

Available online at [GSC Online Press Directory](http://www.gsonlinepress.com)

GSC Biological and Pharmaceutical Sciences

e-ISSN: 2581-3250, CODEN (USA): GBPSC2

Journal homepage: <https://www.gsonlinepress.com/journals/gscbps>

(RESEARCH ARTICLE)



## Analysis of genetic diversity and bioaccumulation potential of *Juncus acutus* grown in some northern swamp habitats of Egypt

Mansour Hassan <sup>1, 2, \*</sup>

<sup>1</sup> *Biological Sciences Department, Rabigh-College of Science & Art, King Abdulaziz University, Rabigh 21911, Saudi Arabia.*

<sup>2</sup> *Department of Botany, Faculty of Science, Suez Canal University, Ismailia, 41522 Egypt.*

Publication history: Received on 04 October 2018; revised on 05 November 2018; accepted on 17 October 2018

Article DOI: <https://doi.org/10.30574/gscbps.2018.5.2.0111>

### Abstract

*Juncus acutus* is one of main wetland plants, valuable in remediation of wetland environment from heavy metals. Determination of genetic diversity in its natural populations is important for species conservation and ecological restoration. The present study evaluated the genetic diversity of four populations of *J. acutus* growing in Manzala lake coast and inland swamps in Ismailia and Sinai by using random amplified polymorphic DNA (RAPD) technique. Fifteen primers generated a total of 217 RAPD bands (loci) of which 156 (71.9%) were polymorphic across all individuals of the four populations. At Manzala lake coast (i.e. sites 3 and 4, contaminated sites), the genetic diversity measures observed in the populations of the two species showed higher diversity in comparison to the less contaminated sites 1 and 2 (Ismailia and Sinai). This study revealed also the presence of a noticeable accordance between genetic diversity measures of *J. acutus* with some edaphic variables and heavy metal concentration in soil of the studied sites and leaves of the two species and it indicated that populations from sites 3 and 4 respond with increased genetic variation, resulting possibly from new mutations affecting allele frequencies, as a consequences of adaptation to changes or disturbances in the environment. This may indicate that the increased diversity levels may act as a buffer to severe heavy metal stress, which explains the importance of monitoring the genetic diversity of *J. acutus* populations in detecting trends that should alert ecologists to potential problems.

**Keywords:** *Juncus acutus*; Manzala; Sinai; Genetic diversity; Pollution; Bioaccumulation

### 1. Introduction

*Juncus acutus* was considered as one of the major halophyte species of wetland ecosystems in whole over the world, including coastal zones of lakes, along rivers and irrigation/drainage canals, marshlands and anthropogenic habitats where soil is periodically flooded (road side ditches, fields, storm- water retention basin), its geographical distribution outspreads from cold temperate regions to the tropics [1-2].

*Juncus acutus* species are perennial grass like with wide distribution, it is autochthonous monocotyledons thriving in wetland. In Egypt it, usually distributed throughout the running water of the main River Nile streams and its branches, irrigation and drainage canals as well as in the still water of some specific habitats like fresh water swamps and salt marshes [3]. *J. acutus* is used by farmers (in Egypt and many other parts of the world) from ancient periods, for roofing, fencing, mats, and baskets manufacture. Ecologically, *J. acutus* is important for oxygen production - they release high amount of Oxygen in the rhizosphere-, nutrient cycling, control of water quality, sediment stabilization and shelter for aquatic organisms and wildlife [4].

\* Corresponding author

E-mail address: [hmansor@kau.edu.sa](mailto:hmansor@kau.edu.sa)

Wetland plants are potentially studied as “biomonitors” that accumulate contaminants in their tissues and therefore may be analyzed to identify the abundances and bioavailability of such contaminants in aquatic environments. Therefore, the use of *helophyte species* appears to be particularly promising as they can accumulate heavy metals from sediments and water [5]. Along with metals accumulation in the below ground plant parts, phytostabilization has also been reported as another remediation mechanism in the root zone. In addition, recent literature has revealed the potential contribution of *Juncus* sp. on the removal of EDCs and PPCPs.

The main threats facing the management of *J. acutus* are due to the fact that its habitats are subjected to greater stress from various human activities. As a result, large quantities of organic and inorganic materials were introduced into these ecosystems [5]. Understanding the effects of the environmental contaminants on the plant genome is crucial for preserving the evolutionary potential of natural populations, as genetic diversity provides potential to adapt to environmental changes [6]. Many chemical contaminants have been demonstrated to induce genetic mutations and therefore affect the genetic structure of populations [7]. The toxicity of different pollutants and their physical disturbance can influence plant survival, recruitment, reproductive success, mutation rates, and even migration and consequently affect the genetic diversity of exposed populations [8].

In the last few years, the field of molecular biology has provided new tools for studying population structure and genetic diversity in wetland species. For example, cattain (*Typha*) and cordgrass (*Spartina*) were studied for the first time, using allozyme polymorphism [9-11]. Since the 1980s new perspectives in how to study population dynamics in common reed became available with the development of molecular markers [12-13]. One of the most efficient molecular marker methods in terms of ability to produce polymorphic markers within a comparatively short time and with a limited budget is RAPD (random amplified polymorphic DNA). Since its introduction by [14], RAPD has become widely used in various areas of plant research.

Taking into account that the ability of plants to accumulate compounds may be affected by the variation and high levels of contaminants. Therefore, the aims of the present study are to: 1) determine habitat characteristics, 2) assess heavy metals accumulation in the plant parts of *J. acutus*; and 3) describe this plants genetics using random amplified polymorphic DNA (RAPD), focusing on their genetic diversity and genetic differentiation and determine the relations between genetic variation and heavy metals bioaccumulation of the existing sampled populations of *J. acutus*. This study provides some molecular information to understand the genetic background to support the formulation of effective measures for genetic resources characterization, genetic improvement and sustainable utilization of *J. acutus*.

## 2. Material and methods

### 2.1. Plant populations

A total of 60 accessions of *J. acutus* were used in this study. Soil samples and leaves were collected from four populations (see Table 1), namely two populations in the Manzala coastal land (indicated as Manzala lake 1, elgameel and Manzala lake 2, Bahr kuwar), one from the saline in Ismailia (gate of the industrial zone) and one from salt marshes in Sinai, at the east bank of Suez Canal (New Meet Abu elkom village).

**Table 1** Location of the collection sites of the four study populations of *Juncus acutus* and their respective geographic coordinates in Egypt

| Population | Population site            | Longitude (N)  | Latitude (E)   | Elevation (m) |
|------------|----------------------------|----------------|----------------|---------------|
| 1          | Industrial zone, Ismailia  | 30° 34' 20.43" | 32° 11' 51.04" | 15.41         |
| 2          | New Meet abou elkom, Sinai | 30° 23' 57"    | 32° 26' 36.28" | 13.45         |
| 3          | Elgameel, Manzala lake 1   | 31° 17' 12.42" | 32° 12' 42.79" | 9.92          |
| 4          | Bahr kuwar, Manzala lake 2 | 31° 15' 43.57" | 32° 13' 12.16" | 8.69          |

Three soil samples were collected from each stand at a depth of 0-50 cm, mixed, air-dried and passed through a 2-mm sieve for physical and chemical analyses. Soil texture was determined by the use of Bouyoucos hydrometer; organic matter content was determined by Walkely and Black rapid titration method. Calcium carbonate content was estimated in the dry soil samples using Collins Calcimeter. Soil-water extracts (1:5) were used for the estimation of soil salinity (EC) using conductivity meter, soil reaction (pH) was determined using pH-meter, soluble carbonates ( $\text{CO}_3^{2-}$ ) and bicarbonates ( $\text{HCO}_3^-$ ) by titration against standard  $\text{H}_2\text{SO}_4$  using methyl orange and phenol- phenolphthalein as

indicators, chlorides (Cl<sup>-</sup>) by direct titration against standard AgNO<sub>3</sub> solution using K<sub>2</sub>CrO<sub>4</sub> as an indicator, calcium and magnesium were estimated by Versene (EDTA) method. Sodium and potassium were determined using a flame photometer. All these procedures were according to [15- 18].

Heavy metals (Cd, Cr, Mn, Ni, Pb, Co, Cu and Fe) in soil samples were analyzed by the total sorbed metals method according to [19] using atomic spectrophotometer.

## 2.2. Plant analysis

Leaves of *J. acutus* were collected at the four sites for heavy metals (Cd, Cr, Mn, Ni, Pb, Co, Cu and Fe) analysis using Perkin Elmer Atomic Absorption Spectrophotometer (model PYEUNICAM SP9, England) according to [17]. Soil characteristics supporting the four study populations and heavy metal measurements in leaves are shown in Tables 2 and 3.

## 2.3. DNA analysis

Fresh leaves of plants were collected and total genomic DNA was extracted using Wizard genomic DNA extraction kit promega (USA). 10- to 21-mer arbitrary primers were used for RAPD analysis.

Fifteen primers were screened for their amplification (Table 2). PCR amplification was performed in total volume of 25 µl containing 10× reaction buffer, 2.5 mM dNTPs, 5 mM MgCl<sub>2</sub>, 10 pmol/reaction primer, 100 ng of genomic DNA and (0.5 U/ µl) of Taq polymerase (promega, Germany) in Thermocycler Gene Amp 9700 (Applied Biosystems (ABI), USA). After a denaturation step for 5 min at 95 °C, amplification reactions were carried out for 40 cycles. Each cycle comprised of 1 min at 95 °C, 1 min of annealing temperature ranging from 28 to 30 °C and 1 min at 72 °C. The final elongation step was extended to 10 min. Amplification products were separated on agarose gel electrophoresis using 1.5% (w/v) agarose in 0.5× TBE buffer, stained with ethidium bromide and photographed by using gel documentation system. Amplification products were analysed by a 100 to 1000 bp molecular weight marker.

**Table 2** Sequences of the 15 primers used in this study

| Primer | Sequences of primer (5→ 3 ) | Total number of bands | Number of polymorphic bands | Percent of polymorphic bands % |
|--------|-----------------------------|-----------------------|-----------------------------|--------------------------------|
| UBC1   | CCTTCGGCTC                  | 8                     | 5                           | 63                             |
| UBC3   | GGCTTGACCT                  | 5                     | 3                           | 60                             |
| UBC6   | GAAGGCGAGA                  | 10                    | 7                           | 70                             |
| UBC9   | GTCATGCGAC                  | 15                    | 12                          | 80                             |
| UBC13  | CCTGGCACAG                  | 18                    | 13                          | 72                             |
| UBC16  | CCAGACTCCA                  | 28                    | 20                          | 71                             |
| UBC64  | GAGGGCGGGA                  | 30                    | 25                          | 83                             |
| UBC76  | GAGCACCAGT                  | 25                    | 17                          | 68                             |
| UBC77  | GAGCACCAGG                  | 21                    | 15                          | 71                             |
| OPA02  | TGCCGAGCTG                  | 6                     | 5                           | 83                             |
| OPA04  | AATCGGGCTG                  | 4                     | 2                           | 50                             |
| OPA18  | AGGTGACCGT                  | 10                    | 8                           | 80                             |
| OPB01  | GTTTCGCTCC                  | 6                     | 4                           | 67                             |
| OPB05  | TGCGCCCTTC                  | 19                    | 12                          | 63                             |
| OPC08  | TGGACCGGTG                  | 12                    | 8                           | 58                             |
|        | Total                       | 217                   | 156                         | 71.9                           |
|        | Average                     | 15                    | 10                          | 73                             |

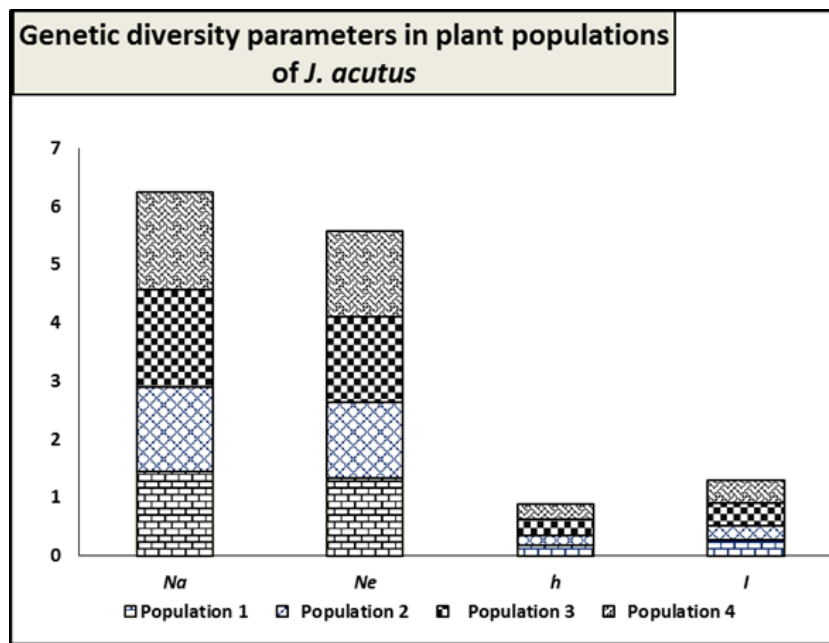
## 2.4. Statistical analysis

RAPD bands were scored as binary presence (1) or absence (0) characters to assemble the matrix of the RAPD data. Then, the indices of genetic diversity, such as percentage of polymorphic loci (PPL), observed number of alleles ( $N_a$ ), number of effective alleles ( $N_e$ ), Nei's gene diversity ( $h$ ), Shanon information index ( $I$ ), the coefficient for gene divergence ( $G_{st}$ ) were estimated using allele frequencies, by POPGENE 3.2 software [20] GenAEx version 6.4 [21].

## 3. Results

Fifteen primers produced a total of 217 RAPD bands (loci), among which 156 were polymorphic. The number of bands per primer varied from 4 to 30 with an average of 15. The average proportion of polymorphic markers across primers was 69%, ranging between 50% (OPA04) and 83% (OPA02) (Table 2).

The genetic diversity parameters (PPL%,  $N_a$ ,  $N_e$ ,  $h$ ,  $I$ ) among populations of *J. acutus* showed that, the population no. (4) of *J. acutus* growing in Bahr Kwar site reached the highest values (PPL = 68.20%,  $N_a$  = 1.6820,  $N_e$  =1.472,  $h$  = 0.264,  $I$  = 0.387) whereas in the population no. (2) of *J. acutus* growing in new Meet abou elkom site, Sinai attained the lowest values (PPL= 44.24%,  $N_a$  = 1.442,  $N_e$  =1.472,  $h$  = 0.164,  $I$  = 0.242), Figure (1).



**Figure 1** Genetic diversity parameters in plant populations of *J. acutus*: observed number of alleles ( $N_a$ ), number of effective alleles ( $N_e$ ), Nei's gene diversity ( $h$ ), and Shanon information index ( $I$ )

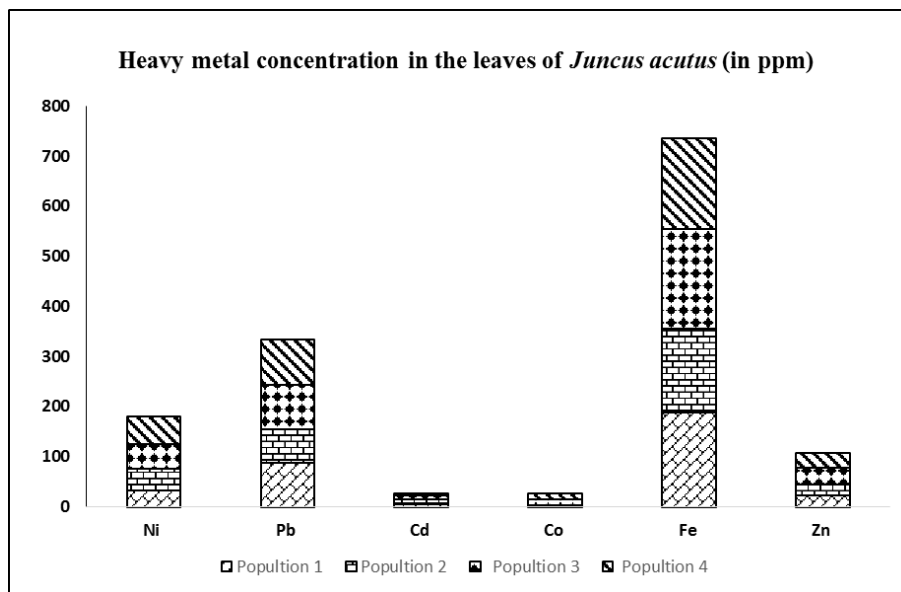
Soil chemical and physical features are in Table 3. As shown, soil of site 1(Industrial zone, Ismailia) had the highest values of pH (10.25) ,  $CO_3$  (22.4 ppm),  $Mg^{++}$  (42.6mg/100 gm soil) and the lowest values of  $HCO_3^-$  (18.34 ppm). Soil of site 2 (Meet abou elkom, Sinai) attained the highest values of silt (4.8%), clay (18.2%), EC (23.2 mm/cm, CL (812.5 ppm),  $Na^+$  (672 mg/100 mg soil and  $K^+$  (16.2 mg/100 mg soil) but the lowest of sand (72%),  $CaCO_3$  (2.8%) and  $Ca^{++}$  (331 mg/100 gm soil). Soil of site 3 (Manzala lake, elgameel) showed the highest values of sand (85%),  $CaCO_3$  (5.88%),  $HCO_3^-$  (27.28) and O.M. (0.70%) and the lowest of pH (8.53). Soils of Site 4 (Manzala lake 2, Bahr kuwar) had the highest values of  $Ca^{++}$  (520 mg/100 mg soil) and the lowest of  $Cl^-$  (104 ppm), Na (48 mg/ 100 mg soil) and Mg (16.6 mg/100 mg soil).

Heavy metals (Iron, Zinc, Nickel, Lead, Cadmium and Cobalt) were recorded in high concentrations in all studied sites. The highest values of Iron and Zinc (22.2 ppm and 12.9 ppm) were recorded in site 1. Lead recorded the highest value (33 ppm) in site 2. The highest values of Cadmium (0.40 ppm) and Cobalt (4.4 ppm) were recorded in Site 4.

**Table 3** The soil characteristics supporting the studied populations of *J. acutus*

| Soil factor                         | Sites |       |       |       |
|-------------------------------------|-------|-------|-------|-------|
|                                     | (1)   | (2)   | (3)   | (4)   |
| Sand (%)                            | 80    | 72    | 85    | 81    |
| Silt (%)                            | 2.5   | 4.8   | 2.4   | 2.4   |
| Clay (%)                            | 15.4  | 18.2  | 14.2  | 14.3  |
| pH                                  | 10.25 | 9.33  | 8.53  | 8.66  |
| CaCO <sub>3</sub> (%)               | 5.24  | 2.8   | 5.88  | 4.24  |
| CO <sub>3</sub> <sup>-</sup> (ppm)  | 22.4  | 4.75  | 2.25  | 2.22  |
| HCO <sub>3</sub> <sup>-</sup> (ppm) | 18.34 | 20.96 | 27.28 | 22.2  |
| O.M. (%)                            | 0.66  | 0.33  | 0.70  | 0.36  |
| EC (ms/cm)                          | 4.29  | 23.2  | 2.66  | 1.93  |
| Cl <sup>-</sup> (ppm)               | 790.8 | 812.5 | 300   | 104.5 |
| Ca <sup>++</sup> (mg/100 gm)        | 380   | 331   | 372   | 520   |
| Mg <sup>++</sup> (mg/100 g)         | 42.6  | 37.6  | 30    | 16.6  |
| Na <sup>+</sup> (mg/100 gm)         | 382   | 672   | 119   | 48    |
| K <sup>+</sup> (mg/100 gm)          | 12.4  | 16.2  | 15.5  | 14.6  |
| P (mg/100gm)                        | 2.2   | 1.3   | 2.4   | 2.6   |
| Fe (ppm)                            | 22.2  | 9.5   | 21.2  | 19.5  |
| Zn (ppm)                            | 12.9  | 5.1   | 5.8   | 9.4   |
| Ni (ppm)                            | 18.6  | 15.2  | 8.6   | 5.4   |
| Pb (ppm)                            | 22    | 33    | 22    | 28    |
| Cd (ppm)                            | 0.08  | 0.24  | 0.33  | 0.40  |
| CO (ppm)                            | 0.95  | 2.9   | 1.9   | 4.4   |

The estimate of heavy metals content in the leaves of *J. acutus* indicated the highest accumulation of Zn (33.9 ppm) , Ni (48.5 ppm) in site 3 and Fe (188.1 ppm) in site 1, Cd (8.2 ppm), Co (12.2ppm), and Pb (91 ppm) in site 4. (Figure 2).



**Figure 2** Heavy metal concentration in the leaves of *Juncus acutus* (in ppm)

---

#### 4. Discussion

The genetic diversity in wetland plant populations has been reviewed in some studies, and a considerable amounts of diversity have been found in most plant species (22-23). Studies on *J. acutus* examining genetic variation showed high levels of genetic differentiation among populations [24- 26].

RAPD is an effective method to detect population variation and is still used widely in many plants [25, 27-30]. Our results also show that RAPD is suitable for genetic diversity assessment in *J. acutus*.

In our study we attempt to apply the data of environmental variations for appropriately interpreting genetic information of *J. acutus*. A number of previous studies have shown that there is a correlation between genetic diversity and environmental heterogeneity *J. acutus* and other related wet land species [31, 30, 32], but very few studies have explicitly tested the causal environmental factors behind the pattern of genetic variation.

In our study the values of the measurements of CaCO<sub>3</sub> and O.M. are in accordance with all the genetic parameters of the *J. acutus* populations. Soil analyses revealed that the coastal sites of Manzala lake (site 3 and site 4) have higher levels of cadmium and cobalt whereas the sites of salines in industrial zone, Ismailia and new Meet Abu Elkoum, Sinai (site1 and site2) consistently grouped as the sites with the significantly least amount of metals.

The present study the genetic diversity parameters in parallel some heavy metals values such as Iron and Cadmium in sites 3 and 4. These findings are in conjunction with the results reported by [33] on isozyme diversity that indicate the population grown in contaminated sites were higher polymorphic than uncontaminated populations. Brian et al., (1999) detected that there are significantly higher genetic diversity at polluted sites [34]. The retention of such elevated levels of genetic diversity within these contaminated populations can be attributed to a number of selective, reproductive and demographic factors. As described by [6] if tolerance to the adverse environmental condition increases as a function of individual heterozygosity and/or if the contaminant is a mutagen, genetic variation within the affected population will remain elevated and may increase. The correspondence between ecological and genetic landscapes may be indicative of the potential role of environmental variables in driving population divergence [35-36]. Possibly, these variations among studied populations will assist in successful management of *J. acutus*.

---

#### 5. Conclusion

In conclusion, the present results demonstrated that *J. acutus* showed high capacity of metal bioaccumulation, moreover higher genetic diversity especially in contaminated sites in studied sites of Manzala lake. Overall, the correspondence between ecological and genetic landscapes may be indicative of the potential role of environmental variables in driving population differences.

---

#### Compliance with ethical standards

##### *Acknowledgments*

The author thank Dr. Hussein Rashed (Egyptian environment Agency,Egypt) for valuable guidance and help during sampling of *Juncus acutus* from the study sites in Elgameel site, Manzala lake.

##### *Disclosure of conflict of interest*

The author have no conflict of interest (only one author for the manuscript).

---

#### References

- [1] Good R. (1974). Geography of Flowering Plants. Longman Group, United Kingdom, 574.
- [2] Den Hartog C, Kvet J and Sukopp H. (1989). Reed: a common species in decline. Aquatic Botany, 35, 1-4.
- [3] Serag MA, Khedr AA, Zahran MA and Willis AJ. (1999). Ecology of some of some aquatic plants in polluted water courses, Nile Delta, Egypt. Journal of Union of Arab Biologists (B), 9, 85-97.
- [4] Mohan BS and Hosetti BB. (1999). Aquatic plants for toxicity assessment (review). Environmental Research, 81, 259-274.

- [5] Zurayk R, Sukkariyah B and Baalbaki R. (2001). Common hydrophytes as bioindicators of nickel, chromium and cadmium pollution. *Water, Air and Soil Pollution*, 127, 373-388.
- [6] Bourret V, Couture P, Campbell PGC and Bernatchez L (2008). Evolutionary ecotoxicology of wild perch (*Perca flavescens*) populations chronically exposed to a polymetallic gradient. *Aquatic Biology*, 86, 76-90.
- [7] Hoffmann AA and Willi Y. (2008). Detecting genetic responses to environmental change. *Nature*, 9, 421-432.
- [8] Deng J, Liao B, Ye M, Deng D, Lan C and Shu W. (2007). The effects of heavy metal pollution on genetic diversity in zinc/cadmium hyperaccumulator *Sedum alfredii* populations. *Plant Soil*, 297, 83-92.
- [9] McNaughton SJ. (1975). R- and k-selection in *Typha*. *American Nature*, 109, 251-261.
- [10] Silander JAJr. (1985). Microevolution in clonal plants. In: Jackson JBC, Buss LW and Cook.
- [11] Raybould AF, Gray AJ, Lowrence MJ and Marshall DF. (1991). The evolution of *Spartina* C-E. Hubbard (Graminae): origin and genetic variability. *Biological Journal of Linnean Society*, 43, 111-126.
- [12] Jackson JBC, Buss LW and Cook RE. (1985). Population biology and evolution of clonal organisms. Yale university press, London.
- [13] De Kroon H and van Groenendael J. (1997). The ecology and evolution of clonal plants, Backbuys Publication, Leiden.
- [14] Williams JGK, Kubelik AR, Livak KJ, Rafalski JA and Tingey S. (1990). DNA polymorphism amplified by arbitrary primers are useful as genetic markers. *Nucleic Acids Research*, 18, 6531-6535.
- [15] Chapman HD and Pratt PF. (1961). Ammonium vandate-molybdate method for determination of phosphorus. In: Methods of analysis for soils, plants and water. 1<sup>st</sup> Ed. California: California University, Agriculture Division, 184-203.
- [16] Jackson ML. (1973). Soil Chemical Analysis. Prentice-Hall of India Pvt. Ltd., New Delhi, India, 38–204.
- [17] Allen SE, Grimshaw HM, Parkinson JA and Quarmby C. (1974). Chemical analysis of ecological materials. Oxford: Blackwell Scientific.
- [18] Baruah TC and Barthakur HP. (1997). A Textbook of Soil Analysis. Vikas Publishing House Pvt. Ltd, 334 pp.
- [19] USEPA (1986). Quality Criteria for Water. EPA-440/5-86-001, Office of Water Regulations Standards, Washington DC, USA.
- [20] Yeh FC, Yang RC, Boyle TBJ, Ye ZH and Mao JX. (1999). POPGENE 3.2, User-Friendly Shareware for Population Genetic Analysis. Molecular Biology and Biotechnology Center, University of Alberta, Edmonton. Available from: <http://ualberta.ca/wfeyeh>.
- [21] Peakall R and Smouse PE. (2006). GENALEX 6: genetic analysis in Excel. Population genetic software for teaching and research. *Molecular Ecology Notes*, 6, 288–295.
- [22] Tsyusko OV, Smith MH, Sharitz RR and Glenn TC. (2005). Genetic and clonal diversity of two cattail species, *Typha latifolia* and *T. angustifolia* (Typhaceae), from Ukraine. *American Journal of Botany*, 92, 1161–1169.
- [23] Diyanat M, Booshehri AAS, Alizadeh HM, Naghavi MR and Mashhadi HR. (2011). Genetic diversity of Iranian clones of common Reed (*Phragmites australis*) based on morphological traits and RAPD markers. *Weed Science*, 59, 366–375.
- [24] Zeidler A, Scheneiders S, Jung C, Melchinger AE and Dittrich P. (1994). The use of DNA fingerprint in ecological studies of *Phragmites australis* (Cav.) Trin. ex Steudel. *Botanica Acta*, 107, 237–242.
- [25] Koppitz H, Ku<sup>hl</sup> H, Hesse KJ and Kohl G. (1997). Some aspects of the importance of genetic diversity in *Phragmites australis* (Cav.) Trin. ex Steudel for the development of reed stands. *Botanica Acta*, 110, 217–223.
- [26] McLellan AJ, Prati D, Kaltz O, Schimd B. (1997). In: de Kroon H. and van Groenendael J (Eds.), Structure and analysis of phenotypic and genetic variation in clonal plants, 185–210.
- [27] Koppitz H. (1999). Analysis of genetic diversity among selected populations of *Phragmites australis* world-wide. *Aquatic Botany*, 64, 209–221.
- [28] Keller BEM. (2000). Genetic variation among and within populations of *Phragmites australis* in the Charles River watershed. *Aquatic Botany*, 66, 195–208.

- [29] Bussell GD, Waycott M and Chappill JA. (2005). Arbitrarily amplified DNA markers as characters for phylogenetic interference. *Perspect. Plant Ecology, Evolution and Systematics*, 7, 3–26.
- [30] Curn V, Kubatova B, Vavrova P, Krivackova-Sucha O and Cizkova H. (2007). Phenotypic and genotypic variation of *Phragmites australis*: comparison of populations in two human-made lakes of different age and history. *Aquatic Botany*, 86, 321–330.
- [31] Hargeby A, Johansson J and Ahnesjo J. (2004). Habitat-specific pigmentation in a freshwater isopod: adaptive evolution over a small spatiotemporal scale. *Evolution*, 58, 81–94.
- [32] Hansen DL, Lambertini C, Jampeetong A and Brix H. (2007). Clone-specific differences in *Phragmites australis*: effects of ploidy level and geographic origin. *Aquatic Botany*, 86, 269–279.
- [33] Bush EJ and Barret SCH. (1993). Genetics of mine invasions by *Deschampsia cespitosa* (Poaceae). *Canadian Journal of Botany*, 71, 1336-1348.
- [34] Brian K, Pelikan S, Toth G, Smith M, and Rogstad S. (1999). Genetic diversity of *Typha latifolia* (Typhaceae) and the impact of pollutants examined with tandem-repetitive DNA probes. *American Journal of Botany*, 86(9), 1226–1238.
- [35] Guo XX and Mrazek J. (2008). Long simple sequence repeats in host-adapted pathogens localize near genes encoding antigens, housekeeping genes, and pseudogenes. *Journal of Molecular Evolution*, 67, 497–509.
- [36] Hancock AM, Alkorta-Aranburu G, Witonsky DB and Di Rienzo A. (2010). Adaptations to new environments in humans: the role of subtle allele frequency shifts. *Philosophical Transactions of the Royal Society B*, 365, 2459–2468.

---

### How to cite this article

Mansour H. (2018). Analysis of genetic diversity and bioaccumulation potential of *Juncus acutus* grown in some northern swamp habitats of Egypt. *GSC Biological and Pharmaceutical Sciences*, 5(2), 74-81.

---