

Nymphaea lotus (Indian Lotus) Analysis with Genetic Algorithm

Dwadasi Venkata Sushma Chandra^{1,*}, Kavirayani Srikanth²

Abstract

There is a significant problem with the availability of medicinal plants for the treatment of various diseases. *Nymphaea lotus* (Indian lotus) is one such plant, which is primarily available in the Indian subcontinent. This paper investigates the analysis of this medicinal plant with the help of a genetic algorithm. Himalayan yew, false black pepper, Indian snakeroot, and Indian lotus are four medicinal plants. These four have some unique medicinal values, which has caused them to be overharvested, bringing them to the verge of extinction. Among the four identified plants the Indian lotus is considered sacred and is extensively used in festivals, temples, and other places, which is causing overharvesting of the plant. The plant being considered sacred in this country has also to be preserved for its medicinal values and hence this paper envisages the same using a varied analysis modifying the population and the possible ways to prevent its extinction in the context of its requirement for recovering full medicinal values if it comes under extinction and the number of generations it would take to retrieve the same. The analysis proved that this genetic algorithm-based analysis will pave way to preserve the plant from extinction and help in reshaping the medicinal timeline of this country for these plants.

Keywords: *Nymphaea lotus* (Indian lotus), genetic algorithm (GA), medicinal plant, algorithm, analysis

INTRODUCTION

The importance of medicinal plants in Indian subcontinent is predominant due to Ayurveda being a backbone of medical research in this region. *Nymphaea lotus* (Indian lotus) is one such plant, which is investigated for potential risk of extinction in this work.

LITERATURE SURVEY

India is a land of rich floral diversity with all exotic endemic species of plants. From the beginning of human life, they were in proximity with these plants, exploiting them for their medicinal use by trial-and error-method. Then this traditional knowledge is passed from generation to generation thereon. As a result, the biodiverse flora is becoming endangered and if left, they might become extinct also. Himalayan yew, false black pepper, Indian snakeroot, and Indian lotus are four medicinal plants. These four have some unique medicinal values, which is causing them to be overharvested bringing them to the verge of extinction. For instance, *Taxus wallichiana*, commonly known as the Himalayan yew, is a tree species that holds medicinal significance. One of its primary medicinal advantages lies in its production of taxol, a potent anticancer compound. Breast, ovarian, and lung cancers are among the many cancers for which taxol is used as a treatment. The bark, needles, and seeds of *Taxus wallichiana* contain taxol and other

*Author for Correspondence

Dwadasi Venkata Sushma Chandra
E-mail: sushma.dwadasi@gmail.com

¹Research Scholar, Department of BioChemistry, Andhra University, Visakhapatnam, Andhra Pradesh, India

¹Assistant Professor, Department of BioChemistry, Gayatri Vidya Parishad College for Degree and PG Courses, Visakhapatnam, Andhra Pradesh, India

²Assistant Professor, Department Electrical and Electronic Engineering, Gayatri Vidya Parishad College for Degree and PG Courses, Visakhapatnam, Andhra Pradesh, India

Received Date: August 28, 2023

Accepted Date: October 05, 2023

Published Date: October 21, 2023

Citation: Dwadasi Venkata Sushma Chandra, Kavirayani Srikanth. *Nymphaea lotus* (Indian Lotus) Analysis with Genetic Algorithm. International Journal of Algorithms Design and Analysis Review. 2023; 1(2): 18–22p.

taxanes, which have shown promising results in inhibiting the growth of cancer cells. Taxol prevents the multiplication of cancer cells by interfering with their ability to divide. *Taxus wallichiana* has been used in traditional medicine to treat conditions like asthma, rheumatism, and bronchitis in addition to its ability to fight cancer. It is thought to have antioxidant, analgesic, and anti-inflammatory effects. In India, *Taxus wallichiana* is primarily found in the western Himalayan region, including states like Jammu and Kashmir, Himachal Pradesh, and Uttarakhand. The forests of these regions serve as natural habitats for this tree species. A perennial aquatic eudicot, *Nelumbo nucifera* is a member of the Nelumbonaceae family, which consists of just one genus and two species. It is a significant horticultural plant that has been extensively used, particularly in Southeast Asia [1], for purposes ranging from ornamental to nutritional to medicinal.

In several regions of India, it has been utilized as a traditional medicinal and functional food. It has a wide range of biological and pharmacological properties, including antioxidant, anti-inflammatory, immune-modulatory, antiviral, hepatoprotective, cardioprotective, and hypoglycemic activities. It contains a variety of phytochemicals, including alkaloids, polyphenols, terpenoids, steroids, and glycosides [2]. The entire *Nelumbo* plant, including its roots, rhizomes, leaves, flowers, and seeds, serves various culinary and medicinal purposes due to its rich phytochemical composition [3–11]. These studies highlight the ecological advantages associated with diverse plant species and the variations in their growth patterns [12]. Furthermore, Souza et al. [13] explore the challenges of detecting associations among rare genetic variants with small minor allele frequencies (MAF), emphasizing the persistent difficulties in addressing modest effects using rare variant association methods. Lastly, Coreus and Oliveto [14] and Chromik and Arnrich [15] delve into the efficiency of steady-state genetic algorithms (GAs), demonstrating that they outperform standard bit mutation-only evolutionary algorithms by 25% in terms of speed for moderate population sizes. This finding offers valuable insights for a wide range of species-related analyses.

Nelumbo nucifera is a diploid with a number of chromosomes $2n = 16$. Flow cytometric analysis has estimated the lotus genome's size to be around 929 Mb. The introduction of third-generation sequencing techniques, which have proven successful in enhancing genome assembly in numerous other species, holds promise for improving the lotus genome assembly in the near future. In this paper, GA-based evolutionary analysis of the plant is done to understand the evolutionary rate and the possibilities in variation in harvesting that can be understood by variation in the population for the *Nymphaea lotus* (Indian lotus) using a Python language-based code to evaluate the genetic variation and the problems associated with the extinction.

The paper aims to emphasize the importance of cultivating and growing the plant in a more methodological fashion, which would be helpful for a balanced availability in the ecosystem across the country for various medical purposes to enable the usage of the plant on need basis.

METHODOLOGY

This work aims at the studies of evolution cycle of the Indian lotus plant based on their chromosome structure. The plant normally appears as shown in Figures 1 and 2.

Experimental Method

- *Step 1:* Identify the plant/shrub which needs to be evaluated for genetic process such as *Nymphaea lotus* (Indian lotus)
- *Step 2:* The GA testing based on standard GA established process.
- *Step 3:* The offspring are further allowed to alter their genetic characteristics completely until full DNA sequencing with all important properties is reflected in the n th generation.
- *Step 4:* The analysis is repeated for the same mutation rate and crossover rate for different plant species indicated fixing the number of maximum iterations and the variation in fitness and computation times by Python codes is evaluated.



Figure 1. *Nymphaea lotus* (Indian lotus).



Figure 2. An enlarged view of *Nymphaea lotus* (Indian lotus).

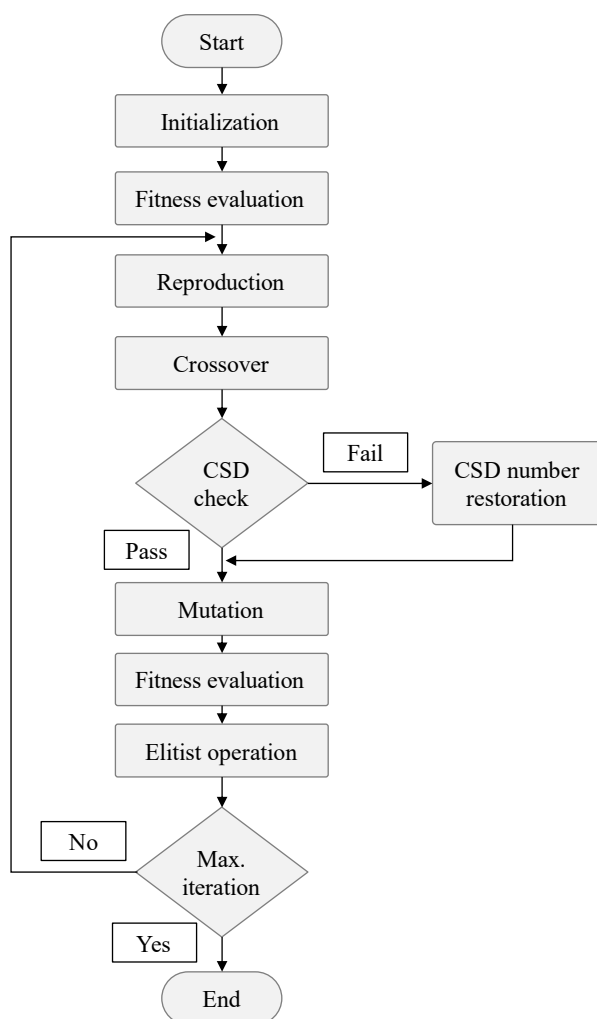


Figure 3. Flowchart of genetic algorithm.

The process implemented can be analyzed by using the flowchart shown in Figure 3.

RESULTS

The analysis for variation taking different populations is as shown in Table 1. The fitness was best with very high initial population in less iterations and as the population decreases as in case 1, it would take at least 893 generations to reach a fitness of 85%, which clearly indicate the necessity for the plant to be preserved from extinction.

Table 1. Analysis of *Nymphaea lotus* (Indian lotus).

S.N.	Initial population	Generation	Fitness
1	20	893	85.71
2	2000	7	100
3	200000	6	100

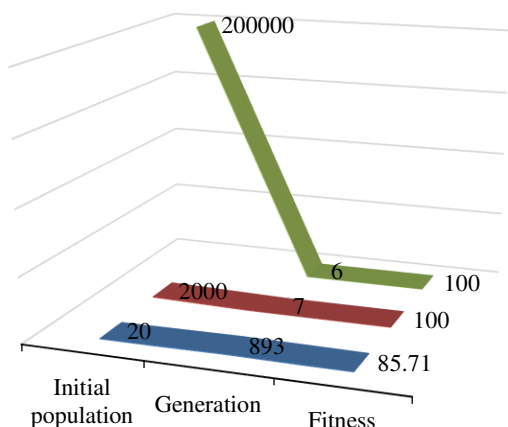


Figure 4. Genetic analytics of *Nymphaea lotus* (Indian lotus).

Figure 4 presents the analytical view of the data represented in Table 1 which clearly indicate that if the initial population is high the fitness is the best DNA possibility with full medical values can be obtained for the *Nymphaea lotus* and if the initial population were less, we would require 800 generations of plant evolution to get its full medicinal values. So, it clearly indicates the need for preserving the plant from extinction.

CONCLUSION

This work explores the GA-based analysis of the *Nymphaea lotus* (Indian lotus), which has medicinal value. The extinction of such a plant will cause a problem for the farmer depending on it. If proper evolution with full fitness is not done, the plant might become extinct, and we might be at loss of some important medicines which are otherwise available as traditional medicine in the Indian subcontinent. Indian lotus thus needs to be preserved from extinction and it is very important to analyze this plant and other medicinal plants on the verge of extinction to preserve and restore the full medicinal values of these plants so that these can be used in future medicines, which would help restore health of individuals in the shortest time. The breakthrough mechanisms of evolutionary analysis of the Indian lotus are very important to sustain the medicinal prosperity of a country like India, which has a huge population where the requirements are demanding and pressing every second in the context of millions requiring medical care at affordable cost.

REFERENCES

1. Lin Z, Zhang C, Cao D, Damaris RN, Yang P. The latest studies on lotus (*Nelumbo nucifera*) – an emerging horticultural model plant. *Int J Mol Sci.* 2019; 20 (15): 3680.
2. Purohit SR, Rana SS, Idrishi R, Sharma V, Ghosh P. A review on nutritional, bioactive, toxicological properties and preservation of edible flowers. *Future Foods.* 2021; 4: 100078.
3. Carod-Artal FJ. Hallucinogenic drugs in pre-Columbian Mesoamerican cultures. *Neurología (Engl Ed).* 2015; 30 (1): 42–49.
4. Altaf M, Javid A, Khan AM, Khan MS, Umair M, Ali Z. Anthropogenic impact on the distribution of the birds in the tropical thorn forest, Punjab, Pakistan. *J Asia Pacific Biodiversity.* 2018; 11 (2): 229–236.

5. Balakrishnan P, Ajayan S, Mukkudakkattu S, Nechiyil K, Nambi N. Review of unique ophthalmic formulations in Vaidya Manorama: a traditional Kerala Ayurveda literature. *J Ayurveda Integr Med.* 2022; 13 (2): 100576.
6. Serag MS, El-Hakeem A, Badway M, Mousa MA. On the ecology of *Azolla filiculoides* Lam. in Damietta district, Egypt. *Limnologica – Ecol Manage Inland Waters.* 2000; 30 (1): 73–81.
7. Aumeeruddy MZ, Mahomoodally MF. Global documentation of traditionally used medicinal plants in cancer management: a systematic review. *South Afr J Botany.* 2021; 138: 424–494.
8. Nimrouzi M, Jaladat AM, Zarshenas MM. A panoramic view of medicinal plants traditionally applied for impotence and erectile dysfunction in Persian medicine. *J Tradit Complement Med.* 2020; 10 (1): 7–12.
9. Suroowan S, Pynee KB, Mahomoodally MF. A comprehensive review of ethnopharmacologically important medicinal plant species from Mauritius. *South Afr J Botany.* 2019; 122: 189–213.
10. Ajao AA, Sibiyi NP, Moteetee AN. Sexual prowess from nature: a systematic review of medicinal plants used as aphrodisiacs and sexual dysfunction in sub-Saharan Africa. *South Afr J Botany.* 2019; 122: 342–359.
11. Khan SU, Anjum SI, Ansari MJ, Khan MH, Kamal S, Rahman K, Shoaib M, Man S, Khan AJ, Khan SU, Khan D. Antimicrobial potentials of medicinal plant's extract and their derived silver nanoparticles: a focus on honey bee pathogen. *Saudi J Biol Sci.* 2019; 26 (7): 1815–1834.
12. Song W, Huang C. Mining high utility itemsets using bio-inspired algorithms: a diverse optimal value framework. *IEEE Access.* 2018; 6: 19568–19582.
13. Souza MG, Vallejo EE, Estrada K. Detecting clustered independent rare variant associations using genetic algorithms. *IEEE/ACM Trans Comput Biol Bioinform.* 2019; 18 (3): 932–939.
14. Corus D, Oliveto PS. Standard steady state genetic algorithms can hillclimb faster than mutation-only evolutionary algorithms. *IEEE Trans Evolution Comput.* 2017; 22 (5): 720–732.
15. Chromik J, Arnrich B. Optimal deployment in emergency medicine with genetic algorithm exemplified by lifeguard assignments. In: 2021 43rd Annual International Conference of the IEEE Engineering in Medicine & Biology Society (EMBC), Mexico, November 1–5, 2021. pp. 1806–1809.