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ORIGINAL ARTICLE

PHENOPLASTICITY AND KARYOTYPING OF *CONVOLVULUS ARVENSIS* L., 1753 (SOLANALES, CONVOLVULACEAE) GENOTYPES

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ABSTRACT

Convolvulus arvensis L., 1753 (Solanales, Convolvulaceae) is a cosmopolitan polymorphic perennial herb and one of 15 noxious crop weeds. The species has notable phenoplasticity among its populations. This study aimed to assess phenoplasticity in 20 morphologically distinct populations collected from the same habitat in Egypt to understand this feature in terms of chromosome number and karyotyping. A total of 55 morphological characters were studied, and the similarity values were assessed using Jaccard's similarity coefficient. The morphological characters were distinguished into five groups with variations in chromosome counting and karyotyping. Accordingly, they were treated as genotypes. These genotypes include two distinct ploidy levels: tetraploids (2n = 32) and hexaploids (2n = 48). The hexaploid genotypes had a higher intrachromosomal asymmetry index A1 value than the tetraploids. Significant chromosomal differences among the studied genotypes were revealed through an ANOVA test, indicating that quantitative genomic alteration has an essential role in *C. arvensis* diversification. The study concluded that the studied phenoplasticity of the populations of this species was genetically controlled and not attributed to ecological factors. The importance of cytological studies in assessing the phenoplasticity of *C. arvensis* populations is highlighted in this study, especially for those grown in the same habitat.

Keywords: Genetic diversity, Hexaploids, Karyotyping, phenoplasticity, Tetraploids.

INTRODUCTION

Convolvulus arvensis L., 1753, family Convolvulaceae, is a polymorphic perennial herb native to Europe and grows extensively in Mediterranean climates, temperate, and tropical regions in a wide range of habitats with worldwide distribution (Austin, 2000; Preston, 2012; Sunar *et al.*, 2015; Moustafa *et al.*, 2019; Sosnoskie *et al.*, 2020). *C. arvensis* is considered as one of the most harmful weed species in orchards, cultivated fields, roadsides, wasteland, and apportioned habitats (Austin, 2000; Gianoli, 2004). Worldwide, *C. arvensis* is one of the 15 noxious weeds that cause severe problems for about 32 different crops in more than 44 countries (Sunar *et al.*, 2015). Its weeding is exceptionally difficult due to its twining growth

habit, and its capability to reproduce sexually producing seeds, and vegetatively by root or rhizome fragments (Sosnoskie *et al.*, 2020). *C. arvensis* has been reported to have high (96%) pollen grain fertility (Ashfaq *et al.*, 2020).

Many biotypes and ecotypes were reported in *C. arvensis* worldwide (Gianoli, 2001, 2004; Mehrafarin *et al.*, 2009; Moustafa *et al.*, 2019). In Europe, more than 60 varieties were identified, and many intermediates of these varieties were traced to the USA. However, researchers were discouraged from applying a specific name to them (Moustafa *et al.*, 2019). The phenotypic plasticity of this species extended to its chromosome number, where several chromosome counts were detected, 2n = 32 (Vij and Singh, 1976) and 2n = 24, 48, 50, and 78 (IPCN Chromosome Reports, 2015). In Egypt, *C. arvensis* is one of 20 species of the genus *Convolvulus* (Boulos, 2009).

The presence of notable phenoplasticity in this species was revealed after field and herbarium observations. Some of these different phenotypes were traced to the same habitats. However, this phenotypic plasticity has not yet been subjected to a detailed study regarding chromosome counting and karyotyping. Variations in chromosome traits could cause morphological variation (Agbo and Ukwu, 2010), where genome duplication often causes a complex pattern of genetic diversity and phenotypic outcome (Marques *et al.*, 2014). Accordingly, increasing our knowledge of the chromosome traits of different populations of C. *arvensis*, together with morphological variation, and could serve as an essential guide in the planning of a future successful control program for such a noxious crop weed.

Phenotypic plasticity is the ability of a species to adapt to different forms depending on the environment or the ability of a given genotype to develop different states of character or groups of characters in a different environment (Nayar, 2014; Oldroyd *et al.*, 2018). Plants respond by phenotypic plasticity as an adaptive response to heterogeneous environments rather than genetic differentiation, where phenotypic plasticity is expected in varying environments (Gianoli, 2004). Phenoplasticity is associated with environmental selection and is more significant in stressful environments (Wang and Althoff, 2018). Genetic differentiation and ecotype formation are expected in more homogeneous environments. However, the ecological significance of this pattern has not been explained (Gianoli, 2004). According to Çalişkan (2012), genetic diversity provides information about the adaptation of species to changing environments, understanding hybridization, and clarifying the gene flow among populations. Finally, phenoplasticity is essential to the adaptability and survival of populations.

The current study represents a detailed study of different populations of *C. arvensis* in Egypt. It aims to (1) assess the phenotypic plasticity and its supporting chromosome traits among the morphologically distinct populations, (2) delimit the genetic diversity of the studied morphologically distinct populations in terms of chromosome counting and karyotype, and (3) check whether the phenoplasticity in *C. arvensis* populations is related to ecological factors or whether it may be genetically controlled.

MATERIALS AND METHODS

Plant material: A total of 20 fresh morphologically distinct populations were collected from the same habitat between 2022-2023 from the experimental garden of the Agriculture Research Center in Giza, Egypt (to exclude environmental variability). Herbarium specimens deposited in Cairo University Herbarium (CAI) and the specimens on the JSTOR (Global Plants database). The identification was according to the contribution of earlier taxonomic treatments (Täckholm, 1974; Boulos, 2000, 2009). Then, the studied populations were grouped into five distinct morphotypes (based on the 55 morphological characters). Acronyms were according to Thiers (2019). Voucher specimens were deposited in the Cairo University Herbarium (CAI).

Chromosome counting and karyotyping: The identified morphotypes were subjected to chromosome study. Seeds from 10 individuals/ morphotype were germinated for chromosome counting and karyotype investigation. Actively growing root tips were pretreated with 8-hydroxyquinoline (0.002 mol) for 3 h and then fixed in the fixative Carnoy solution (1 acetic acid: 3 ethanol) for 24 h at room temperature. Afterward, the root tips were washed thoroughly using distilled water, and hydrolyzed in 60ºC 1N HCl for 5 min. Then, they were stained using 1% Orcien according to Khalifa *et al.* (2017). From each individual, 10 clearly and well-spread mitotic metaphase cells were selected for chromosome counting (i.e., 100 cells/ morphotype) using a light microscope (Leica DM2500, Wetzlar, Germany). The cells were then photographed using Leica CW4000 (Image Processing Analysis System Standard and high-resolution automated karyotyping software). The arrangement of chromosomes was in descending order of length: short arm length (p), long arm length (q), and total length (TL) of each chromosome (p + q) were determined. The total form percentage (TF %) was calculated (sum of short arms/ total chromosome length). In addition, the mean relative length (MRL) was calculated as [TL/ (sumTL) × 100] for each chromosome pair to represent the relative length of a particular chromosome pair. At the same time, the mean centromeric index (MCI) for each chromosome pair was calculated (p/TL × 100) to determine the position of the centromere. Chromosomes were considered metacentric when the value of the centromeric index was 45.0–50.0 and telocentric when the value of the centromeric index was zero (Hassan and Abd El-Gawad, 2013). Karyotype asymmetry was estimated for the relations between the chromosome arms following the equation by Romero Zarco (1986) for intrachromosomal asymmetry (A1):

$$A_1 = 1 - \frac{\sum_{i=1}^{n} b_i/B_i}{n}$$

Where: the number of homologous chromosome pairs (n); average length for short arms in each chromosome pair (bi); and average length for long arms in each chromosome pair (Bi). Additionally, the interchromosomal asymmetry (A2) was used to estimate the variation in chromosome length using the Romero Zarco (1986) index based on Pearson's dispersion

coefficient, as follows: A2 = s/$\bar{X}$; where S represents the standard deviation, and $\bar{X}$ represents the mean length of the chromosome.

Statistical analyses: The morphologically distinct five morphotypes were then identified as five genotypes based on chromosome counting and karyotyping. The studied genotypes were subjected to Jaccard's measure based on their macromorphological characters (a data matrix of 55 characters) to elucidate their similarity. The dendrogram was estimated by combining macromorphological characters with karyotype features (A data matrix of 67 characters) using the SPSS program (version 20 for Windows). A one-way ANOVA and the least significant difference test (LSD) were conducted on the length of chromosomes, length of the long arms, and length of the short arms to admit a significant difference among the studied genotypes (Sheidai and Jalilian, 2008). Moreover, a Pearson's correlation was conducted between the karyotype features of the identified *C. arvensis* genotypes.

RESULTS

Morphological aspects of *C. arvensis*: Twinning or prostrate perennial herb, glabrous to sparsely hairy. Stem 20–80 cm long, branched at base. Leaves simple, 1.4–7 × 0.5–5.4 cm, narrowly linear-oblong, deltoid or elliptic, glabrescent or nearly so; apex subacute-acuminate with diverse intermediates; margin entire or undulate; base haustate-sagittate or auriculate; petiole 4.0–28 mm long. Flower axillary, solitary, or in pairs on pedunculate cymes, peduncle 2.0–3.5 cm long, pedicel 2.0–5 cm long; bracts and bracteoles oblong-elliptic 1–4 × 0.5–1.5 mm; sepals five, slightly unequal, imbricate, 3.5–6 × 1.5–5 mm broadly oblong, glabrous, or occasionally with spreading hairs, margin scarious, apex retuse-mucronulate. Petals five, funnel-shaped, pink-pale pink, or white, 1.5–3.0 cm long, dorsal midpetaline area is often greenish-green or pink, pubescent; stamens five, unequal, glandular below; anther oblong, 2–3.5 × 0.5–2.5 mm; filament 5–12 mm; ovary ovoid with a cup-shaped or annular disc at the base, nearly glabrous 1–1.5 mm width; style 6–12 mm long, filiform; stigma 2–4.5 mm long, cylindrical; fruit capsule 7–10 × 4–7.5 mm, ovoid to sub-globose, nearly glabrous, 1–4 seeded; seeds 3.5–5 × 2.5–3.8 mm, obovoid, tuberculate, orange-brown or black. It grows as a cultivated weed and a cosmopolitan species in all phytogeographic regions in Egypt. Detailed characters distinguishing the identified genotypes are outlined in Plate (1) and Table (1), showing 55 morphological characters. Based on the characters in this table, a morphological key for the identified genotypes was constructed.

The morphologic key of the identified genotypes of *C. arvensis*:

1. Flower in paired; corolla dark pink; midpetaline area pink…….……Genotype 5
   – Flower solitary; corolla not so; midpetaline area pale green…….……2
2. Flower pale pink; anther pink; leaves yellow-green ……..……3
   – Flower white; anther white; leaves blue-green ……..……..…4
3. Leaves narrow linear, up to 2.6 times as long as wide, style up to 10 mm, seeds brown & black…….……..….. Genotype 1
   – Leaves elliptic, up to 1.5 times as long as wide, style up to 6 mm, seeds black …….……..... ..... Genotype 2

4. Leaves elliptic, up to 3 times as long as wide, base sagittate, style up to 12 mm ……..……...…… Genotype 3
   – Leaves deltoid-oblong, up to 1.8 times as long as wide, base hastate-auriculate, style up to 8 mm ……..……...……...… Genotype 4

Statistical analysis based on morphological data: The similarity values between the identified genotypes of *C. arvensis*, based on 55 morphological characters, are shown in (Tab 2). The lowest similarity value (33.3%) was recorded between genotypes 1 and 5, while the highest similarity value (51.2%) was recorded between the two white-flowered genotypes (genotypes 2 and 4). The pink-flowered genotype 5 had low similarity values with the other genotypes, ranging from 33.3% to 39.5%.

Karyotype analysis: Two ploidy levels (tetraploid and hexaploid) were revealed in the chromosome count of the mitotic metaphase of the studied genotypes within *C. arvensis* (x = 8). Genotypes 1, 3, and 5 were tetraploid, having a chromosome set of 2n = 4x = 32. In contrast, genotypes 2 and 4 were hexaploid with a chromosome set of 2n = 6x = 48 (Diag. 1). Satellite chromosome appeared in the second chromosome pair of genotype 3 (Diag. 1). Details of the karyotype analysis of the studied genotypes are presented in Diagram (1) and (App. 1, 2). The arrangement of chromosomes was descending. The first chromosome pair was the longest chromosome of all the studied genotypes. Its length ranged from 4.22 ± 1.53 µm to 6.82 ± 1.24 µm in genotypes 5 and 2, respectively. The last chromosome pair was the shortest of all the studied genotypes. Its length ranged from 1.98 ± 0.96 µm to 3.48 ± 0.73 µm in genotypes 3 and 2, respectively (App. 1). Moreover, the mean relative length (MRL%) of the longest chromosome in all the studied genotypes ranged between 16.61% and 18.60% in genotypes 1 and 3, respectively. At the same time, the mean relative length (MRL%) of the shortest chromosome ranged between 7.74% and 8.93% in genotypes 3 and 4, respectively (App. 2, Diag. 2). The centromeres were metacentric in chromosome pairs (1–4) and telocentric in chromosome pairs (5–8) in the complement of all the studied genotypes (App. 2, Diag. 3). Clearly, the chromosome sets of the studied genotypes (1–5) showed high differences in their karyotype features (Tab. 3). The length of total chromosomes (TL) of the hexaploids ranged between 31.44 µm and 40.11 µm in genotypes 4 and 2, respectively. The length of total chromosomes (TL) of the tetraploids ranged between 24.54 µm and 25.61 µm in genotypes 5 and 3, respectively. Moreover, the hexaploids genotypes 2 and 4 had the highest values of the intrachromosomal asymmetry index A1 (0.86 and 0.85), respectively. At the same time, tetraploids had the lowest A1 values (Tab. 3, Diag. 4). The interchromosomal asymmetry index A2 was slightly different among the studied genotypes, with its highest value (0.29) in genotype 3 and its lowest value (0.21) in genotype 2 (Tab. 3, Diag. 4).

Statistical analysis based on karyotype data: According to the results of the ANOVA, the length of long and short arms of the chromosome pairs 1–8 of the studied genotypes was significantly different in addition to the TL of the chromosome pairs 2–8. At the same time, the LSD test clarified that the tetraploid genotypes had no significant difference in the TL of the chromosomes and the length of the long arm of the chromosome pairs 2–8. Meanwhile, the hexaploid genotypes were significantly different in the TL of the chromosomes and the

length of the long arm of chromosome pairs 6, 7, and 8. The length of the short arm of chromosome pairs 1 and 2 had a significant difference between genotypes 5 (pink-flowered) and 4 (white-flowered). Nonetheless, these chromosome pairs had no significant difference in the length of the short arm between the two pale pink-flowered genotypes (1 and 2, respectively). Also, there was no significant difference between the two white-flowered genotypes (3 and 4, respectively). The Pearson's correlation among the karyotype features of *C. arvensis* genotypes is shown in Table (4). The TL of chromosomes had a significant positive correlation with the length of longest and shortest chromosomes and the mean chromosome length and a significant negative correlation with TF% ($r = -0.907$ and $P = 0.034$). At the same time, the intrachromosomal asymmetry index A1 had a significant positive correlation with the length of the longest chromosome ($r = 0.908$ and $P = 0.033$). The separation of tetraploid genotypes (Cluster I: genotypes 1, 3, and 5) from the hexaploid genotypes (Custer II: genotypes 2 and 4) was revealed by the dendrogram developed from the combined cytological and macromorphological data (Diag. 5).

DISCUSSION

The 20 investigated populations of *C. arvensis* had distinct phenoplasticity in the field (Tab. 1, Pl. 1), leading to the delimiting of five genotypes. These identified genotypes with notable morphological diversity (leaf shape and dimensions, flower color, mid-petaline color, fruit shape, seed texture, and others; Tab. 1) were recorded earlier within and among *C. arvensis* populations (Gianoli, 2001, 2004; Mehrafarin *et al.*, 2009; Sunar *et al.*, 2015; Moustafa *et al.*, 2019). The phenoplasticity of *C. arvensis* was recorded earlier in Europe as more than 60 varieties. Additionally, many intermediates of these species have been identified in the USA (Moustafa *et al.*, 2019).

The presence of five different genotypes of *C. arvensis* that were collected from the same habitat was revealed in this study. Mehrafarin *et al.* (2009) recognized the morphological and genetical variability within *C. arvensis* populations collected from different geographical regions. On the opposite side, Whitesides (1979) described three *C. arvensis* ecotypes with morphological variations grown under similar conditions in Oregon, USA. Also, DeGennaro and Weller (1984) recorded five biotypes with morphological variations on the railroad side of Lafayette in the USA.

The vegetative and floral characteristics of *C. arvensis* are widely contributing to its morphological differentiation and species delimitation (Borba *et al.*, 2002; Ashley, 2015). These characters represented developmental plasticity and agreed with Wood *et al.* (2015), who reported that *C. arvensis* is a very variable species with many forms. Species in the whole Convolvulaceae family have such morphological diversity, which is not restricted to *C. arvensis* (Abdel Khalik and Osman, 2007). The similarity between the recorded genotypes was clarified with Jaccard's similarity coefficient, which uses a proximity matrix by squared Euclidean distance based on the studied macromorphological data (55 characters, Tab. 2). The similarity of these genotypes ranged from 33.3% to 51.2%, and the lowest similarity (33.3%) was reported between genotypes 1 and 5. The highest similarity (51.2%) was noticed between 2 and 4. Moreover, the recorded low similarity values of genotypes 1

and 5 with the other genotypes were expressed in several morphological characters that distinguished genotype 5 (among them: leaf shape, petiole length, flower in pairs, petal color, midpetaline color, and others; Tab. 1). Similarly, the distinctive morphological characters [e.g., leaf shape, epidermal feature, the density of hairs on flower parts, the apex of bracteoles, fruit shape, and seed color (Tab. 1)] delimited genotype 1 from the other identified genotypes. Our results are congruent with contexts proposed by Tominaga and Willer (1992) and Westwood *et al.* (1997). These researchers that reported self-crossing and backcrossing are difficult due to self-incompatibility, and *C. arvensis* can produce many different genotypes by outcrossing. Additionally, the genotype that is ecologically more adapted may be dominant in the habitat.

The current study is a pioneer record for the chromosome number of *C. arvensis* in Egypt, confirming that the morphologically distinct genotypes (20 populations) retain genetic variations expressed as differences in chromosome numbers. Two ploidy levels were observed, the tetraploids (2n = 32) for genotypes 1, 3, and 5, and the hexaploids (2n = 48) in the genotypes 2 and 4, where, the base number is "X = 8" (Khoshoo and Sachdeva, 1961). Congruent results were reported by Vii and Singh (1976) and (IPCN Chromosome Reports, 2015). At the same time, the reported higher number (2n = 50 and 78; IPCN Chromosome Reports, 2015) in *C. arvensis*, postulated by Moore (1973) and Fedorov (1969) as aneuploidy, characterizes the Convolvulaceae family in generic and specific levels.

After combining the retrieved cytological data with the macro-morphological data, the separation of the identified tetraploid genotypes (Cluster I) from the hexaploid genotypes (Custer II) was confirmed with the developed dendrogram (Diag. 5). Moreover, hexaploid genotypes are distinguished by the highest values of the intrachromosomal asymmetry index A1 compared to tetraploid genotypes (Tab. 3, Diag. 4). On the contrary, the interchromosomal asymmetry index A2 (Tab. 3, Diag. 4) had a few differences among the identified genotypes, reflecting the close affinity between these genotypes.

A significant chromosomal difference in the length of total chromosomes and the lengths of the short and long arms (App. 1), among the studied genotypes (1–5) was revealed in the ANOVA results, indicating that quantitative genomic alteration has an essential role in *C. arvensis* diversification. In addition, there was no significant difference between tetraploid genotypes for the TL of the chromosome, and the length of the long arm of chromosome pairs 2–8 was revealed by the LSD test. In contrast, hexaploid genotypes significantly differed in the TL of the chromosome, and the length of the long arm of chromosome pairs 6, 7 and 8. This result confirms the symmetric karyotype of tetraploid genotypes compared to hexaploid ones. Moreover, Westwood *et al.* (1997) mentioned that *C. arvensis* might be controlled genetically by one or more loci, each of which may have multiple alleles.

The length of the short arm of chromosome pairs 1 and 2 had a significant difference between genotypes with different flower colors according to the LSD test. In contrast, these chromosome pairs showed no significant difference in the length of the short arm between

genotypes with similar flower colors. Further investigations are needed to clarify the role of chromosome pairs 1 and 2 in determining corolla color in *C. arvensis.*

Variation in karyotype is essential, as genetic variability represents an important micro-morphological feature for species and is frequently associated with species differentiation (Stebbins, 1971). After using Pearson's correlation among karyotype features of *C. arvensis,* it was clarified that the TL of chromosomes had a significant positive correlation with the length of the longest and shortest chromosomes and the mean chromosome length and a significant negative correlation with TF% (r = – 0.907 and P = 0.034). At the same time, the intrachromosomal asymmetry index A1 had a significant positive correlation with the length of the longest chromosome (r = 0.908 and P = 0.033), reflecting the relatively symmetric karyotype of *C. arvensis*. A similar result was concluded by Sheidai *et al.* (2011). It was revealed in the current study that the reasons behind the growth of five different genotypes of *C. arvensis* in similar environments still need more clarification. *C. arvensis* is self-incompatible (Gianoli, 2004), and the species breeding system is mixed (Sunar *et al.,* 2015). Polyploidy and hybridization constantly contribute to complex patterns of genetic diversity, reproductive isolation, and discrepancies in breeding systems (Marques *et al.*, 2014). Also, Moustafa *et al.* (2019) recorded variations in morphological and anatomical characters accompanied by nucleotide sequences in two forms of *C. arvensis* and stated that such variation might lead to a consequence of mutations in the lineage of *C. arvensis* forms.

Accordingly, our morphological and cytological results revealed that the studied *C. arvensis* populations have genotypic plasticity, confirming that the observed plasticity of *C. arvensis* could be related to other factors rather than ecological factors. Our result is in line with those of Pigliucci (2001), who reported that phenotypic plasticity is not just an environmental phenomenon but is a result of complex genotype-environment interactions. At the same time, the interactions between the genotypes and the environment cause the appearance of an array of discordant genotypes in *C. arvensis*. This may be explained by Westwood *et al*. (1997), who reported that self-incompatibility in *C. arvensis* may have multiple alleles. The length of the short arm of chromosome pairs 1 and 2 had a significant difference between genotypes with different flower colors according to the LSD test. In contrast, these chromosome pairs showed no significant difference in the length of the short arm between genotypes with similar flower colors. Further investigations are needed to clarify the role of chromosome pairs 1 and 2 in determining corolla color in *C. arvensis.*

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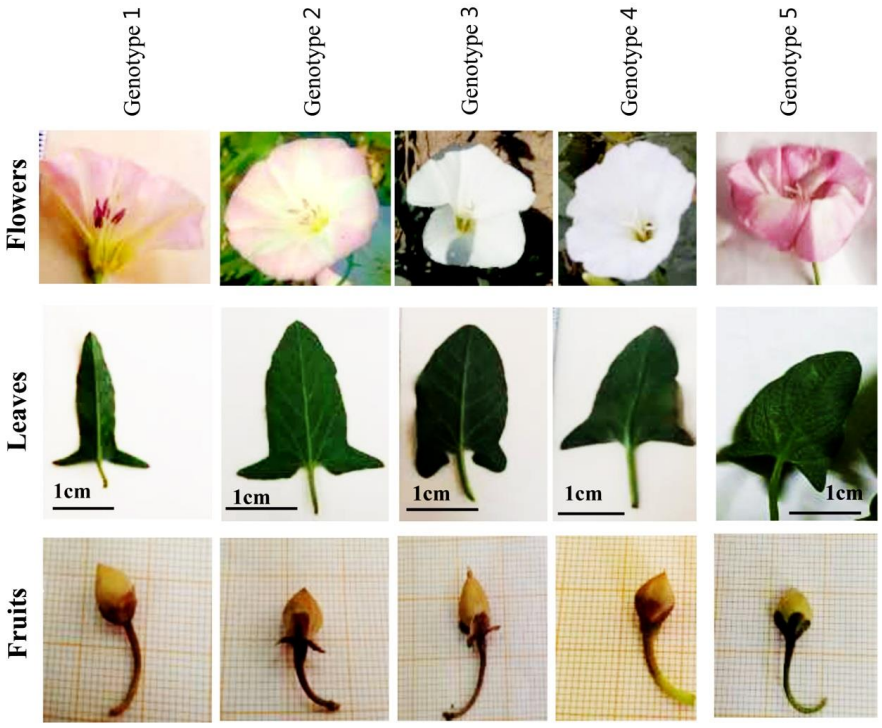

Plate (1): Morphological variations of flowers, leaves and fruits for the identified *Convolvulus arvensis* genotypes. (For each genotype, flower and leaf were photographed using the same scale bar).

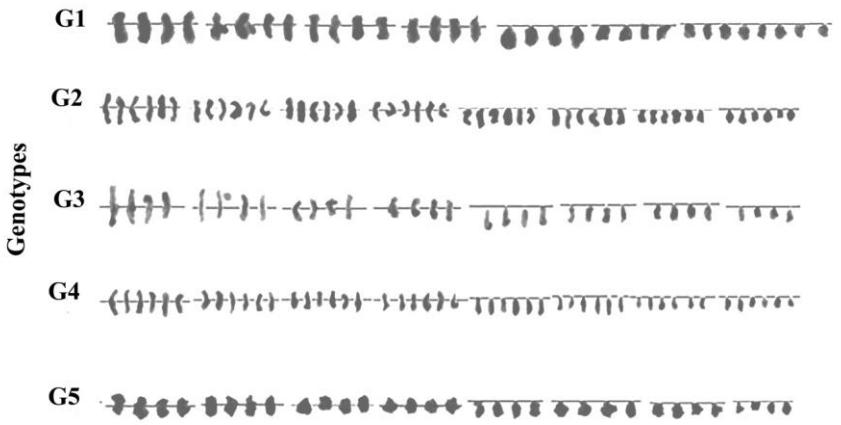

Diagram (1): Karyotypes of the identified *C. arvensis* genotypes.

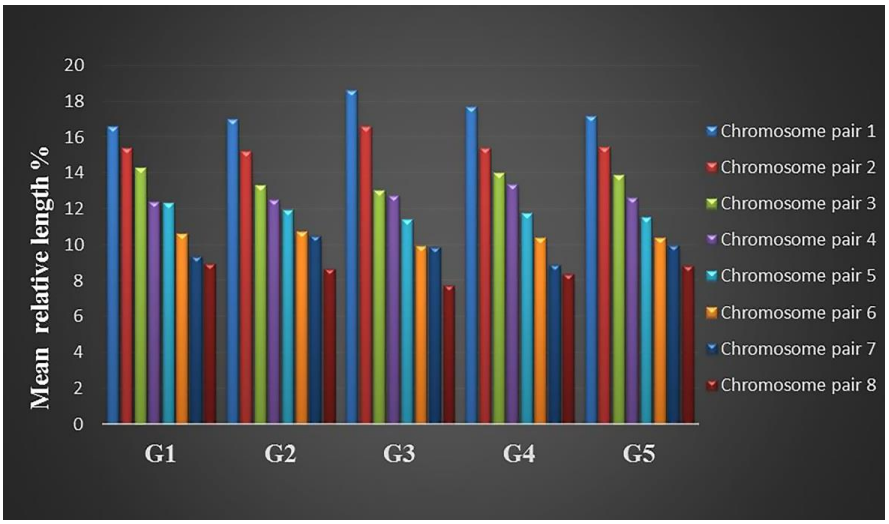

Diagram (2): Mean relative length percentage of each chromosome pair in the complement of the investigated genotypes (G1–G5).

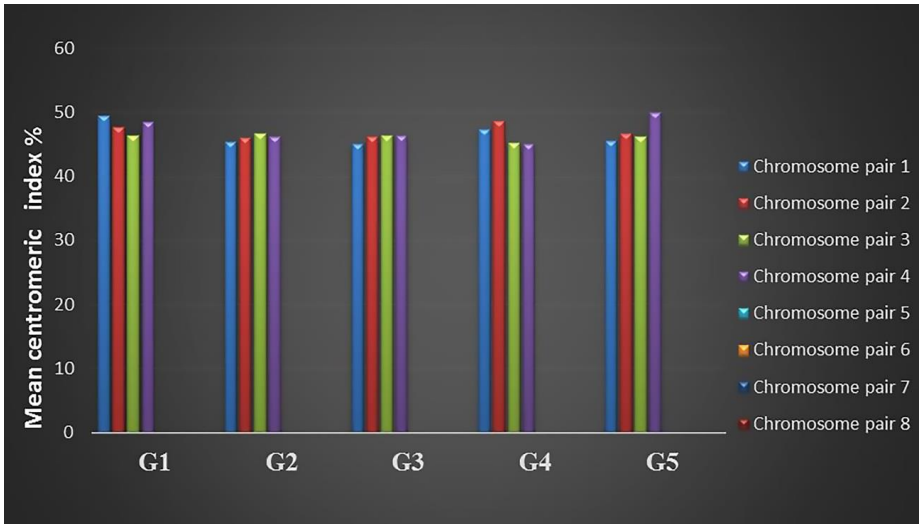

Diagram (3): Mean centromeric index of each chromosome pair in the complement of the investigated genotypes (G1–G5); mean centromeric index is zero for chromosomes (5-8).

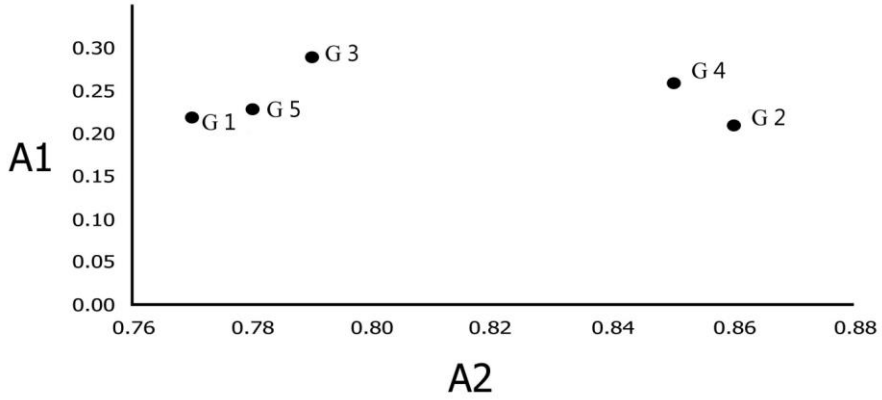

Diagram (4): Scatter diagram showing karyotype asymmetry indexes A1 and A2 among the identified *C. arvensis* genotypes. (G: Genotype).

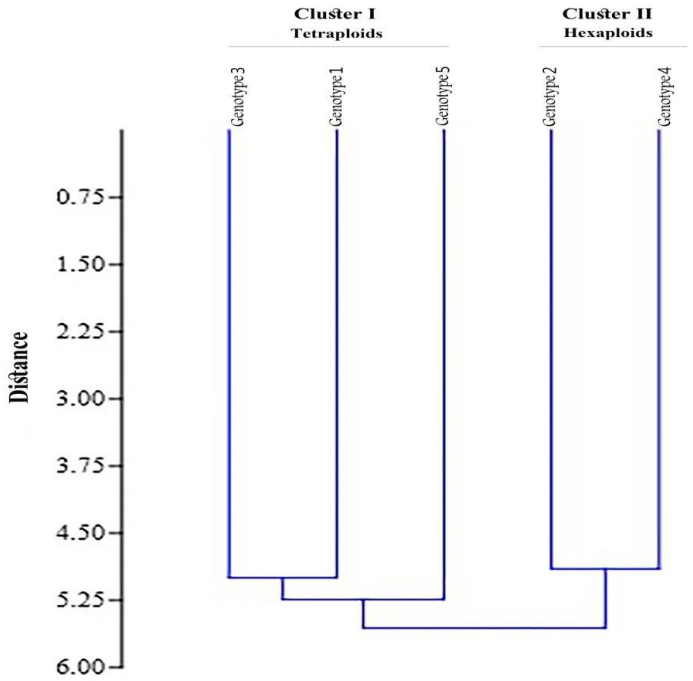

Diagram (5): The constructed dendrogram for the identified *C. arvensis* genotypes (G1-G5) is based on morphological data (55 characters) combined with karyotype features (ten characters).

Table (1): Morphological variation among the identified genotypes of *C. arvensis*.

Characters	Genotype 1	Genotype 2	Genotype 3	Genotype 4	Genotype 5
Leaf characters					
1. L/W ratio	1.3–2.6	1.3–1.5	2.2–3.0	1.1–1.8	1.4- 1.9–(2.6)
2. Shape of leaf	narrow linear	Elliptic	elliptic	deltoid–oblong	linear–oblong
3. Leaf color	Yellow–green	Yellow–green	Blue –green	Blue –green	Blue–green
4. Apex	Acuminate	Acuminate	Subacute–retuse	Obtuse–mucronate	Obtuse–mucronulate
5. Base	haustate	Haustate	sagitate	Haustate–auriculate	Haustate–auriculate
6. Margin	entire	Entire	Entire	Entire	Entire
7. Epidermal feature	Dense papillose	Moderate papillose	Moderate papillose	Moderate papillose	Sparse papillose
8. Hairs on leaf	Occ. on base	Glabrous	Occ. on margin	Glabrous	Occ. on margin, base & midrib
9. Petiole length (mm)	up to 14.0	up to 14.0	up to 14.0	Up to 20.0	Up to 28.0

10. Hairs on petiole	Occasionally	Occasionally	Occasionally	Glabrous	Occasionally
Flower characters					
11. Solitary/ pairs	Solitary	Solitary	Solitary	Solitary	In pairs
12.Pedicle Length (cm)	Up to 5.0	Up to 4.0	Up to 5.0	Up to 5.0	Up to 4.0
13. Hairs on pedicle	Glabrous	Hairy	Hairy	Occasionally hairy	Hairy
14. Density of hairs on pedicle	Non	Moderate	Moderate	Low density	Dense
15. Shape of bracteoles	Oblong	Oblong–elliptic	Oblong	Oblong	Elliptic
16. Bracteoles length (mm)	1.5–3.5	2.0–3.5	2.5–3.5	3.0–4.0	1–3
17. Bracteoles width (mm)	0.5–1.0	0.5–1.0	0.5–1.0	1.0–1.5	0.5–1
18. Bracteoles Apex	Acute–acuminate	Acuminate	Acuminate	Acuminate	Acuminate
19. Density of hairs on bracteoles	Low	Moderate	Dense	Low	Low
20. Length of hairs on bracteoles (mm)	Up to 0.2	Up to 0.2	Up to 0.8	Up to 0.2	Up to 0.2
21. Shape of the sepals	Broad oblong	Broad oblong	Broad oblong	Broad oblong	Broad oblong
22. Apex of sepals	Retuse–mucronulate	Retuse – mucronulate	Retuse – mucronulate	Retuse – mucronulate	Retuse–mucronulate
23. Outer sepals length (mm)	4.0	4.0-5.0	4.0-5.5	3.5-5.0	4.0-4.8
24. Outer sepals width (mm)	1.5–2.0	2.5–3.0	2.0–2.5	2.0–2.5	2.0–3.0
25. Hairs on outer sepals	Glabrous	Hairy	Hairy	Hairy	Hairy
26. Density of hairs on outer sepals	Non	Moderate	Dense	Moderate	Dense
27. Inner sepals length (mm)	4.0–5.0	4.0–5.0	5.0–6.0	5.0–5.0	4.0–5.0
28. Inner sepals width (mm)	4.0–5.0	4.0–5.0	4.0–5.0	3.5–4.0	3.0

29. Hairs on inner sepals	Glabrous	Occasionally	Occasionally	Glabrous	Occasionally
30. Petal length (cm)	2.0–3.0	2.0–3.0	2.5–3.0	2.0–2.5	1.5–2.0
31. Petal width (cm)	2.0–4.0	2.0–4.0	2.5–4.0	2.0–2.5	2.0–2.2
32. Colour of petal	Pale pink	Pale pink	White with pink spots	White	Dark pink
33. Colour of the midpetaline area	Greenish	Greenish	Green	Green	Pink
34. Hairs of the midpetaline area	Moderate	Moderate–dense	Moderate	Moderate	Moderate
35. Stamens number	5.0	5.0	5.0	5.0	5.0
36. Anther length (mm)	3.0–3.5	3.0–3.5	3.0–3.5	2.5–3.0	2.0–3.5
37. Anther width (mm)	0.5–1.0	0.5–1.0	1.0–1.5	1.0–1.5	1–2.5
38. Anther colour	Purple	Purple	White	White	Purple
39. Filament length (mm)	9.0–12.0	6.0–10	5.0–10.0	5.0–10.0	6.0–10
40. Ovary width (mm)	1.5	1.0	1.5	1.5	1.5
41. Hairs on the ovary	Occasionally	Glabrous	Glabrous	Glabrous	Glabrous
42. Style length (mm)	up to 10.0	up to 6.0	up to 12.0	up to 8.0	up to 8.0
43. Hairs on style	Occasionally	Glabrous	Glabrous	Glabrous	Glabrous
44. Stigma length (mm)	3.0–4.5	2.5–3.0	2.0–2.5	2.5–3.0	2.5–3.0
Fruit characters					
45. Fruit length (mm)	7.0–9.0	7.0–9.0	9.0–10.0	7.0–9.0	8.5–10.0
46. Fruit width (mm)	4–5	5–7	5–7	4–6.5	7–7.5
47. Fruit shape	Ovoid to sub-globose	Sub-globose	Ovoid	Sub-globose	Sub-globose
48. Hairs on fruit	Glabrous	Glabrous	Glabrous	Glabrous	Occasionally
49. Number of seeds /fruit	1.0–3.0	1.0–4.0	1.0–3.0	2.0–3.0	1.0–4.0
50. Seeds length (mm)	3.5–4.0	4.0–4.5	5.0	4.5–5.0	3.5–4.5

51. Seeds width (mm)	2.5–3.5	2.5–3.0	3.5	2.5–3.0	2.5–4.0
52. Seed shape	Obovoid	Obovoid	Obovoid	Obovoid	Obovoid
53. Seed texture	Fine	Fine	Moderate	Moderate	Course tuberculate
54. Seed colpus	Not distinct	Distinct	Not distinct	Distinct	Distinct
55. Seed colour	Brown–black	Black	Black	Black	Orange, brown–black

Table (2): The similarity between the identified genotypes of *C. arvensis* was based on morphological data (55 characters; Tab. 1) using Jaccard's similarity index.

Genotypes	**Jaccard's Measure**				
	Genotype 1	**Genotype 2**	**Genotype 3**	**Genotype 4**	**Genotype 5**
Genotype 1	100.00				
Genotype 2	45.00	100.00			
Genotype 3	39.50	42.50	100.00		
Genotype 4	41.50	51.20	50.00	100.00	
Genotype 5	33.30	39.50	37.50	39.50	100.00

Table (3): Karyotype features for *C. arvensis* species, TL: Total length of chromosomes, L: Longest chromosome, S: Shortest chromosome, Ratio: Longest/shortest chromosome, X: Mean chromosome length, A1 and A2: Romero-Zarco indices, and TF%: Total form percentage.

Genotypes	**2n**	**Ploidy level**	**Tl**	**L**	**S**	**L/S**	**X**	**A1**	**A2**	**TF%**
Genotype 1	32	4x	27.97	3.45	1.68	1.86	3.50	0.77	0.22	0.28
Genotype 2	48	6x	40.11	4.80	2.33	2.06	5.01	0.86	0.21	0.27
Genotype 3	32	4x	25.61	2.92	1.52	1.93	3.20	0.79	0.29	0.28
Genotype 4	48	6x	31.44	3.71	1.90	1.96	3.93	0.85	0.26	0.28
Genotype 5	32	4x	24.54	2.84	1.55	1.48	3.07	0.78	0.23	0.28

Table (4): Pearson's correlation among karyotype features in *C. arvensis* species, ** = correlation is significant at the 0.01 level (2-tailed). * = correlation is significant at the 0.05 level (2-tailed).

		TL	L	S	L/S	X	A1	A2	TF%
TL	Pearson Correlation	1	.982**	.965**	.314	1.000**	.853	-.485	-.907*
	Sig. (2-tailed)		.003	.008	.607	.000	.066	.408	.034
	N	5	5	5	5	5	5	5	5
L	Pearson Correlation	.982**	1	.969**	.370	.982**	.908*	-.316	-.880*
	Sig. (2-tailed)	.003		.006	.540	.003	.033	.605	.049
	N	5	5	5	5	5	5	5	5
S	Pearson Correlation	.965**	.969**	1	.130	.964**	.781	-.368	-.935*
	Sig. (2-tailed)	.008	.006		.835	.008	.119	.542	.020
	N	5	5	5	5	5	5	5	5
L/S	Pearson Correlation	.314	.370	.130	1	.314	.711	.126	-.011
	Sig. (2-tailed)	.607	.540	.835		.607	.178	.840	.986
	N	5	5	5	5	5	5	5	5
X	Pearson Correlation	1.000**	.982**	.964**	.314	1	.853	-.487	-.906*
	Sig. (2-tailed)	.000	.003	.008	.607		.066	.406	.034
	N	5	5	5	5	5	5	5	5
A1	Pearson Correlation	.853	.908*	.781	.711	.853	1	-.110	-.668
	Sig. (2-tailed)	.066	.033	.119	.178	.066		.861	.218
	N	5	5	5	5	5	5	5	5
A2	Pearson Correlation	-.485	-.316	-.368	.126	-.487	-.110	1	.547

	Sig. (2-tailed)	.408	.605	.542	.840	.406	.861		.340
	N	5	5	5	5	5	5	5	5
TF%	Pearson Correlation	-.907*	-.880*	-.935*	-.011	-.906*	-.668	.547	1
	Sig. (2-tailed)	.034	.049	.020	.986	.034	.218	.340	
	N	5	5	5	5	5	5	5	5

CONCLUSIONS

The current study is a pioneer record for the chromosome number and karyotype analysis of *C. arvensis* in Egypt. The study revealed five distinct genotypes of *C. arvensis*, with two ploidy levels; the tetraploids (2n = 32) and the hexaploids (2n = 48). This study clarified the importance of cytological studies in assessing the phenoplasticity of *C. arvensis* populations and concluded that phenotypic plasticity in *C. arvensis* populations is genetically controlled and unrelated to environmental factors. This study also clarified the expression of the chromosome polyploidy on the morphological traits of *C. arvensis*. The current study could serve as an essential guide in the planning of a future successful control program for such a noxious crop weed.

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CONFLICT OF INTEREST STATMENT

"The authors declare no conflict of interest".

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Appendix (1): Mean value, standard deviation and ANOVA *F*-ratio & *Sig.* (*P*) values of the chromosome pairs (1–8) in the complement of the identified *C. arvensis* genotypes ** = $P \leq 0.01$, * = $P \leq 0.05$.

Chromo-some pair	Genotype 1	Genotype2	Genotype 3	Genotype4	Genotype5	F-ratio	Sig.
Total chromosome length (µm)							
1	4.65 ± 1.20	6.82 ± 1.24	4.76 ± 2.32	5.57 ± 0.69	4.22 ± 1.53	3.617	0.11
2	4.32 ± 1.25	6.10 ± 0.67	4.25 ± 2.08	4.85 ± 0.67	3.80 ± 1.13	4.469	0.003**
3	4.00 ± 1.12	5.35 ± 0.58	3.34 ± 1.72	4.40 ± 0.60	3.41 ± 1.16	5.385	0.001**
4	3.48 ± 0.95	5.03 ± 0.65	3.27 ± 1.54	4.20 ± 0.55	3.10 ± 0.94	6.414	0.000**

5	3.45 ± 1.09	4.80 ± 0.82	2.92 ± 1.57	3.71 ± 0.57	2.84 ± 0.74	5.257	0.001**
6	2.97 ± 0.98	4.30 ± 0.51	2.55 ±1.11	3.26 ± 0.50	2.55 ± 0.66	8.43	0.000**
7	2.62 ± 0.86	4.22 ± 0.71	2.53 ± 1.15	2.80 ± 0.60	2.45 ± 0.59	11.181	0.000**
8	2.50 ± 0.91	3.48 ± 0.73	1.98 ± 0.96	2.64 ± 0.85	2.17 ± 0.48	6.888	0.000**
Long arm (µm)							
1	2.35 ± 0.59	3.72 ± 0.91	2.61 ± 1.37	2.93 ± 0.49	2.30 ± 0.72	4.012	0.006**
2	2.25 ± 0.61	3.29 ± 0.71	2.28 ± 1.35	2.49 ± 0.32	2.02 ± 0.70	10.404	0.000**
3	2.15 ± 0.96	2.85 ± 0.49	1.79 ± 0.95	2.41 ± 0.49	1.83 ± 0.65	6.311	0.000**
4	1.79 ± 0.47	2.71 ± 0.68	1.75 ± 0.96	2.30 ± 0.53	1.55 ± 0.53	13.569	0.000**
5	3.45 ± 1.09	4.80 ± 0.82	2.92 ± 1.57	3.71 ± 0.57	2.84 ± 0.74	9.161	0.000**
6	2.97 ± 0.98	4.30 ± 0.51	2.55 ± 1.11	3.26 ± 0.50	2.55 ± 0.66	11.978	0.000**
7	2.62 ± 0.86	4.22 ± 0.71	2.53 ± 1.15	2.80 ± 0.60	2.45 ± 0.59	10.863	0.000**
8	2.50 ± 0.91	3.48 ± 0.73	1.98 ± 0.96	2.64 ± 0.85	2.17 ± 0.48	9.296	0.000**
Short arm (µm)							
1	2.30 ± 0.61	3.10 ± 0.58	2.15 ± 1.00	2.64 ± 0.39	1.92 ± 0.87	2.87	0.031*
2	2.06 ± 0.68	2.81 ± 0.49	1.97 ± 0.80	2.36 ± 0.52	1.78 ± 0.46	3.648	0.01*
3	1.85 ± 0.30	2.50 ± 0.35	1.55 ± 0.84	1.99 ± 0.31	1.58 ± 0.64	5.315	0.001**
4	1.68 ± 0.48	2.33 ± 0.38	1.52 ± 0.62	1.90 ± 0.18	1.55 ± 0.53	5.51	0.001**
5	0	0	0	0	0	-	-
6	0	0	0	0	0	-	-
7	0	0	0	0	0	-	-
8	0	0	0	0	0	-	-

Appendix (2): Mean relative length percentage and mean centromeric index of each chromosome pair in the complement of the investigated genotypes.

Chromosome pair	Genotype1	Genotype 2	Genotype 3	Genotype 4	Genotype 5
Mean relative length %					
1	16.61	17.00	18.60	17.71	17.20
2	15.43	15.21	16.61	15.43	15.48
3	14.30	13.34	13.05	14.00	13.90
4	12.42	12.55	12.77	13.37	12.65
5	12.33	11.97	11.41	11.80	11.57
6	10.60	10.73	9.94	10.38	10.40

7	9.38	10.53	9.89	8.90	9.97
8	8.93	8.68	7.74	8.40	8.83
Mean centromeric index %					
1	49.45	45.46	45.17	47.43	45.53
2	47.77	46.05	46.21	48.65	46.73
3	46.34	46.79	46.48	45.23	46.30
4	48.47	46.25	46.41	45.09	49.99
5	0.00	0.00	0.00	0.00	0.00
6	0.00	0.00	0.00	0.00	0.00
7	0.00	0.00	0.00	0.00	0.00
8	0.00	0.00	0.00	0.00	0.00

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المرونة المظهرية و بنية الصبغيات للانماط الوراثية لنبات العليق *Convolvulus arvensis* L., 1753 (الفصيلة المدادية Convolvulaceae، رتبة الباذنجانيات Solanales)

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الخلاصة

نبات العليق (الفصيلة المدادية Convolvulaceae، رتبة الباذنجانيات Solanales) عشب معمر ، متعدد الأشكال، و هو واحد من ضمن 15 نوع من اكثر الحشائش الضارة للمحاصيل. يتمتع هذا النوع بالمرونة المظهرية الملحوظة بين افراده. هدفت هذه الدراسة إلى تقييم المرونة المظهرية بين20 عشيرة نباتية متميزة شكليا، حيث تم جمعها من بئية واحدة في مصر لتقيم هذه الصفة من حيث عدد و بنية الصبغيات. وقد تمت دراسة 55 صفة مظهرية، وتم تقييم قيم التشابه باستخدام معامل تشابه جاكارد الذي أسفر عن تقسيم الصفات المظهرية إلى خمس مجموعات مع وجود اختلافات في عدد و بنية الصبغيات. وبناء على ذلك، تم التعامل معهم على أنهم أنماط وراثية. تشتمل هذه الأنماط الوراثية على مستويين صبغيين متميزين: رباعية الصبغيات (2ن = 32) وسداسية الصبغيات (2ن = 48). كان للأنماط الوراثية سداسية الصبغيات قيمة أعلى لمؤشر عدم التماثل بين بنية الصبغيات (A1) مقارنة بالانماط رباعية الصبغيات. ومن خلال اختبار الأنوفا تم الكشف عن اختلافات كبيرة في بنية الصبغيات بين الأنماط الوراثية المدروسة، مما يشير إلى أن التغيير الكمي في الجينوم له دور أساسي في التنوع الحيوى لنبات العليق. و أكدت هذه الدراسة على أن المرونة المظهرية لعشائر هذا النوع تحكمها عوامل وراثية ولا تعزى إلى عوامل بيئية. تم تسليط الضوء في هذه الدراسة على أهمية الدراسات الخلوية في تقييم المرونة الظاهرية لعشائر نبات العليق، وخاصة لتلك التي تنمو في نفس الموائل.