

(Original Article)



Assessment of Somaclonal Variants of *Salvia splendens* at Different Subcultures Using Molecular Markers

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Abstract

Genetic variability induced by cell and tissue culture techniques provides a new source of diversity for improvement of ornamental plants species. For this purpose, the effect of Thidiazuron (TDZ) on callus induction and number of subcultures of *Salvia splendens* was studied. The results showed that the MS medium supplemented with TDZ (0.5 mg/l) and Indole Acetic Acid IAA (0.1 mg/l) produced the highest percentage for explants producing callus (60%). For shoot multiplication, the best results were achieved when shoot tips were cultured on MS medium supplemented with TDZ (0.2 mg/l) alone. For subculture the same concentration of TDZ (0.2 mg/l) in media of eleven subcultures were performed at 21-day intervals over a total period of 231 days. For molecular variation detection, SCoT molecular markers were employed. Five SCoT primers were used and a total of 24 bands were obtained. The results showed high level of polymorphism between parent and their regenerated plants (subculture No. 11). These markers revealed distinctly different patterns of DNA fragments in all somaclones, and some distinctive bands were linked to the regenerated plants. For rooting, the best rooting percentage (100.00%), highest number of roots/shoot (7.00) and root length (2.58 cm) were observed when the shoots were cultured on MS hormone-free medium supplemented with 15 g sucrose/l. Plantlets were successfully acclimatized on Peat moss + perlite (1:1) with a survival rate of 100 %.

Keywords: *Micropropagation*, *Subcultures cycle*, *SCoT markers*, *Thidiazuron (TDZ)*.

Introduction

The genus *Salvia* (Lamiaceae) consists of about 900 species including shrubs, herbaceous perennials, and annuals (Karousou *et al.*, 2000).

Salvia splendens is commonly known as Scarlet sage (Shanker and Unnikrishnan 2001; Bobbi 2003) and considered as one of the most commonly observed ornamental perennial plants in the landscape (Erv, 2000). It is characterized by a wide color variation, long-lasting flowering, heat tolerance and resistance to pests and diseases (Regnault, 1997; Alberto *et al.*, 2003). *Salvia splendens* is a worldwide popular bedding plant with a significant economic value

and widely cultivated in many countries around the world (Stepankova, 2001). *Salvia splendens* is among the most commonly cultivated herbaceous ornamental plants and frequently planted for edging walkways and borders in gardens, flowerbeds, and by roadsides (Soundararajan *et al.*, 2013). Therefore, it is of great practical importance to breed new varieties to meet the demand of market for new high-quality varieties (Hui *et al.*, 2004; Fu *et al.*, 2009; and Chen *et al.*, 2016).

As a seasonal flower with decorative values and such worldwide importance in landscaping, micropropagation and tissue culture techniques can provide the plant breeders protocols and methods for plant genetic manipulation of *Salvia splendens*. During in vitro culture, many factors may affect the fidelity of the genotypes leading to the occurrence of somaclonal variation i.e., genetic and epigenetic variation (Larkin and Scowcroft 1981; Cassells, 2002; Bairu *et al.*, 2011; Ferreira *et al.*, 2023). These factors include: plant genotypes, the explant source, the type and concentration of plant growth regulators, propagation methods and the number as well as the interval of subcultures (culture age). Such, variations could demonstrate improvement in the quality of genotype and its yield.

Several methods (morphological, cytological, biochemical and molecular methods) have been reported to detect somaclonal variants (Bairu *et al.*, 2011; Ranghoo-Sanmukhiya, 2021). A number of PCR based molecular markers like random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), inter simple sequence repeat (ISSR), simple sequence repeat (SSR) and start codon targeted (SCoT) polymorphism are preferred for the detection of somaclonal variation (Rai, 2022). Because of its many advantageous characteristics, and its many desirable features the start codon targeted (SCoT) polymorphism marker has gained significant importance in plant genetics, genomics, and molecular breeding. Targeted by the SCoT marker is the highly conserved area of plant genes that surrounds the start codon Start codon targeted (SCoT) polymorphism marker. SCoT marker targets the region nearby the start codon, a highly conserved region in plant genes (Collard and Mackill 2009; Rai, 2023).

This study was conducted for assessment the morphological and molecular variation of in vitro-propagated plants of *Salvia splendens* at different subcultures using SCoT molecular markers.

Materials and Methods

This work was carried out at plant tissue culture laboratory, Department of Ornamental Plants and Landscape Gardening, Faculty of Agriculture, Assiut University.

Plant material and in vitro culture establishment

Shoot tips of *Salvia splendens* was collected from recent branches growing in greenhouse of the nursery of ornamental plants Faculty of Agriculture, Assiut University. The healthy shoot tips (0.5cm) were washed thoroughly in running tap water for 30 min. Then, they were transferred to laminar flow hood for sterilization using 30% commercial bleach (5% NaOCl) for 20 minutes. The ends of the shoot

tips were cut and all the explants (0.3- 0.5 cm) were rinsed three times using sterile distilled water and cultured in 250 ml jars containing 30 ml of MS medium (Murashige and Skoog, 1962). The MS medium was supplemented with 3% (w/v) sucrose and 8 g/l agar and the pH of the medium was adjusted to ± 5.8 before autoclaving at 121° C and 1.5 kg/cm² for 20 min. The cultures were incubated at 24 \pm 2° C for 16 hours under light of cool white fluorescent tubes.

Callus induction

Shoot tips (~ 0.3 – 0.5 cm) were used as explants and grown on MS basal medium supplemented with Thidiazuron (TDZ) at different concentrations (0.0, 0.25, 0.5 and 1 mg/l) combined with Indole Acetic Acid (IAA) at 0.00, 0.10 mg/l. The percentage of explant producing callus, its color and texture were observed and recorded after 4 weeks. The factorial experiment (2 \times 4) was carried out in a randomized complete block design (RCBD) with three replicates per treatment and five jars per replicate each jar containing 2 explants.

Adventitious shoot from callus explants

Pieces (~0.5 g) of callus were cultured onto MS medium supplemented with 30 g/l sucrose and different concentrations of TDZ (0.0, 0.1, 0.2, 0.3, 0.4 and 0.5 mg/l). Data were obtained after 4 weeks on percentage of regeneration, Shoots number/ explant and leaf number/ explants of *Salvia splendens*.

An experiment in a completely randomized design (CRD) with three replicates was used. Each replicate comprised five jars, each jar containing two pieces of callus.

Shoot multiplication

Shoot tips (~1 – 1.5 cm) were excised from the regenerated shoots of callus. Two shoots were cultured onto a 250 ml baby-food jar filled with 30 ml MS basal medium supplemented with 30 g/l sucrose and different concentrations of TDZ (0.0, 0.1, 0.2, 0.3, 0.4 and 0.5 mg/l). After 4 weeks of culture, data on regeneration percentage, number of shoots/ explant, shoot length (cm), and number of leaves/shoot were recorded. The plants resulting from this stage were used for next stage.

Subculture cycles during *Salvia splendens* micropropagation

To assess how is the number of subculture cycles affect somaclonal variation? The multiplication rate (expressed as a number of shoots/explant) during micropropagation of *Salvia splendens* shoots were transfer from multiplication stage and subculture on fresh MS medium supplemented with 0.2 mg/l (TDZ). Two shoots were placed in each vessel and five vessels were used per replicate. Regeneration percentage, number of shoots/ explants and shoot length were registered. Over a period of 231 days, eleven subcultures were carried out at intervals of 21 days. The experiment was arranged in a complete randomized design (CRD) with three replicates.

Experimental design and data analysis

For all the experiment, data were subjected to analysis of variance (ANOVA), and mean comparisons were performed using the LSD at probability level of 5% (Gomez and Gomez, 1984).

Detecting of somaclonal variation and molecular assays

The plant samples (0.5 g/ each) were excised from the leaves of mother plant and leaves from shoots grown in each subculture (No.2 to subculture No.11) were used for DNA extraction.

DNA extraction

Total genomic DNA of the studied samples, was extracted from fresh leaves, using Cetyl trimethyl ammonium bromide (CTAB) protocol for plants (Murray and Thompson, 1980). Concentration and quality of DNA was measured at 260/280 nm using a spectrophotometer and checked by separating DNA on 0.8% agarose gel. Each sample was diluted to 50 ng/μl with TE buffer (10mM Tris-HCl, pH 8.0 and 0.1mM EDTA, pH 8.0) and stored at 4 °C for further use.

SCoT markers analysis

Five start codon targeted (SCoT) primers (Table 4), (metabion international AG) were used to amplify the DNA template of our samples. The amplification PCR reactions were carried out in 25μl final volumes, containing (11.0 μl dH₂O, 3 μl of 10x buffer, 3.0 μl of dNTPs (2.5mM) 4 μl of Mg C12 (25 m M), 3.0 μl primer (2.5μl), 0.3 μl of Taq polymerase (5U/ μl) and 2.0 μl of genomic DNA (50 ng/ml). Amplification of SCoT primers was performed in a programmed thermocycler (C-1000) with initial denaturation at 94°C for 3min, 36 cycles of denaturation at 94°C for 1min, primer annealing at 51°C for 1min, extension at 72°C for 1min, and final extension at 72°C for 3min.

Molecular data analysis

Five primers for SCoT provided distinct and robust band patterns. The DNA banding patterns generated by SCoT markers were analyzed and the presence (1) or absence (0) of each band was recorded for each sample for all the tested primers. Using NTsys PC software, a separate cluster analysis based on SCoT data was conducted, and a dendrogram was created according to Jaccard's (1908) coefficient for the unweighted pair-group method with arithmetic averages (UPGMA). Furthermore, data on a dendrogram displaying SCoT markers was also obtained. Moreover, some diversity parameters were calculated from molecular data of all markers, including percentage of polymorphism (%P), polymorphism information content (PIC), primer resolving power (RP), diversity index (DI) and marker index (MI) (Nei, 1987; Prevost and Wilkinson, 1999; Roldan-Ruiz *et al.*, 2000; Varshney *et al.*, 2007).

Rooting stage

The micro-shoots (from each subculture) were tested to induce roots and obtain complete plantlets to be hardened and transferred to the field with a minimum loss. So, shoots of 3-4 cm in length were cultured on half-strength MS

medium without PGRs supplemented with 15 g/l sucrose. Rooting percent, number of roots/plant and root length (cm) were recorded.

Acclimatization stage

The rooted plantlets (~4 cm in length) were gently removed from the culture medium, then the roots were rinsed thoroughly with tap water to remove the excess medium. All the plantlets were transplanted into small plastic pots (10 cm diam.) filled with a mixture of peat moss and perlite (1:1 v/v). Four weeks later, data on the survival rate of the plants was calculated.

Results and Discussion

Effect of PGRs on culture establishment and callus induction

Data presented in Table 1 showed significant effects among concentrations of TDZ with IAA for callus formation of *Salvia splendens*. A green compact callus was induced from shoot tips of *Salvia splendens* cultured on media supplemented with any concentration of TDZ used or when IAA at 0.1 mg/l was combined with TDZ at all concentrations used. Meanwhile, the PGRs-free medium did not produce callus (Table 1). The medium supplemented with TDZ at 0.5 mg/l plus IAA at 0.1 mg/l resulted in the highest percentage for explants producing callus (60%). (Huii *et al.*, 2012) reported that the highest rate of callus induction from leaf and stem explants of *S. splendens* occurred in the medium containing 1.0 mg/L 2,4-D and 1.5 mg/l BAP. On the other hand, (Yu *et al.*, 2015) explained that the whole plantlets of *Salvia splendens* could be rapidly regenerated without intermediate callus stage to avoid the occurrence of any genetic or and epigenetic variation. Many investigations report protocols for direct regeneration by organogenesis and clonal propagation for commercial industry of *Salvia* published by many Authors (Sharma *et al.*, 2014; Kabir *et al.*, 2014; Yu *et al.*, 2015 and Papafotiou *et al.*, 2023).

Table 1. Effect of different concentrations of TDZ and IAA on callus induction of *Salvia splendens* after four weeks in culture

| IAA mg/l | TDZ mg/l | Explants producing callus % | | | | | Visual observations on callus characteristics | | | |
|------------------|-------------|--------------------------------|------|------|------|-------|--|----------------------------|----------------------------|----------------------------|
| | | 0.00 | 0.25 | 0.50 | 1.00 | Mean | 0.00 | 0.25 | 0.50 | 1.00 |
| 0.0 | 0.0 | 0.0 | 10.0 | 30.0 | 40.0 | 20.0 | ----- | Friable and green | green | Friable and green |
| 0.1 | 0.0 | 0.0 | 30.0 | 60.0 | 40.0 | 32.5 | ----- | Compact green callus | Compact green callus | Compact green callus |
| Mean | 0.0 | 20.0 | 45.0 | 40.0 | | | | | | |
| LSD 0.05 | | | | | | | | | | |
| TDZ | | | | | | 7.94 | | | | |
| IAA | | | | | | 5.61 | | | | |
| TDZ x IAA | | | | | | 11.22 | | | | |

TDZ: Thidiazuron, IAA: Indole Acetic Acid



Figure 1. *In vitro*-propagated *Salvia splendens*. (A) Mother plant of *Salvia splendens*; (B) Explant (Shoot tips); (C) callus induction on MS medium with 0.25 mg/l TDZ with 0.1 IAA after 4 weeks; (D) Adventitious shoot multiplication on medium with 0.2 mg/l TDZ after 4 weeks (E). Rooting of isolated single shoot on 1/2 MS medium with 15 g sucrose/l; (F) Acclimatized plantlets transferred to plastic pots filled with Peat moss + perlite (1:1) after 3 weeks.

Effect of TDZ on adventitious shoot from callus explants

Data in Table 2 revealed significant effects on shoots regenerated from callus of *Salvia splendens* when callus was cultured on medium supplemented with different concentration of TDZ (0.0, 0.1, 0.2, 0.3, 0.4 and 0.5 mg/l). The regeneration percentage was ranged from 10% (control treatment without TDZ) to 100% (TDZ at 0.4 mg/l). However, Applying TDZ from 0.2 up to 0.5 mg/l produced the highest regeneration rate with no significance difference among them. TDZ (0.2 mg/l) produced the highest number of shoots (16 shoots/explant), shoot length (3.61 cm) and leaves-number (28 leaves /shoots) with regeneration rate of 90%.

The regenerated shoots look normal and no phenotypic change was observed at this stage. Indirect regeneration methods through the callus induction could

result in morphological genetic and epigenetic variations (Maruthi *et al.*, 2012; and Huii *et al.*, 2012). De Souza *et al.*, 2021 reported that callus formation during micropropagation may have been responsible for the abnormality in 5% of the regenerated plants.

Table 2. Effect of different concentrations of Thidiazuron (TDZ) on shoots regenerated from callus explants of *Salvia splendens* after four weeks in culture.

| TDZ mg/l | Regeneration % | Shoot number/ explant | Shoot length (cm) | Leaves number/ explant |
|-----------------|----------------|--------------------------|----------------------|---------------------------|
| 0.00 | 10.00 | 1.00 | 2.25 | 3.00 |
| 0.10 | 70.00 | 4.20 | 3.34 | 19.00 |
| 0.20 | 90.00 | 16.00 | 3.61 | 28.00 |
| 0.30 | 90.00 | 13.00 | 3.13 | 31.00 |
| 0.40 | 100.00 | 9.00 | 3.44 | 23.00 |
| 0.50 | 90.00 | 5.50 | 4.11 | 17.00 |
| L.S.D 5% | 12.58 | 1.13 | 0.52 | 4.04 |

Effect of TDZ on shoot multiplication

The regenerated adventitious shoots excised from callus formed in the previous stage were multiplied on MS medium supplemented with different concentrations of TDZ (0.0, 0.1, 0.2, 0.3, 0.4 and 0.5 mg/l). It is clear from the results represented in Table 3, that using TDZ (0.2 mg/l) induced the best number of shoots/explant (18.00 shoots), shoot length (5.41 cm) and number of leaves/explant (44.00 leaves) with 100% regeneration. Sharma *et al.*, 2014 mentioned that the ability of *S. splendens* explants to form new shoots varied with the explant's type and cytokinin used. They observed that BA (5.0 μ M) was more effective than other cytokinins (Kinetin, 2-iP and TDZ) in inducing shoot regeneration of *Salvia splendens*. However, they observed that shoot tips when cultured on MS medium with TDZ at 0.1 mg /l produced 3.8 shoots/explant shoot length (1.9 cm) and 82% regeneration. The application of plant growth regulators and endogenous plant hormones are factors that can induce genetic variability. The endogenous accumulation of growth regulators in the explant that favors an increase in the multiplication rate during the subculture cycles may cause inhibition of growth and variation, and subsequently the excess of growth regulators may act as a mutagenic agent (Ferreira *et al.*, 2023).

Sales and Butardo (2014), reported that, several growth regulators, such as NAA, 2,4-D and BAP may be responsible for obtaining in vitro genetic instability. Some studies have shown that TDZ are responsible for somaclonal variants (Bairu *et al.*, 2006; Bidabadi, *et al.*, 2010 and Samarfard *et al.*, 2014).

Table 3. Effect of different concentrations of Thidiazuron (TDZ) on multiplication of shoots of *Salvia splendens* after four weeks in culture

| TDZ mg/l | Regeneration % | Shoot number/ explant | Shoot length (cm) | Leaves number/ explant |
|-----------------|----------------|--------------------------|----------------------|---------------------------|
| 0.00 | 70.00 | 2.00 | 2.15 | 5.00 |
| 0.10 | 90.00 | 11.00 | 4.26 | 32.00 |
| 0.20 | 100.00 | 18.00 | 5.41 | 44.00 |
| 0.30 | 100.00 | 17.00 | 5.23 | 35.00 |
| 0.40 | 100.00 | 12.00 | 3.84 | 25.80 |
| 0.50 | 100.00 | 14.00 | 4.50 | 31.00 |
| L.S.D 5% | 10.27 | 2.91 | 0.87 | 2.67 |

Effect of subculture cycles on shoot multiplication

Eleven subcultures were performed at 21-day intervals over a total period of 231 days. The number and length of shoots showed significant differences among subculture cycles (Fig 2). The reduction in number of shoots per explant was observed from subcultures 9 to 11 (Fig 2 b), while a significant decline in shoot length was observed in subculture 10 and 11 (Fig 2 c). At the phenotypic level, some genotypes remained stable over five subcultures (de Souza *et al.*, 2021). Regarding the regeneration rate, there were no significant differences among subculture cycles from 1 to 10 but at subculture 11 (Fig. 2 a), a significant reduction was observed (80 %) compared to subculture 1 (100%).

Morphological variations in banana plants subjected to micropropagation were observed at 10th subculture cycle (Khan *et al.*, 2011). They observed a reduction in the multiplication rate and an increase in somaclonal variation frequency after eight subcultures. The effect of subculture frequency on genetic variations has been investigated by several researchers (Peng *et al.*, 2015; Graner *et al.*, 2019; Pastelin-Solano *et al.*, 2019 and Hesami *et al.*, 2023). The results obtained in this study showed that subculture cycles have an effect on the regeneration rate, shoot length and number of shoots in *S. splendens* micropropagation. Similar results obtained by Hesami *et al.*, (2023) showed that regeneration rate and shoot length have been shown to decrease as the number of subcultures increases. This may be due to endogenous hormone content (Peng *et al.*, 2015).

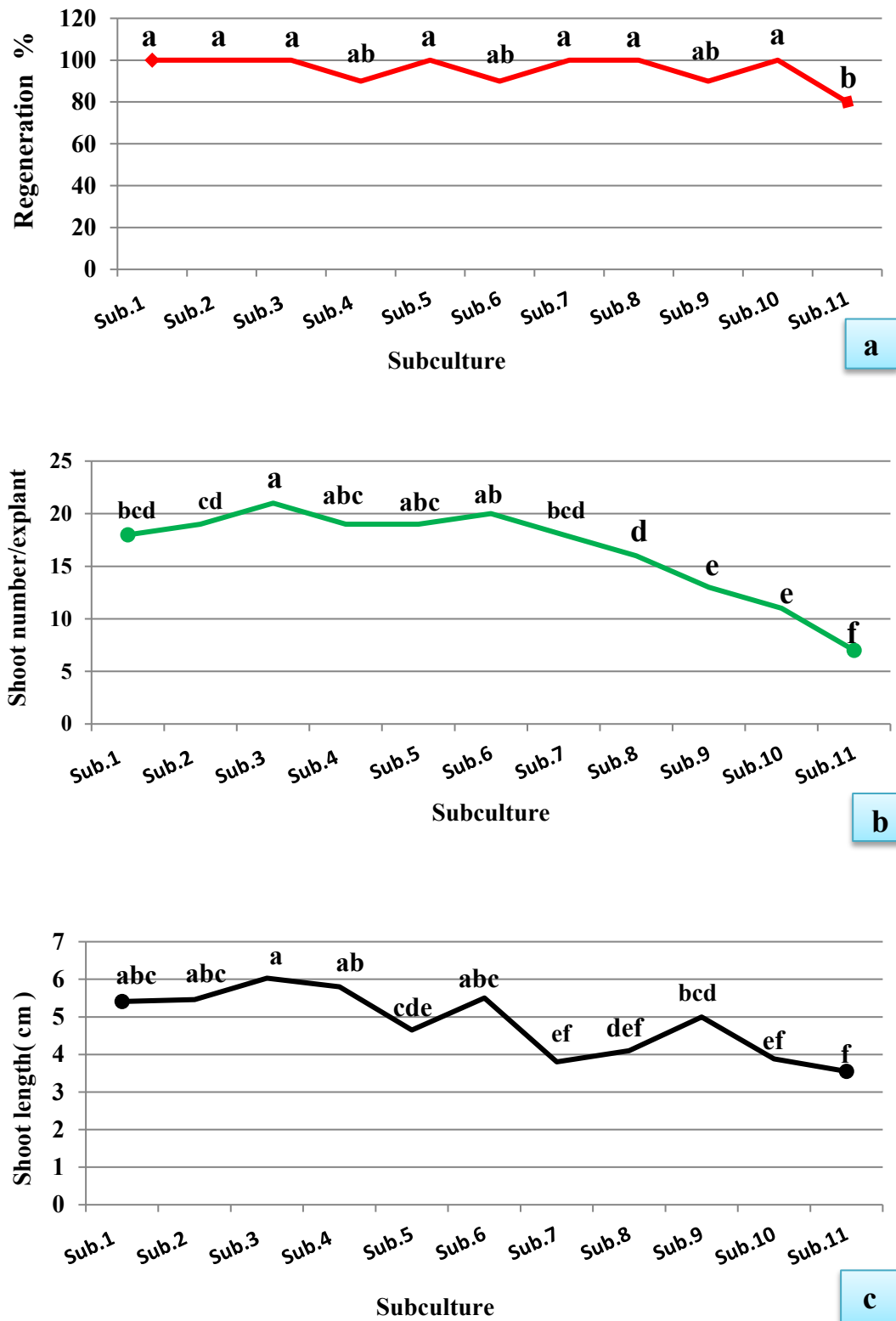


Figure 2. Effect of subculture cycles on shoot regeneration (a), shoot number/explant (b) and shoot length cm (c) during micropropagation of *Salvia splendens* cultured in MS + 0.2 mg/l TDZ. a,b..f: different letters means significant differences at 0.05

Effect of subculture cycles on somaclonal variation and molecular assays

Five SCoT (Table 4) provided repeatable outcomes and polymorphic bands, which were taken into consideration for data analysis. Distinct differences in the reproducible bands obtained from samples (from the mother plant and from subculture No.2, subculture No.11) are shown in Figure 3 and Table 4.

Table 4. Primer sequences and codes used in this study

| Primer codes | Sequence (5' to 3') | Temp. (°C) | |
|--------------|---------------------|--------------------|----|
| SCoT-10 | CAACAATGGCTACCAGCC | 53 | |
| SCoT-18 | ACCATGGCTACCACCGCC | 54 | |
| SCoT | SCoT-22 | AACCATGGCTACCACCAC | 53 |
| | SCoT-28 | CCATGGCTACCACCGCCA | 54 |
| | SCoT-32 | CCATGGCTACCACCGCAC | 53 |

Furthermore, a number of diversity metrics were computed using the marker data, including polymorphism information content (PIC), primer resolving power (RP), diversity index (DI), and marker index (Table 5).

Using several plant entries, SCoT amplified a total of 21 DNA fragments. The molecular size range of the SCoT-PCR products was from 720 bp (SCoT-10) to 1580 bp (SCoT-32) with an average of 4.2 fragments per primer (Figure 3). Out of the 21 fragments scored, 10 bands (48.00%) were found to be polymorphic and 11 loci (52.00 %) were found to be monomorphic in nature with an average of 2.00 polymorphic bands per primer (Table 5).

The polymorphism percentage (% P) ranged between 25.00% (for SCoT-10) and 100% (for SCoT-22). The polymorphic information content (PIC) values for the five SCoT primers varied from 0.11 (SCoT-10) to 0.44 (SCoT-22). The marker index (MI) values ranged from 0.11 (SCoT-10) to 2.20 (SCoT-22). The resolving power of primer (RP) values ranged from 0.66 to 3.30, the SCoT-22 primer gave the highest RP values (3.30) while SCoT-18 exhibited the lowest RP value (0.66) (Table 5). The diversity index (DI) values ranged from 0.37 (SCoT-18) to 1.75 (SCoT-22). These markers revealed distinctly different patterns of DNA fragments in all somaclones and some distinctive bands were linked to the regenerated plants in all of the molecular markers examined. This may be due to somaclonal variations which were notable in their differences from the parents Rai, (2022).

Table 5. Genetic variation parameters produced with SCoT DNA markers⁽¹⁾

| Marker | Primer | TB | NPB | %P | PIC | RP | DI | MI |
|--------|----------------|-----|------|--------|-------|------|------|------|
| | SCoT-10 | 4 | 1 | 25.00 | 0.11 | 0.66 | 0.37 | 0.11 |
| | SCoT-18 | 2 | 0 | 00.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| | SCoT-22 | 5 | 5 | 100.00 | 0.44 | 3.30 | 1.75 | 2.2 |
| SCoT | SCoT-28 | 3 | 2 | 67.00 | 0.29 | 1.32 | 0.75 | 0.58 |
| | SCoT-32 | 5 | 2 | 40.00 | 0.18 | 1.32 | 0.64 | 0.36 |
| | Total | 21 | 10 | -- | -- | -- | -- | -- |
| | average | 4.2 | 2.00 | 46.40 | 0.204 | 1.32 | 0.70 | 0.65 |

⁽¹⁾ TB= Total Bands, NPB= Number of Polymorphic Bands, %P= percentage of polymorphism, PIC= polymorphic information content, RP= Resolving Power, DI= diversity index, MI= Marker Index.

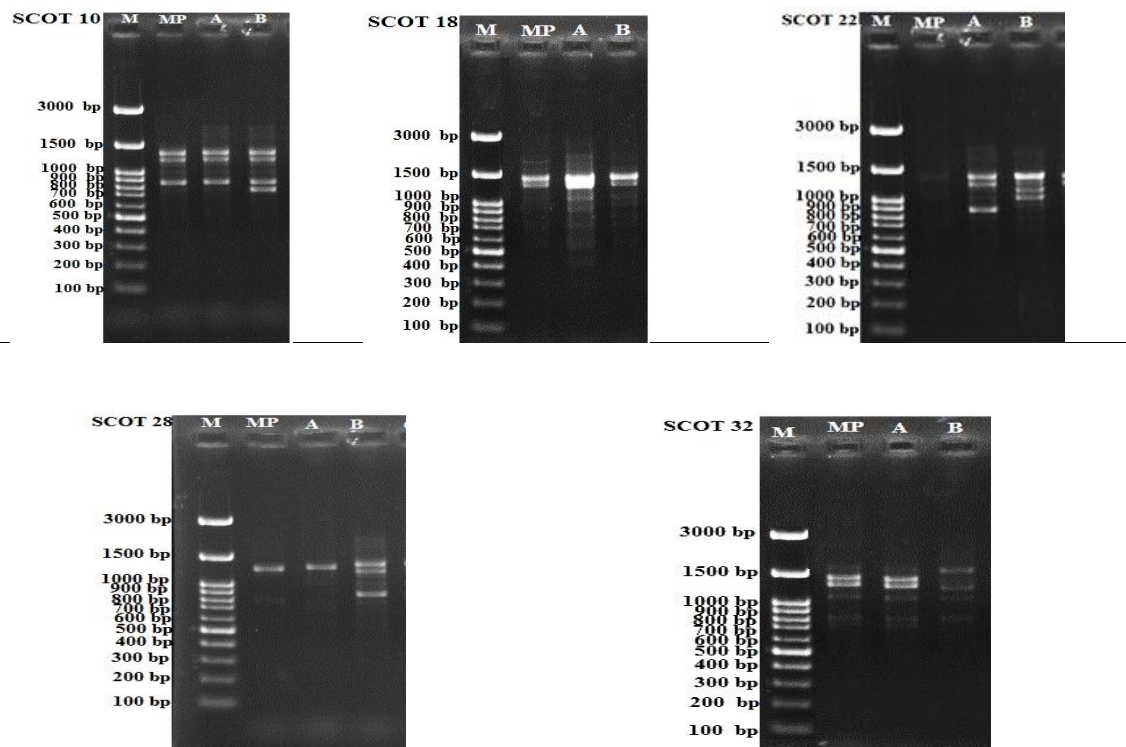


Figure 3. SCoT banding profile of *Salvia splendens*. M: represented the DNA ladder, MP: Mother plant, A: proliferated plants from subculture-2, B: proliferated plants from subculture-11

The three samples were divided into two main groups by the dendrogram (Figure 4). Mother plant (MP) and proliferated plants from subculture-2 (A) with similarity (0.769) are found in group 1. Proliferated plants from subculture-11 (B) with node 1 (MP+ A) and cluster-2 included with a similarity of 0.528.

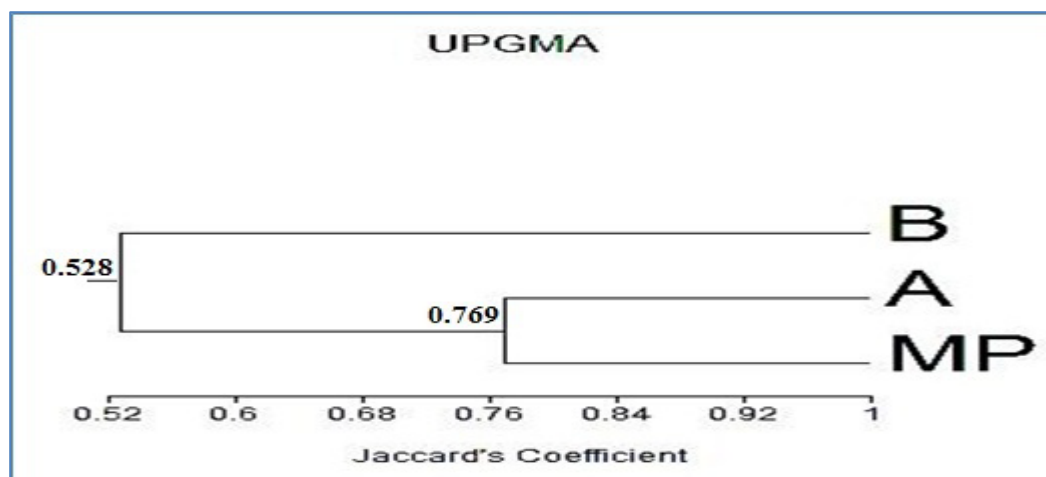


Figure 4. A dendrogram was created by applying UPGMA analysis to the data from five SCoT primers. The scale depends on the coefficients of Jaccard. MP: Mother plant, A: proliferated plants from subculture-2, B: proliferated plants from subculture-11

Molecular analysis has detected somaclonal variation in many species (Pastelín Solano *et al.*, 2019; Tikendra *et al.*, 2021; Gawroński and Dyduch-Siemńska 2022; and Rai 2022). Khan *et al.*, (2011), in *Musa* spp., reported that after subculture eight, the percentage of somaclonal variants was detected using SSR markers. Farahani *et al.*, (2011), in *Olea europea*, observed morphological change and genetic variation among the regenerated plants after subculture seven. Similar results were reported in *Stevia rebaudiana* by Soliman *et al.*, (2014) and *Pistacia lentiscus* by Kılinc, *et al.*, (2015), in which the greatest genetic instability was detected in the highest number of subcultures. Somaclonal variation has been detected in many micropropagated plant species using ISSR markers (Bello-Bello *et al.*, 2014; Martínez-Estrada *et al.*, 2017; Babu *et al.*, 2018). However, SCoT markers are gaining popularity over other dominant DNA marker systems like RAPD and ISSR for higher polymorphism and better marker resolvability (Gorji *et al.*, 2011; Satya *et al.*, 2015; Shalan *et al.*, 2023). Moreover, Antony *et al.*, (2015) used start codon targeted polymorphism (SCoT) DNA markers for the identification of somaclonal variation in cryopreserved *Dendrobium* Bobby Messina.

Rooting and Acclimatization of regenerated shoots

As shown in Figure 1 E shoots were easily rooted (100%) after 3 weeks when cultured on half-strength MS medium supplemented with sucrose at 15 g/l. Acclimatization of plantlets is a vital step in the micropropagation protocol of any plant species. It involves the transfer of plantlets from tissue culture containers to *ex vitro* conditions. In the present study, a plantlet of *Salvia splendens* was acclimatized as shown in Figure 1 F. The plantlets were transferred to plastic pots with peat moss and perlite (1:1 v/v) after four weeks. Plantlets were successfully acclimatized with 100 % survival rate.

Conclusion

In conclusion, the subculture number affects somaclonal variation and in vitro development of *Salvia splendens*. In our study, the polymorphism found after the eleven subculture in MS medium supplemented with 0.2 mg/l TDZ suggests that it could be a promising protocol for plant breeders. However, if the objective is to maintain high genetic fidelity during micropropagation for commercial purpose, it is recommended that in shoot multiplication stage no more than five subcultures. For further studies of micropropagation of *Salvia splendens* on a commercial scale, it is recommended that number of subculture must be mentioned.

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تقييم الاختلافات الوراثية لنبات السالفيا الحمراء عند دورات إكثار مختلفة باستخدام الواسمات الجزيئية

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الملخص

يوفر التباين الوراثي الناتج عن زراعة الخلايا والأنسجة مصدرًا جديدًا للتنوع لتحسين أنواع نباتات الزينة. لذلك كان الهدف دراسة تأثير الثيديازيرون (TDZ) على تحفيز إنتاج الكالس وكذلك تم دراسة عدد دورات النقل الي البيئات والإكثار لنبات السالفيا الحمراء.

وقد أشارت النتائج إلى أن الوسط المغذي الذي يحتوي على TDZ بتركيز 0.5 ملجم/لتر مع IAA بتركيز 0.1 ملجم/لتر أدى إلى أعلى نسبة لإنتاج الكالس (60%).

بالنسبة لتضاعف الأفرع، تم الحصول على أفضل النتائج عندما تمت زراعة قمة الفرع على بيئة (MS) موراشيغ وسكوج المضاف إليها الثيديازيرون TDZ بتركيز 0.2 ملجم/لتر.

بالنسبة لدورات الإكثار، تم استخدام نفس تركيزات TDZ عند 0.2 ملجم / لتر وتم نقل الأفرع القمية لعدد إحدى عشر (11) دورة إكثار على فترات 21 يومًا خلال فترة إجمالية قدرها 231 يومًا.

للكشف عن الاختلافات الوراثية، تم استخدام الواسم من النوع SCoT وتم استخدام خمس بادئات SCoT وتم الحصول على إجمالي 24 حزمه. أظهرت النتائج وجود تعدد أشكال عالي بين النباتات الأم ونباتاتها المتجددة من دورة الإكثار رقم (11). أظهرت الواسمات عن تعدد أشكال الذي يظهر أنماطًا مختلفة بشكل واضح لشظايا الحمض النووي، وقد لوحظت بعض الحزم الجديدة في النباتات المتجددة في جميع الواسمات الجزيئية التي تمت دراستها.

بالنسبة للتجذير، لوحظ أن أفضل نسبة تجذير (100%)، وأعلى عدد للجذور/ فرع (7.00) وطول الجذر (2.58 سم) عند زراعة الأفرع في وسط موراشيغ وسكوج (MS) خالي من الهرمونات والمضاف له 15 جرام سكروز/لتر. وقد تم أقلمة النباتات بنجاح باستخدام بيئة تحتوي علي البيتموس + البيرلايت (1:1 علي اساس الحجم) بمعدل بقاء 100%.