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# Genetic Diversity Analysis of BARI Released Potato Varieties through Sequence Repeat Markers

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## Abstract

Potato (*Solanum tuberosum*) is one of the most important staple crops worldwide and understanding the genetic diversity is critical for breeding improved varieties with desirable traits. In Bangladesh, the Bangladesh Agricultural Research Institute (BARI) has released numerous potato varieties; however, molecular-level insights into their genetic diversity remain scarce. This study aimed to evaluate the genetic diversity of 36 BARI-released potato varieties using simple sequence repeat (SSR) markers to identify genetically divergent genotypes for breeding and improvement programs. The study conducted from October 2020 to November 2022 at the Institute of Biotechnology and Genetic Engineering (IBGE) and the Advanced Plant Breeding Laboratory, Gazipur Agricultural University (GAU), nine SSR primers (STM 1049, STM 2022, STM 2013, STM 1104, STM 1106, STM 0037, STM 0030, STM 0019, and STM 1031) were employed. A total of 10.56 alleles per locus were detected, with STM 0030 producing the highest number of alleles (13) and STM 1104 the least (6). The polymorphic information content (PIC) values ranged from 0.44 (STM 1104) to 0.90 (STM 2013 and STM 0030), indicating the high discriminatory power of these markers. Genetic distance analysis revealed significant diversity, with the highest inter-genotypic distance observed between BA-40 and BA-46 (0.8571) and the lowest between BA-91 and BA-41 (0.33). These results demonstrate the effectiveness of SSR markers,

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particularly STM 2013 and STM 0030, in differentiating potato genotypes. The findings provide critical insights for designing breeding strategies and highlight the potential for leveraging genetic diversity to develop resilient and high-yielding potato varieties.

**Keywords:** Genetic distance, Genetic diversity, Molecular markers, Polymorphic information content, Varietal improvement

## Introduction

Potato (*Solanum tuberosum* L.), a key tuber crop from the Solanaceae family, serves as both a staple food and a versatile vegetable. Originating in the Andean region of South America (Keeps, 1999), potatoes are rich in carbohydrates, protein, essential vitamins, minerals, and trace elements, making them vital for global nutrition and food security (Horton, 1987; Karim et al., 2010).

Bangladesh stands as the seventh-largest potato-producing country globally and ranks second in crop production after rice (FAO, 2021). In the 2022-23 season, the country produced approximately 10.43 million metric tons of potatoes over an area of 455,523 hectares, with an average yield of 22.9 tons per hectare (BBS, 2023). Potatoes are predominantly cultivated during winter but are available in markets throughout the year, primarily consumed as a vegetable.

In Bangladesh, while the production area of potatoes has expanded significantly over the past few decades, the yield per unit area has remained stagnant (BBS, 2010). Factors contributing to this stagnation include the limited availability of high-yielding varieties, reliance on indigenous seeds and traditional cultivars, scarcity of disease-free seed tubers, and the use of inferior seed materials.

Despite the crop’s commercial importance, Bangladesh lacks comprehensive genetic information on potatoes. This poses challenges in ensuring cultivar purity. Since many desirable traits exhibit low heritability and are genetically complex, relying on visual markers for cultivar identification is neither efficient nor reliable. In contrast, DNA-based molecular markers, such as simple sequence repeats (SSRs), offer a more accurate and dependable alternative (Raghunathachari et al., 2000). Evaluating genetic diversity and relatedness among species, populations, and individuals is an integral part of any agricultural production system, ensuring the effective utilization and protection of plant genetic resources (Weising et al., 1995; Paterson et al., 1991).

Molecular markers (RAPD, SCAR, ISSR, and SSR) which are identifiable DNA sequences whose inheritance can be easily tracked, have been effectively used to assess genetic diversity and evolutionary relationships among species. SSR markers are highly preferred due to their high polymorphism, codominance, simplicity, and cost-effectiveness.

The first application of SSR markers in potatoes was by Veilleux et al. (1995), who analyzed the genetic makeup of plants derived from a potato clone using five polymorphic SSRs identified from published potato sequences. Subsequently, Kawchuk et al. (1996) examined 252 *Solanum tuberosum* sequences, detecting 24 alleles and establishing a DNA product database for cultivar identification. Milbourne et al. (1997) expanded the scope by using SSRs alongside three other PCR-based marker systems to study genetic relationships within the potato gene pool, successfully differentiating 16 cultivars. Over time, additional SSR sites have been identified in the potato genome, including highly informative microsatellites (Ghislain et al., 2004).

SSR markers have since been employed for diverse applications, such as identifying French potato cultivars (Moisan-Thiery et al., 2005), analyzing germplasm in the INIA Chile breeding program (Mathias et al., 2007), developing rapid SSR-based cultivar identification methods (Reid and Kerr, 2007), creating a genetic identity kit for potato (Ghislain et al., 2009), and studying genetic relationships in Spanish cultivars (de Galarreta et al., 2011). These efforts have significantly contributed to the understanding and conservation of potato genetic resources. A key study by Ghislain et al. (2006) at the International Potato Center (CIP) demonstrated that SSR markers outperform RAPD markers in detecting polymorphism. SSR technology, along with single nucleotide polymorphism (SNP) techniques, is now regarded as one of the most efficient tools for developing core collections and fingerprinting cultivars. SSR markers provide high-resolution insights into genealogical relationships and genetic diversity while requiring fewer markers to differentiate genotypes (Borem and Caixeta, 2006). Potato is a highly heterozygous crop that is commercially propagated through vegetative reproduction or tubers (Bradshaw, 2007). Among molecular tools, microsatellites, or simple sequence repeats (SSR) DNA markers, have proven invaluable for assessing genetic diversity, genetic structure, and classification (Spooner et al., 2007). They have been used for tracing germplasm migrations (Rios et al., 2007), fingerprinting (Moisan-Thiery et al., 2005), genetic linkage mapping (Feingold et al., 2005), establishing core collections (Ghislain et al., 2006), and identifying duplicate collections across gene banks (Del Rio et al., 2006). SSR markers are currently regarded as one of the most effective tools for studying genetic relationships due to their ease of use, codominant inheritance, multiallelic nature, and high polymorphism (Spooner et al., 2005).

Genetic diversity is a fundamental tool for quantifying genetic variability in both cross-pollinated and self-pollinated crops (Murty and Arunachalam, 1966; Gaur et al., 1978). This diversity aids in identifying valuable traits and selecting superior parents for breeding programs.

Recognizing the importance of genetic diversity and DNA fingerprinting in potato germplasm management, thirty-six potato varieties developed and released by the Bangladesh Agricultural Research Institute (BARI) were genotyped using SSR markers. The objectives of this study included analyzing the genetic diversity among these varieties and identifying genetically divergent genotypes to support potato improvement programs. This approach provides vital insights for optimizing breeding strategies and ensuring long-term genetic stability and productivity in potato cultivation.

## Materials and Methods

### Sample collection

This study was conducted at the Plant Molecular Laboratory, Institute of Biotechnology and Genetic Engineering, and the Advanced Plant Breeding Laboratory, Department of Genetics and Plant Breeding, Gazipur Agricultural University (GAU), Gazipur, Bangladesh. Thirty-six potato varieties (Table 1) were collected from the Tuber Crops Research Centre (TCRC) of the Bangladesh Agricultural Research Institute (BARI), located in Gazipur and Munshiganj, and used as the experimental material. In vitro-grown micro plants derived from sprouts served as the source of plant material. A total of 155 individuals (five from each variety) were randomly selected for molecular analysis to ensure adequate representation of each genotype.

Table 1. Potato varieties used for molecular evaluation

| Genotype code | Name of genotype | Genotype code | Name of genotype | Genotype code | Name of genotype |
|---|---|---|---|---|---|
| Gen-1 | BA-41 | Gen-13 | BA-40 | Gen-25 | BA-73 (CIP-127) |
| Gen-2 | BA-54 (Musica) | Gen-14 | BA-13 (Granola) | Gen-26 | BA-50 (7.86) |
| Gen-3 | BA-46 | Gen-15 | A-lrusset | Gen-27 | BA-62 (9.112) |
| Gen-4 | BA-53 | Gen-16 | BA-48 | Gen-28 | BA-89 (13.7) |
| Gen-5 | BA-91 (Carolous) | Gen-17 | BA-63 (9.125) | Gen-29 | BA-25 (Asterix) |
| Gen-6 | BA-37 | Gen-18 | BA-72 (CIP-139) | Gen-30 | BA-86 (12.13) |
| Gen-7 | BA-52 (Labadia) | Gen-19 | BA-12 (Dheera) | Gen-31 | BA-31 (Sagetta) |
| Gen-8 | BA-28 | Gen-20 | BA-60 (Vivaldi) | Gen-32 | BA-81 |
| Gen-9 | BA-90 (Alouette) | Gen-21 | BA-66 (Pamela) | Gen-33 | Innovator |
| Gen-10 | BA-7 (Diamant) | Gen-22 | BA-81 (CIP-10) | Gen-34 | Owatta |
| Gen-11 | BA-29 (Courage) | Gen-23 | BA-83 Cimega | Gen-35 | BA-88 (CIP-123) |
| Gen-12 | BA-57 | Gen-24 | BA-71 (Dolly) | Gen-36 | BA-78 (CIP112 |

Abbreviations: Gen: Genotype, BARI: Bangladesh Agricultural Research Institute

### SSR marker selection

Nine SSR markers were selected to analyze the genetic diversity of the 36 potato cultivars. The SSR markers, along with their sequences and annealing temperatures, are detailed in Table 2.

Table 2. SSR markers used in molecular evaluation of potato genotypes

| Serial no | Marker | Sequence (Forward/Reverse) | Annealing Temperature (°C) |
|---|---|---|---|
| 1 | STM1049 | F: CTACCAGTTTGTTGATTGTGGTG | 55 |
| | | R: AGGGACTTTAATTTGTTGGACG | |
| 2 | STM2022 | F: GCGTCAGCGATTTCAGTACTA | 50 |
| | | R: TTCAGTCAACTCCTGTTGCG | |
| 3 | STM2013 | F: TTCGGAATTACCCTCTGCC | 55 |
| | | R: AAAAAAAGAACGCGCACG | |
| 4 | STM1104 | F: TGATTCTCTTGCCTACTGTAATCG | 55 |
| | | R: CAAAGTGGTGTGAAGCTGTGA | |
| 5 | STM1106 | F: TCCAGCTGATTGGTTAGGTTG | 50 |
| | | R: ATGCGAATCTACTCGTCATGG | |
| 6 | STM0037 | F: AATTTAACTTAGAAGATTAGTCTC | 50 |
| | | R: ATTTGGTTGGGTATGATA | |
| 7 | STM0030 | F: AGAGATCGATGTAAAACACGT | 58 |
| | | R: GTGGCATTTTGATGGATT | |
| 8 | STM0019 | F: AATAGGTGTACTGAACTCTCAATG | 50 |
| | | R: TTGAAGTAAAAGTCCTAGTATGTG | |
| 9 | STM1031 | F: TGTGTTTGTTTTTCTGTAT | 55 |
| | | R: AATTCTATCCTCATCTCTA | |

Abbreviations: F: Forward, R: Reverse

## DNA extraction

Genomic DNA was extracted using a modified Cetyl Trimethyl Ammonium Bromide (CTAB) method (Ferrari et al., 2007). Potato leaves were first cut into small pieces and crushed using a mortar and pestle. To the crushed tissue, 700 µl of extraction buffer was added and ground into a fine paste. The mixture was then transferred to a 1.5 ml micro centrifuge tube, and 40 µl of 20% SDS was added. The tube was shaken gently and incubated at 65°C in a boiling water bath for 10 minutes. Following incubation, 100 µl of 5M NaCl and 100 µl of 10X CTAB were added, and the mixture was shaken and re-incubated at 65°C for another 10 minutes. After the second incubation, the sample was centrifuged at 12,000 rpm for 5 minutes. The supernatant was carefully transferred to a new micro centrifuge tube, and 900 µl of a chloroform: isoamyl alcohol mixture (24:1) was added. The tube was mixed vigorously and centrifuged at 12,000 rpm for 5 minutes. The resulting supernatant was transferred to a clean 1.5 ml tube, and isopropanol (equal volume to the supernatant) pre-chilled at −20°C was added. The tube was inverted to mix and placed at −20°C overnight for DNA precipitation. The next day, the sample was centrifuged at 13,000 rpm for 30 minutes, and the supernatant was discarded, leaving the DNA pellet at the bottom. The pellet was washed with 70% ethanol and centrifuged at 12,000 rpm for 5 minutes. Finally, the DNA pellet was re-suspended in 150 µl of 1X TE buffer and stored at −20°C.

### PCR preparation and amplification

The PCR preparation was performed using a 10X reaction buffer without $MgCl_2$, which was stored in the refrigerator and thawed with gentle vortexing before use. dNTPs, each at a concentration of 10 mM, were either supplied individually or as a premixed solution, with each dNTP at 100 mM. Due to their sensitivity to freeze-thaw cycles, the dNTPs were kept at −20°C and thawed gently before use. Primers, both forward and reverse, were lyophilized and reconstituted in 100 µM stock solutions by adding 10 µl of 1X TE buffer, then stored at 4°C overnight for complete chelation. Working solutions were prepared by diluting the stock primers with water, which were then thawed gently before PCR. Taq polymerase (5 U/µl) was stored at −20°C and added to the PCR master mix by pipetting. The PCR reactions were set up in a total volume of 10 µl, containing 3 µl of DNA template, 1 µl of 10X PCR buffer, 2 µl of 25 mM $MgCl_2$, 0.8 µl of 25 mM dNTPs, 0.5 µl of each 10 µM forward and reverse primers, 0.2 µl of Taq polymerase, and 2 µl of distilled water. The PCR cycle conditions included an initial denaturation at 95°C for 5 minutes, followed by 36 cycles of denaturation at 95°C for 45 seconds, annealing at 55°C for 45 seconds, extension at 72°C for 1 minute, and a final extension at 72°C for 5 minutes, with storage at 15°C if needed.

### Agarose Gel Electrophoresis and Visualization

For agarose gel electrophoresis, 3.6 g of agarose was dissolved in 240 ml of 1X TAE buffer and mixed with 9 µl of ethidium bromide for DNA visualization. The agarose solution was heated gently until fully dissolved, avoiding boiling to prevent degradation. After cooling to approximately 50°C, the solution was poured into a gel casting tray with a comb inserted to form wells for sample loading. Once the gel solidified, 10 µl of PCR product was mixed with 2 µl of 10X loading dye, and the mixture was briefly centrifuged at 3600 rpm for 1 minute to ensure proper mixing and removal of air bubbles.

The gel was placed in an electrophoresis chamber filled with 1X TAE buffer, and electrophoresis was performed at 180 volts for 40 minutes. A DNA size marker was loaded in a separate well as a reference. After the run, the DNA bands were visualized under UV light, enabling size determination based on the marker.

### SSR data scoring and analysis

After electrophoresis, SSR marker bands were observed and analyzed. Molecular weight markers (1 kb and 50 bp DNA ladders) were used to estimate the sizes of amplified products by comparing fragment migration distances with known marker sizes. Each distinct band was assigned an identification number based on its gel position and scored visually as present (1) or absent (0) for each primer. Scores from all primers were compiled into a data matrix for further analysis of polymorphic loci, gene diversity, and genetic distance.

Major allele frequency, gene diversity, and polymorphic information content (PIC) for each SSR locus were calculated using Power Marker v3.25 (Liu and Muse, 2005). Genetic distances between varieties were computed and used to form clusters. A neighbor-joining dendrogram was constructed using DARwin 6.0 (Perrier and Jacquemoud-Collet, 2006) to illustrate the genetic relationships among the varieties.

## Results and Discussion

### Gel run data:

The gel profiles for primers STM1049, STM2022, STM2013, STM1104, STM1106, STM0037, STM0030, STM0019, and STM1031 are presented in Figures 1, with each primer tested across 36 genotypes.

The genotypes include BA-41, BA-54 (Musica), BA-46, BA-53, BA-91 (Carolous), BA-37, BA-52 (Labadia), BA-28, BA-90 (Alouette), BA-7 (Diamant), BA-29 (Courage), BA-57, BA-40, BA-13 (Granola), A-lrusset, BA-48, BA-63 (9.125), BA-72 (CIP-139), BA-12 (Dheera), BA-60 (Vivaldi), BA-66 (Pamela), BA-81 (CIP-10), BA-83 (Cimega), BA-71 (Dolly), BA-73 (CIP-127), BA-50 (7.86), BA-62 (9.112), BA-89 (13.7), BA-25 (Asterix), BA-86 (12.13), BA-31 (Sagetta), BA-81, Innovator, Owatta, BA-88 (CIP-123), and BA-78 (CIP-112).

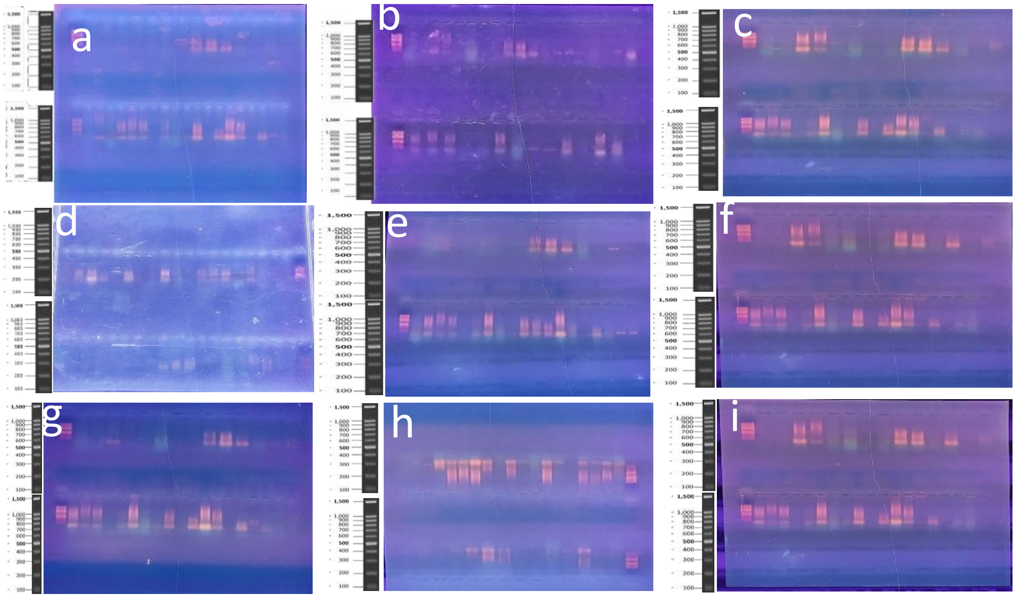

Fig. 1. Gel electrophoresis profile of 36 genotypes amplified with primers STM1049, STM 2022, STM2013, STM1104, STM1106, STM0037, STM0030, STM0019 and STM1031denoted a to i respectively.

## Genotypic distance

The inter-genotypic distances among 36 potato cultivars were analyzed to assess genetic diversity. The highest distance, 0.8571, was observed between BA-40 and BA-46, indicating significant genetic variation between these cultivars. Other notable pairs with high inter-genotypic distances included BA-62 and BA-66 (Pamela), with a distance of 0.8182, ranking 10th in Table 3, which presents all genotypic combinations in descending order of distance.

In contrast, the lowest inter-genotypic distances are summarized in Table 4. The smallest distance, 0.3333, was recorded for the pairs BA-91 (Carolous) vs. BA-41 and BA-91 (Carolous) vs. BA-54 (Musica). Additional pairs with slightly higher distances (0.5556) included BA-13 (Granola) vs. BA-41, BA-73 (CIP-127) vs. BA-12 (Dheera), BA-83 (Cimega) vs. BA-72 (CIP-139), BA-25 (Asterix) vs. BA-12 (Dheera), and BA-63 (9.125) vs. BA-57. These findings highlight varying levels of genetic diversity among the potato cultivars, highlighting significant differences as well as close genetic relationships within specific pairs.

Table 3. The ten highest inter genotypic distances among the 36 potato cultivars

| Serial No | Genotypic combinations | Distances |
|---|---|---|
| 1 | BA-40 vs BA-46 | 0.8571 |
| 2 | Alrusset vs BA-46 | 0.8462 |
| 3 | BA-81 (CIP-10) vs BA-46 | 0.8462 |
| 4 | Innovator vs BA-46 | 0.8333 |
| 5 | BA-31 (Sagetta)vs BA-90 (Alouette) | 0.8333 |
| 6 | BA-29 (Courage) vs BA-7 (Diamant) | 0.8333 |
| 7 | BA-63 (9.125) vs BA-48 | 0.8333 |
| 8 | BA-50 (7.86) vs BA-48 | 0.8333 |
| 9 | BARI Alu-48 vs BA-48 | 0.8333 |
| 10 | BA-62 (9.112) vs BA-66 (Pamela) | 0.8182 |

Table 4. The ten lowest inter genotypic distances among the 36 potato cultivars

| Serial No | Genotypic combinations | Distances |
|---|---|---|
| 1 | BA-91 (Carolous) vs BA-41 | 0.3333 |
| 2 | BA-91 (Carolous) vs BA-54 (Musica) | 0.3333 |
| 3 | BA-25 (Asterix) vs BA-66(Pamela) | 0.4 |
| 4 | Innovator vs BA-66(Pamela) | 0.5 |
| 5 | BA-13 (Granola) vs BA-90 (Alouette) | 0.5385 |
| 6 | BA-13 (Granola) vs BA-41 | 0.5556 |

| Serial No | Genotypic combinations | Distances |
|---|---|---|
| 7 | BA-83 (Cimega) vs BA-72 (CIP-139) | 0.5556 |
| 8 | BA-73 (CIP-127) vs BA-12 (Dheera) | 0.5556 |
| 9 | BA-25 (Asterix) vs BA-12 (Dheera) | 0.5556 |
| 10 | BA-63 (9.125) vs BA-57 | 0.5556 |

### Factorial analysis via scatter diagram

The factorial analysis provided insights into genetic distances among 36 potato cultivars, as illustrated in Figure 2. The analysis revealed both substantial genetic diversity and close genetic relationships among the cultivars. The highest genetic distance, 0.190, was observed between BA-54 (Musica) and BA-66 (Pamela), indicating notable genetic dissimilarity, highlighting its distinct genetic makeup. Conversely, the lowest genetic distance, 0.018, was recorded between BA-88 (CIP-123) and BA-13 (Granola), as well as between BA-63 (9.125) and BA-57, reflecting their close genetic relationships.

The 36 cultivars were grouped into three distinct clusters based on their genetic relationships:

**Group 1 (14 genotypes):** BA-41, BA-54 (Musica), BA-46, BA-53, BA-91 (Carolous), BA-37, BA-52 (Labadia), BA-28, BA-90 (Alouette), BA-7 (Diamant), BA-29 (Courage), BA-57, BA-40, and BA-13 (Granola).

**Group 2 (18 genotypes):** A-lrusset, BA-48, BA-63 (9.125), BA-72 (CIP-139), BA-12 (Dheera), BA-60 (Vivaldi), BA-66 (Pamela), BA-81 (CIP-10), BA-83 (Cimega), BA-71 (Dolly), BA-73 (CIP-127), BA-50 (7.86), BA-62 (9.112), BA-89 (13.7), BA-25 (Asterix), BA-86 (12.13), BA-31 (Sagetta), and BA-81.

**Group 3 (4 genotypes):** Innovator, Owatta, BA-88 (CIP-123), and BA-78 (CIP-112).

The clustering analysis supports the conclusion that genotypes within the same group share closer genetic relationships than those in different clusters. These findings align with prior research on potato genetic diversity. For instance, Rahman et al. (2016) similarly demonstrated that cultivars from distinct clusters exhibit marked differences, while those within the same cluster show fewer variations. The consistency between these results and previous studies underscores the robustness of the current analysis and its implications for understanding potato genetic diversity.

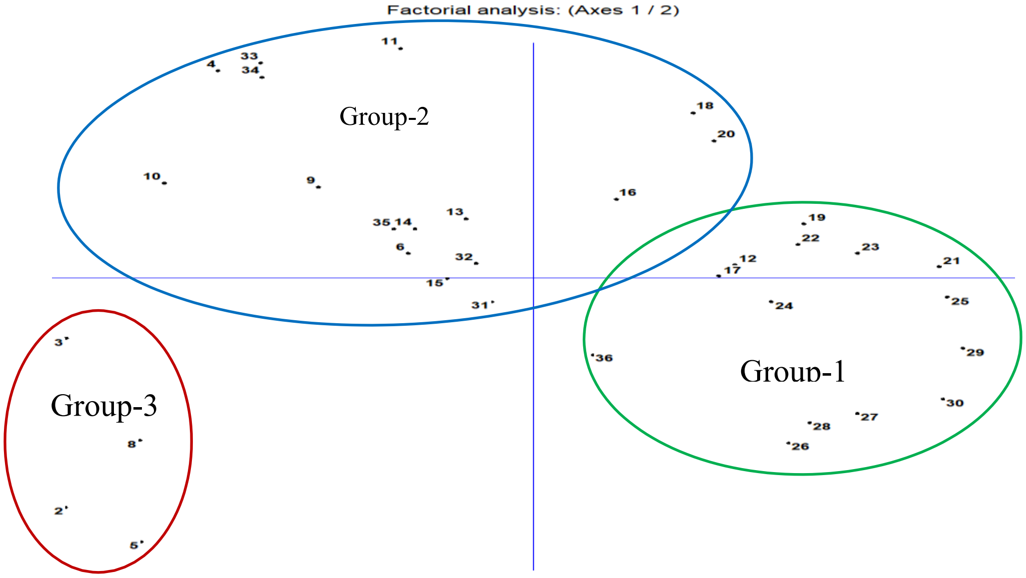

Fig. 2. Scatter plot from factorial analysis illustrating the genetic distribution of 36 potato cultivars.

### Clustering of genotypes using SSR data

An unweighted neighbor-joining dendrogram constructed using DARwin software 6.0 (Figure 3) depicted the genetic relationships among 36 potato genotypes based on nine SSR markers. The analysis grouped the genotypes into three distinct clusters based on their genetic similarities:

**Cluster I:** Included three genotypes (BA-29, BA-57, and BA-40) with closely related genetic backgrounds.

**Cluster II:** Comprised 17 genotypes, including BA-48, BA-63 (9.125), BA-72 (CIP-139), BA-12 (Dheera), BA-60, BA-66 (Pamela), BA-81 (CIP-10), BA-83 (Cimega), BA-71, BA-73 (CIP-127), BA-50 (7.86), BA-62 (9.112), BA-25 (Asterix), BA-86 (12.13), and others.

**Cluster III:** Included 16 genotypes such as BA-41, BA-54 (Musica), BA-46, BA-53, BA-91 (Carolous), BA-37, BA-52 (Labadia), BA-28, BA-90 (Alouette), BA-7 (Diamant), BA-13 (Granola), Alrusset, BA-31 (Sagetta), Innovator, Owatta, and BA-88 (CIP-123).

The dendrogram provides valuable insights into the genetic relatedness of the genotypes, offering a foundation for effective crop improvement strategies. The clustering patterns help identify genetically diverse genotypes, which are critical for breeding programs aimed at enhancing genetic variability and introducing desirable traits. This analysis underscores the utility of SSR markers in elucidating genetic diversity and informing the selection of breeding components.

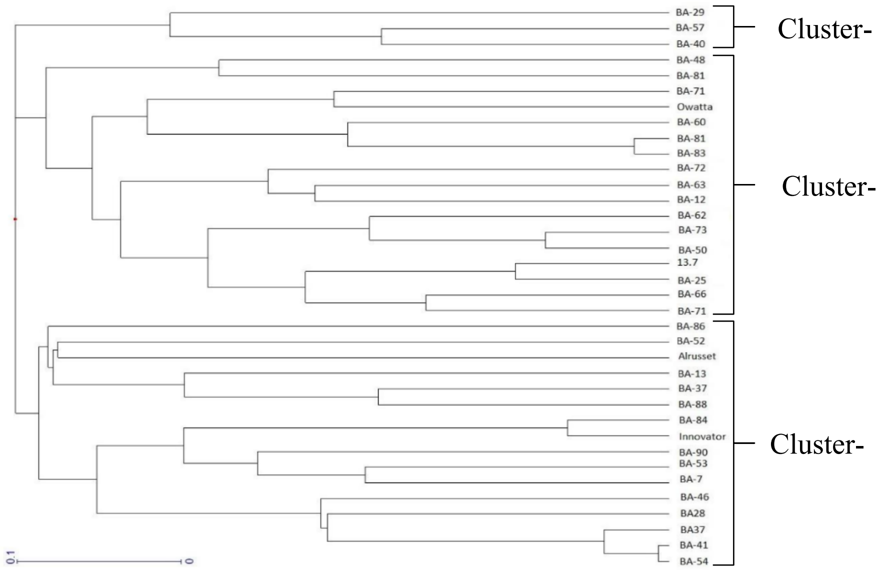

Fig. 3. Unweighted neighbor jointing genetic relationship among 36 potato genotypes based on SSR allele data.

In this study, nine SSR markers were utilized to assess polymorphism across different potato varieties. The polymorphism information content (PIC) values ranged from 0.43 to 0.90, with a mean of 0.80, while genetic diversity values varied between 0.44 and 0.90, with an average of 0.81. These findings highlight the effectiveness of SSR markers in capturing genetic variation.

Similar research has also explored potato genetic diversity. For instance, Liao et al. (2014) evaluated potato cultivars from Yunnan Province using 24 SSR markers. The PIC values ranged from 69.31% to 93.67%, with a mean of 86.47%. Genetic similarity among these cultivars ranged between 0.5987 and 0.7632, suggesting relatively low genetic diversity. Similarly, Galani et al. (2015) characterized Indian potato varieties for cold-induced sweetening using SSR markers, reporting pair-wise genetic similarity values from 0.390 (DSP 287 and Kufri Himsona) to 0.889 (Kufri Lauvkar and Kufri Bahar), with an average similarity of 0.671. Close parental relationships, such as DSP 287 and DSP 186, showed higher genetic similarity (0.714).

In the current study, the maximum genetic distance of 0.190 was observed between BARI Alu-56 and BARI Alu-35, indicating significant genetic dissimilarity. Conversely, the lowest genetic distance, 0.018, was recorded between BARI Alu-36 and BARI Alu-45 (Steffi), indicating close genetic relatedness.

Previous studies have also employed dendrogram analyses for clustering potato varieties. Chimote et al. (2007) grouped 32 Indian potato varieties into three major and five minor clusters. Consistently, this study categorized 36 potato varieties developed by the Bangladesh Agricultural Research Institute (BARI), Gazipur, into three major clusters. Among the markers, STM0030 and STM2013 exhibited the highest genetic diversity, with PIC values of 0.90. These results underscore the wide genetic diversity present in BARI-developed potato varieties. The findings reaffirm the utility of SSR markers as a reliable tool for assessing genetic diversity, which is crucial for breeding programs and the development of improved cultivars.

## Conclusion

This study evaluated the molecular diversity of 36 potato genotypes using nine SSR markers, revealing significant genetic variation. Eight of the markers were highly polymorphic, amplifying a total of 95 alleles, with STM2013 and STM0030 demonstrating the highest polymorphism (90%) and gene diversity (90%). The cluster analysis based on SSR markers identified three main genetic groups, which were further supported by factorial analysis, grouping the genotypes into three distinct clusters based on genetic distance. The results underscore the substantial genetic diversity present within the studied genotypes, highlighting the potential for utilizing this variation in potato breeding programs. The findings also demonstrate the effectiveness of SSR markers, particularly STM2013 and STM0030, as valuable tools for genetic studies and germplasm evaluation in potato.

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