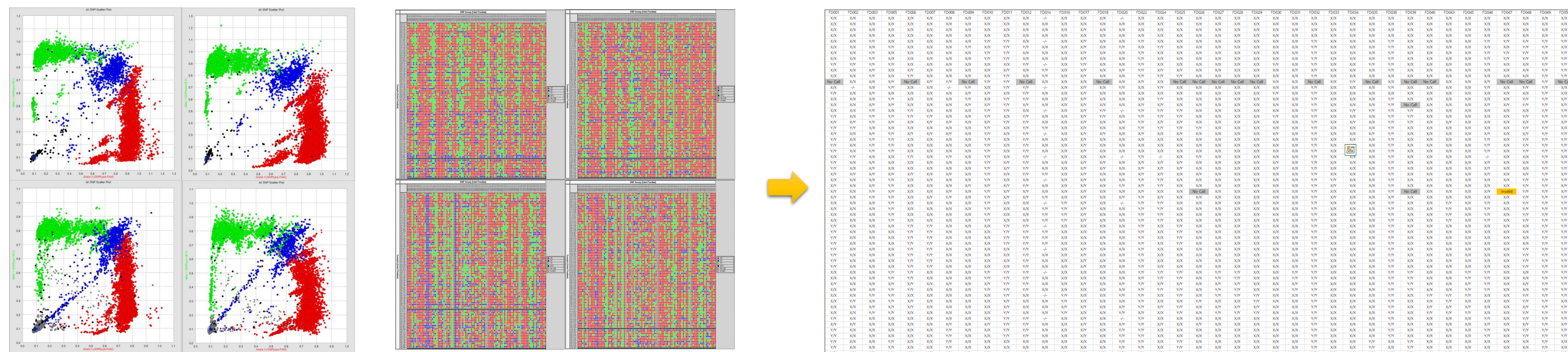


Figure 2. Geographical distribution of 271 wild-simulated ginsengs collected from 22 regions in Korea.

Application of Fluidigm SNP Chips



Genotype distribution

Call performance by chip

Genotype analysis results

1. Genotype analysis of wild-simulated ginseng samples collected by regions using Fluidigm 96.96 Dynamic Array IFC.
2. Check the genotype information collected according to the manual and treat the sample as incorrect (orange dot ●) if the genotype is at the boundary between different clusters and too far away from the cluster.
3. If genotype analysis is difficult because it is not amplified enough, process no call (gray dot ●).
4. Genetic distance analysis is performed using UPGMA trees and population structures, except for samples or markers that do not have sufficient genotypes in the experimental results.

A total of 345 samples were used in the experiment, including 15 ginseng cultivars (K-1, Gowon, Gopung, Geumseon, Geumjin, Geumpung, Seonun, Seonwon, Seonpung, Seonhyang, Yeonpung, Jeongseon, Cheonpung, Cheonhyang, Kumwen), 14 violet-stem variants and wild-simulation ginsengs. The 15 ginseng cultivars were experimented with four samples each, and 60 samples were collected, and 271 samples were collected for wild simulation ginseng. Ginseng cultivars were provided by Rural Development Administration, and wild-simulated ginseng were sampled from 22 regions of Korea.

Results

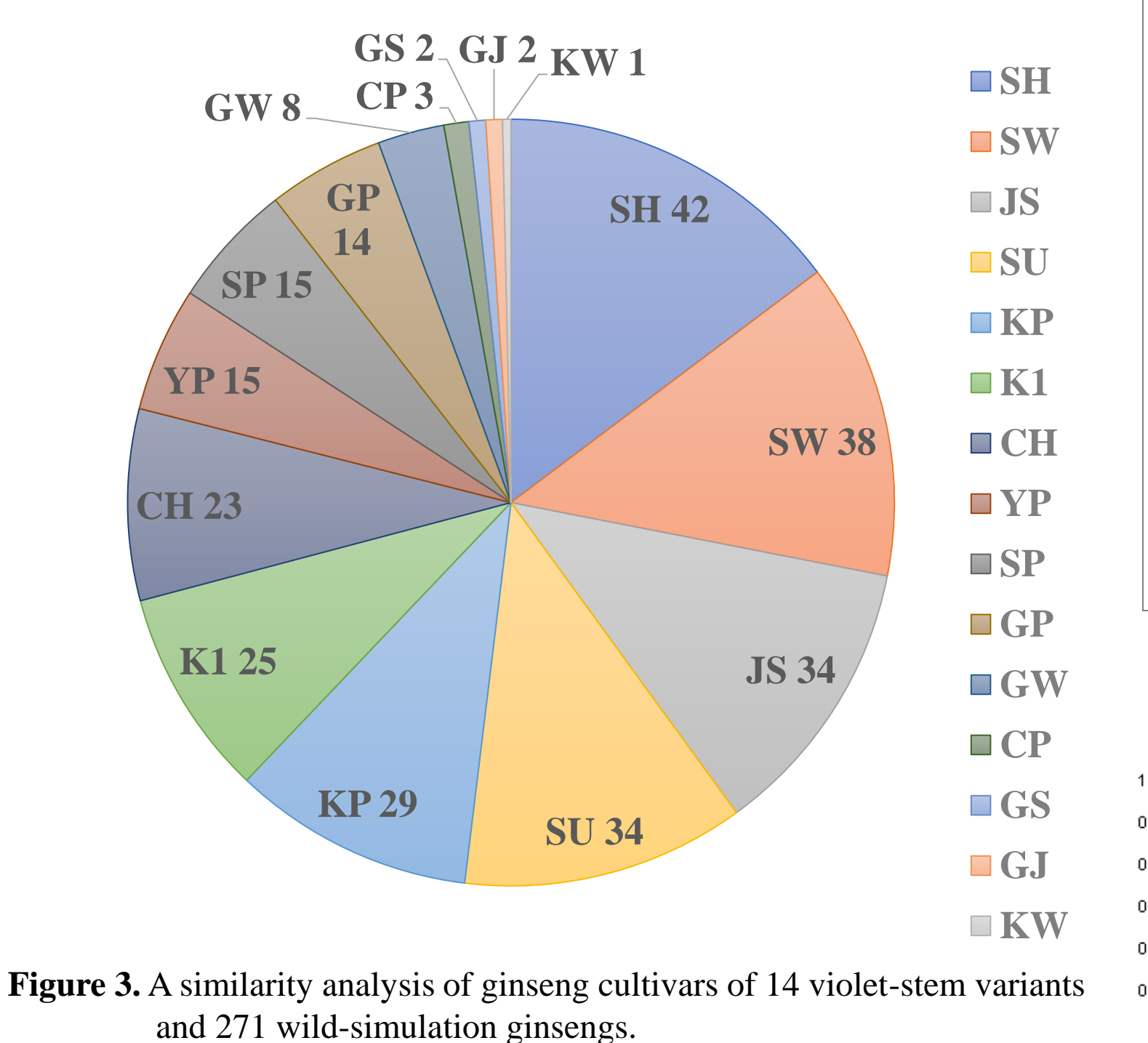


Figure 3. A similarity analysis of ginseng cultivars of 14 violet-stem variants and 271 wild-simulation ginsengs.

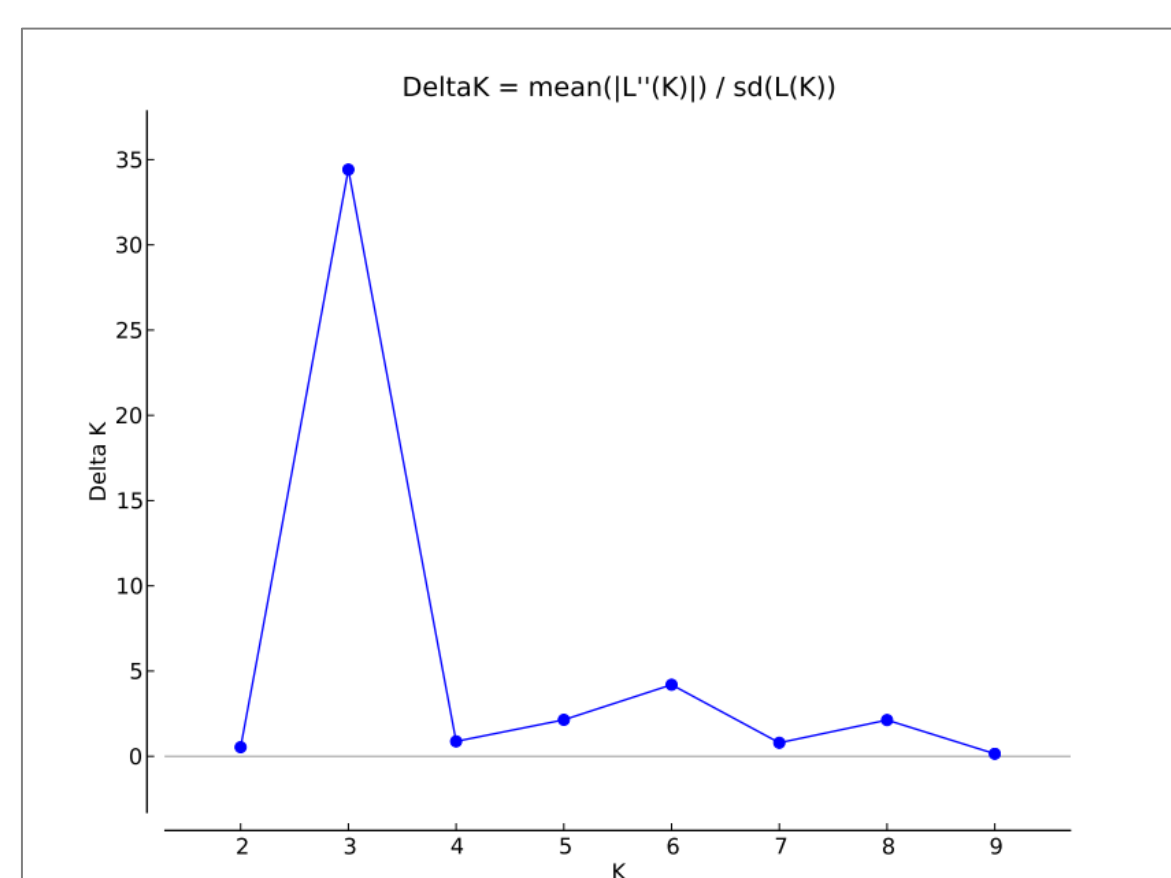


Figure 5. As a result of calculating the exact value of Delta K in the Pyeongchang region, Delta K = 3.

K	Reps	Mean LnP(K)	Stdev LnP(K)	Ln'(K)	Ln'(K)	Delta K
1	5	-20607.26	0.626897	—	—	—
2	5	-19501.88	8.679401	1105.38	4.64	0.534599
3	5	-18391.86	12.012202	1110.02	413.42	34.41667
4	5	-17695.26	45.429209	696.6	39.78	0.875648
5	5	-17038.44	33.013528	656.82	70.66	2.140335
6	5	-16452.28	99.568002	586.16	418.14	4.199542
7	5	-16284.26	929.374356	168.02	736.5	0.792469
8	5	-15379.74	177.254176	904.52	377.08	2.127341
9	5	-14852.3	118.439246	527.44	17.56	0.148262
10	5	-14342.42	40.257074	509.88	—	—

Table 2. Mean LnP(K), Stdev LnP(K), Ln'(K), |Ln'(K)| and Delta K in Pyeongchang region according to clusters (K) value.

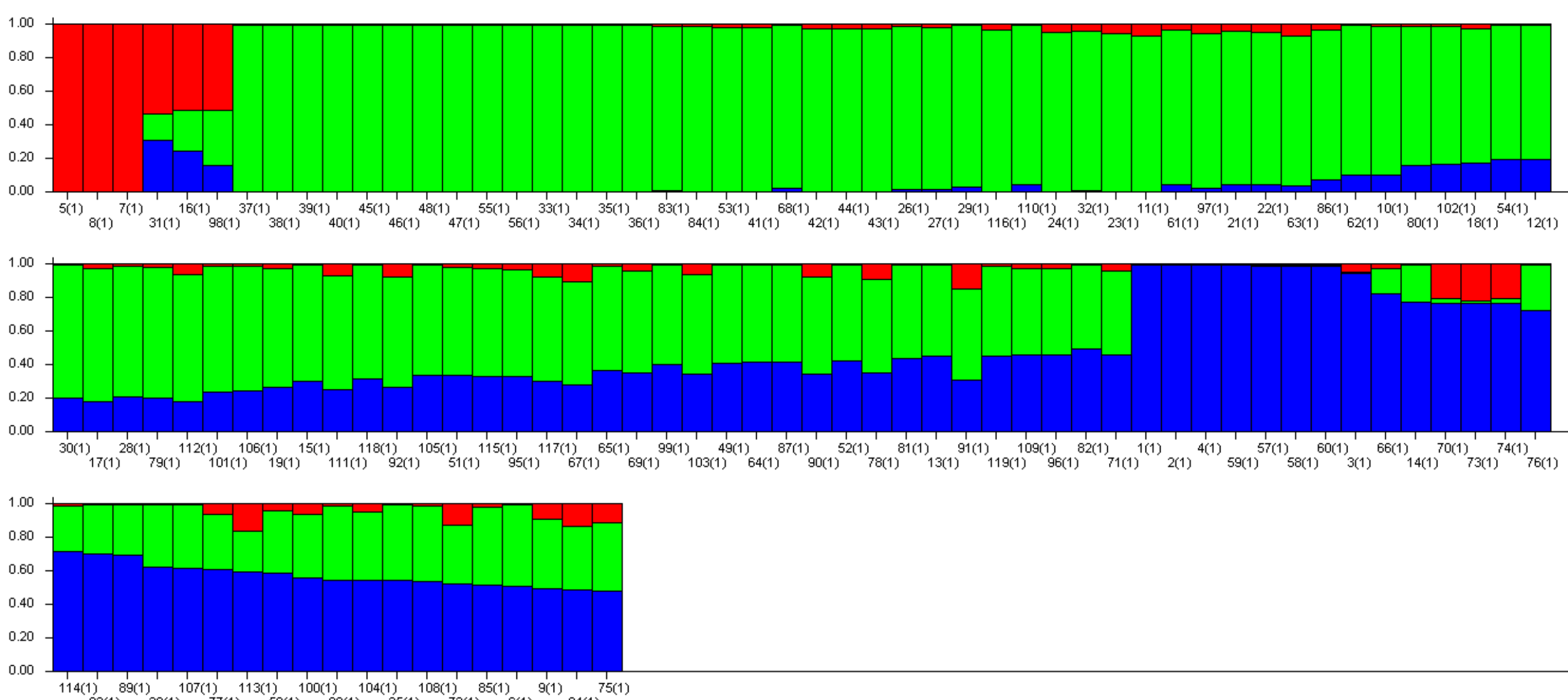


Figure 6. Model-based ancestry of 119 P. ginseng including 45 wild ginseng in Pyeongchang region with cluster numbers K=3. Pop1=red; Pop2=green; Pop3=blue.

- As a result of analyzing the similarity of violet-stem variants wild-simulation ginsengs, it is distributed in the order of 'Seonhyang (SH), Seonwon(SW), Jeongseon (JS), Seonun (SU), Geumpung (KP), K-1 (K1), Cheonhyang (CH), Yeonpung (YP), Seonpung (SP) Gopung (GP), Gowon (GW), Cheonpung (CP), Geumseon (GS), Geumjin (GJ), Kumwen (KW)' (Figure 3).
- In a genetic diversity analysis using 191 Fluidigm SNP Chips, *P. ginseng* was not grouped together according to the collection region. It also showed high genetic diversity (Figure 4).
- Population structures were analyzed using model-based STRUCTURE software (version 2.3.4) using the following parameters: number of clusters (K) set = 1 to 10; number of iterations = 5; length of burning period = 100,000; number of MCMC (Markov Chain Monte Carlo) Reps after Burnin = 100,000.
- In the population structure analysis conducted by region, *P. ginseng* was generally classified into three populations (Table 1).

Reference

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