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## Contents

## Vietnam

# Assessment of genetic diversity of sesame varieties(*Sesamum indicum* L.) by SSR and SRAP markers

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**Abstract**: The genetic relationship analysis of sesame is very inportant for genetic conservation and development. In this research, we presented the results on analysis of genetic diversity of 56 sesame accessions. The experiment used 15 markers (10 SSR and 5 SRAP markers), including 3 monomorphic and 12 polymorphic marker with a total of 34 alleles, an average of 2.3 alleles per locus. Proportion of polymorphic band ranged from 66.7% to 100.0% and reached 80.9% on average. Genetic similarity coefficient of 56 sesame cultivats ranged from 0.52 to 0.97, at 0.70 similarities divided 56 seed samples into 7 groups, including the largest group with 35 cultivars, followed by group 2 with 17 cultivars.

**Key words**: sesame; SSR marker; genetic diversity

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## 0 Introduction

Sesame(*Sesamum indicum* L.) is an important tree in the family oil Pedaliaceae. Species sesamum consists of 30 species(Kobayashi et al., 1990). Sesame is considered the "queen" of oil plants based on excellent advantages of sesame oil(Falusi and salako, 2001). The average oil content in sesame seeds to nearly 50%, and ranged from 34.4% to 59.8%(Ashri, 1998). According to FAOSTAT, the world has about $9.4\times10^6$ ha of sesame, which has $4.38\times10^6$ ha in Asia and Africa $4.74\times10^6$ ha. Average yield sesame period 2009-2013 to reach about 5.74 kg/ha, of which China is the leader in terms of yield of 13.25 quintals/ha, followed by Ethiopia reached 7.64 t/ha. The average total production of sesame exports in the last 3 years to reach about $1.05\times10^6$ t with an average value of about $1539.35\times10^6$. In Vietnam, sesame is cultivated in all the ecological zones of the country with an area varying from 40000-50000 ha, production is estimated at 22000 t. Overall, sesame productivity in Vietnam is low due to lack of improved varieties, the seed is usually sensitive to pests, diseases and environmental conditions. Information on genetic diversity and the relationship between the sesame seeds are the important information in the hybrid program. Currently, the research in this direction in the sesame in Vietnam is very limited, only works by Pham et al.(2009); Nguyen and Nguyen(2011). The study of genetic diversity can be identified based on the characteristics of agricultural biology and morphology and isozyme analysis and DNA directive(Geleta et al., 2008). However, the characteristics of agricultural biology and morphology often heavily influenced by environmental factors and the cultivation conditions. Thus, the study by molecular she can limit the downside on. Today, PCR-based techniques such as AFLP, SSR, ISSR, RAPD SRAP,etc., and can be used in the study of genetic diversity in sesame(Pham et al., 2009). In particular, SSR and SRAP directives are instructed high polymorphism and stability, has been widely used and most effective way to beat wild tree genetic resources (Zhang et al., 2012;Wu et al., 2014). In this study, SSR and SRAP markers used to assess the genetic diversity of 56 samples were collected in sesame seeds and exotic country to cater to the sesame breeding program

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in the future.

# 1 Materials and methods

## 1.1 Materials

Sesame seed samples of 56 different origin(Tab.1) included: 31 sesame seed samples collected in Nghe An, 6 samples collected in Ha Tinh, 3 samples collected in Thanh Hoa, Quang 4 samples collected average, 2 samples collected in Quang Tri, 2 samples collected in Laos and 8 samples collected in Thailand. Sesame seeds are sown seed samples in the experiment group, not repeated, area 2 $m^2$ plots in the summer-autumn crop in 2015 in Nghe An. When this wild tree from the 3-5 leaves separated conduct DNA sampling. 10 SSR primer pairs(Wu et al., 2014) and 5 SRAP primers(Zhang et al., 2012) was used to assess the genetic diversity of sesame seed samples(Tab.2).

**Tab.1 List of seasam varieties used in this study**

| No. | Variety name | Original location | No. | Variety name | Original location |
|---|---|---|---|---|---|
| 1 | $VTC_1$ | Thanh Chuong-Nghe An | 29 | $VDLC_{10}$ | Do Luong-Nghe An |
| 2 | $VTL_2$ | Chiang Mai, Thailand | 30 | $VBTB_2$ | Vien KHKTNN BTB |
| 3 | VQL | Quynh Luu-Nghe An | 31 | $VQB_1$ | Quang Phuong, Quang Binh |
| 4 | $VDL_1$ | Do Luong-Nghe An | 32 | $VQB_2$ | Quang Phuong, Quang Binh |
| 5 | $VTL_1$ | Ratchasima, Thailand | 33 | $VQT_1$ | Gio Linh, Quang Tri |
| 6 | $VDL_2$ | Do Luong-Nghe An | 34 | $VDLC_3$ | Do Luong-Nghe An |
| 7 | $VTL_3$ | Chiang Mai, Thailand | 35 | VL2 | Xieng Khoang, Laos |
| 8 | $VDHK_1$ | Huong Khe-Ha Tinh | 36 | $VDLC_9$ | Do Luong-Nghe An |
| 9 | VTTH | Hoang Hoa-Thanh Hoa | 37 | $VBTB_{8HH}$ | Vien KHKTNN BTB |
| 10 | VDVQ | Vu Quang-Ha Tinh | 38 | $VBTB_{4HH}$ | Vien KHKTNN BTB |
| 11 | VNL | Nghi Loc-Nghe An | 39 | $VTC_3$ | Thanh Chuong-Nghe An |
| 12 | VHH | Hoang Hoa-Thanh Hoa | 40 | $VQB_3$ | Quang Phuong, Quang Binh |
| 13 | $VTL_4$ | Ratchasima, Thailand | 41 | $VTL_8$ | Chiang Mai, Thailand |
| 14 | $VTL_5$ | Ratchasima, Thailand | 42 | $VDHK_2$ | Huong Khe-Ha Tinh |
| 15 | $VTL_6$ | Ratchasima, Thailand | 43 | $VAS_4$ | Anh Son-Nghe An |
| 16 | $VDL_3$ | Do Luong-Nghe An | 44 | $VTC_4$ | Thanh Chuong-Nghe An |
| 17 | $VDL_4$ | Do Luong-Nghe An | 45 | $VBTB_3$ | Vien KHKTNN BTB |
| 18 | $VTC_2$ | Thanh Chuong-Nghe An | 46 | $VDLC_8$ | Do Luong-Nghe An |
| 19 | $VAS_1$ | Anh Son-Nghe An | 47 | $VDLC_{2-1-2}$ | Do Luong-Nghe An |
| 20 | $VBTB_6$ | Vien KHKTNN BTB | 48 | VTH | Hoang Hoa-Thanh Hoa |
| 21 | VCL | Can Loc, Ha Tinh | 49 | $VDLC_{3-1}$ | Do Luong-Nghe An |
| 22 | VLH | Loc Ha-Ha Tinh | 50 | $VBTB_4$ | Vien KHKTNN BTB |
| 23 | $VL_1$ | Xieng Khoang, Laos | 51 | $VDLC_{10-1}$ | Do Luong-Nghe An |
| 24 | $VTL_7$ | Chiang Mai, Thailand | 52 | $VDLC_{2-2}$ | Do Luong-Nghe An |
| 25 | $VDL_5$ | Do Luong-Nghe An | 53 | $VQT_2$ | Gio Linh, Quang Tri |
| 26 | $VDLC_1$ | Do Luong-Nghe An | 54 | $VBTB_5$ | Vien KHKTNN BTB |
| 27 | $VDLC_{2-1}$ | Do Luong-Nghe An | 55 | $VQB_4$ | Quang Phuong, Quang Binh |
| 28 | $VBTB_1$ | Vien KHKTNN BTB | 56 | VDHS | Huong Son-Ha Tinh |

## 1.2 DNA isolation

Young leaf genomic DNA of sesame seed samples were extracted and purified operation method CTAB (cetyl Trimethyl Ammonium Bromide) by Doyle(1987), have improved under JICA-JST Laboratory, Institute of Agriculture Vietnam, as follows: warm the CTAB solution in an incubator at 65 ℃. 100 mg crushed leaves with liquid nitrogen with a mortar pestle. Add 700 L 2× CTAB buffer solution, 20 L β-mercathoethanol and mashed again. Translated into 1.5 mL eppendoft tubes. Incubate samples at 65 ℃ for 30 minutes. Add 500 L CIA(24 chloroform: 1 isoamylalcohol) shake for 30 min. 14000 rpm centrifuge for 15 min at 20 ℃ and then sucked into the upper part supernatant new tube. Add 1 V equivalent isopropanol and 15 min set in stone. 14000 rpm centrifuge for 10 min at 4 ℃. Pour off the liquid. Add 500 L of 70% ethanol to wash the precipitate. 14000 rpm centrifuge

at 4 ℃ for 5 min, then discard the solution. Drying ethanol remaining in the tube. Add 30 L 0.1× TE solution into each tube to dissolve the precipitate.

## 1.3 PCR reaction

The PCR amplification was carried out on a PCR machine (firm ABI) in 20 L, including 10 μL buffer solution Go Green Master Mix 2× *Taq*, 1 L for each component of the 4 types of dNTPs, 1 L for DNA mold, 2 L/ Predator 10 micron and 5 L nuclease-Free Water.

**Tab.2 SSR and SRAP used in this study**

| TT | Name | Primer sequence(5′- 3′) | Annealing tempreature | Type |
|---|---|---|---|---|
| 1 | HS233 | F-CGTCCCGTGTTGTCTCTATG<br>R-GCGGAGAATATGCCGTTATT | 55 ℃ | SSR |
| 2 | Me07 & Em09 | F-TGAGTCCAAACCGGTCC<br>R-TGAGTCCAAACCGGACG | 45 ℃ | SRAP |
| 3 | Me07 & Em07 | F-TGAGTCCAAACCGGTCC<br>R-GACTGCGTACGAATTCAA | 45 ℃ | SRAP |
| 4 | HS189 | F-CTCCAACCCCCATAAATCAC<br>R-GCTTCTGGAGAGGAGATTGC | 55 ℃ | SSR |
| 5 | Me07 & Em06 | F-TGAGTCCAAACCGGTCC<br>R-GACTGCGTACGAATTGCA | 45 ℃ | SRAP |
| 6 | HS94 | F-CATGTGTTCTCTCCCACCAC<br>R-TCTTGACCATGTTTTCCACC | 55 ℃ | SSR |
| 7 | HS07 | F-AGAGTACAGCCACGGGAAT<br>R-CAACAAGACAACGGTTTTGG | 55 ℃ | SSR |
| 8 | HS216 | F-TGAGAGAGGTTAATTGGGGG<br>R-TGGCTCCCATGTATTTACCA | 55 ℃ | SSR |
| 9 | HS53 | F-GAAGCTTGAAGAGAGGAGGG<br>R-ATGGAACTTCTCCGATCACC | 55 ℃ | SSR |
| 10 | HS21 | F-CGGAATTCCTGAAAGAAGGA<br>R-CAGTGAATTTCTCAACCCGA | 55 ℃ | SSR |
| 11 | HS207 | F-TGCCCATGGATTCAATTTTT<br>R-CAGAGGTCACCATTGACGAG | 55 ℃ | SSR |
| 12 | Me08 & Em08 | F-TGAGTCCAAACCGGTGC<br>R-GACTGCGTACGAATTCTG | 45 ℃ | SRAP |
| 13 | HS270 | F-TGCCCATGGATTCAATTTTT<br>R-CAGAGGTCACCATTGACGAG | 55 ℃ | SSR |
| 14 | HS259 | F-AAAGCCTCCCATACGATCAC<br>R-ACCGACGGAAACAACTAAGC | 55 ℃ | SSR |
| 15 | Me05 & Em05 | F-TGAGTCCAAACCGGAAG<br>R-GACTGCGTACGAATTAAC | 45 ℃ | SRAP |

The PCR product was agarose gel electrophoresis on 4% at voltages of 150 V, 200 mA current intensity during 50-70 min. The gel was stained with ethidium bromide directly. Using standardized scale of Sigma-Aldrich 100 bp(USA). Results are shown electrophoresis and UV light is captured by a reader gel, its capture and print photos ATTO Corporation.

## 1.4 Data analysis

Isomorphic genetic indicators(GS): GS= $2N_{ij}/(N_i+N_j)$, in which the $N_{ij}$ is a sample of SSR alleles $i$ and $j$, $N_i$ and $N_j$ is the total number of seed samples observed allen $i$ and $j$. Phylogenetic tree constructed using methods unweighted pair group UPGMA and analysis software with 2:10 NTSYS-pc version. Results using SSRs and SRAP electrophoresis arena were scored(0) and(1). 0 ie no allen, allen point 1 in a position on the line.

# 2 Results and analysis

## 2.1 Polymosphism of SSR and SRAP in the sesame varieties

The results in Tab.3 show that, out of 15 indicators used to study the genetic diversity of the line/sesame seeds 12 instructed the 3 allele polymorphism and polymorphism directive does not(HS21, and HS270 HS259). The directive does not make sense in the study of polymorphism. Allen number fluctuates from 1 to 5 allen. Me 07 and Em 07 multiplied with 5 allen, allen including 4 polymorphism(Fig.1). Next it's directive and directives

HS94 Me08–Em08 with 4 allen allen and 4 are both polymorphic(Fig.2 and Fig.3). The number of alleles per locus on sesame seed samples at 2.8 and the average number of polymorphic alleles at 2.3. The percentage of polymorphic band of instructs varied from 66.7% to 100.0%. 7 instructed the polymorphic allele is 100.0% indicating the HS233, Me07–Em09, HS94, HS07, HS53, HS207 and Me08–I08. There are two directives (HS189 and Me07–Em06) for polymorphism rate lowest, reaching 66.7%. Total of 15 directives allen multiply is 42, of which 34 allelic polymorphism, averaged 80.9% rate of allelic polymorphism. The results of this study for lower allelic polymorphism results of Wu et al.(2014) when studying the genetic diversity of sesame seed samples with average values of 3.65 alleles per locus, however the rate of ice higher polymorphism results of Wu et al.(2014) with a 36.50% average value. Thus, some polymorphic alleles obtained very high, this is significant in the study of genetic diversity at the molecular level of DNA.

**Tab.3　No. of alleles that were generated by SSR and SRAP markers**

| Marker | No. of alleles | No. of polymorphic alleles | Polymorphic percentage(%) |
|---|---|---|---|
| HS233 | 2 | 2 | 100.0 |
| Me07–Em09 | 2 | 2 | 100.0 |
| Me07–Em07 | 5 | 4 | 80.0 |
| HS189 | 3 | 2 | 66.7 |
| Me07–Em06 | 3 | 2 | 66.7 |
| HS94 | 4 | 4 | 100.0 |
| HS07 | 2 | 2 | 100.0 |
| HS216 | 4 | 3 | 75.0 |
| HS 53 | 3 | 3 | 100.0 |
| HS21 | 1 | 0 | 0.0 |
| HS207 | 3 | 3 | 100.0 |
| Me08–Em08 | 4 | 4 | 100.0 |
| HS270 | 1 | 0 | 0.0 |
| HS259 | 1 | 0 | 0.0 |
| Me05–Em05 | 4 | 3 | 75.0 |
| Total | 42 | 34 | – |
| Average | 2.8 | 2.3 | 80.9 |

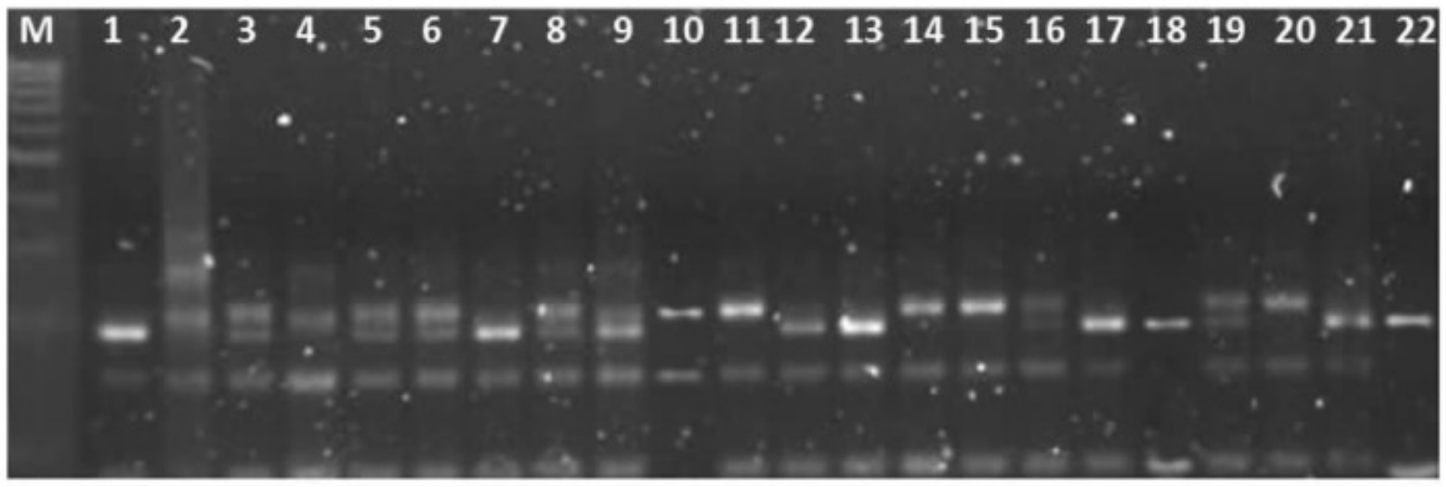


**Fig.1　PCR products of sesame varieties of SRAP(Me07–Em07)**

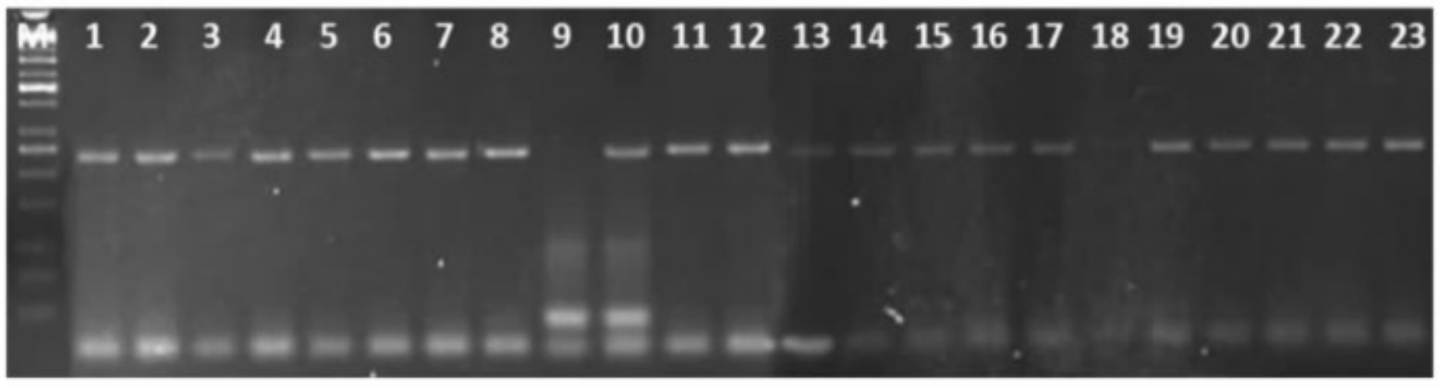


**Fig.2　PCR products of sesame varieties of SSR(HS189)**

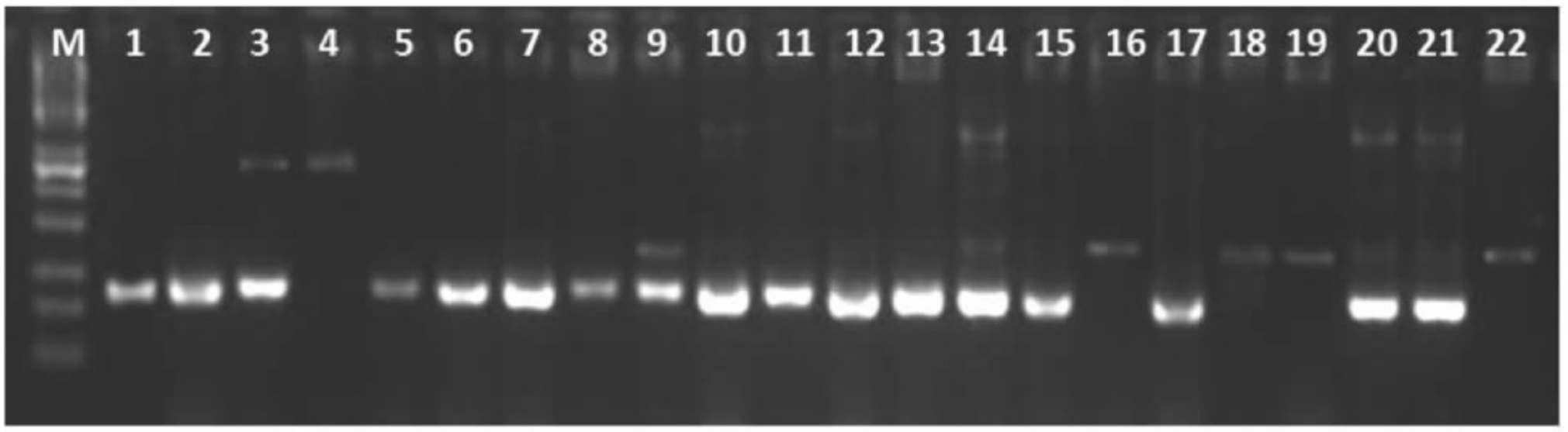


**Fig.3 PCR products of sesame varieties of SRAP(Me08–Em08)**

## 2.2 Genetic relationship between sesame seed samples studied

Genetic relationship between sesame seed samples were analyzed by software NTSYS 2:10, thereby determining the genetic similarity coefficient and genetic tree of sesame seed samples(Fig.4). Genetic similarity coefficient of 56 seed samples ranged from 0.52 to 0.97, the two varieties have similar genetic system is the lowest form of 39 varieties originating in Thanh Chuong district, Nghe An province and the same sample number 28 is derived from the Institute of Agricultural Science for north central, hit. 235. Two seed samples of genetic similarity coefficient is the highest form of the 35 varieties originating in Xieng Khouang province, Laos and No. 41 seed samples originating from Thailand Chiang Mai province, reached 0.97. Two samples of this same general characteristics as the result of biological agriculture with 4 rows of beads, 1 fruit/axillary, deciduous completely when ripe, the leaves grow symmetrically. The results of this research for the genetic similarity coefficient higher than the findings of Pham et al. (2009). Two studies have shown genetic similarity coefficient of sesame seed samples based on RAPD oscillating indicator corresponding to 0.38 and 0.03 from 0 to 0.43. However, results of this study similarities di coefficient equivalent pure research results of Nguyen and Nguyen(2011) to assess the genetic diversity of black sesame seeds by directive RAPD. Results of this study showed the genetic similarity coefficients ranged from 0.42 to 0.81.

In the breeding work, parental pairs as far apart genetically as for high heterosis. If the genetic distance between the parents too big(genetic similarity coefficient of less than 0.4), hybrids are often difficult to survive or pollination. If the genetic distance between the parents too small(genetic similarity coefficient greater than 0.7), hybrids usually no heterosis(Le, 2011). Thus, the genetic similarity coefficient of 0.7 indicates on the genetic tree(Fig.4) we split the 56 samples studied sesame seeds into 7 groups.

– Group 1 included 25 samples with the same degree of genetic similarity of about 70.6%, the same templates specifically 1, 3, 21, 8, 33, 37, 35, 45, 34, 35, 41, 40, 38, 42, 5, 7, 11, 12, 9, 6, 27, 28, 32, 30 and 31. During the same 25 samples, 21 samples have been collected in the same North Central, 3 seed samples collected from Thailand and 1 seed samples collected in Laos.

– Group 2 included 17 samples similar to the degree of genetic similarity of about 70.6%, the same templates specifically 13, 46, 55, 14, 16, 20, 43, 18, 17, 54, 52, 44, 47, 49, 51, 48 and 50. this group includes the majority of the sample varieties that are branching, leaf angle stand, fruit and seeds 4 to 8 per axillary line with results from 1 to 3. Especially two of 47 and 49 seed samples have similar characteristics as they are collected from Do Luong district, Nghe An province, branching tree, every fruit has 4 seeds, black seeds, each leaf axils 3 results.

– Group 3 consisted of 4 models with the same degree of genetic similarity of about 73.0%, specifically No.2 seed samples originating from Thailand, the No.4 seed samples derived from Luong district, Nghe An province, the same sample No.19 is derived from Anh Son district, Nghe An province and No.23 seed samples derived from Xieng Khouang province, Laos. This group has many common features as they are 4 rows seeds, stems with

square cross section, the leaf angle stand.

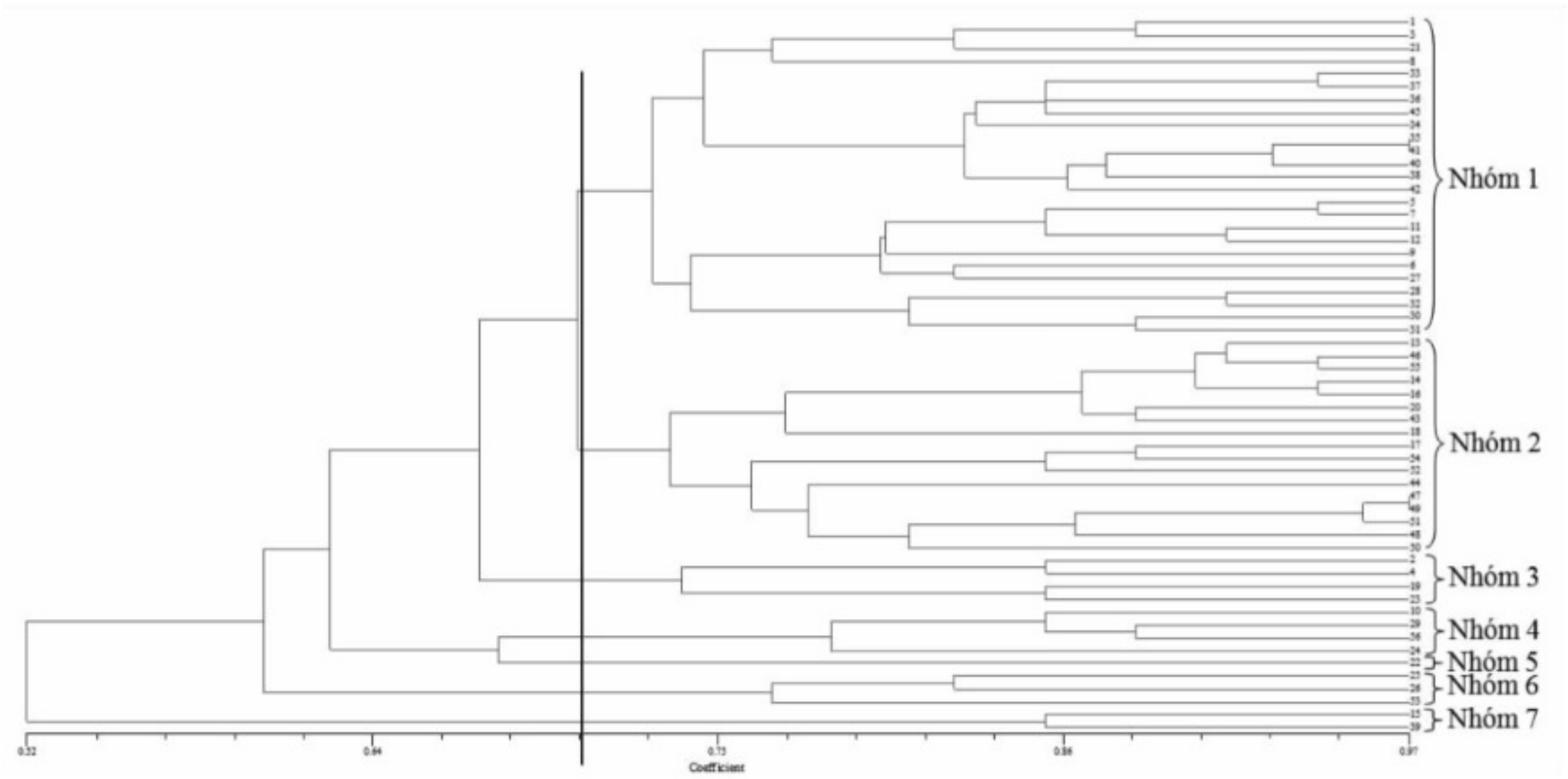


**Fig.4　Trees clustering genetic diversity of 56 sesame seed samples based on molecular markers**

– Group 4 consisted of 4 models with the same degree of genetic similarity of 78.0%, namely the same sample of 10, 29, 56 and 24. The same pattern has many morphological and biological farmers alike as tree ramified burning below, with black beads, feathers on a smooth result, average growth time(from 75 to 78 days).

– Group 5 with only a No.22 seed is the seed samples derived from Loc Ha district, Ha Tinh province.

– Group 6 included 3 samples with the same degree of genetic similarity of about 77.0%, namely the same sample numbers 25, 26 and 53. The denominator of this same pattern has many agricultural and biological characteristics similar pattern as 4 rows fruit seeds, black seeds, tree branching and branching in the lower combustion, long fruit(>3.0 cm), each with 3 axillary fruits, seeds easily separated when dried fruit, smooth leaves, stems have square cross section.

– Group 7 included a sample size of sample 2 of 15 native varieties of Thailand and No.19 seed samples originated in Thanh Chuong district, Nghe An province. Two samples of this variety have some common characteristics such as branching trees, fruit beads 4 rows, each with 3 results axillary, smooth leaves, leaf angle stand and fall completely when ripe, green body and is square.

Results grouped based on genetic distance above shows, sesame seed samples corporations is available at Vinh University has high polymorphism, is an important material for research and breeding sesame energy high interest in Vietnam in general and in particular in the north central region. The groups may form hybrid varieties together to heterosis occurs without sterility in hybrids.

## 2.3　Results evaluated several agricultural biological traits and yield components

Tab.4 showed the past, growth time of 56 sesame seed samples varied from 60 to 87 days. Plant height ranges from 84.9 to 171.5 cm. Some fruit on the trees ranged from 12.56 to 68.40. Number of particles on the results varied from 58.67 to 164.89 grains. Weight of 1000 seeds ranges from 2.12 to 3.51 g. Grain rows on the results varied from 4–12 every county, including 36 samples with 4 rows seed beads, 13 beads form 8 rows seed, 4 seed samples from 6–8 every bead, 1 seed bead 10 rows and 2 seed samples of 12 seeds each.

Some fruit on the leaf axils indicators closely correlated with sesame and productivity are important criteria in breeding programs sesame(Osman, 1989). Some results on axillary varied from 1–3 result, with the same 25 samples(representing 44.64%) 3 results/axillary and 31 seed samples(representing 55.36%) have 1 fruit/leaf axils. Evaluation results sesame genetic resources of Turkey shows that only 2.9% of the genetic resources of the 103 samples collected 3 results/axillary(Furat and Uzun, 2010).

**Tab.4 Some agricultural biological characteristics and yield components of sesame seed samples in the summer–autumn crop in 2015 in Nghe An**

| TT | Varieties name | Growth duration (d) | Plant height (cm) | No. of primary branch 1 | No. of fruit per plant | No. of seed row | No. of fruit/ nách lá | No. of seeds per fruit | 1000 grain weight (g) | Yield (g/plant) | Seed color |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | $VTC_1$ | 83 | 112.3 | 0.0 | 36.5 | 6–8 | 3 | 126.7 | 2.32 | 8.56 | 3 |
| 2 | $VTL_2$ | 81 | 171.5 | 2.7 | 35.2 | 4 | 1 | 65.5 | 2.61 | 5.12 | 1 |
| 3 | VQL | 85 | 128.3 | 0.0 | 33.9 | 4 | 1 | 73.3 | 3.14 | 5.47 | 3 |
| 4 | $VDL_1$ | 69 | 115.4 | 0.0 | 61.6 | 4 | 3 | 81.3 | 2.71 | 9.12 | 3 |
| 5 | $VTL_1$ | 78 | 131.3 | 0.0 | 54.3 | 4 | 1 | 81.5 | 3.31 | 8.45 | 4 |
| 6 | $VDL_2$ | 75 | 117.5 | 0.6 | 51.6 | 4 | 3 | 74.7 | 2.96 | 8.12 | 3 |
| 7 | $VTL_3$ | 82 | 159.6 | 5.1 | 53.4 | 4 | 1 | 72.3 | 3.02 | 7.32 | 4 |
| 8 | $VDHK_1$ | 68 | 95.3 | 0.0 | 51.7 | 4 | 3 | 68.4 | 2.51 | 5.36 | 3 |
| 9 | VTTH | 75 | 105.7 | 1.9 | 28.7 | 10 | 1 | 125.8 | 2.24 | 4.78 | 2 |
| 10 | VDVQ | 78 | 96.2 | 1.6 | 51.2 | 4 | 3 | 82.7 | 2.89 | 8.43 | 3 |
| 11 | VNL | 76 | 121.5 | 1.5 | 37.9 | 4 | 1 | 80.6 | 2.91 | 6.54 | 4 |
| 12 | VHH | 82 | 119.2 | 1.6 | 51.2 | 4 | 3 | 69.5 | 2.81 | 7.12 | 3 |
| 13 | $VTL_4$ | 81 | 122.7 | 0.0 | 45.7 | 4 | 1 | 64.6 | 2.51 | 5.32 | 1 |
| 14 | $VTL_5$ | 82 | 140.1 | 1.1 | 49.9 | 4 | 1 | 78.3 | 3.12 | 8.34 | 3 |
| 15 | $VTL_6$ | 87 | 125.5 | 1.3 | 38.2 | 4 | 3 | 77.6 | 3.51 | 7.57 | 4 |
| 16 | $VDL_3$ | 65 | 105.4 | 0.5 | 29.1 | 8 | 3 | 129.5 | 2.43 | 6.32 | 3 |
| 17 | $VDL_4$ | 70 | 112.5 | 1.9 | 38.9 | 8 | 1 | 113.7 | 2.28 | 8.12 | 3 |
| 18 | $VTC_2$ | 75 | 84.6 | 1.7 | 41.5 | 4 | 3 | 83.6 | 2.68 | 6.05 | 3 |
| 19 | $VAS_1$ | 85 | 95.5 | 0.0 | 38.9 | 4 | 3 | 73.2 | 2.61 | 5.23 | 3 |
| 20 | $VBTB_6$ | 78 | 89.8 | 2.1 | 35.5 | 8 | 1 | 94.7 | 2.31 | 4.13 | 2 |
| 21 | VCL | 84 | 105.8 | 0.0 | 41.6 | 6–8 | 1 | 132.5 | 2.68 | 9.23 | 3 |
| 22 | VLH | 74 | 116.5 | 3.1 | 31.2 | 8 | 1 | 115.9 | 2.58 | 7.12 | 4 |
| 23 | $VL_1$ | 70 | 141.3 | 2.6 | 24.6 | 4 | 1 | 73.6 | 3.41 | 4.78 | 1 |
| 24 | $VTL_7$ | 65 | 106.3 | 1.8 | 38.9 | 4 | 1 | 73.9 | 2.79 | 5.28 | 4 |
| 25 | $VDL_5$ | 85 | 116.2 | 1.6 | 55.6 | 4 | 3 | 76.5 | 2.73 | 7.26 | 3 |
| 26 | $VDLC_1$ | 75 | 112.5 | 2.6 | 42.8 | 8 | 3 | 129.5 | 2.38 | 8.42 | 3 |
| 27 | $VDLC_{2-1}$ | 68 | 131.7 | 0.0 | 27.7 | 4 | 1 | 75.1 | 3.18 | 4.21 | 3 |
| 28 | $VBTB_1$ | 82 | 127.1 | 1.5 | 21.5 | 4 | 1 | 71.3 | 3.08 | 2.87 | 4 |
| 29 | $VDLC_{10}$ | 65 | 105.1 | 2.5 | 58.4 | 4 | 3 | 74.4 | 2.56 | 8.25 | 3 |
| 30 | $VBTB_2$ | 85 | 121.1 | 1.8 | 25.5 | 8 | 1 | 106.5 | 2.34 | 4.87 | 4 |
| 31 | $VQB_1$ | 65 | 115.5 | 1.1 | 24.6 | 8 | 1 | 112.8 | 3.08 | 5.12 | 2 |
| 32 | $VQB_2$ | 78 | 99.8 | 1.7 | 47.3 | 4 | 3 | 67.6 | 2.79 | 5.02 | 3 |
| 33 | $VQT_1$ | 60 | 87.1 | 1.1 | 12.6 | 12 | 1 | 164.9 | 2.12 | 3.11 | 2 |
| 34 | $VDLC_3$ | 72 | 128.5 | 2.9 | 63.6 | 4 | 3 | 91.2 | 2.95 | 8.23 | 3 |
| 35 | $VL_2$ | 85 | 137.2 | 3.8 | 37.1 | 4 | 1 | 71.5 | 2.67 | 4.87 | 4 |
| 36 | $VDLC_9$ | 70 | 121.2 | 2.1 | 49.6 | 8 | 3 | 131.1 | 2.51 | 7.56 | 3 |
| 37 | $VBTB_{8HH}$ | 65 | 118.5 | 2.8 | 28.7 | 8 | 1 | 123.6 | 2.41 | 6.24 | 3 |
| 38 | $VBTB_{4HH}$ | 70 | 131.6 | 1.1 | 41.8 | 4 | 1 | 79.6 | 2.87 | 7.12 | 3 |
| 39 | $VTC_3$ | 85 | 118.9 | 2.4 | 43.0 | 4 | 3 | 71.5 | 2.79 | 5.32 | 3 |
| 40 | $VQB_3$ | 75 | 108.5 | 2.6 | 26.8 | 12 | 1 | 134.7 | 2.27 | 4.56 | 2 |
| 41 | $VTL_8$ | 83 | 111.0 | 0.0 | 34.1 | 4 | 1 | 71.0 | 3.01 | 5.46 | 3 |
| 42 | $VDHK_2$ | 70 | 106.7 | 0.0 | 51.7 | 4 | 3 | 71.2 | 2.51 | 6.12 | 3 |
| 43 | $VAS_4$ | 85 | 117.4 | 1.8 | 38.7 | 8 | 1 | 138.7 | 2.58 | 7.81 | 3 |
| 44 | $VTC_4$ | 65 | 125.1 | 1.2 | 39.8 | 8 | 1 | 112.6 | 2.28 | 5.67 | 3 |
| 45 | $VBTB_3$ | 60 | 95.5 | 1.8 | 34.7 | 6–8 | 1 | 115.7 | 2.68 | 6.58 | 3 |
| 46 | $VDLC_8$ | 70 | 101.2 | 1.7 | 26.7 | 8 | 1 | 121.2 | 2.25 | 4.67 | 3 |
| 47 | $VDLC_{2-1-2}$ | 85 | 121.7 | 0.9 | 45.6 | 4 | 3 | 74.4 | 2.41 | 5.12 | 3 |
| 48 | VTH | 75 | 116.1 | 0.0 | 42.5 | 4 | 3 | 71.5 | 3.06 | 7.14 | 3 |
| 49 | $VDLC_{3-1}$ | 70 | 131.1 | 2.8 | 55.1 | 4 | 3 | 93.5 | 2.98 | 7.69 | 3 |
| 50 | $VBTB_4$ | 78 | 115.6 | 3.1 | 35.8 | 6–8 | 1 | 109.5 | 3.01 | 6.61 | 3 |
| 51 | $VDLC_{10-1}$ | 60 | 125.2 | 3.7 | 68.4 | 4 | 3 | 76.1 | 2.61 | 10.11 | 3 |
| 52 | $VDLC_{2-2}$ | 78 | 116.2 | 0.9 | 44.9 | 4 | 3 | 82.2 | 2.79 | 8.14 | 3 |
| 53 | $VQT_2$ | 75 | 108.2 | 1.6 | 53.6 | 4 | 3 | 84.7 | 3.07 | 10.43 | 3 |
| 54 | $VBTB_5$ | 70 | 125.5 | 2.8 | 45.2 | 4 | 3 | 58.7 | 2.78 | 5.98 | 3 |
| 55 | $VQB_4$ | 82 | 135.5 | 3.1 | 45.7 | 4 | 1 | 63.7 | 2.21 | 4.53 | 4 |
| 56 | VDHS | 75 | 99.5 | 1.8 | 35.9 | 8 | 1 | 95.4 | 2.18 | 5.01 | 3 |
| ±SD | | 7.56 | 16.31 | 1.2 | 11.4 | – | – | 25.1 | 0.33 | 1.72 | – |
| R | | 27 | 86.9 | 5.1 | 55.8 | – | – | 106.2 | 1.39 | 7.56 | – |
| Max | | 87 | 171.5 | 5.1 | 68.4 | – | – | 164.9 | 3.51 | 10.43 | – |
| Min | | 60 | 84.6 | 0 | 12.6 | – | – | 58.6 | 2.12 | 2.87 | – |
| Average | 75.25 | 116.9 | 1.6 | 41.2 | – | – | 91.7 | 2.71 | 6.46 | – | |

SD: Standard deviation; R: Variation interval

Individual productivity ranged from 2.87 to 10.43 g/tree, which has two models of 51 and 53 have the same individual productivity reached 10.11 and 10.43, respectively grams/plant. These are the same branching pattern

with many fruit/tree. Every fruit has 4 seeds, 3 fruits/axillary, black seeds. 2 samples can yield varieties of fish is very low seed samples and samples of 28 varieties of 33. reaching 2.87 and 3.11, respectively g/tree. They are characterized with 1 fruit/axillary, the fruit on the tree less(from 12.6 to 21.5 fruits/tree), branching tree.

Thus, the results of agricultural biological characteristics and yield components showed similarities in the genetic relationships based on molecular markers.

## 3 Conclusions

Of the 10 SSR markers and 5 SRAP markers used to assess genetic diversity of 56 sesame seed samples originated in the north central region and exotic genetic resources. 12 instructed by DNA polymorphism in 12 loci obtained 34 different allelic polymorphism. Polymorphic allele number ranged from 2–4 and reached an average of 2.3 alleles/locus.

The percentage of polymorphic band of 12 primers ranged from 66.7% to 100.0% and averaged 80.9%, with the proportion of couples each polymorphic band 100.0%.

Genetic similarity coefficient of 56 sesame seed samples ranged from 0.52 to 0.97. At the genetic similarity of 70.0%. 56 sesame seed samples are divided into 7 groups. including the largest group with 25 samples 1 seeds. followed by groups of 2 to 17 varieties.

Luong black sesame seeds(51 samples) and black sesame seeds Quang Tri(53 samples) with high yield. trials should continue to develop production.

The results of the genetic polymorphism of sesame seed samples in the north central region and exotic genetic resources is important information for the evaluation, selection and creation in the future.

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