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Genetic Composition of Korean Ginseng Germplasm by Collection Area and Resource Type

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Received: 24 September 2020; Accepted: 22 October 2020; Published: 26 October 2020

Abstract: To improve crops, it is important to secure plant genetic source material and evaluate the genetic diversity. Ginseng (Panax ginseng C.A. Meyer) has long been used as a medicinal herb in Korea and China. Since ginseng originated from wild ginseng with low genetic diversity, it is also expected to have low genetic diversity. In this study, the genetic diversity of 451 ginseng accessions conserved in the National Agrobiodiversity Center (NAC) at Korea was analyzed using 33 SSR markers. Another objective was to establish a strategy for NAC to manage ginseng germplasm based on these results. The 451 accessions were collected from 22 cities in six provinces in South Korea. Among the 451 ginseng accessions, 390 (86.5%) and 61 (13.5%) were landraces and breeding lines, respectively. In the STRUCTURE results for the accessions, there was no relationship between assigned genotypes and collection areas, but there was a population genetic structure. In addition, genetic differentiation within populations of each analysis was low, indicating that the ginseng accessions conserved at NAC are extensively dispersed throughout the collection areas. The results of this study suggest that NAC should increase the genetic diversity of ginseng accessions for breeding programs, and alternatives are needed for securing ginseng genetic resources.

Keywords: ginseng; genetic composition; genetic diversity; SSR

1. Introduction

Plant breeding in agriculture has decreased the diversity of many crops, which has caused bottlenecks in crop domestication, dispersal, and modernization. Researchers, in particular, have identified significant negative effects of plant breeding on diversity following the modernization bottleneck [1]. The loss of crop variation caused by the modernization of agriculture has been described as genetic erosion [2]. Since loss of genetic variation could decrease the potential of species to persist in the face of abiotic and biotic environmental changes, genetic erosion could pose a severe threat to long-term global food security [3]. Crop improvement largely depends on immediate conservation of genetic resources for their effective and sustainable utilization. For this, it is necessary to conserve and breed the vast genetic variation found in populations of the wild progenitors and landraces of cultivated plants [4,5].

Plant genetic resources are the most important components of agro-biodiversity, which encompasses primitive forms of cultivated plant species and landraces, modern and obsolete cultivars, breeding lines and genetic stocks, weedy types, and related wild species [6]. Since the International Board for Plant Genetic Resources was established in 1974, over 1750 gene banks have been activated worldwide, about 130 of which hold more than 10,000 accessions each [7,8]. In Korea,
The National Agrobiodiversity Center (NAC) was established in 2008, and the center now has conserved 258,984 accessions of 3126 species [9].

The *Panax* genus of the Araliaceae family comprises 17 species, of which *P. ginseng*, *P. notoginseng*, and *P. quinquefolium* are widely cultivated for medicinal value [10,11]. The Korean ginseng, *P. ginseng* C.A. Meyer, is an important medical plant, which is well-known for its remarkable pharmacological effects [10–14]. Generally, the origination area and time of *P. ginseng* are known to be in Sangdang, China and the first century B.C during the Han dynasty, era (Chinese origin theory of ginseng). However, it is fairly obvious that this theory does not answer appropriately to the fundamental questions of the origin of ginseng; (1) why ginseng suddenly appeared in that time, Han China, (2) how explain clearly the formation of ginseng character. Since *P. ginseng* naturally exists in only three regions: Korea (33.7°–43.1°), Manchuria (43°–47°), and the Littoral province of Siberia, it is sometimes referred that the originating place is not Shangdang of Shansi area of China, but Manchuria and Korea [15].

Many previous researchers have studied the medical and pharmacological effects and genetic diversity of *P. ginseng* [16–23]. Based on the growing environment and the method of cultivation, commercial trade ginseng is classified into three grades: cultivated, mountain cultivated, and mountain wild [24]. In general, the cultivated ginseng is known to have originated from wild ginseng, a rare, endangered plant [25]. The genetic consequence of rare or endangered species is increased genetic drift and inbreeding, and these increased phenomena contribute to a reduction in genetic diversity [26,27].

Geographic differences in the distribution of genetic diversity are extremely common. Populations can vary in all aspects of diversity such as number of alleles, identities of alleles, and the effect on the characteristics in the population. The breeding system of the species is very important in determining the differences between populations from different geographic locations [28]. In a previous study, the researchers reported on narrow genetic diversity among 1109 ginseng accessions conserved in the NAC, but there was a lack of sufficient information on the genetic diversity of ginseng accessions such as the collection site [29]. In this study, the genetic diversity of 451 Korean ginseng accessions with information on the collection area was analyzed; in particular, each accession was genetically differentiated and sorted by the collection area. Based on these results, this study includes proposals for how to efficiently manage the ginseng germplasm in NAC.

2. Materials and Methods

2.1. Plant Materials

A total of 451 ginseng accessions were obtained from the NAC at the Rural Development Administration in South Korea (Table S1).

2.2. DNA Extraction

Genomic DNA was extracted from the leaves of ginseng accessions using Qiagen DNA extraction kit (Qiagen, Hilden, Germany). DNA quality and quantity were measured using 1% (w/v) agarose gel and a spectrophotometry (Epoch, BioTek, Winooski, VT, USA). Extracted DNA was diluted to 30 ng/µL and stored at −20 °C until further PCR amplification.

2.3. SSR Genotyping

For SSR (simple sequence repeat) analysis, a total of 33 SSRs were selected previous studies [30,31] (Table S2). They were fluorescently labelled (6-FAM, HEX, and NED) and used to detect amplification products. PCR reactions were carried out in a 25 µL reaction mixture that contained 30 ng template DNA, 1.5 mM MgCl₂, 0.2 mM of each dNTPs, 0.5 um of each primer, 1 U Taq polymerase (Inclone, Yongin, Korea). The amplification was performed under the following cycling conditions: initial denaturation at 94 °C for 5 min, followed by 35 cycles of denaturation at 95 °C for 30 s, annealing at 55 °C for 30 s, extension at 72 °C for 1 min, and a final extension step at 72 °C for 10 min. Each amplicon was resolved
on an ABI3500 DNA sequence (Thermo Fisher Scientific Inc., Wilmington, DE, USA) and scored using Gene Mapper Software (Version 4.0, Thermo Fisher, Wilmington, DE, USA).

2.4. Genetic Diversity Analysis

The number of alleles (Na), the number of genotypes (Ng), Shannon-Wiener index (H), Nei’s genetic diversity (I), Eveness, polymorphic information content (PIC) were calculated using R software [32]. Analysis of molecular variance (AMOVA) within and between gene pools was performed using GenAlEx software v. 6.5 [33].

2.5. Population Structure Analysis

Population structure was analyzed using STRUCTURE v.2.3.4 [34]. In STRUCTURE analysis, Bayesian clustering was performed; three independent runs were tested with K from 1 to 15, each run with a burn-in period of 50,000 iterations and 500,000 Monte Carlo Markov iterations, assuming an admixture model. The output was subsequently visualized with STRUCTURE HARVESTER v.0.9.94 [35].

3. Results

3.1. Distribution of Collection Areas in Korean Ginseng Accessions

The 451 ginseng accessions in this study were collected from 22 cities in six provinces in South Korea (Figure 1 and Table S3). The collection areas were four cities in Gangwon (GW), five in Gyeonggi (GG), two in Gyeongsangbuk (GB), two in Jeollabuk-do (JB), five in Chungcheongnam (CN), and four in Chungcheongbuk (CB). Among 451 ginseng accessions, 203 (45.0%) were collected from CN, 124 (27.5%) from GW, 70 (15.5%) from GG, 24 (5.3%) from JB, 20 (4.4%) from CB, and 10 (2.2%) from GB. Of 22 cities, the largest ginseng accessions were collected from Geumsan (19.3%), followed by Hoengseong (14.4%), with less than 10% collected from other cities. Among the 451 accessions, 390 (86.5%) and 61 (13.5%) were landraces and breeding lines, respectively. All 61 breeding lines were collected from Geumsan in CN.

3.2. Profiling of SSR Markers in Korean Ginseng Accessions

A total of 226 alleles were detected among the 451 ginseng accessions (Table 1 and Table S4). Polymorphic information content (PIC) of 33 SSR markers ranged from 0.025 (GM104) to 0.770 (GM116), with an average of 0.469. In the 390 landraces and 61 breeding lines, there were 223 and 148 alleles, respectively. The number of observed alleles (Na) ranged from 2 to 24, with an average of 6.85, of which there were 6.76 and 4.49 ginseng landraces and breeding lines, respectively. The number of genotypes (Ng) ranged from 2 to 100, with an average of 17.79, of which there were 16.83 and 6.18 landraces and breeding lines, respectively. The Shannon-Wiener index (H) showed the range from 0.06 to 1.998, with an average of 0.92. Observed heterozygosity (Ho) and Nei’s genetic diversity (GD) ranged from 0.02 to 1.00 (mean: 0.88) and 0.02 to 0.80 (mean: 0.52), respectively. H, Ho, and GD were similar in the ginseng landraces and breeding lines.

Table 1. Genetic diversity parameters of 33 SSR markers in 451 ginseng accessions.

| No. Acc | Total Alleles | Na ¹ | Ng | H ² | Ho ² | GD ² |
|---------|---------------|------|----|-----|------|------|
| Landraces | 390           | 223  | 6.76 ± 5.72 | 16.83 ± 23.14 | 0.92 ± 0.43 | 0.88 ± 0.27 | 0.52 ± 0.16 |
| Breeding lines | 61 | 148 | 4.49 ± 3.97 | 6.18 ± 7.02 | 0.93 ± 0.43 | 0.88 ± 0.30 | 0.52 ± 0.16 |
| Total    | 451           | 226  | 6.85 ± 5.82 | 17.79 ± 24.60 | 0.92 ± 0.43 | 0.88 ± 0.27 | 0.52 ± 0.16 |

¹ Na, Number of observed alleles; Ng, Number of genotypes; H, Shannon-Wiener index; Ho, observed heterozygosity; GD, Nei’s gene diversity.
Figure 1. Distribution of collected areas in 451 ginseng accessions. CB, Chungcheongbuk; CN, Chungcheongnam; GB, Gyeongsangbuk; GG, Gyeonggi; GW, Gangwan; JB, Jeollabuk.

3.3. Population Structure of Korean Ginseng Accessions

To understand the pattern of the population structure, a Bayesian clustering analysis in STRUCTURE was performed. The STRUCTURE results suggested the best grouping number (K = 2) based on the delta K (Figure 2A). Population 1 (Pop 1) and 2 (Pop 2) consisted of 211 and 240 accessions, respectively. In pop I, 20 accessions are breeding lines and 191 are landraces. In pop II, 41 accessions are breeding lines and 199 are landraces. By collection site, the western region (GG, CN, and JB) in South Korea showed a high rate of ginseng accessions in Pop I and the eastern part (GW and GB) had a
A high percentage of accessions in Pop II, while CB showed the same number of accessions as Pop I and Pop II (Table S1).

![Graph of Delta K](image)

**Figure 2.** Population structure of 451 ginseng accessions based on 33 SSRs markers. (A) Estimation of population using LnP(D) derived ΔK. (B) Seven population sorted by Q, which represent estimated membership probabilities of the individual to inferred populations. Each accession is represented by a thin vertical line. (C) The population structure showed by different types of germplasms in Korea. (D) The population structure showed by accessions from different geographic regions in Korea. CB, Chungcheongbuk; CN, Chungcheongnam; GB, Gyeongsangbuk; GG, Gyeonggi; GW, Gangwan; JB, Jeollabuk.

Because of the further increase of LnP(D), simulation was performed, and LnP(D) was maximized at K = 7 (Figure 2A). All the ginseng accessions could be grouped into seven populations: POP1, POP2, POP3, POP4, POP5, POP6, and POP7 (Figure 2B); the clusters contained, respectively, 93, 52, 58, 77, 55, 30, and 86 accessions. The population structure was separately analyzed to reveal the differentiation between breeding lines and landraces (Figure 2C); all showed complex population
structures. Among the 61 breeding lines, 14 accessions (23%) were assigned to POP4, followed by 12 (19.7%) in POP2, and 11 (18%) in POP6, while only one (IT239306) was in POP5. The 390 ginseng landraces could also be assigned into the seven population clusters: 84 accessions (21.5%) in POP1, 76 (19.5%) in POP7, and 63 (16.2%) in POP4. The population structure was also estimated to display the regional differentiation of ginseng accessions (Figure 2D). Results showed that 26 (21.0%) and 24 (19.4%) of the ginseng accessions collected from GW clustered into POP4 and POP5, respectively. Among the 70 accessions from GG, 22.9% and 24.3% were in POP1 and POP7, respectively. In GB, 50% were in POP7, 30% were POP2 and 20% were in POP4. Among the 24 ginseng accessions from JB, 33.3% were in POP6 and 20.8% were in POP5. In CN and CB, 25.1% of the accessions in POP1 and 35.0% were in POP7.

In the ginseng landraces, STRUCTURE determined 2 to be the best grouping number based on the delta K (Figure 3A). Population 1 (L-Pop 1) and 2 (L-Pop 2) consisted of 201 and 189 accessions, respectively. Due to the further increase of LnP(D), simulation was performed, and LnP(D) was maximized at K = 12 (Figure 3A). All the ginseng accessions could be grouped into 12 populations, L1 to L12 (Figure 3B), ranging from 2 (L6) to 53 (L9) accessions; the distributions of the 12 groups varied by region (Figure 3C). Among 12 groups, L6 was in GG and JB only. All groups could be found in GG, there were 11 in GG and CN (excluding L6). JB contained ten groups (not L1 and L10), and there were seven in CB: L2, L3, L4, L7, L9, L10, and L11. GB showed the fewest groups, L1, L2, L3, L4, L8, and L11.

![Figure 3](image_url)

**Figure 3.** Population structure of 390 ginseng landraces based on 33 SSRs markers. (A) Estimation of population using LnP(D) derived ΔK. (B) Twelve populations sorted by Q, which represent estimated membership probabilities of the individual to inferred populations. Each accession is represented by a thin vertical line. (C) Distribution of twelve populations in each collection area.

In ginseng breeding lines, STRUCTURE proposed 2 as the best grouping number based on the delta K (Figure 4A). Breeding lines population (B) 1 and 2 consisted of 33 and 28 accessions, respectively (Figure 4B).
3.4. Genetic Diversity and Population Differentiation of Korean Ginseng Accessions

AMOVA was collected for the genetic differentiation among and within the ginseng accession populations by collection area and STRUCTURE results (Table 2). In the collection area findings, AMOVA revealed that 97% of the total genetic variation was attributable to differences within populations, which were notably and significantly greater than the 3% total variation found among populations. PhiPT and gene flow (Nm) for 451 ginseng accessions were 0.028 \((p < 0.0001)\) and 17.213, respectively. Pairwise population PhiPT for four clusters ranged from 0.007 (GG–CB) to 0.085 (CB–JB) (Table S5). Pairwise population estimates of Nm for the four clusters ranged from 5.395 (CB–JB) to 67.845 (GG–CB) migrants per cluster. In the STRUCTURE analysis, 97% of the total genetic variation was again attributable to differences within populations. PhiPT and Nm for the 451 accessions in these results were 0.031 \((p < 0.0001)\) and 15.431, respectively. Pairwise population PhiPT for the four clusters ranged from 0.000 (POP1–POP2) to 0.106 (POP6–POP7) (Table S6). Pairwise population estimates of Nm for the four clusters ranged from 4.223 (POP6–POP7) to 39.744 (POP1–POP3) migrants per cluster. In results of, POP1 and POP2 showed no genetic differentiation in PhiPT and Nm.
Table 2. Analysis of molecular variance (AMOVA) of ginseng accessions.

| Source                  | df | SS    | MS    | Est. Var. | %   | PhiPT       | Nm    |
|------------------------|----|-------|-------|-----------|-----|-------------|-------|
| Collection area of total ginseng accessions |    |       |       |           |     |             |       |
| Among Pops             | 5  | 236.102 | 47.220 | 0.487     | 3%  | 0.028       | 17.213 |
| Within Pops            | 445| 7466.739 | 16.779 | 16.779    | 97% | (p < 0.001) |       |
| Total                  | 450| 7702.840 | 17.267 | 100%      |     |             |       |
| STRUCTURE of total ginseng accessions |    |       |       |           |     |             |       |
| Among Pops             | 6  | 305.185 | 50.864 | 0.54      | 3%  | 0.031       | 15.431 |
| Within Pops            | 444| 7397.655 | 16.661 | 16.661    | 97% | (p < 0.001) |       |
| Total                  | 450| 7702.84  | 17.201 | 100%      |     |             |       |
| STRUCTURE of ginseng landraces |    |       |       |           |     |             |       |
| Among Pops             | 11 | 385.070 | 35.006 | 0.578     | 3%  | 0.034       | 14.322 |
| Within Pops            | 378| 6255.419 | 16.549 | 16.549    | 97% | (p < 0.001) |       |
| Total                  | 389| 6640.490 | 17.126 | 100%      |     |             |       |
| STRUCTURE of ginseng breeding lines |    |       |       |           |     |             |       |
| Among Pops             | 1  | 19.859  | 19.859 | 0.178     | 1%  | 0.012       | 40.761 |
| Within Pops            | 59 | 854.239 | 14.479 | 14.479    | 99% | (p < 0.028) |       |
| Total                  | 60 | 874.098 | 14.656 | 100%      |     |             |       |

1 df, degree of freedom; SS, sum of squares; MS, mean squares; Est.Var, estimates of variance; %, percent of variance, PhiPT, genetic differentiation; Nm, gene flow.

In the ginseng landrace AMOVA findings, 97% of the total genetic variation was contributed by differences within populations (Table 2). PhiPT and Nm for the 390 landraces were 0.034 (p < 0.0001) and 14.322, respectively, and the Pairwise population PhiPT for four clusters ranged from −0.097 (L1–L6) to 0.084 (L7–L11) (Table S7). Pairwise population estimates of Nm for the four clusters ranged from 5.455 (L7–L11) to 403.3 (L1–L5) migrants per cluster.

In ginseng breeding lines, AMOVA revealed that 99% of the total genetic variation was attributable to within- rather than across-population differences (Table 2). PhiPT and Nm for 61 ginseng breeding lines were 0.012 (p < 0.0001) and 40.761, respectively.

4. Discussion

4.1. Distribution of Korean Ginseng Accessions

The collection areas for the ginseng accessions used in this study were mainly distributed in northern and central Korea. In South Korea, the ginseng cultivation area is from 36° to 38° N [14]. According to the 15th-century Korean history book Sejong Silokjiriji, Korean ginseng is native to all of Korea except Jeju Island. In the Joseon Dynasty, agriculturalists began cultivating ginseng in areas where native ginseng was found and gradually expanded cultivation throughout the country. However, based on differences in quality, ginseng is cultivated mainly in CN, CB, and GG [13]. The collection for the 390 ginseng landraces used in this study were distributed across six provinces (Figure 1 and Table S3); among them, the main areas were CN (36.4%), GW (31.8%), and GG (17.9%).

At the NAC, the seeds of plant germplasm are generally collected from farmers in the main cultivation areas of the target crops, except wild relatives. CN and GG are main ginseng production areas in the south, centered around Daejeon (CN), and in the north, the major area, bounded by the demilitarized zone and the two coasts (GG) [14]. GW is a mountainous region and is famous for mountain cultivated ginseng, while ginseng in GG and GN is cultivated in the field using shading systems [25–39]. Three provinces accounted for 40.3% of all ginseng production in South Korea in 2018 [40]. In traditional agriculture, farmers create and conserve new varieties, the preponderance of which are landraces. They decide which materials to conserve or discard, and they recycle seed on their farms, which are very often quite small. Such systems are highly dynamic in terms of genetic content and adaptation of the landraces [41].
4.2. Genetic Differentiation of Korean Ginseng Accessions

Although all of the ginseng accessions could be clustered into one of seven populations using STRUCTURE software, the accession clustering did not show clear separation according to geographic origin (Figure 2). In addition, AMOVA showed low genetic differentiation (PhiPT) and gene flow (Nm) between collection area (PhiPT = 0.028, Nm = 17.213) and STRUCTURE group (PhiPT = 0.031, Nm = 15.431) (Table 2). The ginseng landraces also showed low PhiPT (0.034) and high Nm (14.322), although STRUCTURE divided them into 12 groups.

Ginseng seed and seedlings necessarily originate from wild ginseng [42], and wild ginseng, which is rare, has been increasingly endangered because of high demand [43]. Natural populations of rare and threatened species are typically small and geographically isolated [44], and the growth and persistence of small populations are highly influenced by stochastic events such as genetic drift and inbreeding; such events result in reduced genetic diversity and fitness [45,46]. Karron [47,48] reported that some species with restricted distributions showed less genetic diversity than congeneric species with widespread distributions, but Cole [49] observed that it is not clear that rare plant species will necessarily have less gene flow than common species. Ellstrand [44] summarized arguments for expecting that gene flow might increase in rare plant populations, resulting in less differentiation.

In Korea, farmers have been cultivating, self-seed gathering, and seed-selling the ginseng shoots themselves [50,51], and it seems that this method of ginseng cultivation is responsible for the low PhiPT and Nm in the Korean ginseng landraces at NAC. Cultivated ginseng seeds obtained from a few wild ginsengs are amplified and self-seed gathered by local farmers, and then they are sold on the ginseng market. As this cycle repeated over time, ginseng seeds of the same genetic background would have spread to other regions; it is assumed that this is the reason the ginseng landraces collected from different regions showed low PhiPT and high Nm.

The ginseng breeding lines also showed low PhiPT (0.012) and high Nm (40.761), although STRUCTURE divided the breeding lines into only two groups. Interestingly, both groups included two ginseng varieties—gumpoong and chunpoong. The two varieties, which were registered in 2002 (cv. Chunpoong) and 2003 (cv. Gumpoong), were bred by selecting individual plants from Korean landraces [11]. In Korea, 27 ginseng varieties have been registered with the Korea Seed & Variety Service, and all were bred by selecting individual plants from landraces [52]. In general, selecting individual plants is more common for developing new ginseng varieties than is crossbreeding because of the long generation period and small number of seeds with plant selection [11–53]. However, these varieties were selected for their excellent root form, but their genetic background has been little analyzed [11]. Meanwhile, the low genetic diversity in ginseng breeding lines might be because plants have been selected for morphological traits only; because morphological traits are easily affected by environmental conditions [54], their gene profiles could be similar in spite of their different phenotypes.

4.3. Increasing the Genetic Diversity of the NAC’s Ginseng Germplasm

As mentioned above, the population of Korean ginseng landraces is expected to be very small, and it has been reported that small populations increase genetic drift and inbreeding [26], which could in turn influence these small populations by changing patterns of genetic diversity. One concerning drift-induced genetic change is this erosion of genetic variation; loss of genetic variation may decrease the potential for a species to persist in the face of abiotic and biotic environmental change [55,56]. The primary solution to the genetic impoverishment of crop germplasm is genetic conservation and utilization in breeding the vast genetic variation found in populations of the wild progenitors and landraces of cultivated plants [3]. However, it is very difficult to collect wild ginseng because it is such a rare plant. To overcome the shortage of genetic diversity in ginseng, researchers in Korea have attempted crossing interspecies, tissue culture, and mutation breeding [11]. Ahn et al. [57] and Kim et al. [58] attempted to cross P. ginseng and P. quinquefolius, but they did not get seeds from F2 plants. Kim et al. [56] studied the tissue culture of F1 plant propagation in a ginseng hybrid (P. ginseng × P. quinquefolius) to solve the seedless problem. In addition, some research groups have attempted
mutation breeding using irradiation or chemicals, but they did not develop new ginseng varieties; they did confirm plants with high ginsenosides [59–63].

Bang et al. [11] highlighted the need to develop new varieties that are strong against abnormal weather conditions and reflect different trends. To develop such new varieties, NAC should attempt to secure the genetic diversity of ginseng. Collecting and securing P. ginseng and related species will be required for increasing the diversity, and the effort will also require collaboration with other ginseng research institutes to establish effective breeding methods.

Supplementary Materials: The following are available online at http://www.mdpi.com/2073-4395/10/11/1643/s1; Table S1. List of 451 ginseng accessions in this study; Table S2. List of 33 SSR markers in this study; Table S3. Distribution of collected areas in 451 ginseng accessions; Table S4. Genetic diversity parameters of 33 SSR markers; Table S5. Pairwise population PhiPT values (above diagonal) and Nm values based on 999 permutations (below diagonal) from AMOVA using collection area. All PhiPT values were significantly greater than 0 (p < 0.0001); Table S6. Pairwise population PhiPT values (above diagonal) and Nm values based on 999 permutations (below diagonal) from AMOVA using STRUCTURE result of 451 ginseng accessions. All PhiPT values were significantly greater than 0 (p < 0.0001); Table S7. Pairwise population PhiPT values (above diagonal) and Nm values based on 999 permutations (below diagonal) from AMOVA using STRUCTURE result of 39 ginseng landraces. All PhiPT values were significantly greater than 0 (p < 0.0001).

Author Contributions: Conceptualization, K.J.L. and D.Y.H.; data curation, K.J.L. and D.Y.H.; formal analysis, K.J.L. and R.S.; resources, M.K.; investigation, S.-H.K., E.Y., and S.L.; writing—original draft, K.J.L.; writing—review and editing, D.Y.H.; funding acquisition, G.-T.C. All authors have read and agreed to the published version of the manuscript.

Funding: This research was funded by the [Research Program for Agricultural Science and Technology Development, National Institute of Agricultural Sciences, Rural Development Administration, Republic of Korea], grant number [PJ01355701].

Conflicts of Interest: The authors declare no conflict of interest.

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