Cluster Analysis and Dendrogram Mapping of 51 Silkworm Varieties based on Phenotypic Data

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Abstract: In different breeding programs, knowledge of inbreeding and genotype similarities and differences of various varieties is necessary. In many breeding projects, hybridization planning and in different crosses, there is a need to exist varieties with far and close genetic characteristics to each other. Based on this, it is necessary to identify the similarities between various breed. This experiment aiming to sort Japanese varieties group of Iran silkworm gene bank and to investigate genetic relationships between them based on individual economic characteristics was designed and planned. Data of the mentioned traits had been recorded based on performance tests. In order to group lines based on several important economic traits, Cluster analysis with UPGMA method performed on the studied genotypes using Ntsys-pc software. For each of concerned economic traits, the matrix analogous indicates Japanese varieties distance to each other had been determined and according this phylogenic diagram of this varieties that expressing near or far different varieties of Iran Japanese silkworm based on individual economic traits was drawn. According to the results from this research, the studied varieties can locate in different groups, accurately, and express their distance to each other.
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1. Introduction

Silkworm is an insect that is important in economic point of view in the world. Farmers are attempting to produce wet cocoon and also increasingly some of them are working in the complementary sectors of silkworm such as drying silk cocoons, silk dyeing, silk weaving, design and texture of silk carpets, traditional silk production, trade carpets, etc. are active.

In recent years, carrying various research projects the phenotypic potential of Iranian Silkworm genetic resources recognized and has been recorded, scientifically. But considering the vast number of genetic stocks is still not an experiment for grouping varieties to individual economic traits separately and attribute this variety to each economic. Genetic relationships between varieties can be identified by exploring characters. Revealing these relationships, the field for such a breeding projects such as appropriate cross and selection is provides.

Cluster analysis is to encompass a set of mathematical methods to find the similarities between the materials used in a set. The goal of cluster analysis is to find the real categories of people and also to reduce the number of data. Also, after the grouping by cluster analysis, the question is whether a group can separate into sub-groups having significant difference (Frshadfar, 2005).

The main goal of silkworm breeding is gradual improvement of traits which have economic value for animal interests, and increase profits of cocoon producers and other sectors of silkworm industry (Mirhosseini et al, 2005; Sing et al, 1998). Commercial varieties of silkworm in a limited population sizes had been grown and put under breeding programs and high selective pressures. After several generations so that their genetic structure in a result of increased random genetic drift is subject to change. Revealing these relationships, the field for performing breeding projects such as designing appropriate crosses and selection is provides.

Among the animal species, genetic diversity is often a dramatic range among many generations and species. Races are defined as populations within a species whose members can be determine by a series of characteristics about that the race. Although there are many varied definitions, the definition by FAO expressed that in the phenotype of traits, there is a clear boundary between the populations. It may be true in Europe where separating two types of same generations is a specific process that was common by providing cattle husbandry books about two hundred years ago. In other regions such as Africa, a specific

definition of the same generations is not always possible and this depends on the mixing of race between populations. Determine the type of animals for the same generations in these areas can be objective and questionable.

Phylogenic trees are graphical symbols or designs of the matrix of the distance between populations. As we discovered, trees are not phylogenic trees, because the difference in effective population size and migration between species may be diverted this image. However, there are different methods for drawing distance matrix trees. Nei (1983) discussed and compared different ways. Most known methods, are UPGMA and NJ (Takazaky and Nei, 1996) that generally have been associated with good results.

In cross systems it is trying to provide desired gene bank for future generations selecting the concerned parents and through the actions of different cross systems, this bank will be brought to the desired level. Currently, the most common methods in breeding is doing in silkworm research and breeding section that ultimately will lead to the synthesis of new lines. About selection systems in the world now, continuous methods, eliminating the independent level and the index is considered which based on this parents choose in proper, accurate and consistent and leads to improve quality and quantity of various performance in breeding processes, in a way that today parameters such as the genetic variance and covariance, correlation coefficient, and heritability and finally economic coefficient traits are helping (Kalpana, 1992; Li, 1996).

In the study conducted by Mirhosseini et al (2005) dendrogram obtained from cluster analysis of silkworm groups based on morphological traits of samples were divided into two groups of indigenous varieties and imported varieties and also each of Chinese and Japanese varieties were located in the two groups related to their. In differentiation in Chinese and Japanese races, mainly morphological traits such as cocoon shape, color eggs, the larval period was considered. In reviews conducted by Balvasi (2003) to compare two groups of Chinese and Japanese varieties different results was obtained. Varieties 32 and 107 in one group, as well as varieties 110 and varieties 31 and 103 in other groups were located and varieties 104 formed a separate group. In the study conducted by Alitalesh (2007) using ten AFLP primer for 90 individuals a total of 208 polymorphism indicator were produced. Results related to the number of positions polymorphism gene variation, the average percentage of polymorphism, the percentage of genetic similarity inter-variety, and the average effective number of alleles was present. But the study by Dalirsefat and Mirhoseini (1998) using AFLP markers on the indigenous masses, the masses of indigenous native had more inter diversity, while the distance between varieties were small. However, the distances between imported varieties were many. There is little genetic diversity in this research into the varieties. Because these varieties are used to generate hybrid, so their in-group diversity should be reduced a lot.

This experiment aimed at classification the Japanese group varieties of silkworm gene bank of Iran and relations between them based on individual genetic traits were designed and planned. Informed of the potential and relative relationship of genetic reserves of silkworm play an important role in the development of silkworm breeding programs is to improve their performance. The purpose of this study was classification of 51 varieties of Japanese silkworm gene bank of Iran based on the silkworm phenotypic data available in the country Silkworm Research Center. This information may consider as the basis of scientific recognition of existing varieties and design future breeding programs.

2. Material and Methods

It is used 51 varieties of Iran silkworm germplasm in this experiment. Fifty one studied varieties included 107-K, 119-K, 113-K, 105, 31, 51, 103, BH-2, B2-09, 1003-4, 1003-5, 1005, M2-6-22-2, M2-6-18(109), M-1-2(5), M2-6-22(107), M2-6-18.3, 307-300-2, 202A-204B, I 20, 101433-9-5, 101433-1-4, 101433-6-6, 1126 (111), 113 (2029), 151 (103×M-1-1), Xihang 2.3, Xihang 3.3, 153 (Xihang-1), 5118×10133-2-2, 5118×10133-3-3, Black-White, 101×F6, F6×101, Kinshu, M-1-1×31, 31×M-1-1, M-1-1×103, 103 Poly Marking, Shaki, 101, T1-J, T5-M, 236, 1524, 1433-15, 1433-9, 7409, N19, White Larvae- Yellow Cocoon, and Black Larvae-White Cocoon.

Also, fifty three studied economical traits included larval weight at 1 day of 5th instar (g), larval weight at 3rd day of 5th instar (g) and larval weight at last day of 5th instar (g), hatchability percentage (%), number of laid eggs, number of fertilized eggs, number of un-fertilized eggs, and number of un-hatched eggs. Larval duration (hr), feeding larval duration (hr), molting larval duration (hr), 1-3 instars larval duration (hr), 1-3 instars feeding larval duration (hr), 1-3 instars molting larval duration (hr), 4-5th instars larval duration (hr), 4-5th instars feeding larval duration (hr), 4-5th instars molting larval duration (hr), 5th instar feeding larval duration (hr), number of total produced cocoons, number of good produced cocoons, number of alive good produced cocoons, number of died good produced cocoons, number of middle produced cocoons, number of alive middle produced cocoons,

number of fertilized cocoons, number of low produced cocoons, number of alive low produced cocoons, number of double produced cocoons, number of alive pupae in double cocoons, number of died pupae in double cocoons, pupae vitality percentage (%), cocoon weight (gr), shell cocoon weight (gr), shell cocoon percentage (%), male cocoon weight (gr), male shell cocoon weight (gr), male shell cocoon percentage (%), female cocoon weight (gr), female shell cocoon weight (gr), female shell cocoon percentage (%), good cocoon weight of 250 larvae (gr), middle cocoon weight of 250 larvae (gr), middle cocoon weight (gr), low cocoon weight of 250 larvae (gr), low cocoon weight (gr), double cocoon weight of 250 larvae (gr), double cocoon weight (gr), total cocoon weight of 250 larvae (gr), total cocoon weight of 10000 4th instar larvae (gr), cocoon number per liter, cocoon weight per liter (gr), pupae weight (gr) and male pupae weight (gr).

Data were collected based on three replications for each variety. It is calculated mean of three replications for each variety using Excel. Meanwhile data was processed using NTSYSpc software (Rolf, 1998) based on economical traits in order to cluster analysis and dendrogram plotting.

3. Results

The cluster analysis and grouping

To perform cluster analysis and grouping Japanese varieties based on 56 economic traits the method of analysis based of UPGMA cumulative was used. Individuals who are in one group, favor more in-group similarity and less out-group similarity. Therefore, about inbreeding and outbreeding of individual and choice of appropriate and parents together for cross in order to obtain high heterosis, made more accurate and safer decisions. Because the distance of genotypes is greater, in the separated generations, making hybridization will create more diversity and offspring that are more desirable will provide and the possibility of collecting more desirable genes in progeny increases. In general, progenies from genotypes cross which are located in two distinct group will develop more heterosis than genotypes in one group.

Grouping with the UPGMA method by the NTSYSpc software

In this study, NTSYSpc software (Ralph, 1998) was used to grouping 51 varieties. Its benefits were the ability of grouping with various methods with different distance measures.

Larval weight at 1 day of 5th instar

Phylogenic tree using the UPGMA method was formed for attribute larval weight at 1 day of 5th instar instars. In cross section 1.83 phylogenic tree was divided into two main clusters. Main clusters contain a number of varieties (1, 39, 40, 49, 48, 3, 51, 14, 35, 27, 38 and 50) and other varieties were located at the other major clusters. Another major cluster subdivided into two smaller clusters. The first cluster contains varieties 2, 11, 18, 4, 20, 32 and the second cluster contain the other varieties.

Larval weight at 3rd day of 5th instar

Grouping was performed according to age, of larval weight at 3rd day of 5th instar UPGMA method separately with the above method. This test showed that in cutting 4.11 varieties were divided into two clusters. In a single cluster only variety (24) was used. Other varieties were placed in other clusters. In cutting 1.7, varieties subdivided into two smaller clusters. One cluster contains varieties 2, 8, 19, 9, 24 and 29 and another cluster was containing other varieties.

Larval weight at last day of 5th instar

Grouping using the UPGMA method was performed for attribute larval weight at last day of 5th instar between Japanese varieties of silkworm gene bank. In cutting 2.89, varieties were divided into two main clusters. The first cluster contains varieties 28, 41, 10, 51 and 39. The second cluster contained the other varieties. A variety interval in the second major cluster was relatively low (about 0.72). Also this cluster was divided into two smaller clusters.

Hatchability percentage

By grouping with varieties of silkworm gene bank of Iran in Hatchability percentage, it became clear that varieties (28, 41, 10, 51 and 39) were located in a major cluster. Another major cluster in cutting about 0.8 was divided into two smaller clusters. One of the two clusters containing varieties (1, 24, 8, 31, 36, 30, 40, 38.7, 49 and 50) and another cluster containing the other varieties.

Number of laid eggs

Grouping with the UPGMA method for attribute number of laid eggs was performed between Japanese varieties of silkworm gene bank. In cutting 2.86, varieties were divided into two main clusters. The first cluster contains variety 14. Between 1.55 distances second cluster was divided into two clusters. A variety interval in the second major cluster was relatively low. Also this cluster was divided into smaller clusters.

Number of fertilized eggs

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of number of fertilized eggs in cutting (Euclid distance) 1.73 two main clusters was formed. One of these clusters in cutting 1.35 was divided into two smaller clusters. A cluster was consists of varieties (14, 44 and 49) and another including 16 varieties. In cutting 1.07 the tree divided into two smaller cluster

contain varieties (25, 28 and 51) on one side and other varieties on the other hand.

Number of un-fertilized eggs

Result from grouping varieties of Japanese silkworm of Iran gene bank showed that for the number of un-fertilized eggs in cutting 2.14 two main clusters were formed. One cluster contains varieties 3, 48, 49, 39, 8, 46, 31, 38, 10 and 29. Another cluster was divided into two main clusters, and so into smaller clusters that contain more varieties.

Number of un-hatched eggs

Phylogenic tree using the UPGMA method was formed for the number of un-hatched eggs. In cutting 2.60 phylogenic tree was divided into two main clusters. Main clusters contain a number of varieties (28, 41, 10, 39 and 51) and other varieties were the other major clusters. Other major clusters in cutting 1 were divided into two smaller clusters. These clusters are also were divided into clusters with several different intervals.

Larval duration

Analysis of silkworm strains for larval duration performed under UPGMA approach. Cluster divided varieties into tow sub-group in distance of 2.8. One of clusters was including variety of 41. Other varieties were in second main cluster. Varieties divided into tow sub-group in distance of 2. First group was including (2, 8, 43, 28, 24, 50, 26, 48, 7 and 3) varieties and another cluster were including remained varieties.

Feeding larval duration

Hierarchical agglomerative clustering preformed based on UPGMA method for trait of feeding larval duration. The variety of number 1 located in distance of 9.99 from others. One of main clusters divided into four sub-groups. One of clusters was including variety of 10.

Molting larval duration

Analysis of silkworm strains for molting larval duration performed under UPGMA approach separately. Varieties divided into tow sub-group In distance of 5.75. Other varieties were in tow main clusters. Fewer clusters were including varieties of 47 and 49.

1-3 instars larval duration

Hierarchical agglomerative clustering preformed based on UPGMA method for 1-3 instars larval duration. In distance of 3.46 the phylogenic tree was divided into tow main clusters. In a single cluster only variety (40) was used. Other varieties were placed in other clusters. Another major cluster subdivided into two smaller clusters in distance of 1.73.

1-3 instars feeding larval duration

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of 1-3 instars feeding larval duration in cutting (Euclid distance) 1.90 two main clusters was formed. A cluster was consists of varieties (1, 3, 16, 18, 20, 51, 8, 28, 15, 19 and 49) and another including another varieties. One of these clusters in cutting 1.3 was divided into two smaller clusters. These clusters are also were divided into clusters with several different intervals.

1-3 instars molting larval duration

Result from grouping varieties of Japanese silkworm of Iran gene bank showed that for the 1-3 instars molting larval duration in cutting 5.02 two main clusters were formed. One cluster contains variety of 49. Another cluster was divided into two main clusters including variety of 1 and another cluster that contain more varieties.

4-5th instars larval duration

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of 4-5th instars larval durationin cutting (Euclid distance) 3.17 two main clusters was formed. One of these clusters was consists of variety of 3 and another cluster that contain more varieties. In cutting 1.58 the tree divided into two smaller clusters contain varieties. These clusters are also were divided into clusters with several different intervals.

4-5th instars feeding larval duration

Phylogenic tree using the UPGMA method was formed for attribute 4-5th instars feeding larval duration. In cross section 2.55 phylogenic tree was divided into two main clusters. One of these clusters was consists of varieties (47 and 49) and other varieties were located at the other major cluster. in distance of 1.6 Another major cluster subdivided into two smaller clusters. The first cluster contains varieties 2, 40, 8, 50, 28, 26, 48, 30, 44 and 3 and the second cluster contains the other varieties.

4-5th instars molting larval duration

Phylogenic tree using the UPGMA method was formed for attribute 4-5th instars molting larval duration. In cross section 2.45 phylogenic tree was divided into two main clusters. Main clusters contain a number of varieties (12, 41 and 51) and other varieties were located at the other major clusters. Another major cluster subdivided into two smaller clusters. These clusters are also were divided into clusters with several different intervals.

5th instar feeding larval duration

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of 5th instar feeding larval duration cutting (Euclid distance) 2.55 two main clusters was formed. One of these clusters was consists of varieties of 3,

50 and 26 and another cluster that contain more varieties. In cutting 1.65 the tree divided into two smaller clusters contain varieties. The first cluster contains varieties 9, 16, 21,15, 42, 45, 24, 3, 49, 50 and 26 and the second cluster contain the other varieties.

Number of total produced cocoons

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of number of total produced cocoons (Euclid distance) 1.4 two main clusters was formed. One of these clusters was consists of variety of 38 and another cluster that contain more varieties

Number of good produced cocoons

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of number of good produced cocoons (Euclid distance) 2.68 two main clusters was formed. One of these clusters was consists of variety of 38 and another cluster that contain more varieties.

Number of alive middle produced cocoons

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of number of alive middle produced cocoons cutting (Euclid distance) 1.72 two main clusters was formed. One of these clusters was consists of varieties of 8, 46, 25, 29 and 38 and another cluster that contain more varieties.

Number of alive good produced cocoons

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of number of alive good produced cocoons cutting (Euclid distance) 1.72 two main clusters was formed. One of these clusters was consists of varieties of 10, 12 and 29 and another cluster that contains varieties 8, 46, 25, 29 and 38 and the second cluster contain the other varieties.

Number of died good produced cocoons

Phylogenic tree using the UPGMA method was formed for attribute number of died good produced cocoons. In cross section 2.62 phylogenic trees was divided into two main clusters. Main clusters contain a number of varieties (10, 11, 12, 30 and 42) and other varieties were located at the other major clusters. In distance of 1.1. Other major cluster subdivided into two smaller clusters.

Number of middle produced cocoons

Phylogenic tree using the UPGMA method was formed for number of middle produced cocoons. In cross section 2.82 phylogenic tree was divided into two main clusters. Main clusters contain a number of varieties (2, 6 and 9) and other varieties were located at the other major clusters with close distances.

Number of alive middle produced cocoons

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of number of alive middle produced cocoons cutting (Euclid distance) 3.75 two main clusters was formed. One of these clusters was consists of variety of 2 and another cluster In cross section 1.5 phylogenic tree was divided into two main clusters.

Number of fertilized cocoons

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of number of fertilized cocoons cutting (Euclid distance) 3.47 two main clusters was formed. One of these clusters was consists of variety of 6 and another cluster In cross section 1.6 phylogenic tree was divided into two main clusters.

Number of low produced cocoons

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of number of low produced cocoons cutting (Euclid distance) 4.51 two main clusters was formed. One of these clusters was consists of variety of 30 and another cluster In cross section 1.3 phylogenic tree was divided into two main clusters.

Number of alive low produced cocoons

Grouping using the UPGMA method was performed for number of alive low produced cocoons between Japanese varieties of silkworm gene bank. In cutting 4.53, varieties were divided into two main clusters. The first cluster contains variety (30). another cluster In cross section 1.3 phylogenic tree was divided into two main clusters.

Number of double produced cocoons

Phylogenic tree using the UPGMA method was formed for number of double produced cocoons. In cross section 2.24 phylogenic tree was divided into two main clusters. Main clusters contain a number of varieties (40, 14, 40, 26, 39, 50 and 48) and other varieties were located at the other major cluster. Another cluster In cross section 0.85 phylogenic tree was divided into two main clusters.

Number of alive pupae in double cocoons

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of number of alive pupae in double cocoons cutting (Euclid distance) 2.25 two main clusters was formed. Main clusters contain a number of varieties (8, 9, 14, 12, 50, 26, 39, 40 and 48) and another cluster In cross section 0.9 phylogenic tree was divided into two less clusters. Other varieties were located at the other major clusters with close distances.

Number of died pupae in double cocoons

Phylogenic tree using the UPGMA method was formed for number of died pupae in double cocoons. In cross section 3.31 phylogenic tree was divided into two main clusters. Main clusters contained tow varieties (3 and 14) and other varieties were located at the other major cluster. Another

cluster in cross section 0.85 phylogenic tree was divided into two main clusters.

Pupae vitality percentage

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of pupae vitality percentage divided to two main clusters. Main clusters contain a number of varieties (10, 30, 42, 11, 45 and 12). Another cluster In cross section 1.19 phylogenic tree was divided into two less clusters. Other varieties were located at the other major clusters with close distances.

Cocoon weight

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of cocoon weight in cross section 7.11 divided to two main clusters. The first cluster contains variety (13). Other varieties were located at the other major clusters with close distances.

Shell cocoon weight

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait shell cocoon weight represented a single main cluster. It represents close genetic distances between varieties for this trait.

Shell cocoon percentage

Phylogenic tree using the UPGMA method was formed for shell cocoon percentage. In cross section 3.28 phylogenic tree was divided into two main clusters. Main clusters contain tow varieties (19 and 20) and other varieties were located at the other major cluster.

Male cocoon weight

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of male cocoon weight in cross section 7.14 divided to two main clusters. The first cluster contains variety (8). Other varieties were located at the other major clusters with close distances.

Male shell cocoon weight

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of male shell cocoon weight cutting (Euclid distance) 1.1 two main clusters was formed. One of these clusters was consists of varieties (3,40,19,7,34,18,39,20,31,50,38 and 48) and another cluster was divided into two main clusters.

Male shell cocoon percentage

Phylogenic tree using the UPGMA method was formed for male shell cocoon percentage. In cross section 2.24 phylogenic tree was divided into two main clusters. One of these clusters was consists of varieties (8, 9, 40, 12, 14, 26, 50, 29 and 48) and other varieties were located at the other major cluster.

Female cocoon weight

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of female cocoon weight cutting (Euclid distance) 7.07 two main clusters was formed. One of these clusters was consists of variety of 42 and another cluster was divided into two main clusters.

Female shell cocoon weight

Phylogenic tree using the UPGMA method was formed for female shell cocoon weight. In cross section 5.30 phylogenic tree was divided into two main clusters. One of these clusters was consists of variety of 18 and other varieties including varieties 18, 19, 24, 15, 29 and 11 were located at the other major cluster.

Female shell cocoon percentage

Hierarchical agglomerative clustering preformed based on UPGMA method for trait of female shell cocoon percentage. The variety of 19 was separated from others. One of main clusters divided into tow sub-group including varieties 2, 40, 18, 50, 42 and 20 and other varieties.

Good cocoon weight of 250 larvae

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of good cocoon weight of 250 larvae cutting (Euclid distance) 2.39 two main clusters was formed. One of these clusters was consists of varieties of 48 and 39 and another cluster was divided into a number main clusters.

Middle cocoon weight of 250 larvae

Phylogenic tree using the UPGMA method was formed for middle cocoon weight of 250 larvae. In cross section 4.30 phylogenic tree was divided into two main clusters. One of these clusters was consists of variety of 2 and other varieties were including other varieties. In cross section 2.14 phylogenic tree was divided into two less clusters including (2 and 8) and other major cluster.

Middle cocoon weight

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of middle cocoon weight cutting (Euclid distance) 1.70 two main clusters was formed. One of these clusters was consists of 18 varieties and another cluster was divided into a number main clusters.

Low cocoon weight of 250 larvae

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of low cocoon weight of 250 larvae cutting (Euclid distance) 5.01 two main clusters was formed. One of these clusters was consists of variety of 30 and another cluster was divided into tow less clusters.

Low cocoon weight

Phylogenic tree using the UPGMA method was formed for low cocoon weight. In cross section 2.98 phylogenic trees was divided into two main clusters. One of these clusters was consists of

varieties of 4, 5, 10, 16, 8, 11, 13, 22, 39, 24 and 47 and other clusters were including other varieties.

Double cocoon weight of 250 larvae

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of double cocoon weight of 250 larvae cutting (Euclid distance) 2.24 two main clusters was formed. One of these clusters was consists of varieties of 8, 9, 14, 50, 12, 26, 40, 39, 24 and 49. Other clusters were including other varieties.

Double cocoon weight

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of double cocoon weight cutting (Euclid distance) 2.31 two main clusters was formed. One of these clusters was consists of varieties of 30, 34, 41, 35, 41, 35, 42, 46, and 43. Other clusters were including other varieties.

Total cocoon weight of 250 larvae

Phylogenic tree using the UPGMA method was formed for total cocoon weight of 250 larvae. In cross section 1.98 phylogenic trees was divided into two main clusters. One of these clusters was consists of varieties of 1, 48, 39, 3, 51, 33, 41 and 35 and other clusters were including other varieties.

Total cocoon weight of 10000 4th instar larvae

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of total cocoon weight of 10000 4th instar larvae cutting (Euclid distance) 1.81 two main clusters was formed. One of these clusters was consists of varieties of 8, 11, 24, 15, 19, 20, 26, 18, 32, 25 and 29. Other clusters were including other varieties.

Cocoon number per liter

Phylogenic tree using the UPGMA method was formed for Cocoon number per liter. In cross section 1.67 phylogenic trees was divided into two main clusters. One of these clusters was consists of varieties of 16, 44, 9, 16 and 6 and other clusters were including other varieties. One of these clusters was consists of varieties of 1, 7, 19, 18, 3, 49, 11, 21, 48, 33, 38 and 42.

Cocoon weight per liter

Analysis of silkworm strains for Cocoon weight per liter performed under UPGMA approach. Cluster divided varieties into tow sub-group in distance of 2.8. One of clusters was including varieties of 7 and 32. Varieties divided into tow sub-group in distance of 2. First group was including (2, 18, 19, 20 and 42) varieties and another cluster was including remained varieties.

Pupae weight

Phylogenic tree using the UPGMA method was formed for Cocoon number per liter. In cross section 2.24 phylogenic tree was divided into two main clusters. One of these clusters was consists of varieties of 2, 42, 19, 18 and 20 and other clusters were including other varieties. One of these clusters was consists of varieties of 1, 31, and 29.

Male pupae weight

The test results showed that in grouping the Japanese varieties of Iran silkworm gene bank with a trait of male pupae weight cutting (Euclid distance) 2.24 two main clusters was formed. One of these clusters was consists of varieties of 2, 48, 38, 12, 31, 19 and 29. Other clusters were including other varieties.

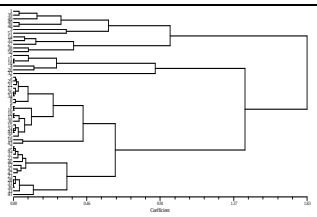

Figure 1- Cluster analysis of 51 studied silkworm varieties for included larval weight at 1 day of 5th instar

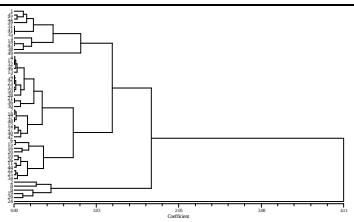

Figure 2- Cluster analysis of 51 studied silkworm varieties for larval weight at 3 th day of 5th instar

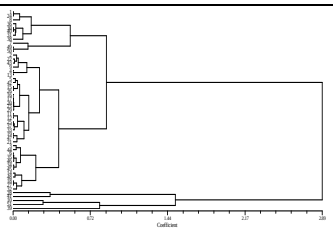

Figure 3- Cluster analysis of 51 studied silkworm varieties for and larval weight at last day of 5th instar

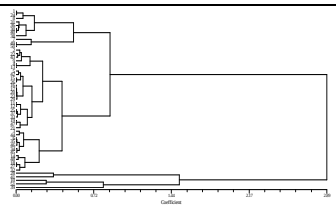

Figure 4- Cluster analysis of 51 studied silkworm varieties for Hatchability percentage

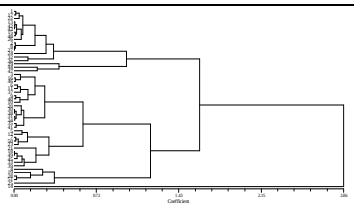

Figure 5- Cluster analysis of 51 studied silkworm varieties for number of laid eggs

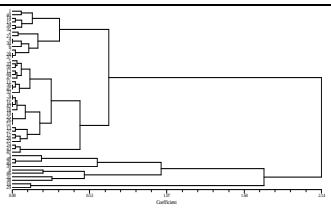

Figure 6- Cluster analysis of 51 studied silkworm varieties for number of fertilized eggs

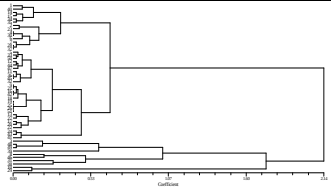

Figure 7- Cluster analysis of 51 studied silkworm varieties for number of un-fertilized eggs

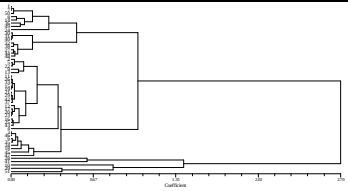

Figure 8- Cluster analysis of 51 studied silkworm varieties for number of un-hatched eggs

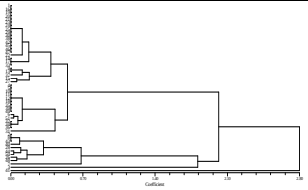

Figure 9- Cluster analysis of 51 studied silkworm varieties for larval duration

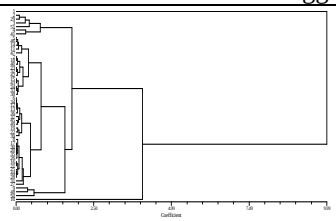

Figure 10- Cluster analysis of 51 studied silkworm varieties for feeding larval duration

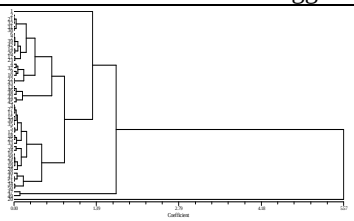

Figure 11- Cluster analysis of 51 studied silkworm varieties for molting larval duration

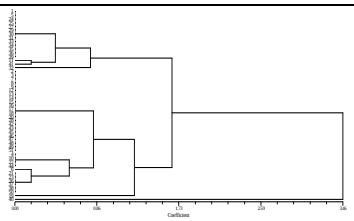

Figure 12- Cluster analysis of 51 studied silkworm varieties for1-3 instars larval duration

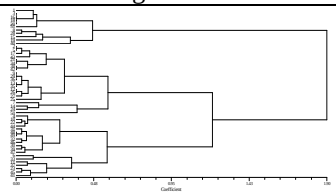

Figure 13- Cluster analysis of 51 studied silkworm varieties for1-3 instars feeding larval duration

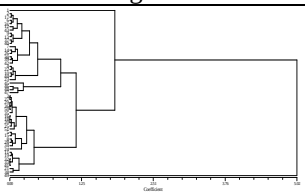

Figure 14- Cluster analysis of 51 studied silkworm varieties for1-3 instars molting larval duration

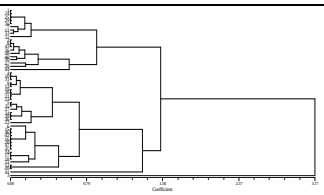

Figure15- Cluster analysis of 51 studied silkworm varieties for4-5th instars larval duration

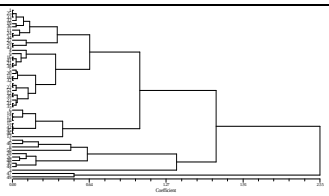

Figure 16- Cluster analysis of 51 studied silkworm varieties for 4-5th instars feeding larval duration

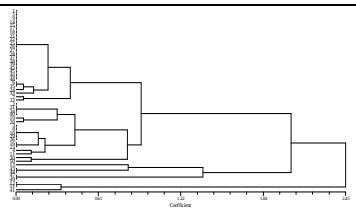

Figure 17- Cluster analysis of 51 studied silkworm varieties for 4-5th instars molting larval duration

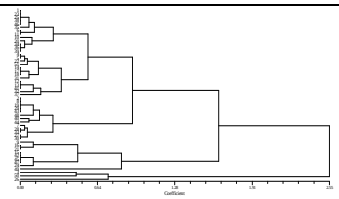

Figure 18- Cluster analysis of 51 studied silkworm varieties for5th instar feeding larval duration

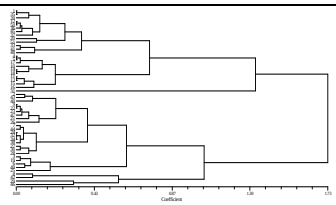

Figure 19- Cluster analysis of 51 studied silkworm varieties for number of total produced cocoons

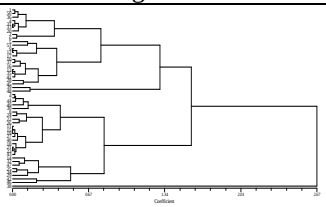

Figure 20- Cluster analysis of 51 studied silkworm varieties for number of good produced cocoons

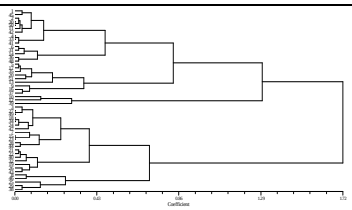

Figure 21- Cluster analysis of 51 studied silkworm varieties for number of alive good produced cocoons

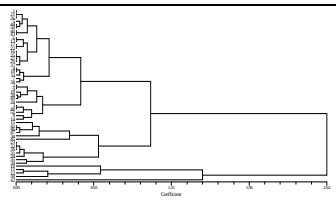

Figure 22- Cluster analysis of 51 studied silkworm varieties for number of alive good produced cocoons

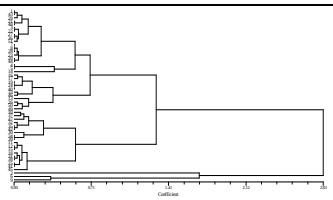

Figure 23- Cluster analysis of 51 studied silkworm varieties for number of died good produced cocoons

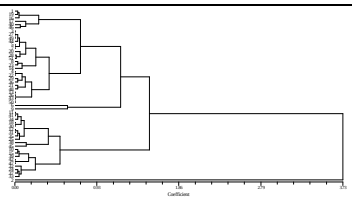

Figure 24- Cluster analysis of 51 studied silkworm varieties for, number of middle produced cocoons

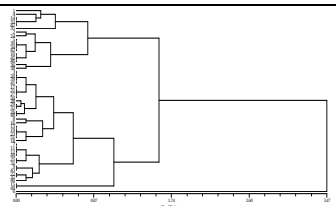

Figure 25- Cluster analysis of 51 studied silkworm varieties for, number of alive middle produced cocoons

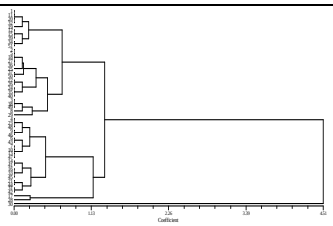

Figure 26- Cluster analysis of 51 studied silkworm varieties for number of died middle produced cocoons

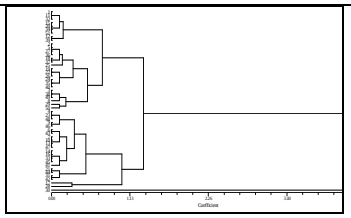

Figure 27- Cluster analysis of 51 studied silkworm varieties for number of low produced cocoons

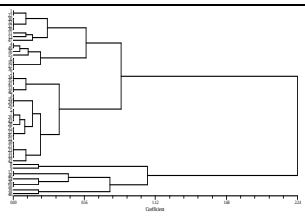

Figure 28- Cluster analysis of 51 studied silkworm varieties for number of double produced cocoons

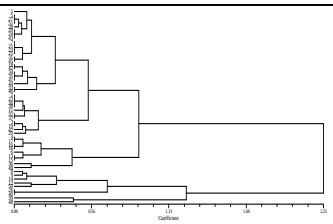

Figure 29- Cluster analysis of 51 studied silkworm varieties for number of alive pupae in double cocoons

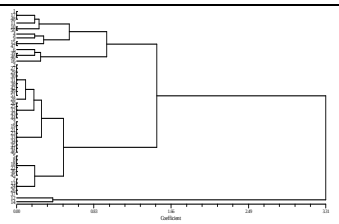

Figure 30- Cluster analysis of 51 studied silkworm varieties for number of died pupae in double cocoons

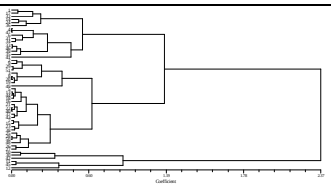

Figure 31- Cluster analysis of 51 studied silkworm varieties for number of died pupae in double cocoons

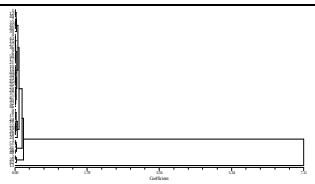

Figure 32- Cluster analysis of 51 studied silkworm varieties for male shell cocoon weight

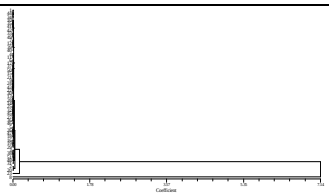

Figure 33- Cluster analysis of 51 studied silkworm varieties for male shell cocoon percentage

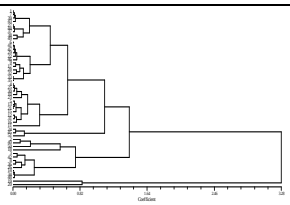

Figure 34- Cluster analysis of 51 studied silkworm varieties for female cocoon weight

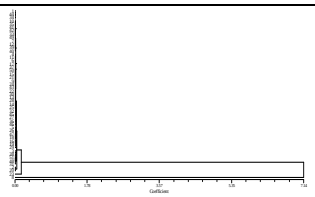

Figure 35- Cluster analysis of 51 studied silkworm varieties for female shell cocoon weight

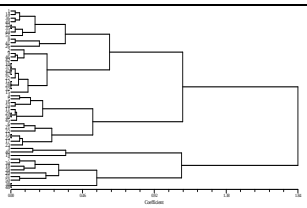

Figure 36- Cluster analysis of 51 studied silkworm varieties for female shell cocoon percentage

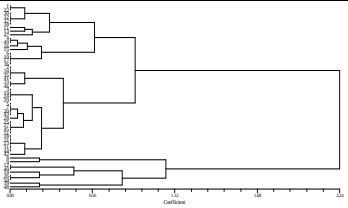

Figure 37- Cluster analysis of 51 studied silkworm varieties for cocoon weight of 250 larvae

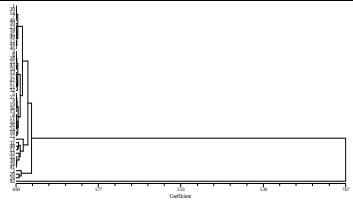

Figure 38- Cluster analysis of 51 studied silkworm varieties for middle cocoon weight of 250 larvae

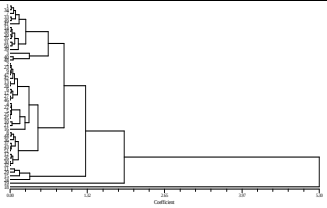

Figure 39- Cluster analysis of 51 studied silkworm varieties for middle cocoon weight

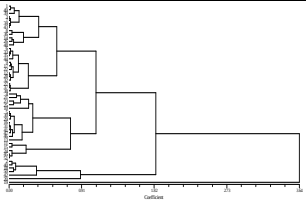

Figure 40- Cluster analysis of 51 studied silkworm varieties for low cocoon weight of 250 larvae

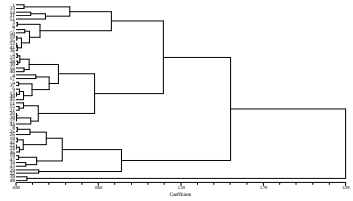

Figure 41- Cluster analysis of 51 studied silkworm varieties for low cocoon weight

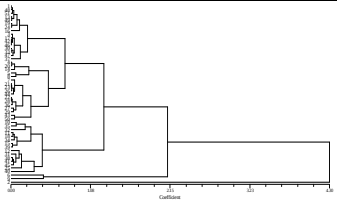

Figure 42- Cluster analysis of 51 studied silkworm varieties for double cocoon weight of 250 larvae

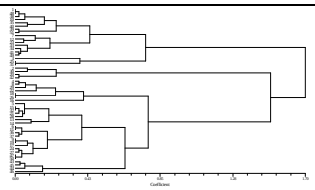

Figure 43- Cluster analysis of 51 studied silkworm varieties for double cocoon weight

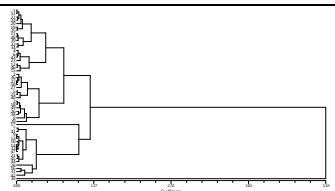

Figure 44- Cluster analysis of 51 studied silkworm varieties for total cocoon weight of 250 larvae

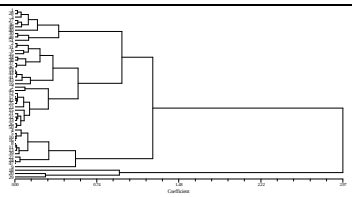

Figure 45- Cluster analysis of 51 studied silkworm varieties for total cocoon weight of 10000 4th instar larvae

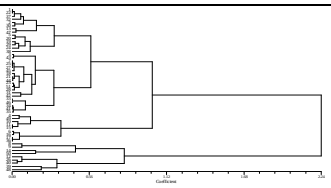

Figure 46- Cluster analysis of 51 studied silkworm varieties for low cocoon weight

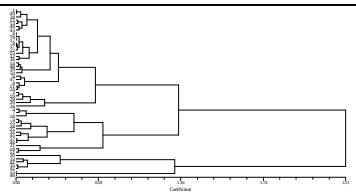

Figure 47- Cluster analysis of 51 studied silkworm varieties for double cocoon weight of 250 larvae

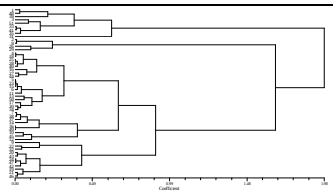

Figure 48- Cluster analysis of 51 studied silkworm varieties for double cocoon weight

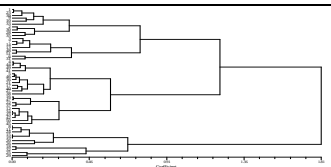

Figure 49- Cluster analysis of 51 studied silkworm varieties for total cocoon weight of 250 larvae

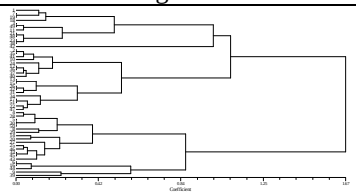

Figure 50- Cluster analysis of 51 studied silkworm varieties for total cocoon weight of 10000 4th instar larvae

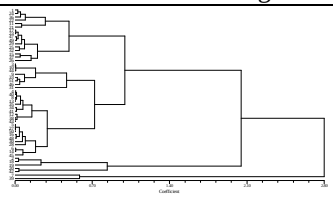

Figure 51- Cluster analysis of 51 studied silkworm varieties for cocoon number per liter

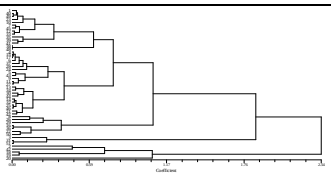

Figure 52- Cluster analysis of 51 studied silkworm varieties for cocoon weight per liter

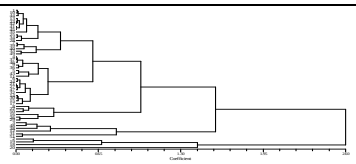

Figure 53- Cluster analysis of 51 studied silkworm varieties for male pupae weight

4. Discussion

This study examines the 51 Japanese varieties of silkworm gene bank in terms of genetic relationships. For this purpose, data Silkworm Research Institute of the country were used. Excel software were used to transfer data, calculate the mean records and data standardization. Also Ntsys software was used for clustered analyzing of data with UPGMA procedure. Software (NTSYSpc) was used for grouping with the UPGMA procedures. The purpose of this experiment was to assess the in-breeding ties of varieties to reduce silkworm gene bank size with making candid some of them for merging with each other. Also separate groupings were done for individual traits, and finally 53 phylogenic trees were obtained.

Genetic potential of each variety is different according to various genetic traits. For example, when certain groups based on traits such as reproductive traits are analyzed, and grouping relevant dendrogram and grouping done by the UPGMA method with different characteristics, is different. This has caused to observe different grouping for separate traits.

Many varieties have a common origin and affinity. Various dendrogram showed that some varieties in many of these grouping which conducted based on different characteristics were in one cluster. This relationship led to place some varieties with a low distance within one cluster together with the large distances with other varieties between clusters.

Scientific knowledge of the studied varieties can be a potential for future research work and use their genetic ability in future breeding programs in the Research Center. The large number of varieties had been recorded in this center. Therefore it is necessary with identify their abilities, the breeding programs for improved production traits and genetic advances should be used. The research has provided suitable area for this study.

Due to the large Japanese silkworm varieties of the countries, costs, problems of management, maintenance and breeding problems in them is high. Grouping can be done based on clusters of small candidates to be merged together in terms of reduced costs and better manage and also can be work on mixed varieties in breeding point of view. Because if we want to arrange some crosses without consider to the relationship between varieties a series of 51 × 51 crosses is necessary which according to the three replications for each around 8000 crosses should be done. This can cause operational and administrative costs. The higher number of to higher updated cross also the experimental error is inevitable. However, if parents have candidate a smaller number of varieties

this work take place easier and the more accurate results will be obtained. (Bizhannia and Seidavi, 2008).

UPGMA is a grouping method that was used in this study. Nevertheless, research conducted by Dalirsefat and Mirhosseini (2007), to assess genetic diversity at least thirty individuals for each varieties and 50 marker as gene locus was used to estimate genetic diversity. In addition, UPGMA method was used for grouping (Nei, 1983). Tree dendrogram of, genetic distance index was drawn by this method. It is obvious that, the AFLP markers which used in this study had enough the ability to detect Khorasan native breed from Japanese commercial breed. Separate grouping of Khorasani and Japanese race reflected, geographic origin and morphological quality and quantity characteristics, which are differ in that two race. Lemon and orange Khorasani races has been located in a classification and located separately with purple which were in accordance with grouping based on morphological characteristics (Mirhosseini, 1998).

For heterosis, those varieties should be selected that have a maximum distance and lower in-breeding coefficient. For this purpose information from their out-breeding and inbreeding (according to mentioned grouping) is important. Because the maximum heterosis occurs in the farthest varieties which have the most distance to each other and the least in-breeding.

In some target cases, breeding is in some traits or particular traits and other traits are not considered for the grower. For this purpose, clusters could identify varieties distance for each attribute (Nei, 1983).

This study had been examined the 51 varieties of Japanese silkworm. Origin of many Chinese and Japanese varieties may be the same. Study the genetic relationships of Chinese silkworm varieties of Iran can help us with superior genetic characteristics of each of these two groups, have attempted to hybridization as well as to prevent from the occurrence of the loss from it. Having this information can also maximize heterosis between the two groups. Silkworm races around the world have emerged, and through some Changes in Phenotype and genotype in a long period, different races had been generated. With the assumption that all races over a long period derived Chinese varieties with an annual laying period (Chatterjee and Datta, 1992).

Iranian native silkworm varieties have some useful and valuable features. For example, genes related to resistance and environmental compatibility which had been institutionalized as a result of long periods of natural selection and evolution in native silkworm. With proper design of crosses between indigenous varieties and those of Japanese varieties that have high production potential, but are weak in terms of disease resistance, hybrids consistence with environment and commercial can be obtained.

This study examines 53 economic traits of silkworm payment. Also, a review conducted with smaller number of economic characteristics of silkworm. Including silk cocoon weight (SGW), larval weight (LBW), larval length (LBL), cocoon length (CL), cocoon weight (CW), width of cocoon (CWD), shell weight (SW) and the percentage of raw silk (RSP), which plays an important role in the selection races and have a continuity with the traits of silkworm cocoons and silkworm net.

According to the field for more research on silkworm genetic resources, there are high potential for complementary research. Therefore, it is suggested to perform similar studies on the other genetic stocks of the country silkworm varieties such as Chinese silkworm gene bank in the future. On the other hand it is possible to use molecular techniques such as using genetic markers for the study of silkworm genetic resources on the country. In this study, 56 economic traits of silkworm were investigated. It is recommended to invest on the varieties K-119 and BH-2 that in this study along with two other varieties, gained the highest rank. That is, the obstacles facing genetic varieties such as general and specific combining ability to be remove as well as needed reviews in climate accommodation and resistance to disease to introduce these varieties as the varieties. Also, it is suggested to perform similar studies in the context of other traits, such as biochemical characteristics. We hope that this study provide appropriate context for other studies and breeding programs such as the establishment different mating systems, selection based on varieties performance and so.

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