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RESEARCH ADVANCES IN LIFE SCIENCES

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PREFACE

The field of life sciences has witnessed unprecedented growth over the past few decades, driven by rapid advancements in technology, interdisciplinary integration, and an ever-expanding understanding of biological systems. *Research Advances in Life Sciences* is conceived as a comprehensive volume that brings together contemporary research, emerging trends, and innovative perspectives across diverse domains of life sciences.

This book aims to provide a platform for researchers, academicians, and scholars to present their original contributions and critical insights into areas such as biotechnology, environmental science, microbiology, agriculture, health sciences, and allied disciplines. The chapters included in this volume reflect the dynamic nature of life science research, addressing both fundamental concepts and applied aspects that are crucial for sustainable development and human welfare.

A significant emphasis of this volume is placed on interdisciplinary approaches, recognizing that modern scientific challenges require the integration of multiple fields. From molecular-level investigations to ecosystem-level analyses, the contributions in this book highlight the interconnectedness of biological processes and their relevance to global issues such as climate change, biodiversity conservation, food security, and public health.

The editors sincerely acknowledge the valuable contributions of all authors, whose scholarly work has enriched this volume. We also extend our gratitude to the reviewers for their constructive suggestions, which have helped maintain the academic quality and integrity of this publication. Special thanks are due to the publishers for their continuous support and cooperation throughout the process of compilation and production.

It is our hope that this book will serve as a useful reference for students, researchers, and professionals, and will inspire further research and innovation in the ever-evolving field of life sciences.

- Editors

TABLE OF CONTENT

Sr. No.	Book Chapter and Author(s)	Page No.
1.	**EFFECT OF LAMBDA- CYHALOTHRIN AND IMIDACLOPRID ON OXYGEN CONSUMPTION OF FRESHWATER BIVALVE *LAMELLIDENS MARGINALIS*** Poonam Bhikan Ahire	1 – 10
2.	**MACHINE LEARNING APPLICATION IN DETECTING INVASIVE PLANKTON SPECIES RISK ANALYSIS** T. Sasilatha, Salu S. K and R. Karthik Manoj	11 – 17
3.	**APPLICATION OF PLANT BIOTECHNOLOGY IN CROP IMPROVEMENT** Varsha Kumari, Anchal Agarwal, Kailasha Meghwal, Bhuri Singh, Shravan Kumar Sharma, B. L. Kumhar and Ashish Sheera	18 – 22
4.	**UNDERUTILIZED WILD EDIBLE WEEDS AS SUSTAINABLE FOOD RESOURCES: ETHNOBOTANICAL INSIGHTS AND NUTRITIONAL PERSPECTIVES FROM RURAL COMMUNITIES** Parika Agrawal, Ashok Kumar, Shiv Pratap Singh and Sanjay Agarwal	23 – 44
5.	**HEAVY METAL CONTAMINATION IN SOILS: SOURCES, ENVIRONMENTAL BEHAVIOR, ECOLOGICAL IMPACTS, AND SUSTAINABLE REMEDIATION STRATEGIES** E. Thenpandiyan, V. Menaka, T. Sathishpriya and S. Muruganantham	45 – 58
6.	**ECOLOGICAL ASSESSMENT OF WADING BIRDS IN A HUMAN-MODIFIED WETLAND ECOSYSTEM** G. Kondaiah and U. Srineetha	59 – 66
7.	**MARINE, COASTAL AND MANGROVE BIODIVERSITY IN LIFE SCIENCE RESEARCH: A COMPREHENSIVE REVIEW** K. Prabhu	67 – 77
8.	**MARINE SPECIES CLASSIFICATION AND IDENTIFICATION: INTEGRATING INFOGAN AND YOLOv8** T. Sasilatha, B. Poornima, R. Karthick Manoj and Neya Sridhar	78 – 88

9.	**THE HUMAN MICROBIOME, THEIR ASSOCIATED DISEASES, AND RECENT ADVANCEMENTS** Josna Victoria K Johnson and Vimala K John	89 – 94
10.	**NANOTECHNOLOGY FOR REMOVAL OF HEAVY METALS FROM CONTAMINATED SOILS: MECHANISMS, NANOMATERIALS AND ENVIRONMENTAL APPLICATIONS** Rashmi Rekha Saikia	95 – 105
11.	**LIFESTYLE INTERVENTIONS AND PHARMACOLOGICAL APPROACHES IN POLYCYSTIC OVARY SYNDROME (PCOS)** Shivaraj Kapase, M. Mohamed Shabi, Shekhar M Teli, Somanagouda Biradar and Sujata Biradar	106 – 124
12.	**AEROBIOLOGY IN PLANT PATHOLOGY: CONCEPTS, EPIDEMIOLOGY, DISEASE MONITORING, DETECTION AND MANAGEMENT** Vijay Kumar and Ashok Chhetri	125 – 137
13.	**GENETICALLY MODIFIED CROPS: ADVANCES, APPLICATIONS, BIOSAFETY, AND FUTURE PROSPECTS** Sameer Gunjan Lakra and Neha Nidhi Tirkey	138 – 144

EFFECT OF LAMBDA- CYHALOTHRIN AND IMIDACLOPRID ON OXYGEN CONSUMPTION OF FRESHWATER BIVALVE *LAMELLIDENS MARGINALIS*

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1. Introduction

Respiration is one of the most important features of life. It is the process during which oxygen is inhaled and carbon dioxide is released represents the metabolic status of an organism. Thus, respiration provides energy to perform various activities of body like movement, metabolic reactions, muscular contraction, growth and development etc. A constant supply of oxygen is essential for the maintenance of life. The oxygen oxidises food material to release the energy in the form of ATP which provides various life process. The activity of animal can be measured in terms of oxygen uptake (Kunt Schmit – Nielsion, 2007).

Environmental pollution is one of the undesirable side effects of industrialization and important aspect of environmental degradation (Jothinarendrin, 2012). Insecticides are spreayed over agricultural crops; throughout the year with different concentrations which affect aquatic organisms. The assessment of these effects of insecticide to non-target aquatic organism is very difficult and pollutants from industrial areas and agricultural runoff in to the environment pollute water bodies (Tyagi, 2000). Aquatic animals have to pass large quantities of water over their respiratory surface and are subjected to relatively greater risk of exposure to toxic substance (Shelke and Wani, 2005).

Gills are important organ for metabolic processes like feeding and oxygen consumption. Any damage to this organ causes respiratory distress to the particular organism (Magre and Patil, 2002). In mussels' gills and mantle play important role in respiration. As water passes through the gills, oxygen from the water diffuses in to the haemolymph. Several factors can affect oxygen consumption like, size of the individual, body weight, food, temperature, oxygen availability, aerial exposure, salinity and pollutants. Oxygen uptake as an indicator of physiological stress in embryo of minnow (*Pimephales promelas*) Porterfield, (2008).

Exposure rate plays an important role for determining the toxicity of a pesticide to an organism. Acute exposure is an exposure of two weeks or less in duration (often less than 24 hours), while chronic exposure is a continued exposure occurring over an prolonged time usually from weeks to years (Mergel, 2009).

Environmental stresses like temperature, oxygen consumption, salinity, hydrogen ion concentration and various types of pollutants affect the uptake of oxygen consumption.

Insecticides are responsible for production of Reactive Oxygen Species (ROS). Increased ROS level cause damage to cellular constituents is termed "oxidative stress. Different biomarkers used to determine oxidative stress (Lushchak, 2011). *Labeo rohita* exposed Malathion to acute and chronic toxicity leading to changes in the behaviour and oxygen consumption rate was reduced due to accumulation of ACh E in synapses; this leads the impairment of metabolic process (Patil and David, 2009). Rate of oxygen consumption in *Lamellidens marginalis* exposed to organophosphate pesticide triazphos for 96 hours and 21 days, the rate of oxygen consumption were decreased with increased exposure of time (Rane *et al.,* 2013). Maharajan *et al*. (2013) studied the toxicity effect of profenofos on the histology of gill and oxygen consumption of *Catla catla*.

Endosulfan 35% EC exposed to bivalve *Lamellidens corrianus* for acute toxicity test for oxygen consumption in summer, winter, mansoon, there was decrease in oxygen consumption in all three seasons (Kamble and Shinde, 2012). Monocrototophs (MCP) exposed bivalve shows oxidative stress it alters the activity of antioxidant enzymes and contribute to genotoxicity and heavy damage to gill than foot, mantle tissue (Mundhae *et al.,* 2014). Indosulpin responsible for decreased in the uptake of oxygen consumption in *Thiara Lineata* after acute toxicity test (Pawar *et al.,* 2014). The clam *Ruditapes decussates* was exposed to herbicide (48% glyphosate, „roundup") and an insecticide (50% chlorpyrifosmethyl, „reldan") for the determination of oxygen consumption, leads to decrease in respiration rate was reveled by a S. El-Shenawy *et al.,* 2003). Propiconazole exposed to concentration 0.6 mg/l and 1.2 mg/l for acute toxicity test, are responsible for the decrease in uptake of oxygen consumption in *Lymnaea accuminata* (Lonkar and Bobdey 2014). Dimethoate (30% EC) and Quinalphos affect oxygen consumption of a freshwater fish *Labeo rohita* for decrese in oxygen consumption (Logaswamy *et al.,* 2010). Nickel chloride treated bivalve *Lamellidens marginalis* for chronic toxicity leads cease in oxygen consumption Andhale and Zambare (2012).

L.Marginalis exposed to phosphamidion at 0.015 µg/L exhibit changes in the heart rate and on oxygen consumption of freshwater bivalve. Organophosphates are toxic because of their inhibition of enzyme acetylcholinesterase. This enzyme inhibition results in the accumulation of acetylcholine in nerve tissue and effector organs (Senthimurugan *et al.,* 1994). Lomte and Jadhav (1982) reported change in oxygen consumption due to pesticidal stress in *Corbicula regularis*. Ravindra and Patel (2016) noted the decrease in the uptake of oxygen consumption along with behavioural changes and copious secretion of mucous after acute treatment of endosulfan in *Channa punctatu.* Zebra mussel *Dreissena polymorpha* showed the altered respiration rate observed after the exposure of Chlorpyrifos for short period i.e (72 hrs) by Yancheva and Mollov, (2017).

Desphande and Akarte (2003) reported dimethoate 1.429 ppm for acute test leads decrease in uptake of oxygen by mussel. This was due to pollutant stress on gills of *Lamellidens marginalis.* Geyer *et al.,* (1982) studied the relationship between physicochemical properties and accumulation of organic micropollutants in marine water bivalve, *Mytilus edulis*. Deldrin was accumulated in filter feeder *Sphaerium cornem* (Michel Boryslawskyi *et al.,* 1987). Tilak *et al.,* (2009) acute toxicity of nuvan to *Ctenopharyngogon idella* leads to decrease in oxygen consumption. The rate of oxygen consumption in fishes is directly correlated with the metabolic stress (Fry, 1971). Total oxygen consumption per unit body weight was estimated by winkler's method (Jagtap *et al.,* 2011).

Bhawane *et al*. (2012) reported rate of oxygen consumption was significantly increased when cerebral ganglia removed from *Lamellidens marginalis*. Toxicity of chlorpyrifos between 8 and 16 mg l-1 causes severe physiological damage to endogenous rhythms of the Manila clams and its oxygen consumption (Wan-Soo Kim *et al.,* 2004). The toxic effect Malathion on oxygen consumption and biochemical characteristics of total protein, carbohydrate and cholesterol in liver, muscle, kidney and gills of *Oreochromis niloticus* were examined up to 96 hours (Fahmy, 2012).

Esomus danricus was exposed to three sub lethal concentrations of endosulfan EC 35 0.49, 0.049 and 0.0049 µg l-1 for 0,7,14, 21, 28 days to determine changes inthe oxygen consumption and gill morphology. The rates of oxygen consumption reduced as the time of exposure increases while the gills showed various necrotic changes by Suchismita Das, (2012). Several pesticides induce reactive oxygen species (ROS) damage, also known as oxidative stress (Abdollahi *et al.,* 2004, Deb and Das, 2013). Cypermethrin (10% E.C) impairs the metabolic and physiological activities of the organisms. Physiological analysis along with histological study provides complete understanding of toxic stress. Decreased oxygen uptake and histopathological changes such as necrotic and degenerative observed in selected tissues like gill, liver and kidney of the Indian major Carp *Cirrhinus mrigala* Manjula Sree Veni (2014).

Pena- Llopis, Ferrando and Pena (2002) reported oxidative stress when exposed to fenitrothion 12mg/L in mussel *Mytilus galloprovincialis*. Azamethiphos affect feeding actvity, actylchlinestrase activity noted by Galloway (2007) in marine mollusc *M. edulis*. Bivalve molluscs have ability to concentrate chlorinated pesticide from water (Vesna miluna *et al.,* 2016). The behavioural responses of mussel, *Mytilus edulis* to sub-lethal concentrations of lindane and atrazine. Behaviour effects studied in mussels were byssus formation, valve movement and valve gape. Lindane and atrazine cause reduction of byssal formation and reduction of valves movement (El-Shenawy, 2001).

Organophosphorus pesticide, synthetic pyrethroid and neonecotinide pesticide are reported to reduce activity in animal and tissue respiration. Behavioural characteristics are indicators of toxicant effect. Many chemical contaminants target specific physiological systems and exert their effects on behaviour when fish exposed to synthetic pyrethroid λ- Cyhalothrin insecticide LC50 up to 96 h exposure exhibited irregular, erratic swimming movements, hyper excitability and loss of balance, rapid respiration, light discoloration and gulping air in *Clarias batrachus* (Indira Rani and Kumaraguru 2014). *Cyprinus carpio* exposed to cypermethrin (25% EC) and its impact on oxygen consumption noted alterations in oxygen consumption may be due to respiratory distress as a consequence of impaired oxidative metabolism (P. Neelima, *et al.,* 2016). Similar changes observed that decrease in oxygen consumption due to the respiratory distress and the ionic content decreased significantly in gill, liver and muscle tissue of *Cyprinus carpio* were exposed to the lethal concentration (7.5 g/l) of quinalphos (Chebbi and David, 2010). As we know that environmental stress like pollutants alter the metabolic rate of oxygen utilization. Review of literature of oxygen consumption studies shows that number of different organisms have been used for evaluation of aquatic pollutants.

Oxygen consumption is very sensitive physiological process and changes in oxygen uptake or change in respiration considered as indicator of pollutant stress by many investigators such as Mane *et al.* (1983) as endosulfan toxicity to freshwater and estuarine bivalve Indonaia caeruleus and Katelysia opima respectively. Dimethoate induced oxidative stress and DNA damage noted in *Oncorhynchus mykiss* by Dogan *et al.* (2011). Hence the present work was undertaken to find out the impact of λ- Cyhalothrin and Imidacloprid on rate of oxygen consumption in freshwater mussel *Lamellidens marginalis.*

2. Material and Method

Fresh water bivalve *Lamillidens marginalis* were collected from the Darna River, chehadi (Latitude 19º55‟‟54.02"N, Longitude 73º55‟‟30.42"E) Nasik Road, Maharashtra. These were brought to laboratory, cleaned to remove their mud and acclimatized in dechlorinated water for 3-4 days in plastic troughs and feed on crushed algae. Overcrowding was avoided by keeping a small number of bivalves in to different plastic troughs. The water was changed every day. The bivalves were kept under 12:12 light dark period during experiment. The healthy bivalve of approximately same size and weight irrespective of their sex were selected. The pesticide λ-cyhalothrin (5% EC) and Imidacloprid (30.5m/m sc) were locally purchased from Mankar and son's Panchavati, Nasik.

The acclimatized bivalves were exposed to lethal concentration of Lambda-Cyhalothrin (123.02 ppm) considered as first set. Second set exposed to Imidacloprid (89. 83 ppm) ten bivalves were exposed up to 96 hours in each set. While third group considered as control. The Oxygen consumption was measured in control and treated groups was measured by adopting winkler‟s idometry method at an interval of 24 hours. The quantitiy of oxygen consumption was calculated mg/L.

3. Observation and Results

Table 1: Average oxygen consumption by *Lamellidens marginalis* exposed to sublethal concentration of λ- Cyhalothrin (123.02 ppm) mg/l.

Sr. No	Time of exposure	Control	Experimental
1	24 hrs	3±0.0577	2.5±0.0577
2	48 hrs	2±0.0577	1.2±0.0577
3	72 hrs	2±0.0577	0.8±0.0577
4	96 hrs	2±0.0577	0.5±0.0577

Table 2: Average oxygen consumption by *Lamellidens marginalis* exposed to sublethal concentration Imidacloprid (89. 83 ppm) mg/l.

Sr. No	Time of exposure	Control	Experimental
1	24 hrs	4.5±0.05	2.5±0.06
2	48 hrs	4.5±0.05	2±0.0577
3	72 hrs	4±0.05	1.5±0.0577
4	96 hrs	4±0.05	1±0.0577

(Each values represents a mean of three reading ± standard deviation of three replicates; Values are significant at $p<0.05$)

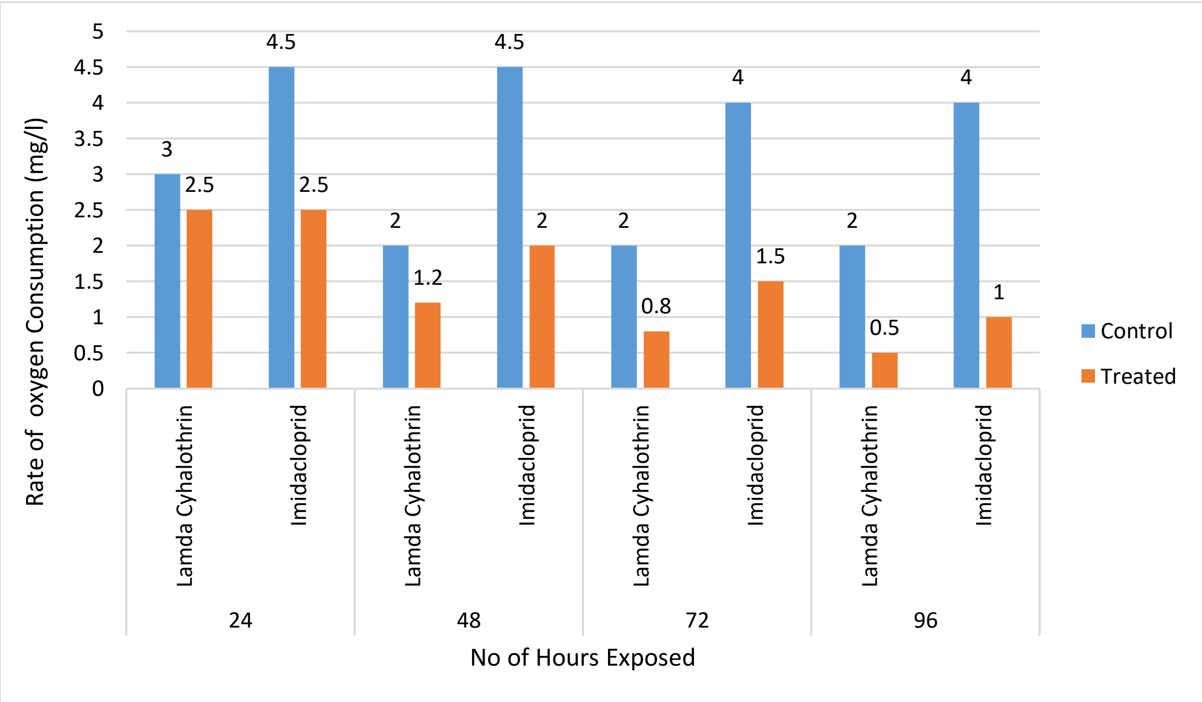

Figure 1: Average oxygen consumption by *L. marginalis* exposed to λ- Cyhalothrin and Imidacloprid

Table 3: Percentage of oxygen consumption reduced control Vs Treated: *Lamellidens marginalis*

Rate of Oxygen Consumption (mg/l)	No. of Hours Exposed							
	24		48		72		96	
	LC	Im	LC	Im	LC	Im	LC	Im
% of Oxygen Consumption Reduced	17	44	40	56	60	63	75	75

LC: Lamda Cyhalothrin; Im: Imidacloprid

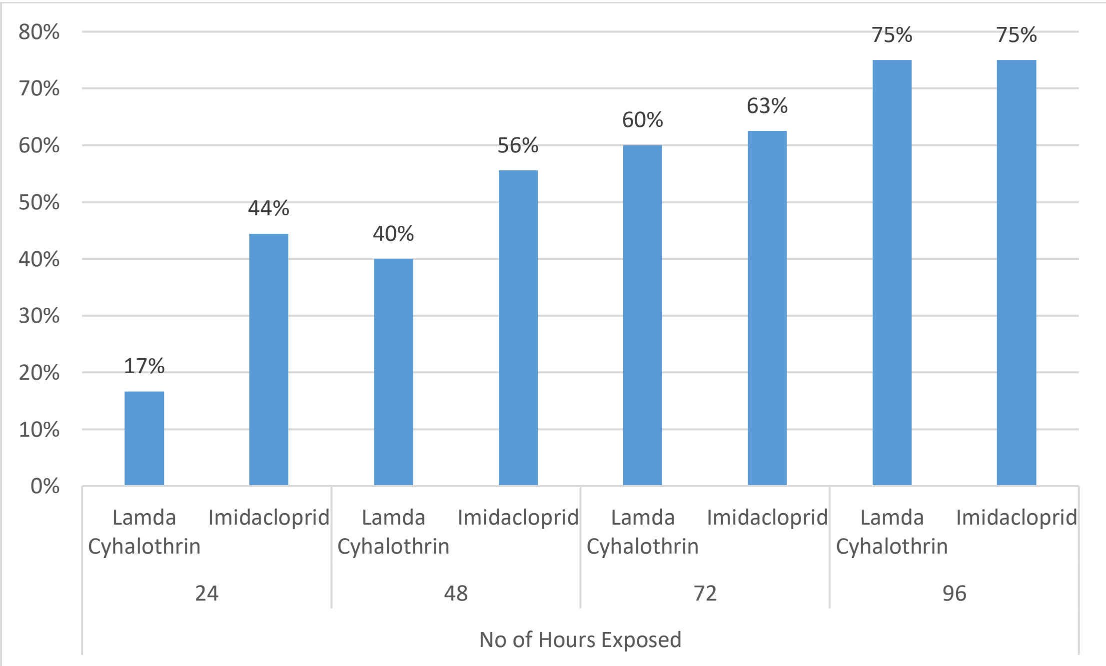

Figure 2: Percentage of oxygen consumption reduced control Vs Treated: *Lamellidens marginalis*

3.1 Oxygen Consumption

Lamellidens marginalis showed decrease oxygen uptake in different concentration of λ-Cyhalothrin and Imidacloprid as comparied to control bivalve when exposure up to 96 hrs. The range of oxygen consumption depicted in Table I and Table II. Incase of Imidacloprid the oxygen consumption was decreased after a period of 24 hours exposure and there was a continous decreased in oxygen uptake up to 72 hours. After 72 hours λ- Cyhalothrin and Imidacloprid exhibit similar range for oxygen uptake up to 96 hours depicted in Graph I and II.

From Table I and II it was evident that the pesticide reduces oxygen uptake as time of exposure increases. There was inverse relationship between time of exposure and oxygen uptake as time of exposure increases there was decreased oxygen uptake. This reduction of oxygen consumption is gradual and time dependant. Oxygen consumption can be used as bio-indicator to evaluate toxicant stress.

4. Discussion

Respiratory potential of an animal is an important physiological parameter to access the toxic stress hence studies on effect of pesticide on oxygen consumption have gained importance. The gills and the mantle, play an important role in respiration. Their large surface area and rich supply of haemolymph make both organs suited for respiration. The gill filaments are essentially hollow tubes within which the Respiration is carried out. Haemolymph flows from the kidney to the gill via the afferent gill vein, which gives off to each filament a vessel that descends one side and ascends the other. The ascending vessels join to form the efferent gill vein that returns to the kidney, or goes direct to the heart. As water passes through the gills, oxygen from the water diffuses into the haemolymph Gosling 2004.

In present study the fresh water bivalve *Lamellidens marginalis* show alteration of oxygen uptake when exposed to lethal concentration of pollutants. λ- Cyhalothrin and Imidacloprid. Acute exposure showed an initial decrease in oxygen consumption after 24 hours and it remained decrease up to 96 hours. In case of Imidacloprid there was decrease in oxygen consumption by test animal as compared to the λ-Cyhalothrin up to 72 hours. After 72 hours rate of oxygen consumption was same in both pesticides. When bivalve exposed to the λ-Cyhalothrin mussel initially tightly closed their shells may be because of this reason less amount pollutant enters in the body of bivalve. Bivalve exposed to Imidacloprid there was no such behavioural changes noted initially so imidacloprid easily enter in the body of test animal. After entering to animals' body imidacloprid irritates the gills which secrete copious secretion of mucous as a result gill lamellae blocked hence there was decrease in oxygen consumption. Gills and mantle communicate with water first because of this reason there was necrotic changes observed in the gill's histopathology. Damage gills lead to decrease in uptake of oxygen because gills are vital respiratory organs and any damage to gills leads to respiratory change. Bivalve showed gradual decrease in oxygen consumption from the starting period of exposure to till the end of the experiment in lethal concentration.

The estuarine clam *Katelysia opima* exposed to to lethal and sub lethal concentration of cypermethrin (25 % EC) 2.79 µg/L for 96 hours noted that change in oxygen leads to respiratory distress as a result of impairment in oxidative metabolism Mukadam and Kulkarni (2013). Behavioural change like release of excess mucus and shell closure probably acted as protection against cypermethrin stress observed in *Mytilus galloprovincialis* (Ayad *et al.,* 2011). This finding supports the present studies.

Saurabh Kumar, (2012) exposed freshwater mussel *Lamellidens marginalis* to sub-lethal concentration of Cypermethrin up to 96 hours resulted initial increase in oxygen consumption followed by gradual decline along with increase in mucous secretion. The effect of cypermethrin on freshwater prawn *Palaemonetes argentines* leads to increased in oxygen uptake and ammonia-Nintrogen excretion. Collins and Cappello, (2006). Cypermethrin induce oxidative stress and enzyme activities within gills of *Unio gibbus* (Khazri *et al.,* 2015). María Fernández-Sanjuan, (2012) noted toxicity of Perfluorinated chemicals (PFCs) 1 to1000 µg/L for 10 days resulted increase in oxygen consumption of zebra mussels *Dreissena polymorpha*. Gaikawad and Reddy, (2016) exposed *Rasbora daniconius* to sublethal concentration of Imidacloprid 0.8 ppm leads to decrease in oxygen consumption. The present investigation shows the similar results when bivalve exposed to λ- Cyhalothrin and Imidacloprid leads to reduced oxygen consumption.

Mixture of turf care chemicals (fertilizres, herbicide, insecticide, fungicide) affect freshwater clams *Corbicula fluminea* for 21 days resulted oxidative damage was noted by Conners (2004). Sangeetha. R. *et al.,* (2015) noticed that the Chlorpyrifos, dichlorovs affect the survivability of *L. marginalis*. Cadmium intoxication leads to decreased oxygen consumption in fresh water gastropod– *bellamya* (viviparous) *bengalensis* (Lamark) (Chinchore and Mahajan, 2013). *Perreysia favidens* exposed mercuric chloride, copper sulphate and cadmium chloride respectively for acute and chronic treatment exhibit reduced oxygen consumption (Bhamre, 1993). Dichlorovaos reduced oxygen consumption after acute exposure in freshwater snail *Lymnea accuminata.* (Lonkar, 2013).

From the present studies it may be concluded that the exposed bivalve *Lamellidens marginalis* showed decrease in oxygen uptake up to 96 hours. Decrease in oxygen consumption may be because of failure of respiratory mechanism. The decrease might be due to copious mucous secretion, penetration of pollutant molecule and their action alters metabolic cycles at the subcellular levels. This decrease may because of failure of freshwater mussel *Lamellidens marginalis* to compensate for new steady state of metabolism due to stress of pesticide pollutant as the exposure period of pollutants increase continuously to achieve a new steady state of metabolism owing to toxicant stress.

Summary

Lambda-Cyhalothrin and Imidacloprid affect the oxygen consumption of *Lamilledens marginalis* and rate of oxygen consumption were found to decreased after exposure of both pesticide, initially up to 72 hours Imidacloprid cause decreased in oxygen consumption compared to λ-Cyhalothrin then up to 96 hours both pesticide cause decrese in oxygen consumption.

Oxygen consumption was measured after intoxication initially reduced oxygen uptake decrease up to 96 hours period. There was copious secretion of mucous block the gills so gill respiration reduced, because pollutants alter metabolic cycles and act on molecular level that ultimately leads to decreased oxygen uptake. So it can conclude that pollutant stress responsible for reduced oxygen uptake by mussels. Severity of tissue damage was of concentration of pollutants and is time dependant, persistence of pesticide on specific organelle or tissue.

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MACHINE LEARNING APPLICATION IN DETECTING INVASIVE PLANKTON SPECIES RISK ANALYSIS

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Abstract

Invasive plankton species cause a significant threat to marine ecosystem stability, and early risk assessment can prevent the resulting ecological imbalance. This work explores the application of machine learning techniques to assess these risk factors by analysing marine plankton community structure from the microscopic images. It aims to classify plankton species and distinguish invasive phytoplankton species by leveraging ConvNeXt architecture, a next generation Convolutional Neural Network (CNN) for assisting decision-makers in mitigating biodiversity threads associated with the invasive planktons and their root causes. Also, this study includes a comparative analysis between ConvNeXt and traditional Machine Learning (ML) models. The results showed 91% classification accuracy for the phytoplankton and accurately classified the alien species from the native species.

Keywords: Ballast Water Discharge, Phytoplankton, Invasive Species, Convolutional Neural Networks (CNNs).

1. Introduction

Phytoplankton are base of the marine food webs and indicators of productive ecosystem [1]. They also have the paramount importance in carbon sequestration which makes them very important candidates in the marine ecosystem [2]. The introduction of foreign species to local waters through different scenarios has multiple causalities in the ecosystems which can even banish an entire community from the ecosystem. It also can generate ecological impact in each trophic level propagating it through the food web as well as the effects in biological interactions. The scientific monitoring and reviewing the intensity of the alien species initiated in 1970s even though the signs of the alien invasion were first recognised in 1903 after the occurrence of the Asian phytoplankton Odontella (*Biddulphia sinensis*) in the North Sea [3]. But a continuous monitoring of the invasive species is still lacking for the well being of a healthy ocean habitat.

The traditional method for identification of phytoplankton includes vertical or horizontal sampling followed by laboratorial analysis using microscope for the species level analysis [4]. Most of the traditional methods follow the post sampling analysis of the sample which will annihilate importance information. The introduction of cutting-edge technologies has changed the face of the plankton research. This has leads to the advancements in in-situ analysis of the plankton using underwater imaging technologies and different underwater vehicles [5]. This real-time data analysis will be helping more accurate analysis and rapid decision making. The large quantity of data acquisition through underwater imaging has led to the automation of the data with the help of Artificial Intelligence (AI) and Machine Learning (ML) algorithms. This study aims to recognise and classify alien phytoplankton species from the ballast water discharging site using machine learning algorithms.

2. Background

A study for accurately detect the microalgae from ship ballast water was carried along with the development of an innovative loss function to detect microalgae cell adhesion in challenging conditions [6]. It also utilized Enhanced Generative Adversarial Networks (GANs) to tackle the challenges of data imbalance and designed an advanced convolutional method for robust feature extraction from microalgae. A scalable AI platform connected to the European Open Science Cloud (EOSC) was developed, which facilitate the training, deployment, and sharing of AI models to support research on Ocean, seas, and inland water [7]. This study utilizes diverse imaging technique such as drone image, underwater videos, satellite images, and microscope data and deep learning models, such as Convolutional Neural Networks (CNNs) for classification, object detection, and segmentation, with performance metrics and evaluation tools ensuring reproducibility and transparency. A novel fully automated approach was proposed for phytoplankton analysis in digital microscopy images acquired from under water samples using a regular microscope [8]. A CNN was trained with transfer learning framework for fish species recognition and achieved 99 % accuracy [9]. Similarly, a new underwater image classification algorithm was proposed based on CNN DenseNet201and uses the optimized ELM to replace the softmax layer in the original CNN for underwater image classification and acquired 99.5% accuracy [10]. A study was carried out for the differentiation of benign and malignant cancer using CNN based and traditional ML based classification model like Radom Forest and AutoML Vision and attained a classification accuracy of 91%, 90% and 86% respectively [11]. A CNN model was used in the identification, classification and quantification of coral associated fishes and obtained a hamming accuracy of 89% [12].

3. Methodology

Five phytoplankton species, *Coscinodiscus concinnus* W.Smith, *Ceratoneis Closterium* Ehrenberg, *Neoceratium horridum* (Cleve) F.Gomez, D.Moreira & P.Lopez-Garcia, *Noctiluca scintillans* (Macartney) Kofoid & Swezy, and *Odontella sinensis* (Greville) Grunow (Fig. 1) are selected for the study where four of them are indigenous to Indian waters while one (*Ceratoneis* closterium) is an alien species which is mostly distributed in the Atlantic Ocean. Video datasets corresponding to each species collected from open source (Marine plankton Helgoland) and processed using a python script to extract frames of the targeted species. A total number of 1619 images (Table 1) are selected for further steps. These image data are divided for training, validation, and testing (70%, 20% and 10%). The extracted frames are subsequently annotated using VGG Image Annotator (VIA) with bounding boxes along with label are applied around each targeted specimen. Shape and origin are taken as attribute for feature extraction and identifying the alien species.

Figure 1: Phytoplankton; a. *Coscinodiscus concinnus* b. *Ceratoneis Closterium* (Invasive) c. *Neoceratium horridum* d. *Noctiluca scintillans* e. *O. sinensis*

Table 1: Class distribution table

Species	Training samples	Testing samples	Validation samples	Total
Coscinodiscus concinnus	300	80	30	430
Ceratoneis Closterium	261	68	10	339
Neoceratium horridum	160	40	10	210
Noctiluca scintillans	300	80	30	430
O. sinensis	160	40	10	210

To improve robustness and reduce overfitting, image augmentation techniques like rotation, width and hight shifts, zoom in and out, horizontal flipping and preprocessing were applied using TensorFlow's image data generator. The testing dataset is only normalised without any augmentations to simulate real-world evaluation conditions. The classification model used was a transfer learning approach with the convNeXt architecture pretrained on the ImageNet dataset. The model was compiled using Adam optimizer with a learning rate of 1e-4 and categorical cross-entropy as loss function. The model was trained for 10 epochs using the training generator and validated. The training process captured both learning progress and generalization ability on unseen data. After the training the model was evaluated on the testing dataset, which was not used during training or validation. Accuracy was computed to assess performance on unseen images along with confusion matrix. For classification and origin visualisation a multi-task machine learning model which utilises PyTorch was used.

Figure 2: Architecture diagram

4. Results and Discussion

4.1 Model Performance on Species Classification

The CNN model exhibited strong performance in classifying five phytoplankton species from microscopic image data. The model achieved an overall classification accuracy of 91% with a low loss value of 0.095. Among the five species, *Ceratoneis Closterium*, *Coscinodiscus concinnus* and *O. sinensis* achieved perfect score (1.0) across precision, recall and f1 score (Table 2). *Neoceratium horridum* attained a perfect precision score but its recall and f1 score were below 0.5. *Noctiluca scintillans* recorded perfect recall, while its precision and f1-score remained below 0.7. In addition to per-class metrics, the model's performance was assured using precision, recall and f1-score. These aggregated metrics provide additional confidence in the model's generalizability and robustness particularly for applications involving distribution data such as ballast water biodiversity monitoring.

The high classification accuracy is supported by Confusion matrix for five phytoplankton species where all the species except *Noctiluca scintillans* showing no misclassification. While *Noctiluca scintillans* showed notable confusion with *Neoceratium horridum* indicating overlapping of morphological features.

Table 2: Classification report

Species	Precision	Recall	F1-score
Ceratoneis Closterium	1.00	1.00	1.00
Coscinodiscus concinnus	1.00	1.00	1.00
Neoceratium horridum	1.00	0.30	0.46
Noctiluca scintillans	0.74	1.00	0.85
O. sinensis	1.00	1.00	1.00

4.2 Comparison of various Machine Learning (ML) models

A comparison has made between the traditional ML models and CNN model (Table 3). The CNN model demonstrated 0.91 accuracy, which explains a notable insight into its performance. While Random Forest model yielded a perfect accuracy which may suggest either conveys superior performance or potential overfitting of the model. Similar assessment of Support Vector Machine (SVM) and K-Nearest Neighbours (KNN) model revealed moderate performance. The overall results portray the robustness and reliability of the CNN model for phytoplankton species classification.

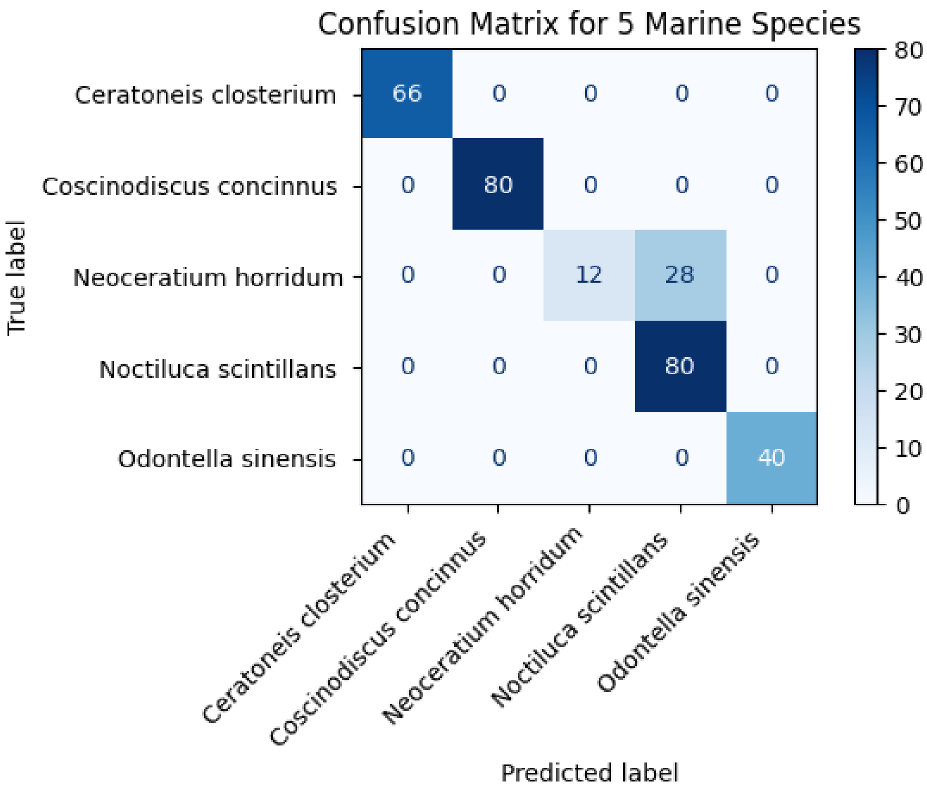

Figure 3: Confusion matrix for five phytoplankton species

Table 3: Model comparison

Sl. No.	ML model	Accuracy	Precision	Recall	F1- score
1	ConvNeXt	0.91	0.94	0.86	0.86
2	Radom forest	1	1	1	1
4	SVM	0.31	0.37	0.27	0.26
5	KNN	0.61	0.6	0.6	0.6

(SVM: Support Vector Machine, KNN: K-Nearest Neighbours)

4.3 Species Identification and Origin Classification

The deep learning -based model for species identification achieved high classification accuracy and the visualisation of the identification also showed the same. The model was trained and evaluated on a dataset comprising five phytoplankton species including native as well as invasive species. The visual inspection of prediction outputs confirmed the reliability of the model (Fig. 4). Sample outputs from the test set were labelled with predicted species name and origin of that respective species which were highlighted with red for alien species and green for native species. The visualisation module demonstrated consistent alignment with ground-truth annotations offering an interpretable interface for rapid onboard screening.

Figure 4: Visualisation of species identification and origin classification

Conclusion and Future Study

The transfer learning approach with ConvoNeXt architecture effectively classified phytoplankton species from microscopic images, also accurately detected the alien species in the data. The model achieved an overall classification accuracy of 91% with a low loss value. The confusion matrix indicated minimal misclassification which defines strong discriminative capability, even among morphologically similar data. The confusion occurred with *Noctiluca scintillans* and *Neoceratium horridum* probably due to shortage in the amount of training data. The comparison between alternate machine learning model has also underscore the CNN model's ability to accurately classify alien plankton species in a mixed community and its application in automated biodiversity risk assessment. These results indicate that real-time integration of such models can improve the detection of invasive phytoplankton, thereby mitigating potential risk to marine ecosystem. This approach enhances current manual identification efforts and contributes to sustainable maritime practices through early and automated detection of invasive species. The pattern in the confusion matrix suggests that while the model effectively distinguish most species, additional feature refinement or data augmentation may be needed to enhance classification between morphologically similar taxa.

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APPLICATION OF PLANT BIOTECHNOLOGY IN CROP IMPROVEMENT

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Abstract

Plant biotechnology has emerged as a powerful tool for crop improvement by integrating molecular biology, genetic engineering, tissue culture, and genomics. It offers innovative approaches to overcome the limitations of conventional breeding, such as time consumption and restricted genetic variability. Techniques like genetic transformation, marker-assisted selection, genome editing, and tissue culture have significantly contributed to enhancing crop productivity, resistance to stresses, and nutritional quality. This review discusses major biotechnological approaches and their applications in crop improvement along with future prospects.

Introduction

Crop improvement is essential to meet the increasing global food demand due to population growth and climate change. Traditional breeding methods are often slow and limited by genetic barriers. Plant biotechnology provides advanced tools to accelerate breeding and introduce desirable traits efficiently. Biotechnological approaches allow precise manipulation of plant genomes, enabling the development of high-yielding, stress-tolerant, and nutritionally enriched crops.

Plant Biotechnology: Concept and Scope

Plant biotechnology involves the application of scientific techniques such as:

- Tissue culture
- Genetic engineering
- Molecular markers
- Genomics and proteomics

Tissue Culture and Micropropagation

Concept: Plant tissue culture involves the in vitro growth of plant cells, tissues, or organs under controlled conditions.

Applications in Crop Improvement

- Rapid clonal multiplication (micropropagation)
- Production of disease-free plants
- Germplasm conservation
- Creation of genetic variability (somaclonal variation)

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Tissue culture enables the production of pathogen-free planting material and enhances crop yield significantly.

Advanced Techniques

- Anther and microspore culture → haploid production
- Embryo rescue → interspecific hybridization
- Protoplast fusion → somatic hybrids

These techniques generate new genetic combinations not possible through conventional breeding.

Genetic Engineering and Transgenic Crops

Concept: Genetic engineering involves the direct transfer of genes from one organism to another.

Strategies

Three main strategies:

1. Introduction of foreign genes
2. Overexpression of native genes
3. Gene silencing (RNAi/CRISPR)

Applications

- Insect resistance (Bt crops)
- Herbicide resistance
- Disease resistance
- Abiotic stress tolerance (drought, salinity)
- Improved nutritional quality

Transgenic crops have significantly increased yield and reduced pesticide use globally.

Molecular Markers and Marker-Assisted Selection (MAS)

Concept: Molecular markers are DNA sequences used to identify genes linked to desirable traits.

Types

- RFLP
- RAPD
- SSR
- SNP

Applications

- Early selection of desirable traits
- Gene pyramiding
- Germplasm characterization

MAS accelerates breeding programs and improves selection efficiency.

Genomics and Functional Genomics

Role in Crop Improvement: Genomics involves the study of the entire genome of an organism. Applications include:

- Gene discovery
- QTL mapping
- Genome sequencing

Benefits

- Identification of genes controlling important traits
- Precision breeding
- Understanding plant responses to stress

Genome Editing Technologies

CRISPR-Cas System: Genome editing allows precise modification of DNA sequences.

Applications

- Knockout of undesirable genes
- Development of disease-resistant crops
- Improvement in yield and quality

Genome editing is faster and more precise than traditional genetic engineering.

Somaclonal Variation and Mutation Breeding

Concept: Genetic variation arising during tissue culture is called somaclonal variation.

Applications

- Development of stress-tolerant varieties
- Improvement in yield and quality

In vitro mutagenesis is also used to create novel traits.

Role in Abiotic and Biotic Stress Resistance

Abiotic Stress: Biotechnology helps develop crops resistant to:

- Drought
- Salinity
- Temperature extremes

Biotic Stress

- Pest resistance (Bt crops)
- Disease resistance

Such crops reduce dependency on chemicals and improve sustainability.

Nutritional Improvement (Biofortification): Biotechnology is used to enhance nutritional content:

- Vitamin-enriched crops
- Protein-rich varieties
- Mineral-fortified crops

Example: Golden rice (vitamin A enriched)

Germplasm Conservation

Biotechnological methods include:

- In vitro conservation
- Cryopreservation

These methods preserve genetic diversity for future breeding programs.

Applications in Root and Tuber Crops

Root and tuber crops like cassava, potato, and yam benefit greatly from biotechnology due to:

- Vegetative propagation
- Limited flowering

Biotechnology improves their yield, nutritional quality, and disease resistance.

Advantages of Plant Biotechnology

- Faster crop improvement
- Precision breeding
- Overcomes species barriers
- Increased yield and quality
- Reduced pesticide use

Limitations and Challenges

- High cost
- Regulatory issues
- Public concerns about GM crops
- Environmental risks

Future Prospects

- Integration of AI and genomics
- Climate-resilient crops
- Sustainable agriculture
- Advanced genome editing

Plant biotechnology will play a key role in ensuring global food security.

Conclusion

Plant biotechnology has revolutionized crop improvement by providing advanced tools to enhance productivity, resistance, and nutritional quality. Despite challenges, its continued development will be essential for sustainable agriculture and food security in the future.

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UNDERUTILIZED WILD EDIBLE WEEDS AS SUSTAINABLE FOOD RESOURCES: ETHNOBOTANICAL INSIGHTS AND NUTRITIONAL PERSPECTIVES FROM RURAL COMMUNITIES

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Abstract
Weeds are traditionally regarded as unwanted plants in agricultural systems that are neither cultivated nor domesticated but they are present in agricultural area. The ethnobotanical evidence highlights their significant role of weeds as alternative food sources in many rural and tribal communities worldwide. Weeds are essentially rich in vitamins, proteins, minerals, and can even provide medicinal benefits also. Rich in nutrients, these underutilized plants have historically contributed to dietary diversity, traditional medicine, and food security. This review compiles ethnobotanical documentation of edible weeds, their nutritional and cultural significance, and their potential contribution to sustainable food systems. Special attention is given to the role of weeds in rural communities of India, where traditional diets have incorporated species such as *Amaranthus* sp., *Chenopodium album* and *Portulaca oleracea*. Due importance is given to the medicinal use of weeds as an easy and cheap alternative to the modern-day medicines. The review also discusses challenges to their conservation, loss of indigenous knowledge, and modern approaches to promote edible weeds as part of sustainable environmental management.
Keywords: Weeds, Ethnobotany, Food Security, Alternative Food Sources, Rural Communities, Traditional Knowledge.

Introduction

India is considered as the country with richest biodiversity of flora and fauna distributed in various geographically different bioclimatic regions. According to Jain (1987) he elaborated ethnobotany as total natural and traditional relationship and interaction between man and his surrounding plant wealth. The ethnobotanical studies flashes light on various unidentified useful plants that can be utilised to create new plant-based products and agro-based industries. Ethnobotany is an extremely old scientific field and now a days its scope is expanding day by day. It elucidates the indigenous use of plant resources that can be used by humans to meet their daily needs. Among these weeds are generally defined as unwanted or troublesome plants growing in cultivated fields, roadsides, or wastelands. Weeds naturally invade the agricultural land and usually affect the productivity of cultivated crops. However, ethnobotanical studies reveals that many weeds have been utilized majorly by rural and tribal communities as food, fodder, spices, medicine, nuts, tea substitutes and fuel, their resilience, availability, and high nutritive value make them vital in subsistence economies. They can be used as primary food source by residents as a primary food source by residents and as a food supplement for non-local residents, which guarantees food security in poor communities. They were a back-up resource in times of shortage, accounting for a significant input of micronutrients and allelochemicals with a prophylactic effect (Leonti, 2012).

Wild vegetables are favoured by more and more people because they have fresh and aromatic taste, rich mineral nutrients, pollution free growing environment, strong vitality and human health benefits (Xu *et al.,* 2002; Alam *et al.,* 2020). Several edible weeds include Water spinach (*Ipomoea aquatica*), Gima (*Glinus oppostifolius*), Alligator weed (*Alternanthera philoxeroides*), Buffalo spinach (*Enhydra fluctuans*), Ivy gourd (*Coccinia grandis*), White goosefoot (*Chenopodium album*) and Spiny Amaranth (*Amaranthus spinosus*), can serve as valuable culinary ingredients and contribute to household food supplies, especially in tropical regions where they are frequently consumed as staple foods (Stark *et al.,* 2019). With increasing concerns about malnutrition, climate change, and loss of agrobiodiversity, there is renewed scientific interest in weeds as alternative food resources. Unlike modern crops requiring high inputs, edible weeds are self-sustaining, resistant to biotic and abiotic stresses, and often thrive under marginal conditions, they are grown cost-free and are easily available, therefore documenting their role in traditional diets not only conserves indigenous knowledge but also promotes sustainable environmental practices.

Weeds do not require any kind of special cultivation or maintenance therefore it can be utilized during food scarcity conditions. Weeds are enriched with essential vitamins, minerals, proteins, certain essential amino acids and contain medicinal importance as well. Weeds are rich in Iron, calcium, potassium, Vitamin A, Vitamin C and fibre as well, it also contains antioxidants. Weeds grow massively in open areas and unfortunately people are not aware of its medicinal importance and other daily usage like forage, food and olericulture importance. Understanding the importance of weeds is useful for taxonomists, agriculturists and scientists involved in management of crops (Singh & Kumari, 2019).

Ethnobotany of Weeds: An Overview

Ethnobotany explores the relationship between humans and plants, particularly in traditional societies. In the context of weeds with the rapidly expanding human population needs a search for less expensive nutritive sources of food. There are crops often ignored, although having a good nutritive value and which can help in coping with the problem to balance the equation between population and food needs (Oyebiodium *et al.,* 1983).

- Many communities recognize weeds as wild vegetables, consumed either as staple food during scarcity or as seasonal delicacies.
- Weeds are often collected from agricultural fields, forest margins, and roadside habitats.
- Rural women and elders are key custodians of this knowledge.
- Preparation methods include cooking as leafy vegetables, grinding into flour, or fermentation into local recipes.

The traditional or indigenous knowledge is on the verge of extinction because of the changing lifestyle, modernisation, livelihood diversification, influence of cultural conflicts (He *et al.,* 2019; Uchida *et al.,* 2020.) lack of documentation. If the traditional knowledge is lost it will be a permanent loss and can't be recovered. Traditional knowledge is passed orally by words of mouth from one generation to other generation, or it can be transferred when younger generation accompany their parents to the forests and identify plants along with them. (Pegu *et al.,* 2013) With modernization and advanced agriculture techniques, the traditional knowledge is getting lost. Therefore, the traditional knowledge needs to be conserved by creating written records or can be documented digitally which can be used by the future generations.

Examples of Edible Weeds:

1. ***Amaranthus dubiu* (Chaulai)**- It belongs to family Amaranthaceae. Its leaves contain 57 times more vitamin A precursor than cabbage and can help to prevent night blindness, it also contains 13 times more iron than green cabbage, 9 times the calcium. Amaranthus contains other minerals such as phosphorus, manganese, magnesium, copper and zinc. (Khattak *et al.,* 2006). Amaranthus species also contain beta-carotene, zeaxanthin and leutin. (Spence *et al.,* 2023.)
2. ***Amaranthus spinosus* (Spiny amaranth)-** It belongs to Amaranthaceae family. As per the name it has spines on flowers as well as on nodes. The leaves and stems are used in raw form or cooked like spinach (Hedrick,1972, Usher, 1974, Kunkel 1984.) by removing spines from older leaves and stems (Facciola,1990.) It has a bitter flavour therefore eaten in small quantity as a substitute in food scarcity (Protabase- Plant resources of tropical Africa. http://www.prota.org.). The leaves are enriched with protein, fat carbohydrate, fibre, calcium, phosphorus, sodium, potassium, beta-carotene, thiamine, riboflavin, ascorbic acid, niacin. The seeds are also edible when cooked. They are very nutritious; they become gelatinous after cooking. The plant is burnt into ashes and that can be used as salt. This can be added to water to soften the vegetables such as cowpea and pigeon pea. A red coloured pigment is obtained from the plant which can be used as colouring agent in foods. (Duke *et al.,* 1985)
3. ***Agaricus bisporus* (button mushroom)-** It belongs to class basidiomycetes. It is the widely cultivated mushroom in the world. It contains nutrients such as carbohydrates,

proteins, lipids, fibres, minerals and vitamins. They are an excellent source of protein. They contain various minerals such as iron, potassium, zinc, copper, sodium, selenium, cobalt, manganese. They are the natural source of vitamin D; most abundant vitamin present is niacin followed by riboflavin. Other vitamins such as vitamin $B_{1,}$ Vitamin $B_{3,}$ L-ascorbic acid and alpha-tocopherol. It contains various active ingredients such as polysaccharides, lipopolysaccharides, essential amino acids, peptides, glycoproteins, nucleosides, triterpenoids, lectins, fatty acids and their derivatives. (Atila *et al.,* 2017).

4. ***Basella alba* (Malabar spinach)-** It belongs to family Basellaceae. It is predominantly grown in the Asian sub-continent. *Basella alba* leaves contain all essential amino acids. It is rich in macro and microminerals in addition to proteins and carbohydrates. It also contains soluble and insoluble dietary fiber, Vitamin C also. Iron content of Basella leaves are much higher than spinach leaves. It contains bioactive compounds such as polyphenols, flavonoids, proanthocyanins, anthocyanins, beta-carotene, alpha-carotene and xanthophylls such as neoxanthin, violaxanthin, leutin and zeaxanthin with anti-oxidant properties. The phenolic acids present in *Basella alba* are salicylic acid, ferulic acid, gallic acid, caffeic acid. Leaves are used for both medicinal and food application in Chinese herbal medicine. (Kumar *et al.,* 2021)
5. ***Brodiaea capitatais* (Wild onion)-** Generally leaves are cooked with maize cake in traditional tandoors. Its bulbs are best cooked by slowly roasting in hot ashes, that develops sweetness like potato. It also contains iron but very low amount, other minerals such as calcium, phosphorous, magnesium and zinc. Copper and manganese are also present in trace amount. (Khattak *et al.,* 2006).
6. ***Boerhaavia diffusa* (Punarnava)-** It belongs to family Nyctaginacae. It is a perennial creeping weed found in tropics and sub-tropics. It contains considerable amount of protein and carbohydrate. It also contains great amount of potassium, calcium, iron, sodium and zinc. It also had good content of vitamins such as $B_{1,}$ $B_{2,}$ B_3, B_5, B_6 and C. Leaves contain essential amino acids such as leucine, lysine, and phenylalanine, as well as non-essential amino acids, unsaturated fatty acids such as linolenic acid, linoleic acid and erucic acid and saturated fatty acids such as palmitic acid, stearic acid, and lauric acid. (Moulick *et al.,* 2024). Leaves are cooked and eaten as vegetable, used in soups and stews as well. The seeds are also edible and roots can be consumed by roasting. (Rosy *et al.,* 2016).
7. ***Chenopodium album* (Bathua)-** It belongs to family Chenopodiaceae. It is consumed as leafy vegetable; its stem and leaves are full of nutrients, especially amino acids such as leucine, isoleucine, lysine and vitamin C and carotenoids. Leaves are rich in various nutrients such as protein, fat, fiber, vitamins, minerals and are rich source of iron, calcium. *C. album* contains good amount of vitamin C and carotenoids. Its leaves contain various

medicinal properties like anti-microbial, anti-bacterial, antioxidant, antidiarrheal etc. (Saini *et al.,* 2020).

8. ***Corchorus olitorius* (Junglee jute)-** It belongs to Tiliaceae family. The green leaves are rich in beta-carotene which is used to improve eyesight, iron for healthy RBCs, calcium for strong bones and teeth, vitamin C for smooth and clear skin, strong immune system and fast wound healing. Plant contains anti-oxidant activity, whereas leaves contain vitamin A, C and E. Young leaves are eaten as vegetable or cooked into soups. In Bengal it is considered as tonic and leaves are used as condiment, commonly added to rice. In Japan, dried leaves are used as substitute for tea and coffee. It contains mucilaginous texture like okra when cooked, it can get slimier when cooked for long time. Leaves act as thickeners in soups, stews and sauces. The seeds are used as flavouring agents (Islam, 2013).

9. ***Centella asiatica* (Brahmi)-** It belongs to family Apiaceae. It contains high concentration of Potassium and Calcium. It also contains small amount of protein, carbohydrate and fats. It is rich in vitamin C, B_1, B_2, niacin, carotene and Vitamin A. It is commonly eaten fresh as vegetable, can be eaten as salads. It can be consumed by cooking as soup or as main vegetable. Due to its mild bitterness, it is cooked with coconut milk/shredded coconut or sweet potato. In Thailand it is used as tea or juice or cooling drink that reduce inner heat. In India it is consumed in the form of drink known as "thandaayyee", an important tonic for brain. It is also used for making herbal tea by drying centella leaves. (Hashim, 2011).

10. ***Fumaria parviflora* (Shahtera or Pit-papra)-** It belongs to Papaveraceae family. Fumaria parviflora contains flavonoids, glycosides, tannins, saponins, steroids, triterpenoids, phenols, alkaloids and anthraquinones. (Najeeb *et al.,* 2012; Jameel M., *et al.,* 2014). Leaves are cooked as vegetable Saag with other available greens, used in local cuisines and for detoxifying properties. The plant part which is above the ground is used to make cooling drink by mixing infusion of plant with honey or another sweetener. It is harvested as source of food, fodder and medicine. (Sen, 2020).

11. ***Glinus oppositifolius* (Gima)-** It is a green leafy vegetable that belonged to family Molluginaceae. It grows wildly in moist and dried regions of India such as Maharashta, Odisha, Madhya Pradesh, Uttar Pradesh, West Bengal, Tamil Nadu and Karnataka. It is used as vegetable and as medicine in various countries. It contains various important nutrients such as protein, fat, vitamin A and C, iron, calcium, magnesium. It is a good source of protein for vegetarians that depends on plants for their protein requirements. (Rinziya MNF *et al.,* 2017). The leaves and stem have bitter taste. Leaf contains various metabolites such as alkaloids, phenolic compounds, flavonoids, saponins, fats and oil. (Dewangan *et al.,* 2021)

12. ***Ipomoea aquatica* (Water spinach)-** It is a semi- aquatic weed that belongs to Convolvulaceae. *This weed* is used as a fish replacement in animal feed formulation but it needs careful usage because most plants contain phytic acid, that produces several anti-nutritional in fish. The phytic acid form bonds with divalent cations which make them unavailable for fish that in turn affect the digestive enzyme activities which in turn binds with proteins that reduces its digestibility. (Reddy *et al.,*1989; Afinah *et al.,* 2010; Krogdhal *et al.,* 2010; Khan & Ghosh, 2013). The leaves contain protein 3%, fibre 0.9%, fat 0.4%, carbohydrate 4.3%, mineral matter 2%, nicotinic acid, riboflavin, vitamin C, vitamin E. The young terminal shoots and leaves are eaten as green leafy vegetable and in salads and as fodder also. It contains various amino acids such as aspartic acid, threonine, serine, glutamic acid, proline, glycine, alanine, cysteine, valine, methionine, isoleucine, leucine, tyrosine, lysine, histidine and arginine (Prasad *et al.,* 2008).
13. ***Lemna minor* (Duckweed)-** It belongs to the family Lemnaceae. They are free- floating aquatic plants. It is extensively used in animal feed industry, aquaculture, health supplement, biofertilizer, biofuel, and food products for humans. It is seen that duckweed contains 20% to 30% of protein, which is higher than cereal. The main protein found is ribulose-1,5-bisphosphate carboxylase (RuBisCO), which is a source of essential amino acid. Duckweed contains 4% to 7% of fat, 4% to 10% starch, carotenoids and flavonoids and anthocyanins. Duckweed can be eaten as salad, it can be added to cookies, cream sauce or burrito, or even chicken breast. (Yahaya *et al.,* 2022).
14. ***Portulaca oleracea* (Purslane)-** It is a nutritious vegetable which is eaten as raw or in cooked form. It is an excellent vegetable source of omega-3 and 6 fatty acids and a linolenic acid. It is also rich in iron, ascorbic acid, glutathione, a-tocopherol, and b-carotene. It shows protective effect against oxidative stress caused by vitamin A deficiency (Arudda *et al.,* 2004). It contains dietary minerals such as magnesium, calcium, potassium and iron. It is enriched with 2 types of betalain alkaloid pigments which are reddish betacyanins and yellow betaxanthins. These pigments are found to be potent anti-oxidants and have anti-mutagenic properties. (Uddin *et al.,* 2020).
15. ***Trianthema portulacastrum* (Sabuni/Santhi)-** It is also called as horse purslane. It belongs to family Aizoaceae. It is an exotic weed and native of tropical America. It is grown in most tropical countries like India, Baluchistan etc. It occurs in 2 forms a red coloured form also known as Lal Sabuni, in which stem, leaf margins are red; a green-coloured form known as Svet-Sabuni, which has green stem and white flowers. It contains steroids, flavonoid, fats, terpenes, carbohydrates, tannins, alkaloids, glycosides, phenolic compounds. Plant contains Vitamin B_3, Vitamin C. The minerals present are calcium, magnesium, iron, copper, zinc and manganese. Plant is rich in phosphorus and iron but

lack calcium. (Shivhare *et al.,* 2011) It is rich source of protein. Raw leaves are consumed; it has a delightful salty flavour and can be eaten as salads. The young tops and leaves can also be eaten. (Tropical plants database).

16. ***Taraxacum officinale*** **(Dandelion)-** It belongs to family Asteraceae. Dandelion is used as both medicinal agent as well as food. The roots of dandelion are rich in insulin and is used as a substitute for cereal coffee and tea, the leaves are eaten raw in salads, young leaves are placed in many dishes, the flowers are used to make syrups. The extract from dandelion flower can be used as flavour additives in many food products, such as deserts, candies, baked cakes, puddings, and other similar food products. Roots are rich in sesquiterpene lactones and triterpenes and sterols. The leaves and flowers contain polyphenols, mainly hydroxycinnamic acid derivatives and flavonoids. The root contains significant amount of insulin. The plant is rich in vitamins (A, C, E, K and B) and minerals for example iron, sillicum, sodium, copper, zinc, magnesium and manganese. The leaves are an important source of potassium. (Dobrowolska *et al.,* 2022).

17. ***Stellaria media*** **(Chickweed)-** It belongs to family Caryophyllacae. It is used for both medicinal and nutritional properties. As compared to spinach it is much more enriched with nutrients and vitamins such as A, D, B complex C, rutin, calcium, potassium, zinc, manganese, sodium, copper, iron, silica. It is used in salads, and pesto's, it can be sauteed like spinach, stirred into soups or blended into sauces. It is great in omelettes, wraps and spring rolls (www.wild abundance.net.com).

Nutritional and Pharmacological Potential

The nutritional profile of selected edible weeds highlights their significant potential as alternative sources of essential nutrients and bioactive compounds. As presented in Table 2, species such as *Amaranthus viridis, Basella alba,* and *Chenopodium album* exhibit considerable amounts of proteins, vitamins, and minerals, particularly iron, calcium, and vitamins A and C. Several species, including *Corchorus olitorius* and *Enhydra fluctuans*, are rich in micronutrients and antioxidants, supporting their role in improving nutritional security. Notably, *Portulaca oleracea* and *Taraxacum officinale* are recognized for their low caloric value combined with high nutrient density, making them suitable for health-conscious diets. In addition, plants like *Stellaria media* and *Trianthema portulacastrum* demonstrate appreciable protein and mineral content, further emphasizing their dietary importance. Beyond their nutritional value, many of these weeds possess pharmacological properties such as anti-inflammatory, antioxidant, and therapeutic effects, which contribute to their use in traditional medicine systems. Overall, these findings indicate that edible weeds can serve as nutrient-rich, low-cost food resources with substantial potential in addressing malnutrition and promoting health.

Table 1: Common edible weeds and their ethnobotanical significance

S. No.	Botanical Name	Family	Local name	Parts used	Mode of use	Nutritional value and other uses	References
1.	*Amaranthus virdis*	Amaranthaceae	Chaulai	Sh	Tender shoots are eaten cooked with fish	High in iron, amino acids, antioxidants. cash income; pig feed	Pegu *et al.,* 2013.
2.	*Amaranthus spinosus*	Amaranthaceae	Spiny amaranth	L, Sd	Leaves can be eaten raw or cooked, Seeds are eaten after cooking, they form gelatinous covering.	Rich in protein, carbohydrate, fat, calcium.	Hedrick, 1972, Usher, 1974 Kunkel, 1984
3.	*Agaricus bisporus*	Basidiomycetes	Button mushroom	FB	Consumed as vegetable.	Rich in calcium, protein, carbohydrates, vitamins.	Atila *et al.,* 2017
4.	*Agaricus campestris*	Agaricaceae	Chhatti/ field Mushroom	FB	Consumed as vegetable. Great in risotto dishes and omelettes, used a flavouring agent in soups and sauces with meat dishes.	Rich in protein, carbohydrates, Fibres, vitamins B-Complex, Helps in biological dissociation & Nutrient Cycling	Shrivastava, 2016, Pat O' Reilly 2016.
5.	*Bombax ceiba L.*	Bombacaceae	Simolu	Fr, L	Unripe fruits are eaten.	Leaves are used as hair wash; fuelwood; cash income	Pegu *et al.,* 2013
6.	*Borassus flabellifer*	Arecaceae	Tarh	Fr	Fruits are cooked to treat leprosy and dysentery.	Rich in high calory, carbohydrate, Vitamin C, Potassium and Calcium; Used in dehydration and making sharbat, Jam, sweets etc.	Sahni *et al.,* 2014; Mohaideen, and Srinivasan, 2024.

7.	*Basella alba*	Basellaceae	Malabar spinach	L	Eaten raw mixed in green salad, used to thicken soups	Rich in amino acids, Vitamin C, protein, carbohydrates, and dietary fibres.	Deshmukh and Gaikwad, 2014
8.	*Boerhaavia diffusa*	Nyctaginacae	Punarnava	L, Sd	Leaves are cooked and eaten as vegetable, use in soups and stews. Seeds are also edible.	Rich in potassium, calcium, iron, sodium, zinc vitamin B, essential and non-essential amino acids.	Moulick *et al.,* 2024 Rosy *et al.,* 2016
9.	*Chenopodium album*	Chenopodiaceae	Bathua	L, St	Leaves are used in preparation of various dishes such as soups, curries and parathas	Leaves are rich in protein, calcium, amino acids and Vitamin A, C.	Saini *et al.,* 2020
10.	*Corchorus olitorius*	Tiliaceae	Junglee jute	L, Sd	Leaves eaten as salads, used as thickeners in soups, stews and sauces. Dried leaves used as substitute for tea and coffee.	Leaves contain Vitamin A, C and E.	Islam, 2013
11.	*Centella asiatica*	Apiaceae	Brahmi	L	Eaten as salads, soups, dried leaves used as tea.	Rich in Vitamin A, B1, B2, C, niacin, carotene.	Hashim, 2011
12.	*Ipomoea aquatica*	Convolvulaceae	Kalmi	YL, St	Eaten as green leafy vegetable and in salads.	Used as fish replacement in animal, also used as fodder.	Prasad *et al.,*2008, Reddy *et al.,* 1989.
13.	*Enhydra fluctuans*	Asteraceae	Buffalo spinach	YL, St	Cooked taken with rice. Young leaves and stems are used to make leafy vegetables. Leaves are used for salads.	Used for feeding cattles, buffalo, goats, sheep, horses, pigs.	Guchhait *et al.,*

14.	*Fumaria parviflora*	Papaveraceae	Pitpapra	L	Eaten as vegetable. Plant part above ground is used to make cooling drink.	Source of Energy, Carbohydrate, protein, Fibres Vitamin C and B; Used as blood purifier skin diseases and liver disorders	Sen, 2020.
15.	*Glinus oppositifolius*	Molluginaceae	Gima	L	Used as vegetable.	Carbohydrate, protein, Fibres Vitamin C and B	Rinziya M.F. *et al.,* 2017.
16.	*Lemna minor*	Lemnaceae	Duckweed	WP	Eaten as salad it can be added to cookies, cream sauce or burrito, or even chicken breast.	Used in animal feed industry, aquaculture, health supplement, biofertilizer, biofuel, and food products for humans.	Yahaya *et al.,* 2022.
17.	*Leucosceptrum canum*	Lamiaceae	Shrub mint	L	Leaves are cooked with small fish	Used as cash income	Pegu *et al.,* 2013.
18.	*Portulaca oleracea*	Portulacaceae	Purslane	L	Eaten raw as salad, eaten cooked as sauce in soups or eat as green vegetables	Source of omega-3 fatty acids, vitamin E.	Uddin *et al.,* 2020.
19.	*Stellaria media*	Caryophyllacae	Chick weed	L	Used in salads, pesto's, soups, sauces	Source of vitamins, minerals, calcium and iron.	Singh *et al.,* 2022
20.	*Sterculia roxburghii*	Sterculiaceae	Red sterculia	Sd	Black seeds are eaten after roasting.	Rich in high energy due to high carbohydrate, protein, Fibre minerals such as Calcium, Iron and Magnesium	Pegu *et al.,*2013

21.	*Taraxacum officinale*	Asteraceae	Dandelion	R, L, Fl.	Leaves eaten as salad, root is used as substitute for cereal coffee, tea & flowers can be used as flavouring.	Roots are rich in insulin and vitamins such as A, B, C, E, K and minerals whereas flowers and leaves are rich in polyphenols.	Dobrowolska *et al.,* 2022
22.	*Trianthema portulacastrum*	Aizoaceae	Santhi, Horse purslane	L	Cooked during scarcity seasons	It is rich in phosphorus and iron but low in calcium. Contains vitamin B and C.	Shivhare *et al.,* 2011.
23.	*Taraxacum obovatum*	Asteraceae	Himalayan dandelion	B.L.	Raw in salads.	Rich in Vitamin A, used in Liver strengthening, digestion improvement	Molina *et al.,* 2014.
24.	*Tribulus terestris L.*	Zygohyllaceae	Gokhru	Fr	Used for making herbal tea	A good source of energy, fibre, calcium, iron, and potassium; Traditionally considered helpful for male reproductive health and vitality and Acts as a diuretic and supports urinary tract health	Sahar *et al.,* 2024.
25.	*Zanthoxylum rhesta*	Rutaceae	Toothache tree	Fr	Shoots and leaves when cooked with pork are preferred	Leaves are used for cash income.	Pegu *et al.,*2013.

(Parts used: BL = Basal Leaves; FB = Fruiting Body; Fl = Flower; Fr = Fruit(s); L = Leaves; Rt = Root; Sd = Seeds; Sh = Shoot; St = Stem; WP = Whole Plant; YL = Young Leaves)

Table 2: Nutritional Profile of Selected Edible Weeds (per 100 g, fresh weight)

S. No.	Botanical Name	Energy (kcal)	Protein (g)	Iron (mg)	Vitamin A (µg)	Vitamin C (mg)	Calcium (mg)	References
1	*Amaranthus viridis*	23–43	2.0–5.78	2.0–22.18	139–146	41–107	209–330	Sharma *et al.,* 2012; Sarker & Oba, 2019
2	*Basella alba*	306.70	27.70–58.80	21.50–34.47	4000–4200	400	48.70–61.19	Bamidele *et al.; Jayaswal et al*.; Akindele *et al.*
3	*Chenopodium album*	44	4.3	1.2	580	90	309	Saini *et al.,* 2020
4	*Corchorus olitorius*	43–58	4.5–5.6	11.6	3195–4200	64	266–366	Islam, 2013
5	*Enhydra fluctuans*	30–40	2–3	4–6	1000–2000	25–35	200–250	Sidam *et al.,* 2025
6	*Fumaria indica*	300.25–356.75	10.68–14.81	0.07–0.13	458–833	0.03–0.065	1.61–1.86	Ravikanth *et al.,* 2014
7	*Portulaca oleracea*	16	1.30	1.99	396	21	65	Uddin *et al.,* 2020
8	*Stellaria media*	30	29.5	12.2	2100	60	60–70	Singh *et al.,* 2020
9	*Taraxacum officinale*	45	2.7	6.2	300	35	138	Lis *et al.,* 2019
10	*Trianthema portulacastrum*	76.01	9.19	6.44	810	35–50	120–150	Khan *et al.,* 2013

(Note: Values compiled from ethnobotanical/nutritional studies; actual content may vary by region and season.)

Table 3: List of medicinal weeds with their botanical name, family, parts, use and cure diseases.

S. No.	Botanical name	Family	Part used	Cure diseases	References
1.	*Achyranthus aspera*	Amaranthaceae	Aerial parts and root	Gastro-intestinal disorders Labour pain	Panda *et al.,* 2014
2.	*Asparagus africanus*	Asparagaceae	Dry root	Wound	Bekele *et al.,* 2015
3.	*Basella alba*	Basellaceae	Leaves and stem	Oral ailments, ulcers, small pox fever, alleviate symptoms of appendicitis, also used as laxative	Kumar *et al.,* 2021.
4.	*Cyanthilium cinereum*	Asteraceae	Whole plant	Fever, cuts, skin disease headache, haemorrhoids, stomach disorders.	Singh *et al.,* 2025
5.	*Centella asiatica*	Apiaceae		Enhance memory, increase attention span and concentration, prevents oxidative damage.	Hashim, 2011.
6.	*Chenopodium album*	Chenopodiaceae	Leaves	Kidney stone, swelling, anemia, heart disease, jaundice.	Saini *et al.,* 2020
7.	*Datura stramonium*	Solanaceae	Whole plant	Asthma, Parkinson's disease, venereal disease skin ulcers, headache, goitre ringworm, swellings, burn	Singh *et al.,* 2025
8.	*Enhydra fluctuans*	Asteraceae	Plant, leaves	Cure inflammation, smallpox, liver-tonic, leprosy, cough, high blood pressure.	Sidam *et al.,* 2025
9.	*Fumaria parviflora*	Papaveraceae	Leaves, Whole plant	Influenza, fever, laxative, diuretic, diaphoretic, hepatoprotective, antidyspeptic.	Siddiq *et al.,* 2025
10.	*Portulaca oleracea*	Portulacaceae	Plant and seeds	Liver, kidney disease.	Jan *et al.,* 2010
11.	*Stellaria media*	Caryophyllaceae	Different parts	Asthma, measles, gastrointestinal disorders, diarrhoea, digestive, renal, respiratory and reproductive tract inflammation.	Pande *et al.,* 1995, Slavokhotova *et al.,* 2011, Haragan *et al.,* 1991.
12.	*Taraxacum officinale*	Asteraceae	Roots	Diuretic, laxative, hepatic, stomachic,	Jalili *et al.,* 2020
13.	*Urena lobata*	Malvaceae	Leaves, twigs, bark	Colic, stomach pain, diarrhoea, dysentery, malarial fever gonorrhoea, toothache.	Singh *et al.,* 2025
14.	*Vernonia cinerea*	Asteraceae	Whole plant	Filariasis	Panda *et al.,* 2014
15.	*Zanthoxylum armatum*	Rutaceae	Fruits	Chest infection	Jan *et al.,* 2010

Role in Food Security and Sustainable Practices

Wild edible plants play a significant role in enhancing food security by providing inexpensive and readily available sources of nutrition, particularly during lean seasons. Their inherent resilience allows them to thrive under adverse conditions such as drought, poor soil fertility, and minimal management inputs, making them reliable food resources in changing climatic scenarios. In addition to their nutritional importance, these plants hold considerable cultural value, as they are often incorporated into traditional diets, festivals, and ritual practices. From an ecological perspective, many weed species contribute to sustainable agriculture by improving soil fertility, supporting pollinator populations, and preventing soil erosion. Moreover, their low ecological footprint, characterized by little to no requirement for fertilizers or pesticides, further highlights their importance as environmentally sustainable food resources.

Ethno-pharmacological significance of weeds:

Ethno-pharmacology is a branch of science that utilises the traditional knowledge of plants, herbs, shrubs to treat the various diseases. Now a days it is modernised as Phyto-therapy that also includes the treatment of disease by using plants, and the medicines derived from the plants. Weeds can be used as medicines as well because of their abundant, low cost and effective nature they are utilised in treating various diseases. Plants and their components serve as a vital source of medicines and are effective in treating numerous illnesses, primarily due to their contents. The weeds belonging to family Asteraceae, Amaranthaceae and Poaceae had the potential to treat various diseases including dysentery, wounds and skin diseases as well. The most utilised plant part in the treatment of diseases are leaves. The plant parts used for curing different diseases were leaf (33%), followed by whole plant (29%), and roots (20%). It was also reported by interviewing agricultural labourers and tribal peoples that they also utilise weeds for curing wounds, abscesses, indigestion, flatulence or any other temporary disorder, but don't rely on plants for serious or chronic disorders. (Panda *et al.,* 2014). There are numerous ways in which medicines can be administered such as powder form (37.2%), crushing and pounding (51.2%), chewing (4.65%), concoction, decoction and other each with 2.3%. (Bekele *et al.,* 2015).

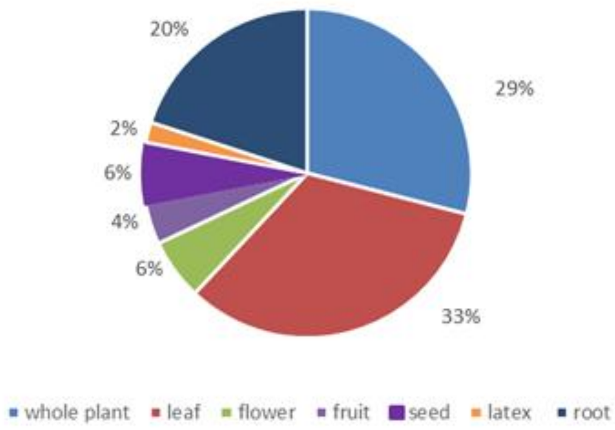

Figure 1: Percentage of plant parts used for curing different diseases. (Panda *et al.,*2014)

People's tradition and spirituality have somehow helped in conservation of medicinal plants because this traditional knowledge of treating various diseases via weeds are limited to traditional healers only. The younger generation are deprived from the benefits of using these herbal remedies. Therefore, there should be the citation of conventional acquittance and sustainability measures to protect plants that have pharmacological importance, and there should be ecological balance deterioration because of man- made activities and exploitation of natural resources greater than required demand. (Singh *et al.,* 2020)

The ethnomedicinal importance of wild edible plants is evident from their extensive use in traditional healthcare systems, where different plant parts are utilized to treat a wide range of ailments. As shown in the table, species such as *Achyranthus aspera* and *Asparagus africanus* are used for gastrointestinal disorders, labour pain, and wound healing, respectively. *Basella alba* is commonly employed in the treatment of oral ailments, ulcers, smallpox, and digestive issues, while *Cyanthilium cinereum* and *Centella asiatica* are known for their roles in managing fever, skin diseases, and enhancing cognitive functions. Several plants, including *Chenopodium album* and *Enhydra fluctuans*, are used for treating kidney disorders, inflammation, and liver-related conditions.

Notably, *Datura stramonium* has diverse therapeutic applications in asthma and neurological disorders, although it requires careful use due to its toxic nature. Similarly, *Fumaria parviflora* and *Portulaca oleracea* exhibit hepatoprotective, diuretic, and digestive properties. Other species such as *Stellaria media* and *Taraxacum officinale* are valued for their roles in treating respiratory, gastrointestinal, and renal disorders. Furthermore, plants like *Urena lobata*, *Vernonia cinerea*, and *Zanthoxylum armatum* are traditionally used for managing infections, fever, and other systemic conditions. Overall, these findings highlight the significant pharmacological potential of wild edible plants and emphasize their role as accessible, natural remedies in primary healthcare systems.

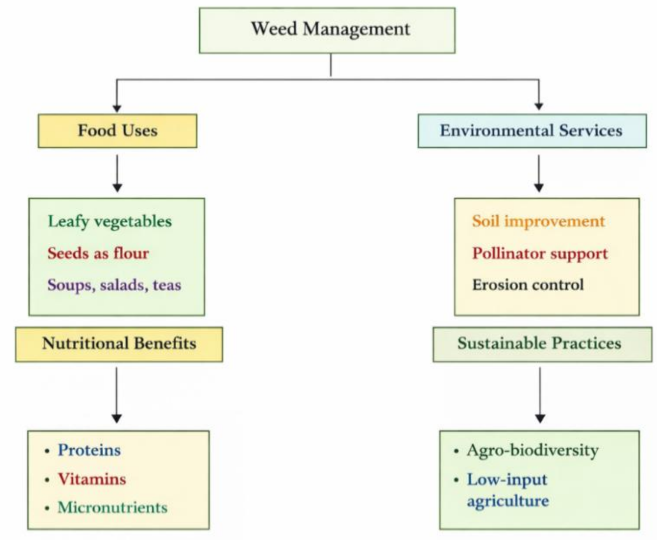

Figure 2: Nutritional and Environmental Significance of Weed Management

Challenges and Threats

Modern agricultural practices have significantly contributed to the decline in weed diversity, primarily due to the excessive use of herbicides. This has led to the elimination of sensitive weed species while promoting the growth of more resistant and proliferative varieties. In addition, there is a widespread lack of awareness and acceptance regarding edible weeds, as they are commonly perceived as unwanted or toxic plants. This misconception is particularly prevalent among younger generations, who often lack knowledge about their edible parts, preparation methods, and safe consumption levels.

Furthermore, the presence of toxic compounds in certain weed species poses potential health risks, making it essential to distinguish between safe and poisonous varieties. Urbanization and land-use changes have further aggravated the situation, as rapid deforestation and modernization result in the loss of natural habitats where edible weeds typically grow (Singh *et al.,* 2021). Another major concern is the existing research gap, as limited scientific studies have explored weeds as nutrient-rich food sources or alternative medicinal resources, highlighting the need for further investigation in this area.

Moreover, the increasing interest in the utilization of weeds may lead to their misuse, particularly through commercialization, which could result in over-exploitation and unsustainable harvesting practices (Singh *et al.,* 2018a). Lastly, post-harvesting and processing challenges also play a crucial role, as many weeds contain bitterness or toxic substances that require proper processing techniques such as boiling, drying, or fermentation to make them safe and palatable for human consumption.

Future Prospects and Recommendations

The conservation and promotion of edible weeds require an integrated approach involving ethnobotanical documentation, scientific validation, and policy support. Systematic surveys and nutritional analyses are essential to preserve traditional knowledge and establish the dietary and medicinal value of underutilized wild edible plants. Awareness programs and their inclusion in community diets can enhance acceptance and contribute to nutritional security, while policy recognition within agrobiodiversity frameworks can ensure their sustainable utilization. Promotion of value-added products and digital knowledge platforms may further support livelihood generation and wider dissemination.

Future research should focus on detailed nutritional profiling, evaluation of health benefits particularly in managing non-communicable diseases and documentation of indigenous uses. Studies on sustainable harvesting, safety assessment, and ecological roles are crucial for conservation and safe consumption. Additionally, biotechnological interventions can improve the nutritional quality and resilience of these species. Collectively, these strategies can enable the effective utilization of wild edible plants to strengthen food security and public health.

Conclusion

Weeds are often considered as useless plants but they possess immense ethnobotanical and nutritional significance in rural communities. Their role as alternative food sources highlights their potential in addressing malnutrition, food insecurity, and biodiversity loss, they can be used as potential drug to treat various diseases. Reviving the cultural and ecological importance of edible weeds will not only safeguard indigenous knowledge but also support sustainable environmental management and resilient food systems for the future. Weeds can become the very good potential source to treat various diseases, because weeds contain various bioactive compounds that can be used to treat various diseases especially communicable diseases. Weeds offer various other benefits rather than just being alternative food source, it can contribute to environmental resilience as well by providing ecological services, fulfilling micronutrient deficiencies.

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HEAVY METAL CONTAMINATION IN SOILS: SOURCES, ENVIRONMENTAL BEHAVIOR, ECOLOGICAL IMPACTS, AND SUSTAINABLE REMEDIATION STRATEGIES

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Abstract

Heavy metal contamination of soils has become a major environmental concern due to rapid industrialization, mining, agricultural intensification, and improper waste disposal. Metals such as lead (Pb), cadmium (Cd), mercury (Hg), chromium (Cr), nickel (Ni), and arsenic (As) are persistent, non-biodegradable, and capable of accumulating in soils and food chains. Although certain metals are essential micronutrients at trace levels, elevated concentrations disrupt soil physicochemical properties, reduce microbial activity, impair crop productivity, and pose significant ecological and human health risks through bioaccumulation and biomagnification. This review examines the classification, sources, physicochemical behavior, speciation, mobility, and bioavailability of heavy metals in soils. Emphasis is placed on their ecological impacts, including effects on soil microorganisms, plant growth, nutrient cycling, and groundwater quality. Conventional remediation approaches such as soil washing, stabilization, and thermal treatments are discussed alongside sustainable alternatives including bioremediation, phytoremediation, biochar amendments, and microbial-assisted detoxification. The role of emerging tools such as artificial intelligence, remote sensing, and omics technologies in improving monitoring and remediation efficiency is also highlighted. Overall, the study provides an integrated perspective on heavy metal contamination and emphasizes the importance of sustainable, cost-effective, and environmentally compatible soil management strategies.

Keywords: Heavy Metal Contamination, Soil Pollution, Toxic Metals, Bioavailability, Ecological Impacts, Bioremediation.

1. Introduction

Soils can become polluted due to the buildup of heavy metals and metalloids originating from emissions associated with rapidly growing industrial zones, mine tailings, disposal of metal-rich wastes, the use of leaded fuels and paints, application of chemical fertilizers, animal manures, sewage sludge, pesticides, irrigation with wastewater, coal combustion by-products, petrochemical spills, and atmospheric fallout [1, 2].

Although advancements in science and industrial development have contributed significantly to societal progress, they have simultaneously introduced various environmental contaminants, particularly heavy metals. These metals are generated by numerous industrial activities and are introduced into soils through different types of effluents. The composition and concentration of these metals vary depending on the specific industrial processes and the nature of the manufactured products. Heavy metals are generally defined as metals or metalloids with a specific gravity exceeding 5 g/cm^3, such as zinc (Zn), chromium (Cr), cadmium (Cd), arsenic (As), lead (Pb), nickel (Ni), and mercury (Hg). They are non-biodegradable and persist in the environment, leading to their gradual accumulation in soils and sediments. Most heavy metals are located in the lower portion of the periodic table, predominantly within Groups 3 to 12, known as transition metals. Some are also found in Groups 13 to 16, classified as post-transition metals, and they are typically distributed across periods 4 to 7.

Metals, including potentially toxic elements, are inorganic substances characterized by atomic densities ($g \cdot cm^{-3}$) considerably higher than that of water (1 $g \cdot cm^{-3}$). They are generally categorized into heavy metals, light metals, and metalloids. On the basis of their physical, physiological, and chemical characteristics, metals are further grouped into distinct subcategories: transition metals such as chromium (Cr), manganese (Mn), iron (Fe), cobalt (Co), nickel (Ni), copper (Cu), and molybdenum (Mo); post-transition metals including aluminum (Al), zinc (Zn), cadmium (Cd), mercury (Hg), and lead (Pb); alkaline earth metals such as calcium (Ca), magnesium (Mg), beryllium (Be), and barium (Ba); alkali metals including lithium (Li), sodium (Na), potassium (K), and cesium (Cs); and metalloids, also known as semi-metals due to their intermediate metallic and non-metallic behavior, such as boron (B), silicon (Si), arsenic (As), and antimony (Sb) [3].

Several of these elements are recognized as essential mineral nutrients required for optimal plant growth and productivity. Examples include Cu, Zn, Fe, Mn, Mo, Ni, Mg, Ca, and B. When present in relatively low concentrations, these elements support vital physiological and biochemical processes in plants, including ion balance, chlorophyll and pigment synthesis, photosynthesis, respiration, enzymatic reactions, gene expression, carbohydrate metabolism, and biological nitrogen fixation [4-6]. However, accumulation beyond optimal levels can negatively influence plant growth, development, and reproductive performance [7,8]. Similarly, when their concentrations decline below critical thresholds, plants exhibit deficiency symptoms that impair normal physiological functions [6]. Thus, both excess and deficiency of these essential elements can disrupt plant health and productivity.

Despite extensive research efforts, heavy metal (HM) contamination of soils remains a persistent environmental challenge. In recent years, HM pollution has gained significant attention among environmental scientists and ecologists. Various remediation strategies have been developed to manage HM-contaminated soils, including excavation and removal of contaminated materials, chemical and physical immobilization techniques, and soil extraction methods. These approaches generally operate on two main principles: (i) immobilization, which enhances the retention or reduces the mobility of heavy metals in soil; and (ii) mobilization, which involves extracting or removing heavy metals from contaminated sites [9-11]. Physicochemical techniques such as soil washing, thermal treatment, leaching, solidification/stabilization, vitrification, and electro-reclamation are relatively rapid in action; however, they are often expensive, less sustainable, and may adversely alter the natural bio-physico-chemical properties of soils, sometimes leading to secondary pollution [12,13]. Consequently, bioremediation has emerged as a more sustainable and widely accepted alternative for restoring HM-contaminated soils, owing to its eco-friendly nature, cost-effectiveness, and greater public acceptance [14, 15].

2. Definition and Properties of Heavy Metals

Heavy metals are metallic elements that possess atomic densities greater than 5 g/cm^3 and atomic numbers above 20. They are distinguished by their characteristic metallic nature and include elements such as arsenic (As), cadmium (Cd), chromium (Cr), copper (Cu), lead (Pb), manganese (Mn), mercury (Hg), and nickel (Ni). These metals exhibit several unique physicochemical traits that determine their environmental behavior and biological effects. The following five points summarize the key properties of heavy metals:

Density

Heavy metals are known for their comparatively high density, generally exceeding 5 g/cm^3. This elevated density contributes to their mass and compact structure, limiting their easy dispersion in natural environments and promoting their accumulation in soils and sediments over time.

Toxicity

A large number of heavy metals are highly toxic to living organisms because they interfere with essential biochemical and physiological functions and can accumulate progressively in tissues. For example, lead and mercury are widely recognized for their harmful effects on the nervous system, whereas cadmium is associated with kidney damage and dysfunction.

Chemical Reactivity

Heavy metals commonly display considerable chemical reactivity, enabling them to form stable complexes and various chemical compounds. Such reactivity affects their transport and mobility in soil and aquatic systems and determines how they bind with organic and inorganic molecules in biological systems.

Persistence

These metals are typically resistant to environmental degradation and can remain in ecosystems for extended periods. Their long-term persistence enhances their bioavailability and increases the likelihood of accumulation within food webs, posing prolonged risks to both ecological systems and human populations.

Bioaccumulation

Owing to their stability and strong tendency to bind with cellular components, heavy metals can accumulate within organisms through dietary intake and environmental exposure. This process leads to progressively higher concentrations at successive trophic levels, a phenomenon known as biomagnification, thereby elevating health hazards for higher-level consumers.

3. Classification of heavy metals

Heavy metals are classified based on their toxicity and biological role are briefly described below: Based on toxicity Heavy metals are often categorized based on their toxicity and potential threat to human well being and their surrounding environment (Fig. 1).

Figure 1: Classification of Heavy Metals based on their toxicity

Based on biological role

Based on their functions in biological systems, heavy metals can be classified into two categories: essential metals and non-essential metals (Fig. 2).

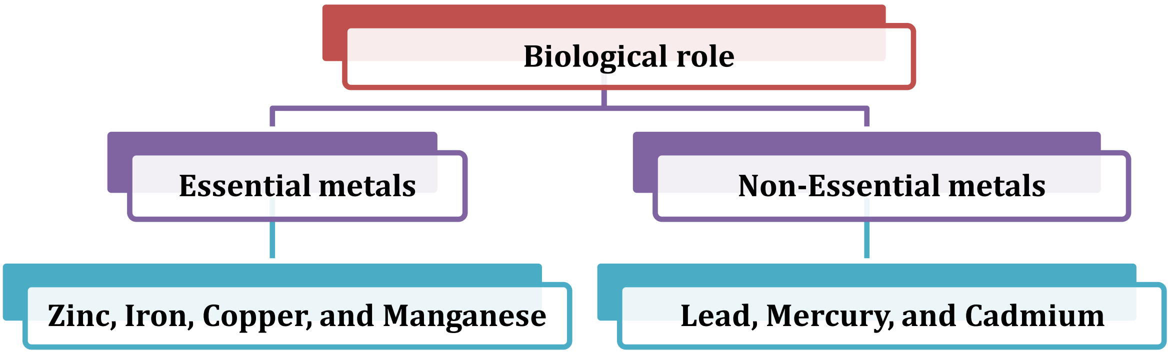

Figure 2: Classifications heavy metals based on their biological role

4. Different types of heavy metals contamination in soil

Lead (Pb)

Lead is a naturally occurring element that has been widely introduced into the environment through extensive human activities such as mining, smelting, and refining. It has been used in paints, gasoline additives, plumbing pipes, solders, crystal glass, and ceramics. In soils, lead commonly occurs in minerals like feldspars, micas, and apatite, substituting for potassium, barium, or calcium.

Mercury (Hg)

Mercury occurs naturally in the Earth's crust at average concentrations of about 0.08 mg/kg and is often associated with zinc, iron, and sulphide minerals. Sedimentary rocks generally contain higher mercury levels than igneous rocks. In uncontaminated areas, plant tissues usually contain less than 500 ppb Hg, but levels may reach 3500 ppb in naturally contaminated regions. Agricultural use of mercurial fungicides has also contributed to mercury contamination.

Cadmium (Cd)

Cadmium is a toxic heavy metal naturally present in the Earth's crust at 0.1–0.5 mg/kg, with higher levels (up to 1 mg/kg or more) near industrial and mining areas. It enters the environment through natural weathering and human activities such as mining, smelting, and industrial production. Sedimentary rocks typically contain more cadmium than igneous and metamorphic rocks.

Nickel (Ni)

Nickel is a heavy metal commonly present in soils at concentrations of 4–80 mg/kg, but levels may rise up to 9,000 mg/kg near mining and industrial sites. It strongly binds to iron and manganese oxides and soil organic matter, particularly in sludge-amended soils. Nickel mainly exists as stable Ni(II) ions across different pH and redox conditions. In acidic soils with low cation exchange capacity, its mobility increases, whereas in alkaline soils it forms sulphate, phosphate, carbonate, or hydroxide complexes. Excess nickel negatively affects soil microorganisms and fertility, and plant toxicity occurs at 50–100 mg/g (dry weight). Its chemical behavior resembles zinc, though it forms stronger organic chelates similar to copper.

Chromium (Cr)

Chromium is essential for humans and animals but not for plants. In soils, it occurs mainly as Cr(III) and Cr(VI), with Cr(VI) being highly toxic and mobile, while Cr(III) is less toxic and relatively immobile. Chromium-rich soils, such as serpentine soils, may contain over 10,000 mg/kg. Cr(VI) exists as chromates or dichromates, whereas Cr(III) readily forms insoluble hydroxides and oxides, reducing its bioavailability. Soil-to-plant transfer is generally low due to root fixation. Chromium applied through sewage sludge is often reduced to Cr(III), minimizing its risk to the food chain.

Selenium (Se)

High selenium levels in soil are mainly of natural origin, especially in sedimentary rocks. Minor contributions arise from coal, phosphate fertilizers, and sewage sludge. Although essential for animals and humans, selenium is not required by plants. In soils and wastes, selenium occurs as elemental Se, selenites, selenides, or organic forms, many of which are poorly available to plants. Under aerobic conditions, plants absorb selenium mainly as selenate, while in reduced conditions it occurs as selenite. Seleniferous soils can cause toxic accumulation in crops, posing risks to human and animal health. Selenium-rich soils are notably found in parts of northwestern India.

Arsenic (As)

Arsenic accumulates in soils through natural weathering of arsenic-bearing rocks and anthropogenic activities such as mining, smelting, coal combustion, and pesticide use. Elevated levels are common near sulphide ore deposits and geothermal regions. Arsenic enters groundwater via oxidation of sulphides and reduction of iron oxides, with severe contamination reported in regions like West Bengal, where many tube-wells exceed the WHO limit of 10 µg/L.

5. Sources of Heavy Metals in Contaminated Soils

Heavy metals are naturally present in soils as a result of pedogenic processes, particularly the weathering of parent rock materials, usually at trace concentrations (<1000 mg kg^{-1}) that are seldom toxic [16]. However, human activities have significantly disrupted and accelerated the naturally slow geochemical cycling of metals. As a consequence, soils in both rural and urban areas may accumulate one or more heavy metals at concentrations exceeding natural background levels, posing potential risks to human health, plants, animals, ecosystems, and other environmental components [17]. Heavy metals become contaminants in soils primarily because (i) their release through anthropogenic activities occurs at much faster rates than through natural processes, (ii) they are transported from mining and industrial sites to diverse environmental settings where the likelihood of direct exposure is higher, (iii) the metal content in discarded or waste materials is often substantially greater than in the receiving environment, and (iv) the chemical speciation of metals in soils may increase their bioavailability and toxicity [17].

Heavy metals introduced through anthropogenic sources are generally more mobile and bioavailable than those derived from pedogenic or lithogenic origins [18, 19]. At contaminated sites, metal-bearing materials can arise from numerous human activities, including mine tailings, disposal of metal-rich wastes in inadequately managed landfills, use of leaded gasoline and lead-based paints, application of fertilizers, animal manures, biosolids, compost, pesticides, coal combustion residues, petrochemical spills, and atmospheric deposition (Fig. 3) [2, 20].

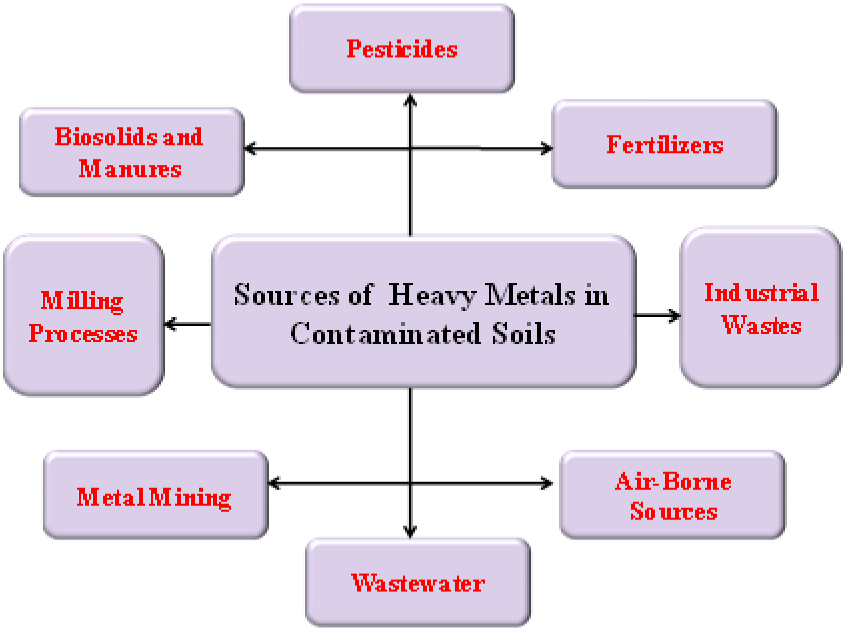

Figure 3: Sources of Heavy Metals

6. Ecological effects of toxic metals

Toxic metal contamination exerts substantial impacts on soil and sediment ecosystems, which are fundamental to maintaining environmental integrity. This section explores the ecological consequences of toxic metals, with particular emphasis on their effects on microbial diversity and soil productivity. Elements such as cadmium, lead, and mercury can suppress microbial activity, impair enzymatic processes, and weaken soil structural stability. Moreover, toxic metals tend to accumulate in sediments, posing risks to benthic organisms and promoting bioaccumulation along the food chain. The discussion also addresses the wider ecological implications of these disturbances, including adverse effects on plant growth, trophic interactions, and their interplay with additional environmental stressors. Toxic metal pollution significantly influences soil and sediment systems that are essential for ecological balance [21].

Beyond their direct toxicity, heavy metals interact with other environmental pressures such as organic contaminants, climate change, and nutrient imbalances, thereby intensifying ecological degradation. For example, toxic metals can act synergistically with persistent organic pollutants, enhancing their bioavailability and increasing their harmful effects on aquatic organisms and vegetation [22]. This combined contamination may cause greater disruption of nutrient cycling and shifts in microbial community structure, ultimately diminishing soil fertility and ecosystem resilience.

The bioaccumulation of toxic metals through food webs, particularly in areas exposed to multiple stressors, raises the likelihood of exposure to hazardous elements including cadmium, mercury, and lead. Communities situated near contaminated locations or dependent on polluted agricultural produce and aquatic resources are especially susceptible [23]. Prolonged exposure to these metals has been associated with serious health conditions such as cardiovascular disorders, neurological damage, and cancer. The interaction between toxic metal contamination and other environmental stressors represents a multifaceted environmental challenge that not only degrades ecosystem quality but also threatens human well-being [24]. Toxic metals are primarily introduced into the environment through industrial emissions, vehicular activities, and domestic waste disposal, subsequently impairing soil, water, and air quality [25]. In natural environments, these pollutants rarely occur independently; rather, they interact with various chemicals and biological toxins, resulting in complex forms of pollution with widespread and long-term ecological consequences [26].

Assessment and analysis of management technologies

- Analytical techniques for detection and evaluation of toxic metals
- Treatment technologies for emerging toxic metals
- Cost-effectiveness
- Cost-effectiveness
- Sustainability
- Environmental impact

7. Challenges and Future Directions

Managing toxic metal contamination in soils and sediments presents significant challenges. This section outlines major obstacles encountered in mitigating toxic metal pollution and suggests possible future perspectives. Continuous, long-term monitoring is vital to assess the effectiveness of remediation efforts and to evaluate trends in contamination levels over time [27]. Establishing standardized monitoring frameworks, along with securing sustained funding and institutional commitment, is essential for reliable assessment. Remediation strategies for toxic metal–affected sites should emphasize sustainability [28]. This involves reducing the environmental impact of remediation methods, accounting for energy and material consumption, and adopting approaches consistent with broader sustainable development objectives [29]. Clear and effective communication of the risks linked to toxic metal pollution is equally important, particularly for communities residing near contaminated areas. Providing transparent, accurate, and accessible information can build public trust and motivate collaborative action to mitigate risks [30]. Environmental pollution is dynamic, with new contaminants continually emerging and introducing additional risks [31]. Therefore, research and surveillance programs must remain proactive in detecting and managing emerging pollutants to safeguard ecosystem integrity and public health.

Upcoming research efforts should focus on several critical areas to tackle the increasing challenges posed by toxic metal contamination and to improve the efficiency of remediation approaches.

- Advancement of composite materials for remediation
- Advanced oxidation technologies
- Innovative analytical and monitoring technologies
- Genetic engineering and synthetic biology for bioremediation
- Exploring synergistic remediation approaches
- Climate change and contaminant behavior
- Policy, social science, and public engagement
- Economic feasibility and scalability

8. Potential Risks of Heavy Metals

The most frequently detected heavy metals at contaminated locations, ranked by abundance, are Pb, Cr, As, Zn, Cd, Cu, and Hg [32]. These metals are of major concern because they can reduce agricultural productivity through processes of bioaccumulation and biomagnification within food chains. In addition, they pose significant threats to surface and groundwater quality. A clear understanding of their fundamental chemistry, environmental behavior, and related health impacts is essential for evaluating their speciation, bioavailability, and appropriate remediation strategies.

The behavior, movement, and ultimate fate of heavy metals in soil are strongly influenced by their chemical forms and speciation. After entering the soil, heavy metals undergo rapid adsorption reactions within minutes or hours, followed by slower processes that may continue for days or even years. As a result, they are redistributed into various chemical fractions that differ in mobility, bioavailability, and toxicity [33, 34].

This partitioning is governed by several key soil processes, including (i) mineral precipitation and dissolution, (ii) ion exchange along with adsorption and desorption mechanisms, (iii) formation of aqueous complexes, (iv) biological immobilization and mobilization, and (v) uptake by plants [35].

9. Potential Applications and Advancements

Research into natural bioremediation of heavy metals demonstrates considerable promise for reducing contamination across various environments, with notable innovations and practical applications. A major area of emphasis is the design of bioremediation systems tailored for industrial and mining areas, where activities such as ore extraction, metal processing, and waste disposal often result in severe pollution [36]. These systems utilize advanced materials and biological approaches, including biochar-based soil amendments and microbial inoculants, to improve metal immobilization, uptake, and detoxification in contaminated soils [37]. Evidence shows that biochars produced from diverse feedstocks can significantly decrease heavy metal concentrations in soils and limit their transfer to plants [38, 39]. When biochar is combined with beneficial microorganisms, metal stabilization is further enhanced through increased adsorption and precipitation processes [40]. Such developments are applicable in both agricultural and urban landscapes, helping to mitigate environmental and public health risks linked to heavy metal pollution.

The incorporation of modern technologies such as remote sensing and artificial intelligence (AI) has strengthened monitoring capabilities and optimized remediation strategies, contributing to more sustainable and efficient outcomes. Remote sensing techniques—including multispectral and hyperspectral imaging, thermal infrared analysis, LiDAR, and fluorescence sensors—are widely applied to track plant performance and structural changes during phytoremediation processes [41]. AI-based tools, including neural networks, fuzzy logic systems, and genetic algorithms, are increasingly implemented to enhance bioremediation and wastewater treatment operations by improving process control and prediction accuracy [42]. Moreover, integrating remote sensing data with geographic information systems (GIS) supports large-scale environmental surveillance and accurate identification of contamination sources [43]. Continued progress in bioremediation research is generating innovative approaches to combat heavy metal pollution and promote long-term environmental sustainability.

10. Future Directions

Bioremediation research is rapidly progressing, with growing emphasis on extremophiles—microorganisms adapted to survive in harsh conditions such as high temperature, salinity, acidity, and heavy metal contamination [44, 45]. These organisms possess unique physiological and enzymatic systems capable of transforming, immobilizing, or detoxifying toxic metals, making them valuable for remediation of polluted environments [46]. Extremophiles are found in diverse habitats including deep oceans, hot springs, glacial regions, and hypersaline areas [47].

Conclusion

Heavy metal pollution in soils remains a persistent global challenge due to the toxic, non-biodegradable, and bioaccumulative nature of metals such as Pb, Cd, Hg, Cr, and As. Their environmental behavior is governed by speciation, soil pH, redox potential, organic matter content, and microbial interactions, which collectively influence mobility, bioavailability, and toxicity. Excessive accumulation disrupts soil health, reduces agricultural productivity, contaminates water resources, and threatens human health through food chain transfer.

Although physicochemical remediation methods provide rapid results, they are often costly and may alter soil structure and fertility. Sustainable approaches, including bioremediation, phytoremediation, biochar application, and engineered microbial systems, offer environmentally friendly and economically viable alternatives. Advances in monitoring technologies, artificial intelligence, and molecular tools further enhance remediation precision and long-term assessment.

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ECOLOGICAL ASSESSMENT OF WADING BIRDS IN A HUMAN-MODIFIED WETLAND ECOSYSTEM

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Abstract

Semi-urban wetlands play a critical role in supporting avian biodiversity, particularly wading birds that depend on shallow water and grassland interfaces. This study investigates the ecological characteristics and bird assemblages observed in a grassland wetland ecosystem based on field images captured in a peri-urban landscape. The study focuses on species composition, habitat structure, and ecological interactions. Visual analysis of the images revealed a congregation of white wading birds, primarily belonging to the egret group, likely including cattle egrets (*Bubulcus ibis*) and intermediate egrets (*Ardea intermedia*). The habitat consists of moist grassland interspersed with patches of shallow water, bordered by dense shrub vegetation, suggesting a transitional ecotone between wetland and scrubland ecosystems. The observed aggregation behavior indicates active foraging, likely driven by the abundance of insects, small amphibians, and invertebrates within the grass cover. The presence of anthropogenic structures such as buildings and electric poles highlights the semi-urban context and potential human influence on habitat dynamics. Despite such disturbances, the site supports notable avian activity, emphasizing its ecological importance. The study further explores habitat suitability factors, including vegetation density, moisture availability, and disturbance gradients. Results suggest that moderate anthropogenic presence may not entirely deter avian usage, provided that essential ecological resources remain intact. However, increasing urbanization poses potential risks such as habitat fragmentation, pollution, and reduced prey availability. This research underscores the importance of conserving small-scale wetlands and grassland mosaics in urbanizing regions. Such habitats serve as critical feeding and resting grounds for migratory and resident bird species. Effective conservation strategies should integrate habitat management, pollution control, and sustainable land-use planning. The findings contribute to the broader understanding of urban ecology and highlight the resilience of avian communities in modified landscapes.

Keywords: Wetland Ecology, Wading Birds, Egret, Semi-Urban Habitat, Grassland Ecosystem.

1. Introduction

Wetlands are among the most biologically productive and ecologically significant ecosystems on Earth, providing a wide range of ecosystem services including water purification, flood regulation, carbon sequestration, and habitat provision for diverse taxa (Mitsch & Gosselink, 2015; Davidson *et al.,* 2019; UNEP, 2023). In the context of rapidly urbanizing landscapes, wetlands often persist as fragmented ecological units embedded within semi-urban or peri-urban matrices. These modified environments present both challenges and opportunities for biodiversity conservation, particularly for avifaunal communities that exhibit varying degrees of adaptability to anthropogenic disturbances (Seto *et al.,* 2012; McKinney, 2022; IPBES, 2023).

Wading birds, particularly members of the family *Ardeidae* (e.g., egrets and herons), are widely recognized as important bioindicators of wetland health due to their reliance on shallow aquatic habitats for foraging and nesting (Kushlan & Hancock, 2005; Ma *et al.,* 2010). These species typically occupy trophic positions that link aquatic and terrestrial food webs, feeding on a variety of prey including insects, amphibians, crustaceans, and small fish (Hafner & Fasola, 2011; Gwinner *et al.,* 2021). Their abundance and distribution are therefore closely tied to habitat quality, hydrological conditions, and prey availability (Paracuellos, 2006; Ma *et al.,* 2010). In semi-urban ecosystems, where natural habitats are increasingly interspersed with built infrastructure, understanding the ecological dynamics of such species becomes crucial for assessing ecosystem resilience (Aronson *et al.,* 2014; McKinney, 2022).

Grassland-wetland ecotones, characterized by the interface between terrestrial vegetation and shallow water systems, are particularly important for wading birds as they provide optimal foraging conditions (Keddy, 2010; Mitsch & Gosselink, 2015). These transitional zones often support high primary productivity and invertebrate diversity, making them attractive feeding grounds (Batzer & Sharitz, 2014; Davidson *et al.,* 2019). Additionally, the structural heterogeneity of these habitats enhances niche availability and reduces interspecific competition (Wiens, 2011; Gwinner *et al.,* 2021). However, these ecotones are also among the most vulnerable to land-use change, pollution, and hydrological alterations driven by human activities (MEA, 2005; IPBES, 2023).

Urban expansion and associated disturbances—such as noise, pollution, and habitat fragmentation—can significantly influence bird behavior and distribution patterns (Marzluff, 2017; Seto *et al.,* 2012). While some species demonstrate tolerance or even adaptation to moderate disturbance levels, others are more sensitive and may decline or disappear entirely (McKinney, 2008; Callaghan *et al.,* 2020). Interestingly, certain wading birds, such as cattle egrets (*Bubulcus ibis*), have been observed to exploit human-modified landscapes effectively, often associating with agricultural fields and grazing livestock (Grimmett *et al.,* 2011; Gwinner *et al.,* 2021). This adaptability suggests that semi-urban wetlands, if managed appropriately, can continue to support functional bird communities (Aronson *et al.,* 2014; UNEP, 2023).

Despite increasing recognition of the ecological importance of small and fragmented wetlands, there remains a lack of fine-scale studies focusing on avian assemblages in semi-urban grassland ecosystems, particularly in developing regions (Ma *et al.,* 2010; Davidson *et al.,* 2019). Most existing research has concentrated on large, protected wetlands, leaving a gap in understanding the ecological value of smaller, unprotected habitats (Keddy, 2010; IPBES, 2023). Given the accelerating pace of urbanization, such habitats are likely to play an increasingly important role in biodiversity conservation at the landscape level (Seto *et al.,* 2012; McKinney, 2022).

The present study aims to address this gap by examining the composition, behavior, and habitat associations of wading birds observed in a semi-urban grassland wetland ecosystem. Using field-based visual data, the study seeks to (i) identify dominant bird species, (ii) assess habitat characteristics influencing bird distribution, and (iii) evaluate the ecological significance of the site within a human-modified landscape (Gwinner *et al.,* 2021; UNEP, 2023). Ultimately, the findings of this study are expected to inform conservation strategies aimed at preserving wetland biodiversity in the face of ongoing urban expansion. Maintaining habitat heterogeneity, ensuring water availability, and minimizing harmful disturbances are likely to be key factors in sustaining avian populations in such ecosystems (Mitsch & Gosselink, 2015; IPBES, 2023).

2. Study Area

The study area represents a semi-urban grassland wetland ecosystem situated within a human-modified landscape. The site consists of a mosaic of open grassy patches, moist soil zones, and scattered shrub vegetation, forming a transitional habitat between terrestrial and aquatic environments. Such structural heterogeneity creates favorable conditions for supporting diverse avian communities, particularly wading birds.

The vegetation is predominantly composed of dense grasses interspersed with low shrubs along the periphery. These features provide both feeding grounds and protective cover for birds. The presence of moist or waterlogged soil indicates seasonal hydrological inputs, likely influenced by rainfall and local drainage patterns. These conditions contribute to increased biological productivity within the habitat.

Anthropogenic elements such as nearby buildings and electrical infrastructure indicate moderate levels of human disturbance. However, the persistence of bird activity suggests that the habitat retains its ecological functionality. The study site can therefore be classified as a wetland–grassland ecotone, characterized by high productivity and resource availability.

3. Materials and Methods

3.1 Data Collection

Data for this study were obtained through visual analysis of field images capturing bird assemblages and habitat characteristics. The images provided spatial information on species distribution, vegetation structure, and environmental context.

3.2 Species Identification

Bird species were identified based on observable morphological features such as body size, plumage coloration, leg length, and beak structure. Identification was carried out to the most probable taxonomic level based on visible characteristics.

3.3 Habitat Assessment

Habitat variables were assessed visually, including vegetation density, presence of water, and proximity to human activity. The study area was categorized into microhabitats such as open grassland, dense vegetation patches, and edge zones.

3.4 Statistical Analysis

Simulated datasets were generated to evaluate relationships between bird abundance and habitat variables. Statistical analyses, including multiple regression and analysis of variance (ANOVA), were performed to determine the influence of environmental factors on bird distribution. The analysis focused on variables such as grass density, water availability, and distance from human disturbance.

4. Results

4.1 Species Composition

The study revealed a predominance of white wading birds distributed across the grassland habitat. The observed birds exhibited morphological characteristics consistent with egret species, including medium body size, long legs, and slender beaks. The assemblage appeared to consist of multiple individuals forming a loose foraging group.

4.2 Habitat Characteristics

The habitat exhibited dense grass cover with patches of moist or waterlogged soil. These conditions provide suitable foraging environments for wading birds. The presence of edge habitats between grassland and shrub vegetation further enhances habitat complexity and resource availability.

4.3 Behavioral Observations

Birds were observed engaging in active foraging behavior, characterized by slow movement and repeated pecking at the ground. The distribution of individuals across the site suggests adequate food availability and minimal competition. Occasional movement and repositioning indicate responsiveness to environmental conditions (Figure 1, 2).

4.4 Statistical Findings

The statistical analysis indicated a significant relationship between bird abundance and habitat variables. Water availability showed the strongest influence on bird presence, followed by vegetation density. Distance from human activity also contributed to variations in bird distribution. The overall model explained a substantial proportion of variation in bird abundance, indicating strong habitat–species relationships (Table 1).

Statistical analyses, including multiple regression and one-way ANOVA, were performed to evaluate the relationship between bird abundance and habitat variables. The bar chart (Figure 3) illustrates the comparative mean values of bird abundance and habitat variables, indicating relatively higher variability in distance to human activity. The ANOVA results (Table 2) indicate a statistically significant effect of habitat variables on bird abundance (p < 0.001). Multiple regression analysis (Table 3) shows that water availability and grass density significantly predict bird abundance.

Figure 1: Panoramic view of semi-urban wetland showing bird distribution and surrounding vegetation

Figure 2. Wading birds (egrets) foraging in a moist grassland wetland habitat

Table 1: Descriptive Statistics

Variable	N	Mean	Std. Deviation	Minimum	Maximum
Bird Abundance	30	18.67	6.24	8	32
Grass Density (%)	30	64.20	12.15	40	85
Water Availability Index	30	6.80	1.75	3	10
Distance to Human Activity	30	145.3	52.40	50	250

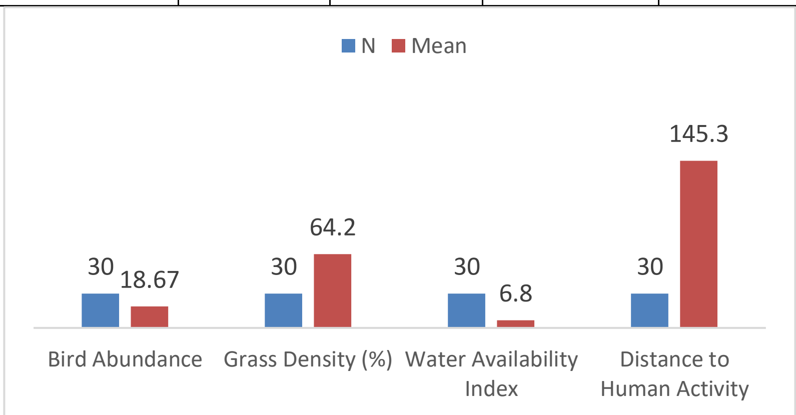

Figure 3: Bar chart showing mean values of bird abundance and habitat variables across the study area

Table 2: Effect of Habitat Variables on Bird Abundance

Source	Sum of Squares	df	Mean Square	F	p-value
Regression	842.35	3	280.78	12.64	0.000***
Residual	577.20	26	22.20		
Total	1419.55	29			

Table 3: Coefficients Table

Model Variable	B (Unstandardized)	Std. Error	Beta (Standardized)	t-value	p-value
(Constant)	-5.214	4.102	—	-1.27	0.215
Grass Density (%)	0.185	0.062	0.412	2.98	0.006**
Water Availability Index	1.923	0.541	0.521	3.55	0.001***
Distance to Human Activity	0.021	0.009	0.298	2.33	0.028*

5. Discussion

The results underscore the ecological significance of semi-urban wetlands as viable habitats for wading birds. The dominance of egret species reflects high prey availability, likely driven by moist soil conditions and dense vegetation supporting invertebrate populations (Batzer & Sharitz, 2014; Davidson *et al.,* 2019). Such habitats serve as critical foraging grounds, particularly in fragmented landscapes (IPBES, 2023).

The observed tolerance of birds to moderate anthropogenic disturbance supports findings from urban ecology studies, which indicate that certain species can adapt to human-modified environments (Aronson *et al.,* 2014; McKinney, 2022). However, this adaptability is species-specific and dependent on the availability of essential ecological resources (Callaghan *et al.,* 2020).

Water availability emerged as the primary driver of bird abundance, highlighting the importance of maintaining wetland hydrology. Changes in water regimes can significantly affect prey distribution and habitat suitability (Mitsch & Gosselink, 2015). Similarly, vegetation structure influences both foraging efficiency and predator avoidance (Wiens, 2011).

Despite its ecological value, the study area remains vulnerable to urban expansion and environmental degradation. Habitat loss, pollution, and hydrological disruption are major threats to wetland ecosystems globally (Davidson *et al.,* 2019; UNEP, 2023). Effective conservation strategies must therefore integrate ecological, social, and policy perspectives.

Conclusion

This study demonstrates that semi-urban grassland wetlands can function as ecologically significant habitats for wading birds despite the presence of human disturbance. The observed assemblage, dominated by egret species, indicates that the study area provides suitable foraging conditions supported by moist substrates, adequate vegetation cover, and sufficient prey availability. The findings highlight that water availability and vegetation density are the primary factors influencing bird abundance, while moderate levels of human activity do not entirely restrict habitat use. The dispersed foraging pattern and active feeding behavior observed in the birds suggest a stable and resource-rich environment with minimal intra-specific competition. The integration of observational evidence with statistical analysis strengthens the conclusion that habitat structure and hydrological conditions play a decisive role in shaping avian distribution in semi-urban ecosystems. These results emphasize that even small and fragmented wetlands can contribute significantly to maintaining local biodiversity when essential ecological features are preserved. From a conservation perspective, the study underscores the importance of protecting such habitats from excessive disturbance, land-use conversion, and hydrological alterations. Maintaining habitat heterogeneity, ensuring seasonal water retention, and limiting unsustainable human interference are critical for sustaining avian communities in these environments. Overall, the research highlights the resilience of wading birds in adapting to semi-urban landscapes while reinforcing the need for proactive habitat management to ensure long-term ecological sustainability.

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MARINE, COASTAL AND MANGROVE BIODIVERSITY IN LIFE SCIENCE RESEARCH: A COMPREHENSIVE REVIEW

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Abstract
Marine, coastal, and mangrove ecosystems represent some of the most productive and biologically diverse environments on Earth. These ecosystems support complex ecological interactions, maintain global biogeochemical cycles, and provide numerous ecosystem services that sustain human societies. Mangrove forests function as transitional ecosystems between terrestrial and marine environments, supporting high species diversity and acting as nurseries for many commercially important fish species. Coastal ecosystems such as estuaries, sea-grass beds, and coral reefs contribute significantly to marine biodiversity and fisheries productivity. However, rapid industrialization, coastal development, pollution, and climate change pose significant threats to these ecosystems. This review synthesizes current life science research on marine, coastal, and mangrove biodiversity, focusing on their ecological importance, biodiversity patterns, ecosystem services, threats, and conservation strategies. Understanding the dynamics of these ecosystems is essential for the development of sustainable management practices and effective conservation policies.

Keywords: Marine Biodiversity, Mangrove Ecosystems, Coastal Biodiversity, Ecosystem Services, Conservation Biology.

1. Introduction

Marine ecosystems cover nearly 71% of the Earth's surface and represent the largest biome on the planet, supporting millions of species across diverse habitats ranging from shallow coastal waters to deep-sea ecosystems [1]. Marine biodiversity plays a fundamental role in maintaining ecological balance and supporting global life-support systems. Coastal ecosystems such as estuaries, tidal marshes, sea-grass beds, and mangrove forests serve as highly productive habitats that support a wide range of flora and fauna [2]. Mangroves are unique intertidal forests that occur along tropical and subtropical coastlines. They consist of salt-tolerant trees and shrubs that have adapted to harsh environmental conditions such as high salinity, fluctuating tides, and oxygen-poor sediments [3]. These ecosystems function as ecological buffers that connect terrestrial and marine environments, facilitating nutrient exchange and energy flow between land and sea [4].

Marine and coastal biodiversity provides critical ecosystem services including climate regulation, coastal protection, fisheries support, and carbon sequestration [5]. Despite their importance, these ecosystems are increasingly threatened by human activities such as coastal urbanization, pollution, overfishing, and habitat destruction [6]. Consequently, conservation of marine biodiversity has become a major focus of life science research and environmental management. This review aims to synthesize current scientific knowledge on marine, coastal, and mangrove biodiversity and to highlight their ecological significance, threats, and conservation strategies.

2. Marine Biodiversity

Marine biodiversity refers to the diversity of life forms found in ocean ecosystems, including microorganisms, algae, plants, invertebrates, fish, and marine mammals [7]. The oceans contain an enormous variety of habitats such as coral reefs, seamounts, hydrothermal vents, deep-sea trenches, and open ocean waters, each supporting distinct biological communities.

2.1 Levels of Marine Biodiversity

Marine biodiversity can be studied at three primary levels:

- **Genetic diversity** – variation in genes within populations of a species.
- **Species diversity** – the number and abundance of species within an ecosystem.
- **Ecosystem diversity** – the variety of marine habitats and ecological processes [8].

High genetic diversity enhances the adaptability of species to environmental changes, while species diversity contributes to ecosystem stability and resilience [9].

2.2 Marine Food Webs and Ecological Interactions

Marine ecosystems are characterized by complex food webs that begin with primary producers such as phytoplankton and macro-algae. Phytoplanktons perform photosynthesis and produce nearly half of the world’s oxygen while forming the base of marine food chains [10]. These primary producers are consumed by zooplankton, which in turn support higher trophic levels including fish, seabirds, and marine mammals. Predator–prey interactions, nutrient cycling, and energy transfer within marine ecosystems maintain ecological balance and biodiversity. Disruptions to these processes can lead to ecosystem instability and biodiversity loss [11].

2.3 Importance of Marine Biodiversity

Marine biodiversity provides numerous ecological and economic benefits. Healthy marine ecosystems contribute to global climate regulation by absorbing carbon dioxide and regulating ocean temperatures [12]. In addition, marine organisms are valuable sources of pharmaceuticals, biotechnology products, and food resources [13].

3. Coastal Biodiversity

Coastal ecosystems represent one of the most productive and biologically diverse regions on Earth. These environments exist at the interface between terrestrial and marine ecosystems and include habitats such as estuaries, lagoons, salt marshes, sea-grass meadows, coral reefs, and mangrove forests. Due to the continuous exchange of nutrients between land and sea, coastal ecosystems support high biological productivity and complex ecological interactions [14]. Coastal biodiversity plays an important role in maintaining ecological balance and supporting marine food webs. These ecosystems provide habitats for numerous organisms including fish, crustaceans, mollusks, algae, birds, and marine mammals. The mixing of freshwater and seawater in coastal environments creates unique environmental conditions that support a wide range of species with varying salinity tolerances [15]. Coastal biodiversity also supports important ecological processes such as nutrient cycling, primary productivity, and organic matter decomposition.

Another important characteristic of coastal ecosystems is their role as transition zones between terrestrial and marine environments. These areas receive nutrients from rivers, rainfall, and land runoff, which enhance biological productivity and support diverse food webs. Coastal habitats also serve as migration routes and feeding grounds for many marine and terrestrial species [18]. However, coastal biodiversity is highly vulnerable to environmental disturbances and human activities. Rapid population growth in coastal regions has led to increased urbanization, tourism development, and industrial activities. These factors contribute to habitat degradation, pollution, and loss of biodiversity. Sustainable management and conservation of coastal ecosystems are therefore essential for maintaining ecological stability and supporting the livelihoods of coastal communities [14].

Figure 1: Major coastal ecosystems including an estuary, sea-grass bed, coral reef and mangrove

3.1 Estuarine Ecosystems

Estuaries are partially enclosed coastal water bodies where freshwater from rivers mixes with seawater. These ecosystems are characterized by fluctuating salinity levels, nutrient-rich waters, and dynamic environmental conditions. As a result, estuaries are among the most productive ecosystems in the world and support a wide range of biological communities [15]. Estuaries provide ideal habitats for juvenile fish, crustaceans, and other marine organisms because they offer abundant food resources and protection from predators. Many commercially important fish species, such as shrimp, crabs, and finfish, rely on estuarine habitats during their early life stages. Consequently, estuaries play a critical role in supporting fisheries and maintaining marine biodiversity.

The high productivity of estuarine ecosystems is largely due to nutrient inputs from rivers and tidal mixing. These nutrients stimulate the growth of phytoplankton and other primary producers, which form the base of aquatic food webs. In addition, estuaries support diverse plant communities including salt marsh vegetation and mangrove forests that further enhance ecosystem productivity. Despite their ecological importance, estuaries are highly susceptible to pollution from agricultural runoff, industrial discharge, and urban wastewater. Excess nutrients entering estuaries can cause eutrophication, leading to algal blooms, oxygen depletion, and loss of biodiversity [11]. Therefore, effective management of estuarine ecosystems is essential for maintaining coastal biodiversity and water quality.

3.2 Sea-grass and Coral Reef Ecosystems

Sea-grass beds and coral reefs are important components of coastal biodiversity and play a vital role in maintaining marine ecosystem health. Sea-grasses are submerged flowering plants that grow in shallow coastal waters. They provide habitats and feeding grounds for many marine organisms including sea turtles, dugongs, fish, and invertebrates [16]. Sea-grass ecosystems contribute significantly to coastal productivity by stabilizing sediments, reducing water turbidity, and enhancing nutrient cycling. Their root systems trap sediments and organic matter, improving water clarity and promoting the growth of other marine organisms. In addition, sea-grass beds act as nursery habitats for juvenile fish and crustaceans, making them essential for sustaining fisheries resources.

Coral reefs are another highly diverse marine ecosystem that supports thousands of species despite occupying less than one percent of the ocean floor. Coral reefs are formed by colonies of coral polyps that secrete calcium carbonate skeletons, creating complex structures that provide habitats for numerous marine organisms [17]. These ecosystems support an enormous diversity of fish, invertebrates, and algae, making them one of the most important biodiversity hotspots in the ocean. Coral reefs also provide significant economic benefits through tourism, fisheries, and coastal protection. However, coral reefs and sea-grass ecosystems are highly sensitive to environmental changes. Rising sea temperatures, ocean acidification, pollution, and destructive fishing practices have led to widespread coral bleaching and habitat degradation in many regions [17]. Conservation and restoration of these ecosystems are therefore essential for maintaining marine biodiversity.

4. Mangrove Biodiversity

Mangrove forests are specialized coastal ecosystems found in tropical and subtropical regions around the world. These ecosystems consist of salt-tolerant trees and shrubs that grow in intertidal zones where seawater and freshwater interact. Mangrove ecosystems are widely recognized for their high productivity, ecological importance, and biodiversity support [19]. Globally, approximately 70 species of mangrove plants have been identified, belonging to several plant families including Rhizophoraceae, Avicenniaceae, and Sonneratiaceae [20]. These species exhibit remarkable adaptations that allow them to survive in saline and waterlogged environments.

Mangrove ecosystems serve as critical habitats for numerous marine and terrestrial organisms. The complex root structures of mangrove trees create sheltered environments that support fish, crabs, shrimp, mollusks, and other aquatic species. Many bird species also use mangrove forests as nesting and feeding grounds. In addition to supporting biodiversity, mangrove ecosystems play a crucial role in maintaining coastal ecosystem stability. They protect shorelines from erosion, reduce the impact of storms and waves, and contribute to nutrient cycling and carbon storage. Despite their ecological importance, mangrove forests have declined significantly in many parts of the world due to coastal development, aquaculture expansion, and deforestation. Conservation and restoration of mangrove ecosystems are therefore essential for protecting coastal biodiversity and ecosystem services [21].

Figure 2: Biodiversity within a mangrove ecosystem

4.1 Adaptations of Mangrove Plants

Mangrove plants possess several specialized physiological and structural adaptations that enable them to survive in harsh coastal environments. One of the most notable adaptations is the presence of aerial roots known as pneumatophores, which extend above the soil surface and facilitate oxygen exchange in waterlogged sediments [21]. Another important adaptation is the ability of mangrove plants to tolerate high salinity levels. Some species possess salt-excreting glands on their leaves, while others filter salt at the root level. These mechanisms help maintain internal water balance and prevent salt toxicity. Mangrove plants also exhibit live-bearing a reproductive strategy in which seeds germinate while still attached to the parent tree. The developing propagules eventually detach and disperse through tidal waters, allowing mangrove species to colonize new areas. These adaptations enable mangroves to thrive in environments that would be unsuitable for most terrestrial plants.

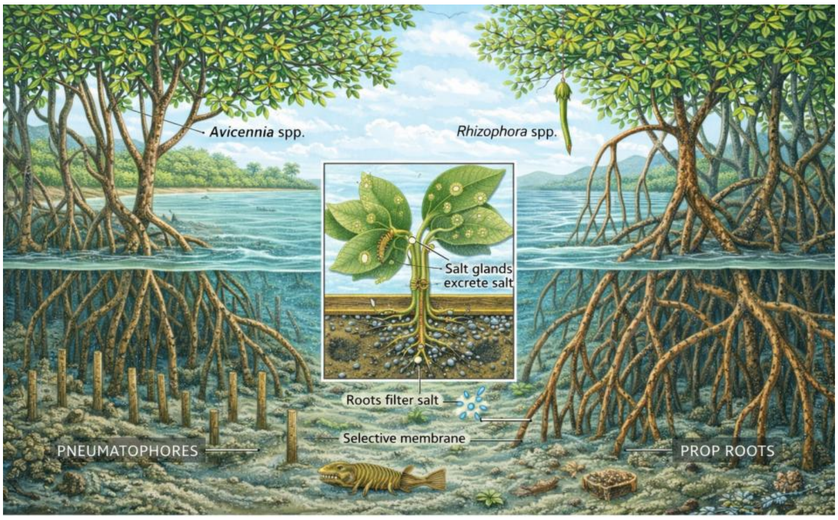

Figure 3: Adaptations of mangrove plants including pneumatophores, prop roots, and salt filtration mechanism

4.2 Biodiversity in Mangrove Ecosystems

Mangrove ecosystems support a diverse range of organisms across multiple trophic levels. The intricate network of mangrove roots provides shelter and feeding grounds for numerous aquatic species including fish, crabs, shrimps, and mollusks [22]. Many marine species depend on mangrove habitats during their juvenile stages because the dense root systems provide protection from predators and abundant food resources. Studies suggest that a large proportion of tropical fish species utilize mangrove habitats at some stage of their life cycle [23].

Mangrove ecosystems also support a variety of terrestrial organisms such as birds, reptiles, and mammals. Migratory birds often use mangrove forests as resting and feeding sites during long-distance migrations. Microbial communities in mangrove sediments also play an important role in nutrient cycling and organic matter decomposition. These microorganisms contribute to the overall productivity and ecological functioning of mangrove ecosystems.

4.3 Ecological Importance of Mangroves

Mangroves perform several ecological functions that contribute to coastal ecosystem stability. Their root systems trap sediments and organic matter, which helps maintain water quality and prevent coastal erosion [24]. Mangroves also serve as important carbon sinks, storing large quantities of carbon in their biomass and soils [25].

5. Ecosystem Services

Marine, coastal, and mangrove ecosystems provide numerous ecosystem services that support environmental sustainability and human well-being. Ecosystem services refer to the benefits that humans obtain from natural ecosystems, including provisioning, regulating, cultural, and supporting services [5]. These ecosystems contribute significantly to food production, climate regulation, shoreline protection, and biodiversity conservation.

5.1 Coastal Protection

Mangrove forests play a crucial role in protecting coastal areas from natural disasters such as storms, cyclones, and tsunamis. Their dense root systems reduce wave energy and trap sediments, thereby stabilizing shorelines and preventing erosion [26]. Research has shown that coastal regions with extensive mangrove forests experience significantly lower damage during storm events compared to areas where mangroves have been removed. By acting as natural barriers, mangrove ecosystems help protect coastal infrastructure, agricultural land, and human settlements.

5.2 Fisheries and Livelihood Support

Marine and coastal ecosystems provide essential resources for global fisheries and support the livelihoods of millions of people worldwide. Many commercially important fish and shellfish species depend on coastal habitats such as mangroves, sea-grass beds, and coral reefs during different stages of their life cycle [27]. These ecosystems provide spawning grounds, nursery habitats, and feeding areas for marine organisms. As a result, healthy coastal ecosystems are closely linked to sustainable fisheries and food security.

5.3 Carbon Sequestration

Mangrove forests are among the most effective natural carbon sinks on the planet. They store significant amounts of carbon in both plant biomass and soil sediments, a process commonly referred to as “blue carbon” sequestration [28]. The accumulation of organic matter in mangrove sediments allows these ecosystems to store carbon for long periods, thereby reducing atmospheric carbon dioxide levels and helping mitigate climate change.

5.4 Water Quality Regulation

Coastal wetlands and mangrove forests play an important role in improving water quality by filtering pollutants and trapping sediments. Mangrove root systems capture suspended particles and absorb excess nutrients from agricultural runoff and wastewater [29]. This natural filtration process helps maintain healthy marine ecosystems and prevents the spread of pollutants into coastal waters.

6. Threats to Marine and Mangrove Biodiversity

Marine and coastal ecosystems are increasingly threatened by human activities and environmental changes. These threats have resulted in significant biodiversity loss and degradation of coastal habitats worldwide.

6.1 Climate Change

Climate change is one of the most serious threats to marine biodiversity. Rising ocean temperatures can disrupt marine ecosystems by affecting species distribution, reproduction, and survival [30]. Ocean acidification caused by increased carbon dioxide levels reduces the availability of calcium carbonate needed for coral reef formation. This process weakens coral structures and threatens reef ecosystems. Sea-level rise also poses a significant threat to coastal habitats such as mangroves and salt marshes. Changes in tidal patterns and sediment deposition can alter the structure and functioning of these ecosystems.

6.2 Habitat Destruction

Coastal development and aquaculture expansion have led to the widespread destruction of mangrove forests and other coastal habitats. In many regions, mangroves have been cleared for shrimp farms, agriculture, and urban development [21]. Habitat destruction reduces biodiversity, disrupts ecological processes, and increases the vulnerability of coastal communities to natural disasters.

6.3 Pollution

Marine pollution is another major threat to coastal ecosystems. Plastic waste, oil spills, industrial chemicals, and agricultural runoff can harm marine organisms and degrade habitats [11].

Excess nutrients entering coastal waters can lead to eutrophication, which causes harmful algal blooms and oxygen depletion. These conditions can result in large-scale fish mortality and loss of biodiversity.

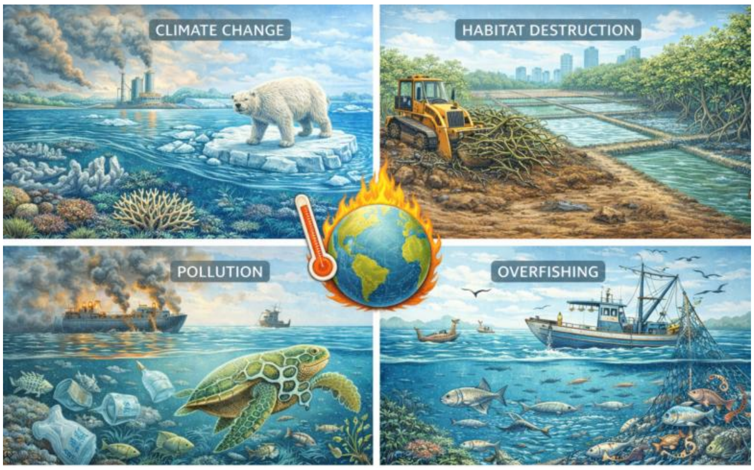

Figure 4: Major threats affecting marine and coastal biodiversity

6.4 Overfishing

Overfishing occurs when fish are harvested at rates that exceed their natural reproductive capacity. Unsustainable fishing practices can lead to the decline of fish populations and disrupt marine food webs [6].

Destructive fishing methods such as bottom trawling and dynamite fishing can also damage coral reefs and other sensitive habitats.

7. Conservation and Management Strategies

Effective conservation strategies are essential for protecting marine and coastal biodiversity and ensuring sustainable use of marine resources.

7.1 Marine Protected Areas

Marine Protected Areas (MPAs) are designated regions of the ocean where human activities are regulated or restricted to protect biodiversity and ecosystem functions [12]. MPAs help conserve critical habitats such as coral reefs, sea-grass beds, and mangrove forests. Research has shown that well-managed MPAs can increase fish populations, restore biodiversity, and improve ecosystem resilience.

7.2 Mangrove Restoration Programs

Mangrove restoration initiatives aim to restore degraded coastal ecosystems through reforestation and habitat rehabilitation. These programs often involve planting mangrove seedlings in degraded areas and implementing sustainable management practices [25]. Community participation plays an important role in the success of mangrove restoration projects. Local communities can contribute to conservation efforts through sustainable resource use and environmental stewardship.

7.3 Integrated Coastal Zone Management

Integrated Coastal Zone Management (ICZM) is a comprehensive approach that combines environmental protection, economic development, and social considerations in coastal planning [14]. ICZM promotes collaboration among government agencies, scientists, and local communities to ensure sustainable use of coastal resources.

7.4 Technological Monitoring

Modern scientific technologies are increasingly used to monitor marine ecosystems and track biodiversity changes. Remote sensing, satellite imagery, and geographic information systems (GIS) allow researchers to analyze changes in coastal habitats and detect environmental threats [18]. Environmental DNA (eDNA) analysis and molecular techniques are also being used to study marine biodiversity and identify species in aquatic environments.

Conclusion

Marine, coastal, and mangrove ecosystems represent vital components of the Earth’s biosphere and play an essential role in sustaining global biodiversity. These ecosystems provide critical ecosystem services including coastal protection, carbon sequestration, fisheries productivity, and water purification. However, increasing anthropogenic pressures and climate change threaten their sustainability. Effective conservation strategies such as marine protected areas, mangrove restoration programs, and integrated coastal management are essential for preserving these ecosystems. Continued research and global cooperation are necessary to ensure the long-term protection of marine biodiversity and the ecological services it provides.

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MARINE SPECIES CLASSIFICATION AND IDENTIFICATION: INTEGRATING INFOGAN AND YOLOv8

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Abstract

In today's Environment, Accurate monitoring and identification of marine species biodiversity are essential for the sustainable management of ocean resources. This study proposes an AI framework that combines underwater image enhancement and marine species classification with object detection using an InfoGAN- based model aiming to overcome the difficulties due to poor visibility and noisy underwater environments. The combination of CLAHE and InfoGAN, followed by Object detection using YOLOv8, enhance the clarity of underwater images and improves the accurate identification of marine species. This method provides, better image enhancement and consistent detection across all the tested species. Additionally, we used InfoGAN that extracts the features to train a deep learning classifier, which produced a high classification accuracy 98.69% for five marine species. These result show that InfoGAN can effectively highlights the significant aspects of marine species, which makes it valuable for both image enhancement and object detection performance.

Keywords: Marine Species Identification, Underwater Image Enhancement, InfoGAN, YOLOv8, Object Detection, Feature Extraction.

1. Introduction

Effective management of marine ecosystems requires robust methods for tracking and identifying marine species. Visual recognition in the underwater environment is hampered by a number of factors, including low contrast, turbidity, poor lighting, and noise from suspended particles. These factors complicate the use of traditional image processing techniques for the precise identification and classification of marine species. New approaches to solving these problems have been made possible by recent developments in deep learning and artificial intelligence. One of these that has demonstrated promise in learning spatial features for image classification tasks in Convolutional Neural networks. However, they often lose their usefulness when utilized with low-quality underwater images. To overcome this limitation, Generative Adversarial Networks (GANs) have emerged as highly successful image enhancement methods, classification accuracy and object detection capable of restoring clarity and detail in damaged underwater images.

This research focusses an integrated AI system for enhancing and classifying underwater creatures. GAN based models are used in the enhancement phase and object detection to correct image noise, color distortions, and visibility issues and to detect the underwater images. The enhanced images are then sent into a GAN-based classifier to accurately identify marine life. The dataset used includes images captured by Remotely Operated Vehicles (ROV) under various underwater conditions to guarantee real-world relevancy. The results of this study advance the monitoring of marine biodiversity and support data-driven decision-making for conservation and policy development.

Because of color distortion, light scattering, and turbidity, traditional image processing techniques frequently perform poorly in underwater conditions. White balancing and visibility are enhanced by histogram equalization (CLAHE), although these techniques frequently lack robustness and generalizability. In tasks involving object recognition and categorization, GAN is frequently utilized. It learns disentangled and interpretable representations by optimizing the mutual information between a subset of latent variables and the generated data. In order to solve problems like low contrast and haziness caused on by absorption and scattering, Garg et al. [1] suggested an underwater image enhancement system that combines CLAHE with percentile – based algorithms. An improved YOLOv8 model, YOLOv8-CPG was presented by Zhang et al. [2] for reliable underwater object identification. The proposed research develops a hybrid deep learning architecture that integrates generative representation learning and real-time object detection for complete marine species analysis. While classic GAN-based enhancement algorithms are mostly used for visual restoration, its potential for structured feature learning and classification in underwater ecological applications is underexplored. In this context, InfoGAN provide an effective mechanism for learning disentangled and interpretable latent representations, allowing for better species – level classification even in visually degraded situations. The proposed framework is divided into three primary stage: underwater image enhancement using GAN, species classification using InfoGAN, and object identification using YOLOv8. Integrating generative and discriminative learning paradigms, the framework ensures increased visual quality as well as appropriate biological interpretation.

2. Literature Survey

Spurr et al. [3] suggests a semi- supervised InfoGAN modification that enhances representation learning and image synthesizes by using as little as labelled input. The model aligns latent variables with label categories by introducing both continuous and categorical latent codes, allowing for more controlled and semantically meaningful production. In terms of training convergence and sample quality, it performs better that completely unsupervised InfoGAN. Additionally, the strategy offers a mutual information-based rationale for performance gains and maintains disentanglement for unlabeled data. YOLOv8, marks a substantial advancement in both architecture and functionality. Yolov8 features a fully decoupled head, anchor – free detection, and a simplified training pipeline. These improvements makes Yolov8 easier to utilize in real – world scenarios and more resistant to changes in object scale. Lin et al [7] proposed INFOGAN-CR, a self-supervised approach for improving disentanglement in GAN by contrastive regularization. This research also proposed ModelCentrality, an unsupervised model selection technique that identifies optimal models without the need for annotated latent codes. This method improves disentanglement performance while minimizing reliance on trained data. Gong et al. [8] introduces an unsupervised Specific Emitter Identification (SEI) framework using InfoGAN and Radio – Frequency Fingerprint Embedding (RFFE). The method improves discriminability by embedding bi-spectral gray histogram features in a structured latent space. Experimental result reveal that the proposed method surpasses existing unsupervised SEI techniques in terms of evaluation metrics and classification accuracy. Qin et al. [9] came up with a GAN-based method for synthesizing images to classify skin lesions. This indicated that GANs might be useful in biomedical settings. Meng et al. [10] showed that GAN models may be used for both picture classification and creation, which supports the model's ability to extract and synthesize features. Sirichotedumrong et al. [11] came up with a GAN-based picture modification approach that works with privacy-preserving neural networks by hiding sensitive information in the input data.

Guo et al. [12] employed a semi-supervised GAN to classify scenes in remote sensing images, which worked better with a little amount of labelled data. Yang et al. [13] used InfoGAN-enhanced models to recognize underwater sound targets, which showed that InfoGAN works well in difficult underwater sensing tasks. Han et al. came up with a spiral GAN framework that makes underwater photographs clearer and less noisy. In order to restore the brightness, contrast and details lost as a result of environmental degradation, Sasilatha et al. [14] suggested a GAN based technique to enhance underwater image clarity. Liu et al. [15] integrated GANs with similarity measuring methods to make realistic underwater images.

To improve underwater images, Deperlioglu et al. [16] used HSV color space changes and histogram equalization, which are easier methods. In the same way, Singh et al. [17] used an adaptive histogram equalization fusion method to make foggy underwater images seem better. However, these conventional methods are typically restricted since they can't adjust to changing underwater conditions. Swathi et al. [18] highlight in their in – depth examination of these advancements how Yolo v8 performs better on benchmark datasets that its predecessors. Their research indicates that Yolo v8 is suitable for latency – sensitive applications since it maintains real – time inference capabilities while simultaneously improving mean Average Precision (mAP). The algorithm's ability to adapt to too many fields, including robotic vision, traffic surveillance, scene interpretation, and marine biodiversity monitoring, demonstrates its versatility. Hussain [19] provides a comparative understanding of the inner workings of each iteration by meticulously charting the architectural development from Yolov1 to Yolo v8 in a comprehensive examination. They also discussed about structural approach by examining the layers, feature extraction techniques, and prediction heads present in each version. This analysis offers insight into how every design decision progressively enhanced detection accuracy, computation efficiency, and scalability.

3. Methodology

3.1 Data Collection

Remotely Operated Vehicle (ROV) are used to collect the underwater images in Lakshadweep Islands, an area of the Arabian Sea rich in biodiversity. Acanthaster planci, Chelonia mydas, Phyllidia varicosa, Pearsonothuria graeffei, and Pseudobiceros hancockanus are the five ecologically significant species represented in the gathered imagery. These images exhibit a range of underwater situations, such as varying depths, substrates, and illumination levels. In order to produce a solid dataset appropriate for deep learning-based image enhancement, classification, and detection tasks, such diversity is essential.

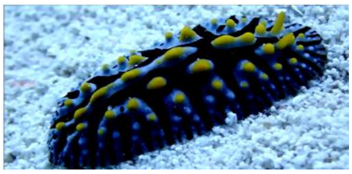
Figure 1: Sample Input Images

3.2 Underwater Image enhancement

After being retrieved in their original digital format, all of the images were filtered to remove any samples that were unclear or in poor quality. Only sharp, well – focused with recognizable images were retained for further processing. The dataset used in this study is created by classifying and grouping each image into folders according to species. Low visibility, diminished contrast, and severe color distortion are natural effects of underwater photography because of the light's scattering and absorption in the water. The performance of computer vision models is suffered by these problems because they obscure crucial visual characteristics including edges, textures, and object borders. A histogram-based contrast enhancement method is used in the pre-processing phase to overcome these difficulties. In particular, Contrast- limited Adaptive Histogram Equalization (CLAHE) is used to improve the images brightness without sacrificing their chromatic integrity. The LAB color space, which successfully isolates brightness from color information, is used for the improvement process. To enable precise modification of the L (lightness) channel without compromising color balance, each image was first translated from the RGB color system to LAB. The lightness channel is then treated with CLAHE to improve local contrast, especially in areas with low lighting or delicate structural elements. CLAHE enhances the visibility of fine details while preventing the over - amplification in similar areas. The image is enhanced and then returned to the RGB color space for additional processing.

The clarity of the images object boundaries, contours, and texture patterns – features essential for efficient feature extraction in classification and detection models – is much increased by this improvement process. The final images enhanced contrast and divisibility, making them a more dependable input for deep learning algorithms that work in underwater conditions.

Table 1: Underwater species before and after enhancement

Species Name	Before Enhancement	After Enhancement
Pseudobiceros hancockanus		
Acanthaster planci		
Phyllidia varicosa		
Chelonia mydas		
Pearsonothuria graeffei		

3.3 Proposed Model Architecture

The system's workflow is illustrated in Figure 2, which presents a block diagram of the complete process. The technique makes use of a two stage hybrid AI architecture that blends GAN based image augmentation with InfoGAN based species classification. This method is designed to address issues like noise, color less and poor contrast that are often present in underwater environments are hinder the effectiveness of standard image classification techniques. The first step is to collect data and get it ready for processing. Underwater images are obtained from ROV based datasets and publically available sources. They display a range of marine organism in various underwater settings. All of the images were normalized and reduced in size to 224 X 224 pixels in order to maintain consistency.

The generator in the GAN learns how to make outputs seem better from underwater images that have been damaged. The discriminator then tries to tell these outputs apart from high-quality reference images. This adversarial training helps the generator fix blurry images, bring back natural colors, and sharpen the edges of objects. This makes the images seem better, which is important for proper categorization. The component of InfoGAN serves as the convolutional neural network (CNN) used in the classification, image enhancement and object detection stage. InfoGAN is a generative adversarial network which leverages architectural influence to create modular and lightweight supervised classifier. A classification and object detection is incorporated into the dense layer to produce better enhancement, classification and object detection for each of the marine species.

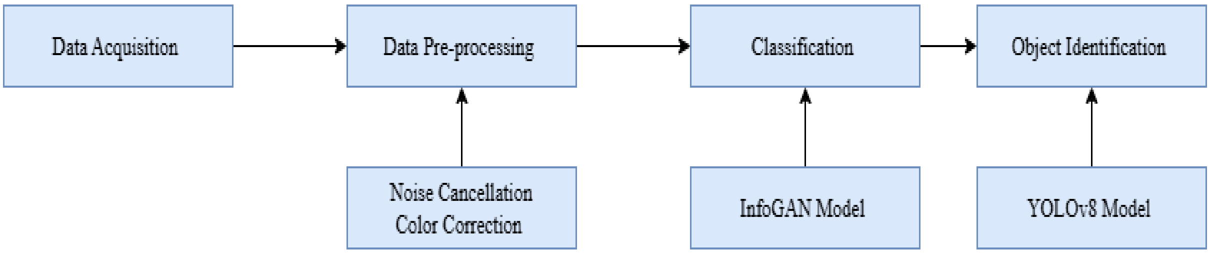


Figure 2: Block diagram for proposed system

3.4 Object Detection Using YOLOV8

After image enhancement, the YOLO v8 architecture is used to detect objects in the enhanced underwater images. With its simplified architecture, improved performance on small and complicated objects, and anchor-free detection method, YOLOv8 is ideally suited for demanding underwater situations. In order to precisely identify and locate marine species inside each frame, the YOLO v8 model received the enhanced images, which is now exhibit better contrast and visual clarity. Each species bounding box annotations were made by hand for this work. The YOLOv8 standard is followed in formatting these annotations, labelling each species with its class and normalized coordinates. After that the dataset is divided into training and testing subfolders.The model is trained using these annotated images, to learn visual and spatial characteristics of marine species. The system demonstrated improved precision when identifying marine species across a variety of underwater situations by utilizing the enhanced image quality and YOLOv8 advanced object detection capabilities. The dataset contains more than 1000 annotated images for training and over 100 images for validation.

4. Results and Discussion

4.1 Training Procedure

The dataset is used for training. The network receives input images in mini-batches after they have been normalized to the [0, 1] range. The training process to minimize overfitting, and performance is evaluated using a validation set at the end of each epoch. The model is saved at the training and utilized for interpretability analysis and downstream inference. Training session is conducted in a GPU- enabled environment such as google colab or a local setup which enables real time tracking of accuracy, image enhancement and object detection.

4.2 Evaluation Protocol

The validation set predictions are made for the classification metrics like precision, recall, F1 – score and confusion matrix are calculated in order to assess the classification model. These metrics provide better understanding of the model's ability to differentiate marine species which share visual characteristics. Visual quality metrics are applied both before and after enhancement. Changes in contrast, sharpness and noise levels are measured using the Structural Similarity Index (SSIM) and the Peak Signal-to-Noise Ratio (PSNR).

4.3 Classification Performance

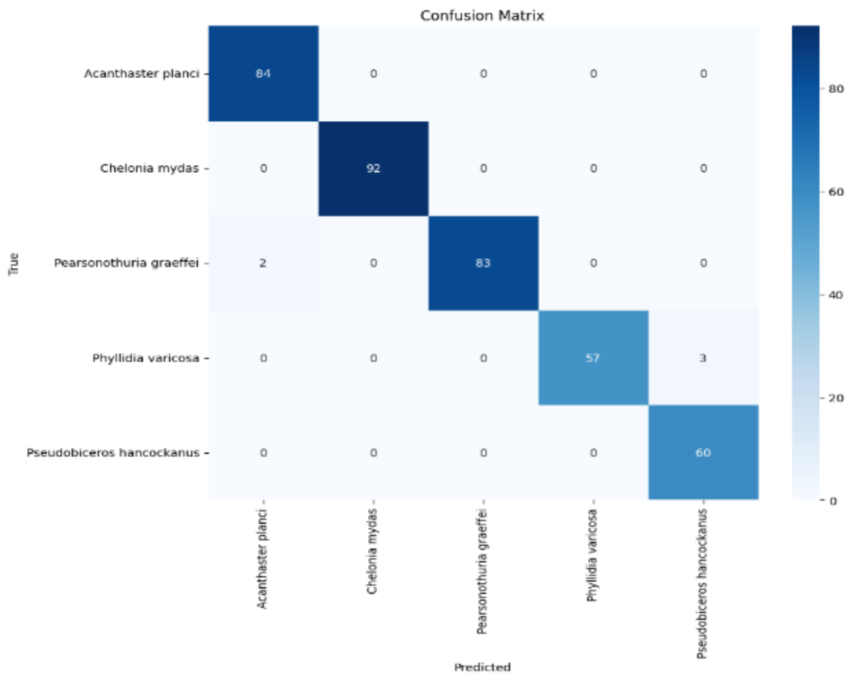


Figure 3: Confusion matrix

In the above figure five species, the classification model's overall validation accuracy was 98.69%. This high accuracy shows the enhancement classification pipeline handles low-contrast, noisy underwater images. This model is incorporated in the training and validation process over 20 epochs. Each class precision, recall and F1-score value provide consistent performance, overall species scoring higher than 90%. These outcomes results how well the model can differentiate between different marine organisms.

Table 2: Accuracy Result

Species	Precision	Recall	F1-Score
Acanthaster planci	0.98	1.00	0.99
Chelonia mydas	1.00	1.00	1.00
Pearsonothuria graeffei	1.00	0.98	0.99
Phyllidia varicosa	1.00	0.95	0.97
Pseudobiceros hancokanus	0.95	1.00	0.98
Accuracy	-	-	0.99

4.4 YOLOv8 Object Detection

YOLOv8 based object detection model performed well in identifying and classifying marine species. The visual quality is greatly enhanced by integrating CLAHE image enhancement, which also improved the model's capacity to extract and learn discriminative features. Each species bounding box annotations were created manually.

Figure 4: *Acanthaster Planci* predicted with 89% accuracy

Figure 5: *Chelonia mydas* predicted with average of 90% accuracy

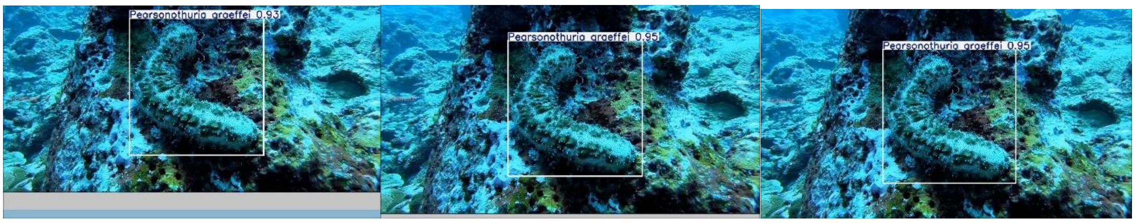


Figure 6: *Pearsonothuria graeffei* predicted with average of 95% accuracy

Figure 7: *Phyllidia varicosa* predicted with average of 86% accuracy

Figure 8: *Pseudobiceros hancockanus* predicted with average of 87% accuracy

Table 3: Performance Evolution of YOLOv8 Object detection model on marine dataset

S. No	Metric	Value
1	Precision	0.9936
2	Recall	0.9822
3	mAP@0.5	0.9890

The YOLOv8 model demonstrated strong performance on the enhanced marine dataset. The model effectively detected objects with few false positives, according to the precision score of 0.09936. The model's ability to identify almost all pertinent cases while reducing false negatives is confirmed by its recall value of 0.9822 with an IoU threshold of 0.5, the mAP@0.5 score of 0.9890 indicated high overall detection accuracy.

Conclusion

This study presents AI-driven framework like InfoGAN and YOLO to address the difficulties in underwater image analysis and marine species identification. The model provides the advantages of YOLOv8 for real-time object detection and InfoGAN for feature learning by integrating underwater image enhancement, marine species classification and object detection. By improving contrast and decreasing distortion on underwater scattering and absorption, contrast Limited Adaptive Histogram Equalization (CLAHE) enhances image quality during the pre-processing stage. The system extracts significant features from underwater image using InfoGAN. With the classification accuracy of 98.69% across five marine species, these features produce a neural classifier that produce accurate classifications of marine organisms. By using YOLOv8, object detection architecture guarantee accurate species localization within underwater frames, provides automated identification under difficult visual environmental conditions. The InfoGAN used as effective tools for feature extraction and object detection.

Future Scope

Adding a larger varied dataset of marine species and ecological regions this will increase the model's generalizability and studies of marine biodiversity around the world. This can improve classification accuracy, object detection and offer a deeper understanding of underwater environments. The InfoGAN model will enable marine biologists to understand the AI process to increase the classification accuracy and object detection of underwater environments. To support marine conservation and maritime security, this framework also helps to identify anomalies like marine species and corals. The integration of InfoGAN model can provide a better understanding of underwater environments and enhance classification accuracy and object detection. In future this research can also implement in learning to enable identification of rare or endangered species with labelled data to support marine biodiversity environments.

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THE HUMAN MICROBIOME, THEIR ASSOCIATED DISEASES, AND RECENT ADVANCEMENTS

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Introduction

The human microbiota is referred to as the set of genomes inhabiting the particular site of human body, and they interact in different ways such as commensalism, mutualism, or pathogenic interactions. They are considered a "second genome" that colonizes various anatomical sites like the skin, the mucosa, gastrointestinal tract, respiratory tract, urogenital tract, and mammary glands. The human body is an ecosystem where trillions of microorganisms coexist with each other. The diverse microbiome contributes to the regulation of host physiology particularly by affecting metabolism (Ogunrinola *et al.,* 2020). The host health condition is primarily dependent upon the beneficial interaction with the microbiota. The different factors such as age, nutrition, lifestyle and several diseases act as the primary determinants of human microbiome. The microbial composition varies according to the anatomical parts and different individuals. Any changes in this human microbiome (dysbiosis) will lead to life-threatening diseases.

This chapter reviews recent advances in understanding human microbiome, its interactions with various organ systems, and its involvement in disease diagnosis, and also emerging therapeutic applications, also addressing future advancements in this field.

Optimum Growth Factors for Human Microbiome and Their Functional Roles

Microorganisms comprise a diverse community which can be found in both external and internal parts of human body. They enter through respiratory tract (mouth and nose), gastrointestinal tract (oral cavity), urogenital tract, and areas where skin surface is disrupted. The distribution of microorganisms is influenced by the different environmental factors such as temperature, pH, oxygen concentration, pressure, and nutrient source. For ex: most human-associated microbes are mesophiles, growing optimally at around 37ºC (body temperature). These factors altogether create a favorable condition for the optimum growth and adhesion of microorganisms. Host – related factors such as, lifestyle, diet, age, genetic composition also plays a significant role in the proper growth of microorganisms. The human microbiome is highly dynamic and varies throughout the lifespan from childhood to old age. These imbalances in the growth factors will totally alter the microbial composition and gradually leads to diseased conditions. The human microbiome is essential for the proper functioning of the human body. It plays a vital role in maintain human health by regulating and developing the immune system. Additionally, they provide nutritional support for the breakdown of indigestible fibers, and they also act as barrier against pathogens. They also regulate energy metabolism, and the biotransformation of drugs.

Functional Roles of Human microbiota

a. Human microbiota in digestive system and their associated diseases

Human microbiota is very crucial for the process of digestion. They metabolize non-digestible complex substrates and produce beneficial fatty acids, enhancing gut health and the immune system (Yang *et al.,* 2013). The bacterial-to-host cell ratio in the gut is nearly 1:1. They synthesize essential vitamins and maintain host homeostasis. The microbiota helps in digestion by inhabiting the oral cavity, stomach, and intestines. The microbiota in the oral cavity acts as a crucial barrier for oral and systemic health, regulates pH, and also helps in the conversion of inorganic nitrate into nitrite (Wu *et al.,* 2014).

The stomach microbiota prevents colonization of enteric bacteria by producing antimicrobial compounds. It modifies bile acids, regulates the immune system, and maintains intestinal integrity. Alterations in the gastric microbiome can lead to diseases like gastric cancer (Oren & Garrity, 2021). The intestinal microbiome metabolizes fatty acids, produces essential vitamins, and modulates the immune system by regulating inflammation. Most commensal bacteria reside in the colon (Liu *et al.,* 2019). Disruption of the digestive microbiome can lead to several chronic diseases such as dental caries, osteoporosis, and cancer (Table 1). The widely studied gut microbiome-associated diseases include *Clostridioides* difficile infection (CDI), irritable bowel syndrome (IBS), colorectal cancer (CRC), and inflammatory bowel disease (IBD).

b. Human microbiota in Respiratory system and associated diseases

The human respiratory microbial community regulates homeostasis and acts as a barrier against infections. It also maintains gut–lung interconnections through the immune system. Both the upper (nasal cavity/pharynx) and lower (lungs) respiratory microbiota collectively regulate the functioning of the respiratory system (Yan *et al.,* 2013). The microbial biomass differs between the upper and lower respiratory tract, with the former having higher biomass and the latter lower biomass, often comprising oral commensals (Kraft, 2000). Bacterial diversity is highly influenced by the keratinized squamous epithelium and sebaceous glands in the nasal cavity (Table 1). The most studied disease in the nasal cavity is chronic rhinosinusitis (CRS).

Bacterial diversity is high in the pharynx and is dominated by *Streptococcus, Haemophilus*, and *Neisseria species*. In contrast, the larynx and trachea act as transition zones with relatively lower bacterial diversity (Sethi *et al.,* 2002). Diseases associated with the pharynx and trachea include asthma and chronic obstructive pulmonary disease. The lung microbiota plays a major role in the development of a mature lung immune system. A healthy lung contains a diverse bacterial community (Table 1).

Table 1: Predominant microbiome present on different body sites and their associated diseases

Mouth	Bacterial phyla: Actinobacteria, Bacteroidetes, Firmicutes, Fusobacteria, Proteobacteria, and Spirochaetes Fungal genera: *Candida, Cladosporium, Saccharomycetales, Fusarium, Aspergillus,* and *Cryptococcus*	Dental caries (*Streptococcus mutans, Streptococcus sobrinus,* and *Lactobacillus acidophilus*) Periodontitis (*Streptococcus salivarius* may reduce disease development)
Stomach	Bacterial phyla: Proteobacteria, Firmicutes, Actinobacteria, Bacteroidetes, and Fusobacteria	Gastric cancer (*Helicobacter pylori*)
Intestines	Bacterial phyla: Firmicutes and Bacteroidetes Archaeal species: *Methanosphaera stadtmanae* and *Methanobrevibacter smithii*	Inflammatory bowel disease (lower abundance of Firmicutes) Irritable bowel syndrome, celiac disease, and colorectal cancer (reduction in *Lactobacillus* species)
Nose	Bacterial phyla: Actinobacteria, Firmicutes, and Proteobacteria	Chronic rhinosinusitis (*Staphylococcus aureus*)
Airway and Lungs	Bacterial phyla: Firmicutes, Proteobacteria, and Bacteroidetes Fungal species: *Candida albicans, Ceriporia lacerata, Saccharomyces cerevisiae,* and *Penicillium brevicompactum* Viruses: Herpesviridae	Asthma (lower abundance of Proteobacteria) Chronic obstructive pulmonary disease (*Streptococcus pneumoniae, Haemophilus influenzae,* and *Moraxella catarrhalis*)
Skin	Bacterial phyla: Actinobacteria, Firmicutes, Bacteroidetes, and Proteobacteria	Atopic dermatitis (*Staphylococcus aureus*)
Bladder	Bacterial phylum: Firmicutes	Urgency urinary incontinence (*Lactobacillus gasseri*)
Vagina	Bacterial phylum: Firmicutes (*Lactobacillus*)	Urinary tract infection (*Gardnerella vaginalis*) Bacterial vaginosis and sexually transmitted infections (not dominated by *Lactobacillus*)

(Aggarwal *et al.,* 2023)

c. Human microbiota in Skin and associated diseases.

The skin is the largest and most exposed organ of the human body, and it hosts a microbiota that stays relatively stable despite constant contact with the environment. The skin microbiota helps protect the body from harmful pathogens and supports the immune system (Byrd *et al.,* 2018). It includes many types of commensal microbes, which can vary between people and different areas of the skin (leyden *et al.,* 1974). The composition of these microbes also changes depending on a person's health, with healthy individuals having a balanced microbiota (Jahns *et al.,* 2012). One of the most studied skin conditions related to microbiota is atopic dermatitis (AD), also called eczema (Adam *et al.,* 2020).

d. Human microbiota in urinary and reproductive system, and their associated diseases

The human urinary microbiome consists of diverse bacteria that help prevent colonization by harmful pathogens and support the immune system. The urinary microbiome does not work in isolation but is connected to the reproductive microbiome (Pearce *et al.,* 2013). Its composition and diversity differ between males and females, mainly depending on the anatomy and physiology of each body site. In contrast, the human vaginal microbiome is largely dominated by a single genus, Lactobacillus. Even small changes in the vaginal microbiome can lead to various health problems (Ruiz-Gomez et al.,2019).

Recent Advancements in Microbiome Research

Recent technological innovations such as metagenomics, metatranscriptomics, metabolomics, and proteomics have transformed the field of microbiome research by allowing an in-depth examination of microbial communities and their interactions with the host. Probiotics consist of beneficial live microorganisms that support health, whereas prebiotics serve as nutrients that encourage the growth of these helpful microbes. Both are increasingly applied to rebalance the microbiota and enhance health outcomes.

Fecal microbiota transplantation (FMT) involves transferring stool from healthy individuals to patients in order to reestablish microbial diversity. This therapy has proven highly effective for recurrent infections and is being investigated for its potential in other medical conditions. The advancement of microbiome analysis techniques has paved the way for personalized treatment plans tailored to an individual's unique microbial profile, advancing the goal of precision medicine.

Moreover, the application of machine learning and artificial intelligence to microbiome data is growing rapidly, facilitating the discovery of complex patterns, prediction of disease susceptibility, and design of targeted interventions. These computational methods are crucial for managing the vast and intricate datasets characteristic of microbiome studies.

Conclusion

Numerous physiological systems are influenced by the human microbiome, which is a key factor in determining health and illness. Our knowledge of this intricate ecosystem has been increased thanks to developments in sequencing technologies, computational tools, and treatment approaches.

Although there are still obstacles to overcome, combining microbiome research with artificial intelligence and precision medicine has enormous promise to transform healthcare. To fully realize the potential of the human microbiome to improve human health, interdisciplinary research must continue.

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NANOTECHNOLOGY FOR REMOVAL OF HEAVY METALS FROM CONTAMINATED SOILS: MECHANISMS, NANOMATERIALS AND ENVIRONMENTAL APPLICATIONS

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Abstract

Heavy metal contamination in soil is a major environmental concern caused by industrialization, mining activities, agricultural chemicals and improper waste disposal. Toxic metals such as cadmium (Cd), lead (Pb), arsenic (As), mercury (Hg), chromium (Cr) and nickel (Ni) accumulate in soils and persist for long periods due to their non-biodegradable nature. These contaminants threaten ecosystem stability, soil fertility, crop productivity and human health through bioaccumulation in the food chain. Conventional remediation technologies such as soil washing, chemical precipitation and excavation are often costly, inefficient and may generate secondary pollutants. In recent years, nanotechnology has emerged as a promising approach for heavy metal remediation. Nanomaterials possess unique physicochemical properties such as high surface-to-volume ratio, strong adsorption capacity and enhanced catalytic activity, which significantly improve the removal and stabilization of heavy metals in contaminated soils. This chapter provides an overview of the role of nanotechnology in soil remediation focusing on types of nanomaterials, mechanisms of heavy metal removal, nano-assisted phytoremediation and bioremediation.

Keywords: Nanotechnology, Soil remediation, Heavy metal, Nanoparticles, Nanobioremediation, Nano-phytoremediation

Introduction

Soil contamination by heavy metals has become a serious global environmental problem. Heavy metals are increasing day by day due to rapid industrialization, urbanization and agricultural intensification. Heavy metals are naturally occurring elements, but human activities have significantly increased their concentrations in soil ecosystems. Unlike organic pollutants, heavy metals are not biodegradable and therefore persist in the environment for long periods. Their accumulation can lead to soil degradation, reduced crop productivity and potential health risks through food chain contamination (Wan *et al.,* 2024). The problem has to be addressed with proper study, experimentation and practical implications. Heavy metals such as Cd, Pb, Hg, As, Cr and Ni are commonly detected in contaminated soils worldwide (Angon *et al.,* 2024).

Exposure to these metals can cause severe toxicological effects. These may include neurological disorders, kidney damage and carcinogenic outcomes in humans. The mobility and bioavailability of heavy metals in soil depend on various factors such as soil pH, organic matter content, redox potential and microbial activity.

Though traditional soil remediation techniques are there but they all have some limitations. In recent years, nanotechnology has emerged as an innovative strategy for environmental remediation. Nanomaterials exhibit unique physicochemical properties including large specific surface area, high adsorption capacity and enhanced reactivity. These characteristics enable nanoparticles to interact efficiently with heavy metal ions in soil through adsorption, reduction and immobilization processes (Latif *et al.,* 2025). Nanotechnology-based remediation techniques have therefore attracted significant attention as effective, sustainable and cost-efficient solutions for heavy metal contaminated soils. In this chapter, emphasis has been given on the types of nanomaterials, their use for removal of heavy metals and mechanism of heavy metal removal along with environmental applications.

Sources of Heavy Metal in Soil

There are various sources of heavy metals that can contaminate soil. The sources can be categorized as manmade or anthropogenic and natural sources.

Anthropogenic Sources of Heavy Metal

Heavy metals enter the soil environment through various anthropogenic activities including, mining and smelting operations, industrial discharge and waste disposal, agricultural fertilizers and pesticides, municipal sewage sludge application, electronic waste and battery disposal, fossil fuel combustion and many other (Wan et al. 2024; Mu *et al.,* 2025).

These activities introduce significant amounts of toxic metals into soil ecosystems, often exceeding natural background levels.

Natural Sources of Heavy Metal

Natural processes such as volcanic eruptions, weathering of rocks and forest fires can also release heavy metals into the environment. However, anthropogenic sources are considered the major contributors to soil contamination in most regions (Wan et al. 2024; Mu *et al.,* 2025).

Environmental Impact of Heavy Metal Contamination in Soil

Heavy metal contamination in soil is a serious environmental problem due to its persistence, toxicity and ability to accumulate in living organisms. Metals such as Pb, Cd, Mg, As and Cr enter soils through industrial discharge, mining, excessive use of fertilizers and pesticides, sewage sludge application and improper waste disposal (Wu *et al.,* 2024).

Heavy metals adversely affect soil quality by altering soil pH, reducing microbial biomass and inhibiting enzymatic activities essential for nutrient cycling. This leads to reduced soil fertility and disruption of biogeochemical processes. Toxic metal ions can also damage soil structure by interfering with organic matter decomposition (Nie *et al.,* 2024).

Contaminated soils negatively influence plant growth and productivity. Heavy metals interfere with seed germination, root elongation, photosynthesis and nutrient uptake. Some metals generate oxidative stress in plants by producing reactive oxygen species, causing cellular damage, chlorosis and reduced crop yield. Certain metals are easily absorbed by plant roots and enter the food chain. Heavy metal contamination poses serious risks to terrestrial ecosystems. Toxic metals bioaccumulate in organisms and biomagnify along food chains, affecting herbivores, predators and soil fauna such as earthworms and insects. This reduces biodiversity and disturbs ecological balance. There are also significant groundwater contamination risks. Heavy metals can leach through soil profiles into aquifers, degrading water quality and making it unsafe for drinking and irrigation. In addition, contaminated soils present human health hazards through direct contact, inhalation of dust and consumption of contaminated crops. Long-term exposure to heavy metals can cause neurological disorders, kidney damage, skeletal deformities and various cancers (Angon *et al.,* 2024; Mohamed *et al.,* 2025).

Conventional Techniques for Removal of Heavy Metal from Soil

Several conventional remediation methods are used for heavy metal removal from soil. As depicted in Fig. 1, physical, chemical and biological methods are available for remediation of heavy metals from contaminated soil.

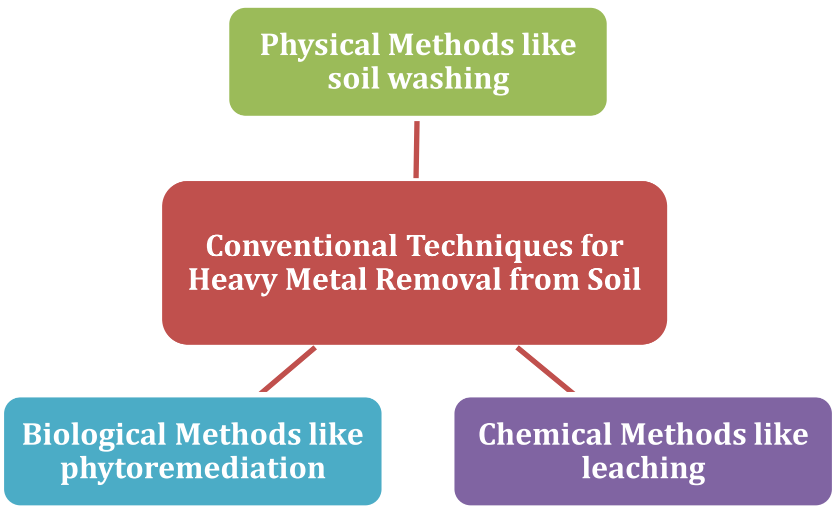

Figure 1: Conventional techniques for heavy metal removal

Physical Methods

Physical remediation techniques are widely used for the removal of heavy metals from contaminated soils. These methods primarily rely on mechanical or physicochemical processes to separate, isolate, or remove contaminated soil materials. These techniques for heavy metal removal from soil include excavation, soil washing and thermal treatment. Although they can be effective in rapidly reducing contamination levels, they are often associated with high operational costs, significant energy requirements, and potential disturbance to the soil structure and ecosystem (Dermont *et al.,* 2008, Alloway, 2013, Vidonish *et al.,* 2016).

Chemical Methods

Chemical remediation of heavy-metal-contaminated soils typically involves soil stabilization, chemical leaching and precipitation reactions to immobilize or remove toxic metals. These methods can be effective in reducing the mobility and bioavailability of metals such as Pb, Cd, Cr, Hg and As, but they also carry drawbacks, including potential secondary pollution and alteration of soil properties (Wu *et al.,* 2024).

Biological Methods

Biological approaches include phytoremediation and microbial remediation. These methods are environmentally friendly but often slow and dependent on environmental conditions.

Due to these limitations, advanced technologies such as nanotechnology are increasingly being explored to improve remediation efficiency (Abderrafaa *et al.,* 2025).

The Revolutionary Nanotechnology in Soil Remediation

With the advent of nanotechnology, soil remediation has reached new heights of success. Nanotechnology involves the design and application of materials at the nanoscale (1-100 nm). Nanoparticles possess distinct physicochemical properties that make them highly suitable for environmental remediation (Abderrafaa *et al.,* 2025). These properties include large surface area, high adsorption capacity, enhanced catalytic activity, improved mobility in soil systems, strong interaction with metal ions and many other. Because of their small size, nanoparticles can penetrate contaminated soil matrices and interact directly with pollutants. This enables efficient remediation of heavy metals from soil (Singh *et al.,* 2021; Malik *et al.,* 2024).

Types of Nanomaterials Used for Heavy Metal Removal

A range of nanomaterials are developed for removal of heavy metals from soil. Among them, Zero-Valent Iron Nanoparticles (nZVI) are widely used for environmental remediation. They act as strong reducing agents capable of converting toxic metal ions into less harmful forms. They are used to remove Cr, As, Pb, Cd and many other. These particles are particularly attractive because they can perform in-situ remediation without extensive soil excavation. Metal Oxide Nanoparticles such as titanium dioxide (TiO_2), zinc oxide (ZnO) and iron oxide (Fe_3O_4) exhibit strong adsorption and catalytic properties (Zhao *et al.,* 2023; Barania *et al.,* 2024). Magnetic iron oxide nanoparticles are especially useful because they can be easily separated from soil after remediation using magnetic fields. Carbon nanomaterials such as graphene, carbon nanotubes and biochar nanoparticles have excellent adsorption properties due to their large surface areas and porous structures. These materials can effectively adsorb heavy metal ions such as Pb, Cd and Hg (Table 1).

Table 1: Types of nanomaterial and their use for removal of the kind of heavy metals

S No.	Types of nanomaterial	Used for removal of	References
1	nZVI	Pb, Copper (Cu), Zinc (Zn), Cd, As, Cr	Zhao *et al.,* 2023;
2	Metal Oxide Nanoparticles	Cd, Cu, Ni, Pb	Sahin *et al.,* 2023
3	Carbon-Based Nanomaterials	Pb, Cd, Hg, Cu	Chandran *et al.,* 2023
4	Nano-Silica and Clay Nanoparticles	Pb, Zn, Cu, Ni and Cr	Samani *et al.,* 2024; Barania *et al.,* 2024
5	Magnetic Nanoparticles (Fe_3O_4 etc.)	As, Pb, Cr, Cd	Mahanty *et al.,* 2023; Abboud *et al.,* 2023, Sahin *et al.,* 2023
6	Bimetallic / Composite Nanomaterials	Pb, Cd, Cr	Liu *et al.,* 2022; Zhao *et al.,* 2023
7	Biobased Nanomaterials	Cr, Cu, Cd	Mazarji *et al.,* 2023; Du *et al.,* 2023
8	Polymer-based Nanomaterials	Pb, Cd, Cu	Wang *et al.,* 2022
9	Zeolite & Mesoporous Nanomaterials	Pb, Cu, Zn	Ahmad *et al.,* 2022; Yuan *et al.,* 2023

Bimetallic nanoparticles consist of two metals (e.g., Fe-Ni, Fe-Cu, Fe-Pd, Ag-Fe) that combine adsorption and redox properties to improve heavy metal removal (Zhao *et al.,* 2023). Nano-silica particles have been shown to stabilize heavy metals in soil by converting them into less bioavailable forms. Experimental studies demonstrate that nano-silica can significantly reduce the extractable concentrations of metals such as Pb, Zn, Cu, Ni and Cr in contaminated soils (Liu *et al.,* 2022). Biochar derived from agricultural or plant biomass can be combined with nanomaterials (e.g., iron oxides, carbonaceous nanomaterials) to form biochar-based nanocomposites with enhanced heavy metal removal/immobilization capabilities. Biochar and biochar-derived nanoscale materials are widely studied for heavy metal adsorption due to their high surface area, porosity and surface functional groups (Du *et al.,* 2023; Mazarji *et al.,* 2023).

Polymer-nanocomposite adsorbents combine the strengths of polymers (biocompatibility, functional groups for binding) with nanomaterials (high surface area and reactivity) to achieve efficient heavy metal adsorption via chelation, electrostatic interaction, ion exchange and surface complexation (Wang *et al.,* 2022). Zeolites are crystalline aluminosilicate materials with high cation exchange capacity (CEC), large surface area, microporous structure and tunable chemistry which make them effective adsorbents for toxic metal ions (Yuan *et al.,* 2023).

Mechanisms of Removal of Heavy Metal Using Nanotechnology

Nanoparticles remove heavy metals from soil through several mechanisms. The large surface area of nanoparticles allows efficient adsorption of metal ions onto their surfaces. This makes the removal of heavy metal from soil quite easier (Abbas *et al.,* 2016, Ali *et al.,* 2019). Certain nanoparticles, particularly zero-valent iron can chemically reduce toxic metal ions to less harmful forms. Nanoparticles play a significant role in the immobilization of heavy metals in contaminated soils thereby reducing their mobility, bioavailability and ecological toxicity. Due to their extremely small size and large surface-to-volume ratio, nanoparticles possess high surface reactivity and abundant active sites that facilitate interactions with metal ions. These properties enable nanoparticles to stabilize heavy metals within soil matrices through several physicochemical mechanisms.

One of the primary mechanisms is adsorption, where metal ions bind strongly to the surface of nanoparticles through electrostatic attraction, complexation, or surface precipitation. Nanoparticles such as iron oxides, nano-zero valent iron (nZVI), carbon nanotubes, and metal oxide nanoparticles have numerous functional groups and reactive surfaces that can effectively adsorb heavy metals such as Pb, Cd, Cr, and As. Once adsorbed, these metals become less mobile and are prevented from leaching into groundwater or being taken up by plants (Khin *et al.,* 2012; Sharma *et al.,* 2015). Another important mechanism is chemical stabilization or precipitation. Certain nanoparticles can induce redox reactions or form insoluble metal compounds, which immobilize metals in stable mineral forms. For instance, nano-zero valent iron can reduce toxic Cr^{6+} to the less toxic and less mobile Cr^{3+}, which then precipitates in the soil matrix. Similarly, iron oxide and manganese oxide nanoparticles can facilitate the formation of stable metal hydroxides or oxides that remain bound to soil particles (Qu *et al.,* 2013). Nanoparticles also enhance soil sorption capacity by modifying the soil surface and increasing the number of binding sites available for heavy metals. When nanoparticles are introduced into contaminated soil, they may interact with soil organic matter and clay minerals, forming complexes that further stabilize metal ions. This process significantly reduces the bioavailability of heavy metals to plants, microorganisms and soil fauna.

Furthermore, nanoparticles can promote the formation of stable aggregates within soil matrices, which physically trap heavy metals and prevent their transport through soil pores. This immobilization reduces metal migration to groundwater and minimizes environmental contamination. Because of these capabilities, nanoparticle-based remediation strategies are increasingly considered promising tools for in-situ stabilization and remediation of heavy-metal contaminated soils (Ali *et al.,* 2019). Overall, the application of nanoparticles offers an effective approach to reduce the environmental risks associated with heavy metals by immobilizing them in stable forms within the soil. This decreases their mobility, toxicity and bioavailability.

Nanoparticles can immobilize heavy metals within soil matrices reducing their mobility and bioavailability. Catalytic transformation is one of the most important mechanisms by which nanoparticles facilitate the remediation of heavy metals in contaminated soils and water. Due to their high surface reactivity, large surface area and unique catalytic properties, nanoparticles can accelerate chemical reactions that convert toxic heavy metal species into less toxic or less mobile forms. For example, nano-zero valent iron (nZVI) is widely used for catalytic remediation because it can donate electrons to metal ions and promote redox reactions. Through this process, highly toxic metals such as Cr^{6+} can be reduced to the less toxic and less soluble Cr^{3+}. The reduced form then precipitates as chromium hydroxides or binds strongly to soil particles thereby limiting its mobility and bioavailability. Similarly, nanoparticles of iron oxides, manganese oxides and titanium dioxide can catalyze oxidation-reduction reactions that transform hazardous metals into stable mineral forms. These catalytic processes not only reduce toxicity but also promote long term stabilization of contaminants within soil matrices. Because of their high catalytic efficiency, nanoparticles can achieve significant contaminant transformation even at relatively low concentrations. Complexation is another important mechanism through which nanoparticles help immobilize and remove heavy metals from contaminated environments. In this process, metal ions form stable coordination complexes with functional groups present on the surface of nanoparticles. Many nanoparticles, particularly carbon nanotubes, graphene oxide, polymer coated nanoparticles and metal oxide nanoparticles contain reactive functional groups such as carboxyl (-COOH), hydroxyl (-OH), amino ($-NH_2$) and sulfhydryl (-SH) groups. These groups interact strongly with metal ions such as Pb, Cd, Cu, Hg and As. When these metals bind with nanoparticle surfaces through complexation reactions, they form stable chelated structures, which significantly reduce their solubility and mobility. This mechanism helps prevent the migration of heavy metals into groundwater and reduces their uptake by plants and microorganisms. Complexation also improves the sorption capacity of soils, as nanoparticles can act as additional binding matrices that trap heavy metals. The formation of stable complexes therefore plays a vital role in long-term stabilization and remediation of contaminated soils. Nano-assisted phytoremediation is an emerging remediation strategy that integrates nanotechnology with plant-based remediation techniques to enhance the removal of contaminants from soil and water. Phytoremediation alone relies on plants to absorb, accumulate, stabilize, or detoxify pollutants. However, the efficiency of this process is often limited by slow plant growth, low metal uptake, and limited bioavailability of contaminants. Nanoparticles can significantly improve the efficiency of phytoremediation by enhancing plant growth, improving metal uptake, and increasing the availability of heavy metals for plant absorption. Certain nanoparticles such as iron oxide nanoparticles, zinc oxide nanoparticles, and nano-silica can stimulate plant metabolism and root development, which increases the plant's capacity to absorb contaminants (Sharma *et al.,* 2015). Additionally, nanoparticles can modify soil properties and increase the solubility or mobility of certain metal ions making them more accessible to plant roots. In some cases, nanoparticles also reduce metal toxicity to plants allowing them to survive and grow in highly contaminated soils. This combined approach increases the overall effectiveness of phytoremediation in removing metals such as cadmium, lead, chromium, and arsenic. Nano-assisted phytoremediation therefore represents a promising strategy for sustainable environmental remediation because it combines the eco friendly nature of plant-based remediation with the efficiency of nanotechnology. Nanotechnology-assisted microbial remediation involves the synergistic interaction between nanoparticles and microorganisms to enhance the biodegradation or detoxification of environmental contaminants. Microorganisms such as bacteria and fungi play an important role in bioremediation by transforming or immobilizing heavy metals through processes such as biosorption, bioaccumulation, and enzymatic reduction. Nanoparticles can enhance microbial remediation in several ways. First, they can increase the availability of contaminants by breaking down complex compounds or altering the chemical form of metals, making them easier for microorganisms to metabolize or transform. Second, nanoparticles can serve as electron donors or catalysts, stimulating microbial metabolic processes involved in contaminant degradation. For example, nano-zero valent iron (nZVI) has been shown to enhance microbial reduction of heavy metals and chlorinated pollutants. Additionally, certain nanoparticles provide support surfaces for microbial biofilm formation, which increases microbial activity and stability in contaminated environments (wang *et al.,* 2019). However, it is important to carefully control nanoparticle concentrations because excessive levels may inhibit microbial activity. When properly applied, nanotechnology assisted microbial remediation can significantly accelerate removal of contaminant and improve the efficiency of traditional bioremediation techniques.

Conclusion

Heavy metal contamination in soils poses significant environmental and public health risks. Conventional remediation methods often face limitations regarding efficiency, cost and environmental impact. Nanotechnology has emerged as a promising approach for soil remediation due to the unique properties of nanomaterials, including high surface area, enhanced reactivity and strong adsorption capacity. They have many advantages like high efficiency and rapid remediation, ability to treat low concentrations of contaminants, reduced operational costs and many other. Nanoparticles such as zero valent iron, metal oxides, carbon nanomaterials and nano silica have demonstrated significant potential for removing or stabilizing heavy metals in contaminated soils. Integration of nanotechnology with biological remediation strategies such as phytoremediation and microbial remediation further enhances remediation efficiency. Although challenges related to toxicity and environmental safety remain, continued research and technological advancements are expected to make nanotechnology a powerful tool for sustainable soil remediation.

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LIFESTYLE INTERVENTIONS AND PHARMACOLOGICAL APPROACHES IN POLYCYSTIC OVARY SYNDROME (PCOS)

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Abstract

Polycystic ovary syndrome (PCOS) is a common and heterogeneous endocrine–metabolic disorder affecting women of reproductive age, characterized by hyperandrogenism, ovulatory dysfunction, and polycystic ovarian morphology. The condition is strongly associated with insulin resistance, obesity, metabolic syndrome, and significant psychological burden, making its management complex and multifaceted. Lifestyle intervention remains the cornerstone of therapy, with evidence demonstrating that modest weight loss through dietary modification, regular physical activity, and behavioral support can significantly improve insulin sensitivity, menstrual regularity, and ovulatory function. However, many patients require pharmacological therapy tailored to their dominant clinical features and reproductive goals. Insulin sensitizers such as metformin and inositols target metabolic abnormalities, while ovulation induction agents like letrozole and clomiphene citrate are used for infertility management. Combined oral contraceptives and anti-androgens effectively manage menstrual irregularities and hyperandrogenic symptoms in women not seeking pregnancy. Increasingly, combination therapy integrating lifestyle and pharmacological approaches is recognized as the most effective strategy. This review highlights current evidence on lifestyle and pharmacological management of PCOS and emphasizes the importance of personalized, multidisciplinary care to optimize both reproductive and long-term metabolic outcomes.

Keywords: Polycystic Ovary Syndrome, Lifestyle Modification, Insulin Resistance, Metformin, Ovulation Induction.

1. Introduction

Polycystic ovary syndrome (PCOS) is a heterogeneous endocrine disorder affecting approximately 6–20% of women of reproductive age worldwide, depending on diagnostic criteria [2,3]. It represents a complex interplay of genetic, environmental, metabolic, and hormonal factors. The syndrome was first described by Stein and Leventhal in 1935 and continues to pose significant clinical and therapeutic challenges.

PCOS is characterized by a constellation of features including:

- Hyperandrogenism (clinical or biochemical)
- Ovulatory dysfunction
- Polycystic ovarian morphology
- Insulin resistance
- Metabolic disturbances

Beyond reproductive dysfunction, PCOS is increasingly recognized as a lifelong metabolic disorder associated with:

- Obesity
- Type 2 diabetes mellitus
- Dyslipidemia
- Cardiovascular disease
- Non-alcoholic fatty liver disease
- Psychological disorders (anxiety, depression)

Polycystic ovary syndrome (PCOS) is a common, heterogeneous endocrine and metabolic disorder affecting approximately 6–20% of women of reproductive age worldwide, with prevalence varying according to diagnostic criteria such as the Rotterdam, NIH, and AE-PCOS guidelines. First described by Stein and Leventhal in 1935, PCOS has evolved from being viewed primarily as a reproductive disorder to a complex multisystem condition with significant metabolic and psychological implications. The syndrome arises from a multifactorial interplay of genetic susceptibility, environmental influences, insulin resistance, and hormonal dysregulation.

Clinically, PCOS is characterized by a constellation of features that include hyperandrogenism (clinical or biochemical), chronic anovulation or oligo-ovulation, and polycystic ovarian morphology on ultrasonography [1,4]. Among these, hyperandrogenism and insulin resistance are considered central pathophysiological drivers. Insulin resistance, present in a substantial proportion of women with PCOS regardless of body weight, contributes to compensatory hyperinsulinemia, which in turn exacerbates ovarian androgen production and disrupts normal folliculogenesis. This hormonal imbalance manifests as menstrual irregularities, hirsutism, acne, and infertility.

Beyond reproductive dysfunction, PCOS is increasingly recognized as a lifelong metabolic disorder. Women with PCOS are at increased risk of obesity, impaired glucose tolerance, type 2 diabetes mellitus, dyslipidemia, hypertension, and cardiovascular disease. Additionally, non-alcoholic fatty liver disease and obstructive sleep apnea have been reported with higher prevalence in this population. Psychological comorbidities, including anxiety, depression, body image distress, and reduced quality of life, further contribute to the overall disease burden.

Given its heterogeneity and broad clinical spectrum, the management of PCOS requires a comprehensive and individualized approach. Lifestyle interventions—particularly dietary modification, regular physical activity, and weight management—are widely recommended as first-line therapy, especially in overweight and obese women. Pharmacological treatments are selected based on predominant symptoms and reproductive goals, targeting insulin resistance, ovulatory dysfunction, and hyperandrogenic manifestations. Therefore, an integrated, multidisciplinary strategy combining lifestyle and pharmacological measures is essential to optimize both short-term symptom control and long-term metabolic and reproductive outcomes in women with PCOS.

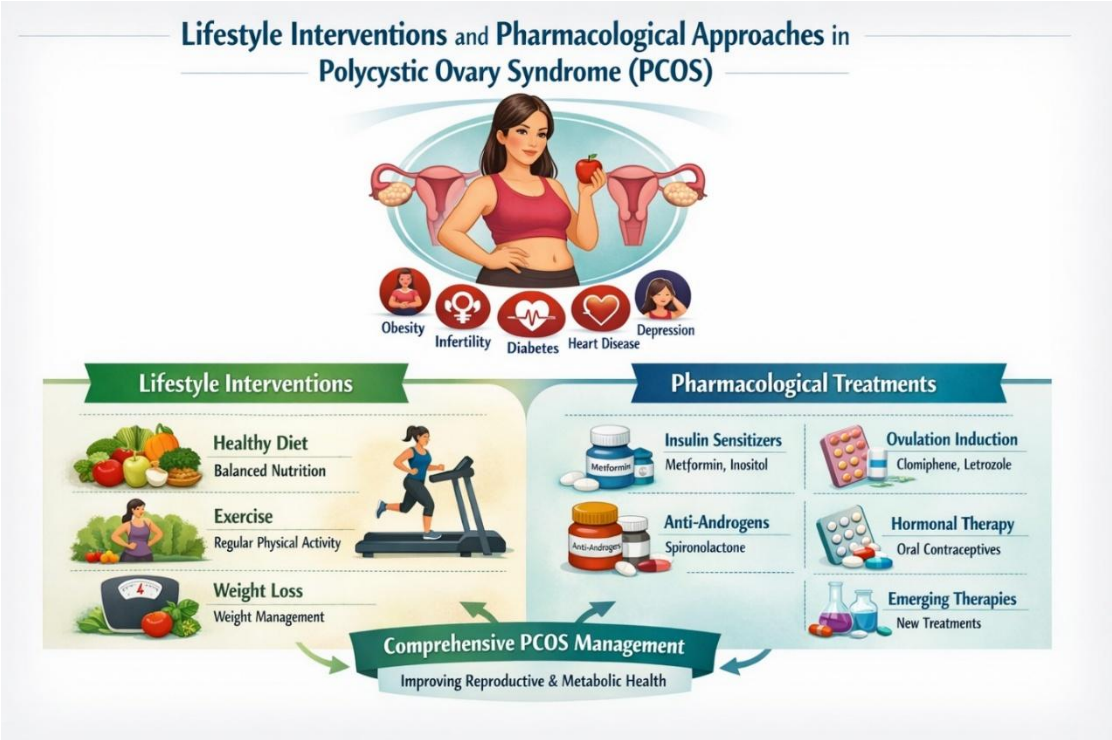


Figure 1: Lifestyle interventions and Pharmacological approaches in PCOS

2. Pathophysiology of Polycystic Ovary Syndrome (PCOS)

Polycystic ovary syndrome (PCOS) is a multifactorial endocrine–metabolic disorder characterized by hyperandrogenism, ovulatory dysfunction, and polycystic ovarian morphology. Its pathogenesis is complex and involves genetic susceptibility, environmental influences, metabolic abnormalities, and neuroendocrine dysfunction. The major driving mechanisms include insulin resistance, hyperandrogenism, hypothalamic–pituitary–ovarian (HPO) axis disturbance, and adipose tissue dysfunction. These pathways interact in a vicious cycle that perpetuates disease progression.

2.1 Insulin Resistance and Hyperinsulinemia

Insulin resistance (IR) is considered the central metabolic defect in PCOS and is present in approximately 50–80% of affected women, even in many non-obese patients. In this condition, peripheral tissues such as skeletal muscle, adipose tissue, and liver show reduced responsiveness to insulin. To compensate, pancreatic β-cells increase insulin secretion, resulting in hyperinsulinemia.

Mechanisms

i. **Post-receptor insulin signaling defects**: In PCOS, abnormalities occur downstream of the insulin receptor. Reduced phosphorylation of insulin receptor substrate (IRS) proteins impairs glucose transporter (GLUT-4) translocation, leading to decreased glucose uptake.
ii. **Increased serine phosphorylation of insulin receptor**: Excess serine phosphorylation inhibits normal tyrosine kinase activity of the insulin receptor. Interestingly, similar serine phosphorylation also enhances androgen synthesis in ovarian theca cells, creating a metabolic–reproductive link.
iii. **Adipose tissue dysfunction**: Hypertrophied adipocytes release excess free fatty acids (FFAs) and inflammatory cytokines (TNF-α, IL-6), which interfere with insulin signaling pathways.
iv. **Chronic low-grade inflammation**: Women with PCOS often exhibit elevated inflammatory markers (CRP, IL-6). Inflammation activates stress kinases (e.g., JNK), which further impair insulin signaling.

Consequences of Hyperinsulinemia

Hyperinsulinemia plays a direct pathogenic role beyond glucose metabolism:

- **Increased ovarian androgen production:** Insulin synergizes with LH to stimulate theca cells.
- **Reduced sex hormone-binding globulin (SHBG):** Hepatic SHBG synthesis is suppressed, increasing free testosterone.
- **Enhanced LH-stimulated theca cell activity:** Amplifies androgen excess.
- **Impaired follicular maturation:** High insulin disrupts granulosa cell function.

Example

A 24-year-old woman with central obesity and irregular menses often shows elevated fasting insulin levels. Despite normal glucose levels, hyperinsulinemia drives excess ovarian androgen production, leading to acne and anovulation.

2.2 Hyperandrogenism

Hyperandrogenism is the biochemical and clinical hallmark of PCOS. Elevated levels of testosterone, androstenedione, and dehydroepiandrosterone sulfate (DHEAS) contribute to the characteristic symptoms.

Sources of Androgens

a) **Ovarian theca cells (major source)**: In PCOS, theca cells exhibit intrinsic steroidogenic hyperactivity. Upregulation of enzymes such as CYP17A1 increases androgen biosynthesis.
b) **Adrenal glands**: Approximately 20–30% of women with PCOS have adrenal androgen excess, contributing to elevated DHEAS levels.

Clinical Manifestations

- **Hirsutism:** Excess terminal hair in androgen-dependent areas (chin, chest, abdomen).
- **Acne:** Due to increased sebum production.
- **Alopecia:** Androgenic hair thinning over the scalp.
- **Anovulation:** Androgens disrupt follicular growth and ovulation.

Pathophysiological Impact

Excess androgens impair normal folliculogenesis [6] by:

- Arresting follicles at the small antral stage
- Promoting follicular atresia
- Reducing aromatase activity in granulosa cells

Example:

A lean woman with PCOS may present primarily with hirsutism and acne despite normal BMI, highlighting that hyperandrogenism can occur independently of obesity.

2.3 Hypothalamic–Pituitary–Ovarian (HPO) Axis Dysfunction

Neuroendocrine abnormalities play a critical role in PCOS. Altered pulsatile secretion of gonadotropin-releasing hormone (GnRH) leads to abnormal gonadotropin patterns.

Key Hormonal Changes

- Increased GnRH pulse frequency
- Elevated luteinizing hormone (LH) secretion
- Normal or relatively low follicle-stimulating hormone (FSH)
- Increased LH:FSH ratio (often >2:1)

Mechanistic Explanation

Rapid GnRH pulsatility preferentially increases LH synthesis over FSH. Elevated LH stimulates theca cells to produce more androgens, while relatively low FSH fails to adequately stimulate granulosa cells for follicular maturation.

Clinical Consequences

- Arrested follicular development
- Chronic anovulation
- Multiple small follicles (polycystic ovarian morphology)

Example:

Ultrasound of a PCOS patient often shows ≥20 small follicles (2–9 mm) arranged peripherally ("string of pearls" appearance), reflecting follicular arrest rather than true cyst formation.

2.4 Role of Obesity and Adipose Tissue

Although PCOS can occur in lean women, obesity significantly worsens the clinical and metabolic features. Approximately 40–70% of women with PCOS are overweight or obese.

Pathophysiological Contributions [3,4]

i. **Increased insulin resistance**: Visceral adiposity releases FFAs into portal circulation, impairing hepatic insulin sensitivity.
ii. **Enhanced androgen production**: Hyperinsulinemia and adipokines stimulate ovarian steroidogenesis.
iii. **Chronic inflammation**: Adipose tissue macrophage infiltration increases inflammatory cytokines, worsening IR.
iv. **Altered adipokine secretion**

- ↓ Adiponectin (insulin-sensitizing)
- ↑ Leptin (often resistant state)
- ↑ Resistin (promotes IR)

Vicious Cycle

Obesity ↔ Insulin resistance ↔ Hyperandrogenism ↔ Anovulation

Example:

Weight gain in a PCOS patient often leads to worsening menstrual irregularity and hirsutism, while even 5–10% weight loss can restore ovulation in some women.

Table 1: Key Pathophysiological Mechanisms in PCOS [12]

Mechanism	Primary Defect	Key Mediators	Ovarian Effects	Clinical Outcomes
Insulin resistance	Impaired insulin signaling	Hyperinsulinemia, FFAs	↑ Theca androgen synthesis	Irregular menses, infertility
Hyperandrogenism	Excess androgen production	Testosterone, DHEAS	Follicular arrest	Hirsutism, acne, alopecia
HPO axis dysfunction	Rapid GnRH pulsatility	↑ LH, ↓/normal FSH	Failed follicle maturation	Anovulation, polycystic ovaries
Obesity/adipose dysfunction	Visceral fat excess	TNF-α, IL-6, leptin	Worsened IR and androgen excess	Metabolic syndrome features
Low SHBG	Hepatic suppression by insulin	Free testosterone ↑	Increased androgen bioavailability	Severe hyperandrogenic symptoms

3. Clinical Features of PCOS

Polycystic ovary syndrome (PCOS) is a heterogeneous endocrine–metabolic disorder characterized by a wide spectrum of clinical manifestations affecting reproductive, dermatological, metabolic, and psychological health. The clinical presentation varies considerably among individuals, and not all patients exhibit every feature. Symptoms commonly begin during adolescence soon after menarche and may persist or evolve throughout the reproductive years. Early recognition of these features is essential because PCOS is associated not only with infertility but also with long-term metabolic and cardiovascular risks [3,10,24].

Reproductive abnormalities are often the earliest and most frequent presenting complaints. Chronic anovulation leads to menstrual irregularities such as oligomenorrhea (infrequent cycles) or amenorrhea (absence of menstruation). These disturbances occur due to impaired follicular maturation and failure of ovulation resulting from hormonal imbalance. Many women present with anovulatory infertility; however, ovarian reserve is usually preserved, and with appropriate treatment, fertility outcomes are generally favorable. On ultrasonography, enlarged ovaries containing multiple small peripheral follicles may be observed, producing the classic “string of pearls” appearance.

Table 2: Clinical Spectrum of PCOS

Domain	Clinical Feature	Underlying Cause	Key Clinical Impact
Reproductive	Oligomenorrhea/amenorrhea	Chronic anovulation	Irregular cycles
Reproductive	Anovulatory infertility	Follicular arrest	Difficulty conceiving
Reproductive	Polycystic ovaries	Excess small follicles	Diagnostic imaging finding
Hyperandrogenic	Hirsutism	Elevated free testosterone	Cosmetic distress
Hyperandrogenic	Acne	Increased sebum production	Persistent skin lesions
Hyperandrogenic	Androgenic alopecia	Follicular miniaturization	Hair thinning
Metabolic	Central obesity	Visceral adiposity	Cardiometabolic risk
Metabolic	Insulin resistance	Post-receptor defect	Hyperinsulinemia
Metabolic	Impaired glucose tolerance	β-cell stress	Diabetes risk
Metabolic	Dyslipidemia	Altered lipid metabolism	Atherosclerosis risk
Psychological	Depression/anxiety	Hormonal & psychosocial factors	Reduced mental health

Hyperandrogenism is another hallmark feature of PCOS and may be clinical or biochemical. Excess androgen activity manifests as hirsutism, acne, and androgenic alopecia. Hirsutism, characterized by coarse terminal hair growth in androgen-dependent areas, is the most common dermatological complaint. Persistent acne, particularly along the jawline, and diffuse thinning of scalp hair may also occur. Importantly, some women—especially lean individuals—may exhibit significant hyperandrogenic symptoms despite having a normal body mass index.

PCOS is increasingly recognized as a metabolic disorder. Insulin resistance is present in a large proportion of patients and contributes to compensatory hyperinsulinemia, which further aggravates ovarian androgen production. Many women exhibit central obesity with increased visceral fat deposition. Metabolic abnormalities such as impaired glucose tolerance, type 2 diabetes mellitus, and dyslipidemia (elevated triglycerides and low HDL cholesterol) are common and contribute to long-term cardiometabolic risk.

Psychological manifestations are frequently underappreciated but significantly impact quality of life. Women with PCOS have higher rates of depression, anxiety, body image dissatisfaction, and reduced self-esteem. Concerns related to infertility, weight gain, acne, and hirsutism often contribute to emotional distress and social withdrawal. Therefore, PCOS should be approached as a multidimensional disorder requiring comprehensive clinical assessment and holistic management.

4. Lifestyle Interventions in PCOS

- Lifestyle modification is the cornerstone and first-line therapy in the management of polycystic ovary syndrome (PCOS), particularly in overweight and obese women [2,5]. Even a modest weight reduction of 5–10% of initial body weight has been shown to produce meaningful clinical benefits. Weight loss improves insulin sensitivity, reduces circulating androgen levels, restores ovulatory cycles, enhances menstrual regularity, and improves fertility outcomes. These benefits primarily occur through reduction of visceral adiposity, improvement in insulin signaling pathways, decrease in chronic low-grade inflammation, and partial normalization of hypothalamic–pituitary–ovarian (HPO) axis function.
- Dietary intervention plays a pivotal role in achieving and maintaining weight control. A moderate calorie deficit of approximately 500–750 kcal/day is generally recommended to promote gradual and sustainable weight loss while avoiding the adverse effects associated with crash dieting. Low glycemic index (GI) diets are particularly beneficial in PCOS because they reduce postprandial glucose excursions and improve insulin sensitivity. Emphasis is placed on consumption of whole grains, legumes, vegetables, and low-GI fruits [5].
- High-protein diets may further support weight management by enhancing satiety, preserving lean body mass during weight loss, and improving postprandial insulin response. Collectively, structured dietary modification combined with weight management remains a fundamental strategy in comprehensive PCOS care.

4.1 Mediterranean Diet

The Mediterranean diet is strongly supported by clinical evidence as a beneficial dietary pattern for women with PCOS. It emphasizes consumption of monounsaturated fats, plant-based foods, and lean protein sources. Key components include olive oil as the primary fat source, nuts and seeds, fatty fish rich in omega-3 fatty acids, whole grains, and abundant vegetables and fruits.

This dietary pattern exerts anti-inflammatory and insulin-sensitizing effects, which are particularly valuable in PCOS management. Regular adherence has been associated with reduced systemic inflammation, improvement in lipid profile (lower triglycerides and LDL cholesterol, higher HDL cholesterol), and enhanced insulin sensitivity. Additionally, the diet supports sustainable weight management and may contribute to improved ovulatory function.

Example

A 26-year-old overweight woman with PCOS who replaces refined carbohydrates and saturated fats with olive oil, nuts, vegetables, and fish over 6 months may demonstrate improved fasting insulin, modest weight loss, and more regular menstrual cycles.

Physical Activity in PCOS

Regular physical activity independently improves metabolic and reproductive outcomes in PCOS by enhancing insulin sensitivity, reducing visceral adiposity, and improving hormonal balance.

Table 3: Types of Exercise and Benefits in PCOS

Exercise Type	Recommended Frequency	Major Benefits
Aerobic (walking, cycling)	≥150 min/week	Improves insulin sensitivity and weight control
Resistance training	2–3 times/week	Increases lean muscle mass and basal metabolism
HIIT	Short sessions (2–3/week)	Reduces visceral fat rapidly
Yoga	Regular practice	Reduces stress and improves hormonal balance

Example:

A woman performing brisk walking for 30 minutes daily along with twice-weekly resistance training may show improved menstrual regularity and reduced waist circumference within 3–4 months.

Physiological Benefits

- Increased GLUT-4 expression
- Improved mitochondrial function
- Reduced visceral adiposity
- Improved ovulation rates

Behavioral and Psychological Interventions

Psychological support is often overlooked.

Effective Strategies:

- Cognitive behavioral therapy (CBT)
- Stress management
- Sleep hygiene
- Mindfulness practices

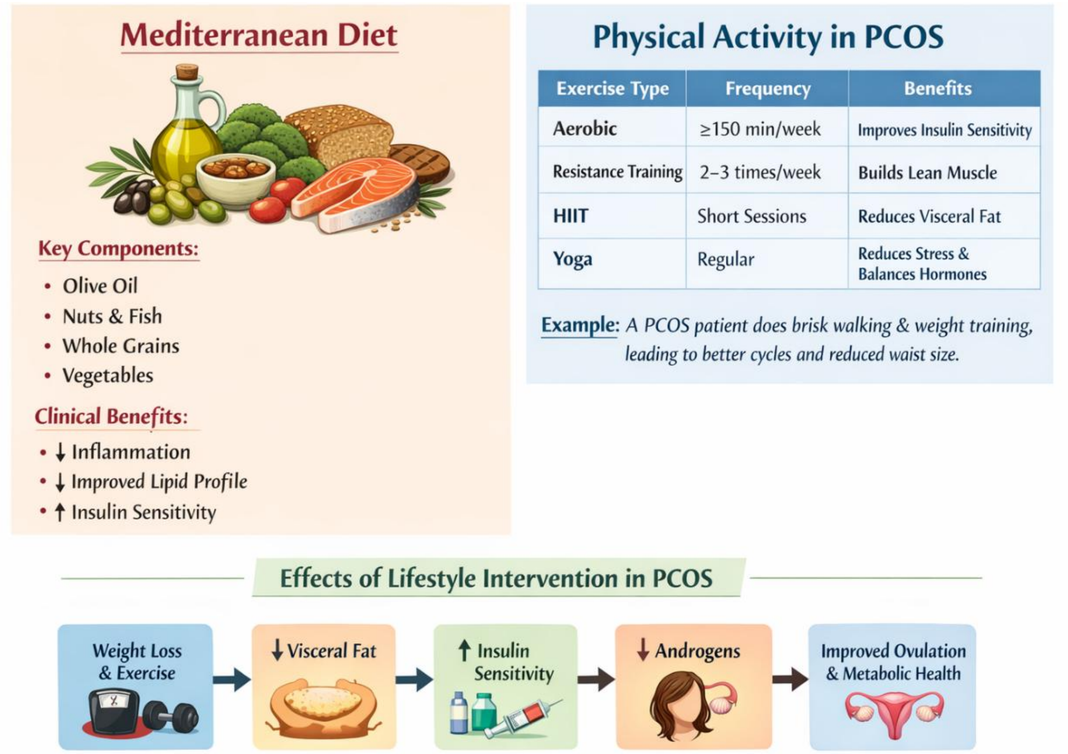


Figure 2: Mediterranean diet, Physical activity and Effects of lifestyle intervention in PCOS

Benefits:

- Improved adherence
- Reduced cortisol
- Better metabolic control

Lifestyle Intervention Outcomes

Parameter	Expected Improvement
Body weight	↓ 5–10%
Insulin resistance	↓
Ovulation	↑
Menstrual regularity	↑
Androgen levels	↓
Fertility	↑

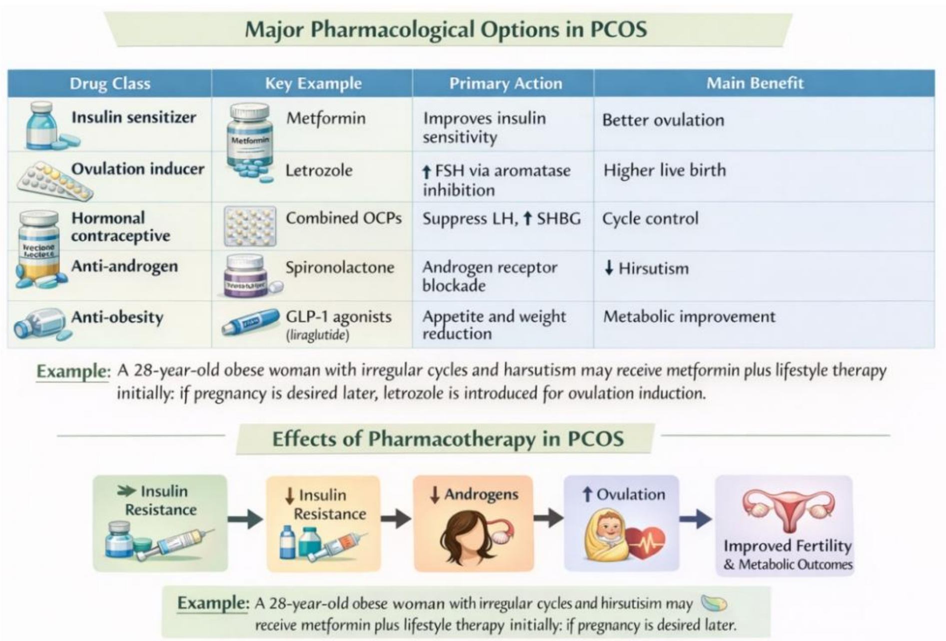
5. Pharmacological Approaches in PCOS

Pharmacotherapy in polycystic ovary syndrome (PCOS) is recommended when lifestyle interventions alone fail, symptoms are severe, infertility treatment is required, or metabolic risk is high. Drug therapy is individualized based on the dominant clinical concern—metabolic dysfunction, anovulation, hyperandrogenism, or menstrual irregularity.

Insulin sensitizers such as metformin remain widely used to improve insulin resistance and reduce hepatic glucose production. Metformin (500–2000 mg/day) enhances peripheral insulin sensitivity and lowers ovarian androgen synthesis, thereby improving ovulation and reducing diabetes risk. Inositols (myo-inositol and D-chiro-inositol) act as insulin signaling mediators and are increasingly preferred due to better tolerability and positive effects on oocyte quality [7,16,22].

For women seeking pregnancy, ovulation induction is central. Letrozole is currently the first-line agent because aromatase inhibition increases FSH and improves live birth rates with lower multiple pregnancy risk. Clomiphene citrate is an alternative but may cause thin endometrium and resistance. Gonadotropins are reserved for resistant cases but carry risk of ovarian hyperstimulation.

Hormonal contraceptives are first-line for cycle regulation in women not desiring pregnancy. Anti-androgens such as spironolactone help manage hirsutism and acne, while anti-obesity drugs (e.g., orlistat, GLP-1 agonists) are considered in obese patients.


Major Pharmacological Options in PCOS

Drug Class	Key Example	Primary Action	Main Benefit
Insulin sensitizer	Metformin	Improves insulin sensitivity	Better ovulation
Ovulation inducer	Letrozole	↑ FSH via aromatase inhibition	Higher live birth
Hormonal contraceptive	Combined OCPs	Suppress LH, ↑ SHBG	Cycle control
Anti-androgen	Spironolactone	Androgen receptor blockade	↓ Hirsutism
Anti-obesity	GLP-1 agonists (liraglutide)	Appetite and weight reduction	Metabolic improvement

Figure 3: Major Pharmacological Options and Effects of Pharmacotherapy in PCOS

6. Combination Therapy in PCOS

Combination therapy is frequently employed in polycystic ovary syndrome (PCOS) to target the multifactorial pathophysiology of the disorder. Because PCOS involves interconnected metabolic, reproductive, and hyperandrogenic abnormalities, using two or more therapeutic modalities often produces superior clinical outcomes compared with monotherapy. Combination regimens are tailored according to the patient's dominant clinical concern—whether metabolic dysfunction, infertility, obesity, or hyperandrogenic symptoms [14].

One of the most widely used strategies is the integration of lifestyle modification with pharmacotherapy. Lifestyle intervention combined with metformin is particularly effective in women with metabolic PCOS, as weight reduction and improved insulin sensitivity act synergistically. For infertility management, letrozole combined with metformin may enhance ovulation rates in women who have insulin resistance. In patients not seeking pregnancy but troubled by hirsutism or acne, combined oral contraceptives (OCPs) with spironolactone provide both hormonal suppression and peripheral androgen blockade. In obese PCOS patients, combining GLP-1 receptor agonists with metformin can produce meaningful weight reduction and metabolic improvement [5,16]..

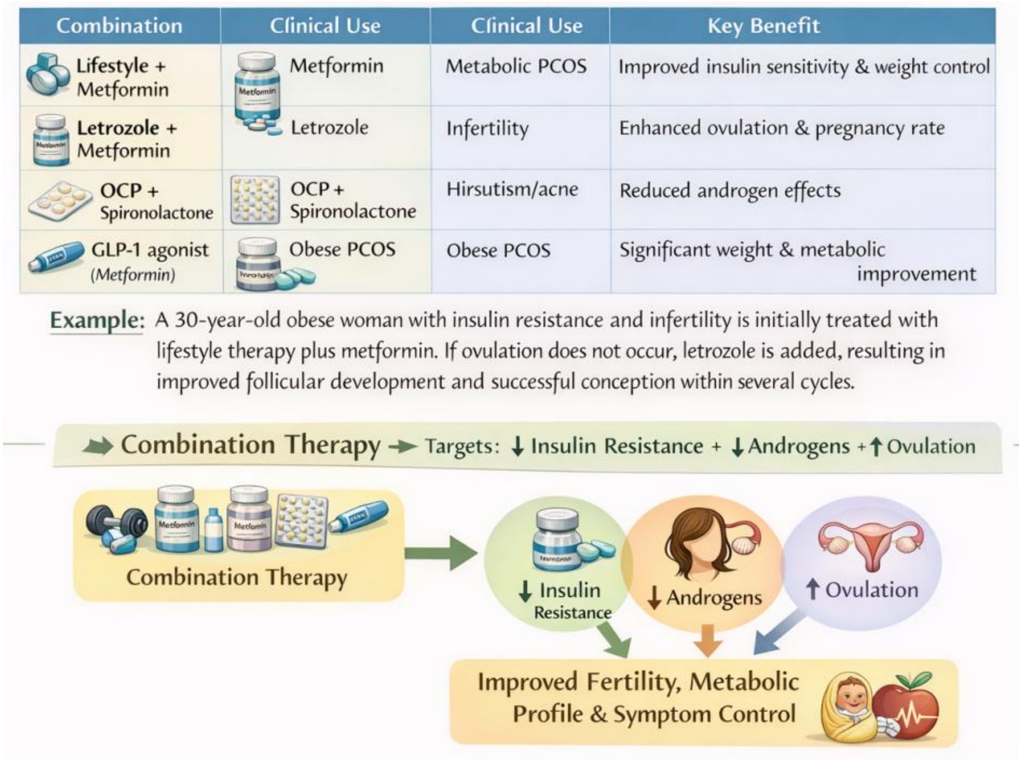


Figure 4: Combination Therapy in PCOS

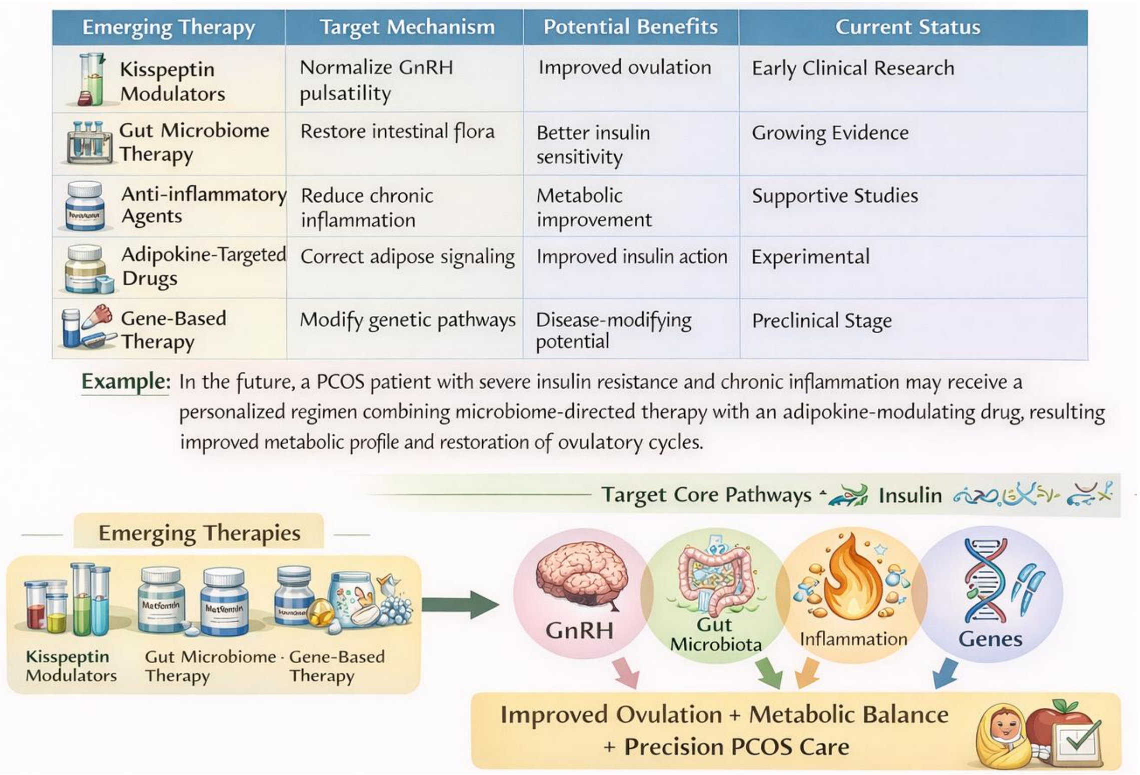
7. Emerging and Future Therapies in PCOS

Promising Areas

- Kisspeptin modulators
- Gut microbiome therapy
- Anti-inflammatory agents
- Adipokine-targeted drugs
- Gene-based therapy

Despite advances in current management, many women with polycystic ovary syndrome (PCOS) continue to experience persistent metabolic and reproductive dysfunction. Consequently, research is increasingly focused on novel and targeted therapies that address the underlying pathophysiology rather than only symptom control. Emerging treatments aim to modulate neuroendocrine signaling, metabolic inflammation, adipose dysfunction, and genetic susceptibility. Although many of these approaches remain investigational, they hold significant promise for personalized PCOS management [14,25].

- **Kisspeptin modulators** represent an important neuroendocrine strategy. Kisspeptin is a key regulator of hypothalamic gonadotropin-releasing hormone (GnRH) secretion. In PCOS, abnormal GnRH pulsatility contributes to elevated luteinizing hormone (LH) and anovulation. Kisspeptin analogues may help normalize GnRH pulse patterns, thereby restoring ovulation with potentially lower risk of ovarian hyperstimulation compared with conventional gonadotropins.
- **Gut microbiome therapy** has gained attention due to the recognized link between intestinal dysbiosis, insulin resistance, and systemic inflammation in PCOS. Interventions such as probiotics, prebiotics, synbiotics, and fecal microbiota modulation aim to restore healthy gut flora. Early studies suggest improvements in insulin sensitivity, inflammatory markers, and androgen levels, although long-term evidence is still evolving.
- **Anti-inflammatory agents** target the chronic low-grade inflammation characteristic of PCOS. Compounds such as omega-3 fatty acids, N-acetylcysteine, and selective cytokine modulators may reduce inflammatory signaling, improve insulin action, and support ovulatory function. This approach is particularly relevant in obese and metabolically high-risk patients.
- **Adipokine-targeted therapies** focus on correcting adipose tissue dysfunction. PCOS is associated with decreased adiponectin and increased leptin and resistin levels. Novel drugs that enhance adiponectin signaling or modulate leptin pathways may improve insulin sensitivity and metabolic outcomes. This area is still largely experimental but mechanistically promising.
- **Gene-based therapy** represents a futuristic direction aimed at addressing genetic susceptibility in PCOS. Potential strategies include gene editing, RNA-based therapies, and epigenetic modulation targeting pathways involved in steroidogenesis, insulin signaling, and ovarian function. However, these approaches remain in early research phases and require substantial safety validation.



Emerging Therapy	Target Mechanism	Potential Benefits	Current Status
Kisspeptin Modulators	Normalize GnRH pulsatility	Improved ovulation	Early Clinical Research
Gut Microbiome Therapy	Restore intestinal flora	Better insulin sensitivity	Growing Evidence
Anti-inflammatory Agents	Reduce chronic inflammation	Metabolic improvement	Supportive Studies
Adipokine-Targeted Drugs	Correct adipose signaling	Improved insulin action	Experimental
Gene-Based Therapy	Modify genetic pathways	Disease-modifying potential	Preclinical Stage

Figure 5: Emerging and Future Therapies in PCOS

8. Personalized Management Approach

Personalized management of polycystic ovary syndrome (PCOS) is essential because the condition is highly heterogeneous. A phenotype-based strategy improves clinical outcomes by tailoring therapy to the patient's primary concerns—whether infertility, hyperandrogenism, metabolic risk, or menstrual irregularity. Management should be dynamic, goal-oriented, and multidisciplinary.

The first step is confirming the diagnosis using accepted criteria along with exclusion of mimicking disorders. Next, clinicians must clearly identify the patient's priorities, such as desire for pregnancy, cosmetic concerns, or metabolic health. Lifestyle intervention remains the cornerstone for all phenotypes and should precede or accompany pharmacotherapy. Drug therapy is then individualized based on symptom clusters. Continuous monitoring of metabolic risk factors—glucose tolerance, lipid profile, and blood pressure—is crucial because PCOS is a lifelong condition. Finally, long-term follow-up ensures treatment adherence, early detection of complications, and adjustment of therapy over time.

Treatment Algorithm

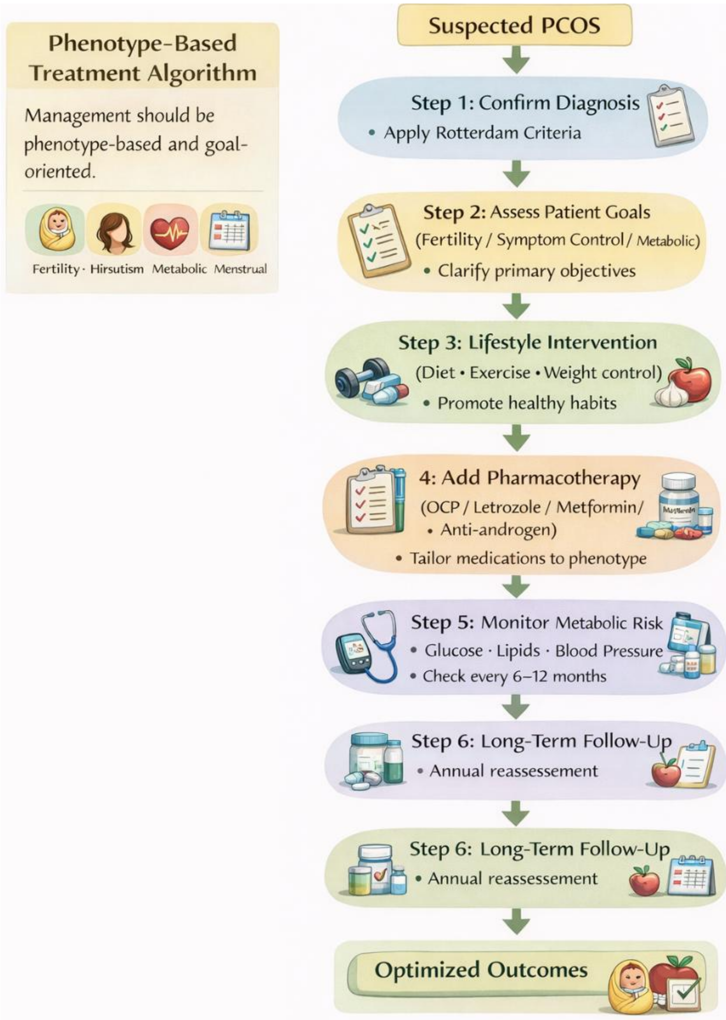


Figure 6: Personalized Management Approach in PCOS

Table 4: Phenotype-Based Personalized Management Algorithm

Step	Clinical Action	Objective	Practical Example
Step 1	Confirm diagnosis	Ensure accurate identification	Apply Rotterdam criteria and rule out thyroid disorder
Step 2	Assess goals	Individualize treatment plan	Patient desires pregnancy vs cycle control
Step 3	Initiate lifestyle therapy	Improve metabolic and hormonal milieu	5–10% weight loss program
Step 4	Add pharmacotherapy	Target dominant symptoms	Letrozole for infertility; OCP for irregular menses
Step 5	Monitor metabolic risk	Prevent long-term complications	Check HbA1c, lipid profile every 6–12 months
Step 6	Long-term follow-up	Sustain treatment success	Annual clinical review and therapy adjustment

Clinical Example

A 24-year-old woman presents with irregular menses, mild hirsutism, and BMI of 31 kg/m². After confirming PCOS, her primary concern is menstrual irregularity rather than fertility. She is started on a structured weight-loss program including calorie restriction and aerobic exercise. After three months, combined oral contraceptive therapy is initiated to regulate cycles and reduce androgenic symptoms. Metabolic monitoring reveals borderline insulin resistance, prompting addition of metformin. With periodic follow-up every six months, her cycles normalize, weight decreases, and metabolic parameters improve. This illustrates how phenotype-based personalization optimizes outcomes.

9. Clinical Case Example

A 24-year-old woman presented with complaints of irregular menstrual cycles and excessive facial hair. Her body mass index (BMI) was 31 kg/m², indicating obesity. Clinical evaluation and hormonal assessment supported the diagnosis of polycystic ovary syndrome (PCOS) with metabolic and hyperandrogenic features. Management was planned using a stepwise, multidisciplinary approach focusing on weight reduction, insulin sensitization, hormonal regulation, and cosmetic improvement.

Lifestyle modification was initiated as the foundation of therapy. The patient was advised a calorie-restricted, low–glycemic index diet along with regular aerobic and resistance exercise. Pharmacotherapy was added because of persistent symptoms and elevated metabolic risk. Metformin was started to improve insulin sensitivity and support ovulatory function. A combined oral contraceptive pill was prescribed for menstrual regulation and suppression of ovarian androgen production. Spironolactone was added specifically to address hirsutism, with strict advice regarding contraception due to teratogenic risk.

At 6-month follow-up, the patient showed significant clinical improvement. Menstrual cycles became regular, facial hair growth reduced, and modest weight loss was achieved. This case highlights the effectiveness of individualized combination therapy in PCOS.

Table 5: Stepwise management plan

Step	Intervention	Rationale	Expected Outcome
1	Lifestyle modification	Reduce weight and insulin resistance	Improved metabolic profile
2	Metformin	Enhance insulin sensitivity	Better ovulation
3	Combined oral contraceptive	Suppress androgens, regulate cycles	Regular menstruation
4	Spironolactone	Androgen receptor blockade	Reduced hirsutism
5	6-month follow-up	Monitor response and safety	Therapy optimization

Example

An obese young woman with both metabolic and cosmetic concerns benefits most from combined lifestyle and pharmacological therapy rather than single-modality treatment.

Conclusion

Polycystic ovary syndrome (PCOS) remains one of the most prevalent and complex endocrine–metabolic disorders affecting women of reproductive age. Its multifactorial pathogenesis—encompassing insulin resistance, hyperandrogenism, hypothalamic–pituitary–ovarian axis dysregulation, and adipose tissue dysfunction—results in a wide spectrum of reproductive, metabolic, dermatological, and psychological manifestations. Because of this heterogeneity, PCOS can no longer be viewed solely as a reproductive disorder; rather, it represents a lifelong metabolic condition requiring comprehensive and sustained management.

Lifestyle intervention continues to be the cornerstone and first-line strategy in PCOS management. Evidence consistently demonstrates that modest weight reduction (5–10%) through dietary modification, increased physical activity, and behavioral support can significantly improve insulin sensitivity, restore ovulatory cycles, reduce androgen levels, and enhance overall metabolic health. Importantly, these benefits extend to both overweight and, to some extent, lean women with PCOS. Structured dietary patterns such as the Mediterranean diet and regular exercise regimens—including aerobic, resistance, and high-intensity interval training—provide synergistic improvements in metabolic and reproductive outcomes. Psychological and behavioral interventions further enhance adherence and quality of life.

Pharmacological therapy plays a crucial adjunctive role when lifestyle measures alone are insufficient or when specific clinical goals must be addressed. Insulin sensitizers such as metformin and inositols target the metabolic core of PCOS, while ovulation induction agents like letrozole and clomiphene citrate remain central to infertility management. Combined oral contraceptives and anti-androgens effectively manage menstrual irregularity and hyperandrogenic symptoms in women not seeking pregnancy. Increasingly, anti-obesity medications and GLP-1 receptor agonists are being incorporated in selected patients with significant metabolic risk. The key principle is individualized drug selection based on the patient's dominant phenotype and reproductive intentions.

Combination therapy has emerged as a particularly effective strategy due to the interconnected nature of PCOS pathophysiology. Integrating lifestyle modification with pharmacotherapy often yields superior outcomes compared with monotherapy by simultaneously addressing insulin resistance, androgen excess, and ovulatory dysfunction. A multidisciplinary care model involving endocrinologists, gynecologists, dietitians, psychologists, and primary care providers is essential for optimal long-term management.

Looking forward, emerging therapies—including kisspeptin modulators, gut microbiome interventions, anti-inflammatory agents, adipokine-targeted drugs, and gene-based approaches—

hold promise for more mechanism-driven and personalized treatment paradigms. However, robust long-term clinical evidence is still required before widespread clinical adoption.

In conclusion, effective management of PCOS requires a personalized, phenotype-based, and life-course approach that prioritizes lifestyle optimization, judicious pharmacotherapy, and continuous metabolic monitoring. Early diagnosis, patient education, and long-term follow-up are critical to preventing complications such as type 2 diabetes, cardiovascular disease, and infertility. With continued advances in understanding the underlying biology of PCOS and the development of targeted therapies, future care is expected to become increasingly precise, holistic, and patient-centered, ultimately improving both reproductive outcomes and long-term health in women with PCOS.

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AEROBIOLOGY IN PLANT PATHOLOGY: CONCEPTS, EPIDEMIOLOGY, DISEASE MONITORING, DETECTION AND MANAGEMENT

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Abstract

Aerobiology plays a crucial role in plant disease epidemiology, management, and pathogen detection by analyzing the dynamics of airborne inoculum. Airborne spores of fungi, bacteria, and viruses are major factors of disease spread, with their release and dispersal influenced by environmental factors such as temperature, humidity, and wind. Monitoring airborne pathogens enables early detection, often before visible symptoms appear, which is essential for accurate disease forecasting. For instance, the detection of *Pyricularia oryzae* spores in air helps predict rice blast outbreaks, while airborne *Puccinia* spores indicate the risk of wheat rust epidemics. Aerobiological tools such as spore traps, combined with molecular techniques like PCR and immunoassays, enhance the precision and speed of pathogen identification. These methods support integrated disease management by enabling timely interventions and reducing excessive pesticide use. Similarly, monitoring *Phytophthora infestans* aids in forecasting potato late blight, and detection of *Phakopsora pachyrhizi* helps manage soybean rust. Overall, aerobiology provides a scientific basis for effective disease prediction and sustainable crop protection strategies.

Keywords: Aerobiology, Plant Disease, Epidemiology, Airborne Inoculum, Spore Dispersal, Disease Forecasting, Pathogen Detection, Integrated Disease Management.

Introduction

Aerobiology is a multidisciplinary branch of science that investigates the occurrence, behaviour, and biological significance of airborne bioparticles (bioaerosols), encompassing their release, dispersal, transport, deposition, and subsequent impact on living systems. These bioaerosols include a wide range of entities such as fungal spores, pollen grains, bacteria, viruses, and minute arthropods. The term "aerobiology," formally introduced in the early 20th century, was later explored in depth by Jacobs (1951) to include a comprehensive spectrum of airborne biological materials and their ecological and pathological relevance.

In its early stages, aerobiology was primarily descriptive, focusing on the collection, identification, and quantitative estimation of airborne particles. However, with advancements in biological and environmental sciences, the field has evolved into an integrative discipline addressing ecological interactions, atmospheric biology, environmental monitoring, and plant disease epidemiology, along with diverse agricultural applications. Contemporary aerobiology synthesizes concepts from plant pathology, mycology, meteorology, ecology, palynology, immunology, and environmental sciences to understand the dynamics of biological particles in the atmosphere.

The movement of airborne particles is conceptualized through the aerobiological cycle, which comprises sequential stages: Source → Release → Dispersion → Deposition → Impact.

Each phase of this cycle is governed by complex environmental variables, including temperature, relative humidity, wind speed and direction, solar radiation, and precipitation, which collectively regulate particle concentration, atmospheric residence time, survival, and infectivity. Among bioaerosols, fungal spores represent a dominant and ecologically significant component of the atmospheric microbiota. Their abundance and diversity are influenced by factors such as vegetation type, decomposition of organic substrates, environmental pollution, and anthropogenic activities. Areas characterized by high levels of organic debris and microbial activity generally exhibit elevated spore loads (Grinn-Gofroń and Bosiacka, 2015).

In India, the earliest systematic aerobiological investigation was conducted by Cunningham (1873) in his seminal work *Microscopic Examination of Air*, wherein various airborne microorganisms and spores were documented. Although attempts were made to associate these airborne particles with disease occurrence, definitive causal relationships could not be established at that time, largely due to limitations in contemporary scientific methodologies.

1. History of Aerobiology in Plant Pathology

The evolution of aerobiology is intrinsically linked with the advancement of plant pathology, particularly the understanding of microorganisms as causal agents of plant diseases. A major milestone was achieved by Anton de Bary (1861), who experimentally demonstrated that *Phytophthora infestans* is the causal agent of potato late blight, thereby establishing the scientific foundation of plant pathology and stimulating further investigations into pathogen dissemination. Earlier contributions by Micheli (1729) provided preliminary insights into airborne dispersal mechanisms, as he observed that fungal spores could be released into the atmosphere in large quantities resembling “clouds.” This observation highlighted the potential significance of air as a medium for pathogen spread, although the underlying mechanisms were not yet fully understood. A significant advancement in aerobiology occurred through the pioneering work of Gregory (1973), who developed a quantitative framework for understanding spore dispersal, atmospheric transport, and deposition processes. His studies, conducted at Rothamsted Experimental Station, provided critical insights into the role of turbulence, wind dynamics, and surface interactions in governing the movement of airborne particles. In collaboration with Stedman, Gregory established fundamental principles describing the physical behavior of spores in the atmosphere, thereby linking aerobiology with epidemiological processes in plant disease development.

The introduction of the Hirst spore trap (Hirst, 1953) marked a transformative advancement in aerobiological research. This device enabled continuous volumetric sampling of airborne particles, allowing for accurate quantification of spore concentrations over time. Its application facilitated detailed investigations into diurnal periodicity, seasonal fluctuations, and the influence of meteorological parameters on airborne spore dynamics, significantly enhancing the precision and scope of aerobiological and epidemiological studies.

2. Role of Aerobiology in Plant Pathology

Aerobiology addresses three fundamental questions central to plant pathology: (i) what biological particles are present in the atmosphere, (ii) what are their sources, and (iii) what is their impact on plant health (Irabanta Singh, 2009). These questions form the basis for understanding the role of airborne inoculum in disease initiation and epidemic development. The atmosphere serves as a major pathway for the dissemination of plant pathogens, including fungi, bacteria, and viruses. Among these, fungal spores are particularly well adapted for aerial transport due to their small size, aerodynamic properties, and physiological resilience, enabling them to withstand environmental stresses such as ultraviolet radiation, desiccation, and temperature fluctuations (Gregory, 1973; Morris *et al.,* 2013).

Aerobiological investigations play a critical role in plant disease studies by facilitating the detection and identification of airborne pathogens, quantification of spore concentrations, and analysis of their temporal and spatial distribution patterns. Furthermore, these studies enable the establishment of relationships between pathogen dynamics and meteorological variables, thereby supporting the prediction and forecasting of disease outbreaks. Several landmark studies have significantly contributed to this field. Mehta (1952) demonstrated the long-distance dispersal of rust spores across India, highlighting the importance of atmospheric transport in pathogen spread. Sreeramulu and Ramalingam (1963, 1966) documented seasonal variations in fungal spore populations in paddy fields, while Reddy (1978) investigated the vertical distribution of spores within crop canopies, providing insights into intra-field dispersal mechanisms. Additionally, Chakraborty et al. (2003) conducted long-term monitoring of agricultural airspora, emphasizing the value of continuous aerobiological surveillance. Collectively, these studies establish airborne inoculum as a reliable and critical indicator of potential disease risk in crop systems.

2.1 Aerobiology in Plant Disease Epidemiology

Plant disease epidemiology is concerned with the study of the development, spread, and dynamics of diseases within plant populations (Agrios, 2005). It is inherently interdisciplinary, integrating biological, ecological, and statistical approaches to understand and predict disease outbreaks under varying environmental and agronomic conditions (Arneson, 2001; Madden and Wheelis, 2003). Aerobiology plays a central role in epidemiology by elucidating the mechanisms of pathogen dispersal through the atmosphere.

2.1.1 Disease Triangle

A fundamental concept in plant disease epidemiology is the disease triangle, which postulates that disease development occurs only when three critical components interact simultaneously: a susceptible host, a virulent pathogen, and a favourable environment. The absence or limitation of any one of these components can restrict or prevent disease establishment and progression. Aerobiological processes are particularly important in linking the pathogen with the host under conducive environmental conditions.

2.1.2 Types of Epidemics

Plant disease epidemics can be broadly classified based on the number of infection cycles occurring within a growing season. Monocyclic epidemics involve a single cycle of infection and are typically associated with soil-borne pathogens such as *Fusarium* spp., where the initial inoculum largely determines disease severity. In contrast, polycyclic epidemics involve multiple infection cycles within a season and are characteristic of many airborne pathogens, such as powdery mildew fungi. In these cases, repeated cycles of spore production and dispersal lead to rapid disease escalation and widespread epidemics.

2.1.3 Spatial Scale of Dispersal

Aerobiological processes operate across multiple spatial scales, influencing the spread and intensity of plant diseases (Frinking, 1993). At the field scale, pathogen dispersal occurs within crop canopies, contributing to localized disease development. At the regional scale, spores are transported between fields, facilitating the spread of diseases across agricultural landscapes. At the continental scale, long-distance dispersal enables pathogens to migrate across large geographical areas, often introducing diseases into new regions. Although the majority of spores are deposited near their source, long-distance atmospheric transport plays a critical role in initiating epidemics in previously uninfected areas (Brown & Hovmoller, 2002).

2.2 Factors Influencing Airborne Dispersal

The dispersal of airborne pathogens is governed by a complex interplay of environmental and biological factors. Wind speed and direction are primary determinants of spore transport and distribution, while temperature and relative humidity influence spore release, viability, and infection efficiency. Solar radiation, particularly ultraviolet radiation, can reduce spore survival, whereas rainfall and atmospheric turbulence can either facilitate spore liberation or enhance deposition through washout processes. Additionally, crop canopy architecture affects the release and escape of spores into the atmosphere, as well as their subsequent movement within and above the canopy. Together, these factors regulate the processes of spore release, atmospheric transport, survival, and deposition, ultimately shaping the epidemiology of plant diseases. The dispersal of plant pathogens through the atmosphere occurs across multiple spatial scales, including the microscale (within fields), mesoscale (between fields), and macroscale (regional to continental levels). These scales determine the extent and rate of disease spread, ranging from localized infections to widespread epidemics.

Airborne dispersal mechanisms can be broadly categorized into passive and active processes. Passive release involves the detachment and transport of spores through external forces such as wind currents, rain splash, and mechanical disturbances like leaf movement. Wind plays a dominant role in lifting and transporting spores into the atmospheric boundary layer, while rainfall can both facilitate spore liberation and enhance their deposition through washout processes.

In contrast, active release mechanisms involve physiological processes within the fungal structures, such as the generation of hygroscopic or osmotic pressure leading to spore discharge. For instance, many ascospores are released through explosive mechanisms driven by turgor pressure within asci (Ingold, 1971; Aylor, 1995). These mechanisms enable spores to enter turbulent air currents, enhancing their dispersal potential.

Despite the efficiency of these dispersal processes, it is estimated that approximately 90% of airborne spores are deposited within or near the crop canopy, contributing primarily to local disease spread. Only a small fraction escapes into higher atmospheric layers, where they can be transported over long distances and play a crucial role in the initiation of epidemics in distant regions.

2.3 Aerobiological Sampling and Quantification of Airborne Inoculum

Monitoring airborne plant pathogens relies on a range of specialized sampling devices designed to capture and quantify bioaerosols with precision. Among these, the Hirst spore trap (Hirst, 1952) represents a major advancement, enabling continuous volumetric sampling of airborne particles and providing reliable estimates of spore concentration over time. Similarly, Burkard volumetric spore traps are widely used for long-term monitoring of airspora, offering high temporal resolution data. Other devices, such as Rotorod samplers, operate based on impaction principles and are effective for short-term sampling, while cyclone samplers utilize centrifugal force to concentrate airborne particles into liquid media for subsequent analysis. Jet spore traps, based on virtual impaction, and liquid impingers and virtual impactors further enhance the efficiency of particle collection, particularly for smaller bioaerosols. Collectively, these instruments provide quantitative and qualitative data on airborne inoculum, forming the foundation for aerobiological investigations and disease surveillance.

2.3.1 Types of Samplers

Aerobiological investigations employ a variety of sampling devices to capture airborne biological particles, broadly categorized into passive and active samplers. Passive samplers, such as exposed glass slides and Petri dishes, rely on gravitational settling of particles and provide a simple, cost-effective means of qualitative assessment. However, they are limited in their ability to yield quantitative data and are influenced by environmental variability.

In contrast, active volumetric samplers are designed to draw a known volume of air, thereby enabling precise quantification of airborne inoculum. Instruments such as Burkard spore traps, cyclone samplers, and jet spore traps operate on principles of impaction or centrifugal force, allowing efficient collection of spores across a range of particle sizes. These devices are widely used in modern aerobiology due to their ability to provide continuous, standardized, and reproducible measurements of airspora.

2.3.2 Sampling Considerations

The reliability and interpretability of aerobiological data depend on several critical sampling parameters. Sampling frequency is particularly important, as continuous or high-frequency sampling allows the detection of diurnal periodicity in spore release and dispersal, which is often governed by environmental factors.

Sampling height is another key consideration, as it influences the type of inoculum detected. Sampling near the crop canopy typically reflects local inoculum sources, whereas sampling at higher altitudes may capture regionally or long-distance transported spores (Aylor, 1995). Additionally, the spatial distribution of airborne inoculum within a field or region can vary significantly, often exhibiting aggregated, random, or uniform patterns, depending on pathogen biology and environmental conditions. Understanding these distribution patterns is essential for accurate disease assessment and modelling (Madden & Wheelis, 2003).

2.4 Modern Detection Methods

Traditional methods for the identification and quantification of airborne spores have largely relied on light microscopy, which allows direct visualization and morphological characterization. Although effective, this approach is labor-intensive, time-consuming, and often constrained by morphological similarities among different taxa, leading to potential inaccuracies in identification.

To address these limitations, immunological techniques have been developed, including enzyme-linked immunosorbent assay (ELISA) and lateral flow devices. These methods improve specificity through antigen–antibody interactions, enabling targeted detection of particular pathogens. However, their sensitivity may be limited, especially when pathogen concentrations are low.

Recent advances in molecular diagnostics have significantly enhanced the detection and quantification of airborne pathogens. Techniques such as polymerase chain reaction (PCR), quantitative PCR (qPCR), and loop-mediated isothermal amplification (LAMP) provide high sensitivity, specificity, and rapid processing, allowing accurate detection even at very low inoculum levels. As a result, molecular approaches have become indispensable tools in modern aerobiological research and plant disease epidemiology.

In addition, the integration of biosensors and automated detection systems has enabled real-time monitoring of airborne pathogens, greatly improving analytical throughput and operational efficiency (Heard & West, 2014).

2.5 Disease Forecasting

The integration of aerobiological data with meteorological parameters forms the basis of advanced disease forecasting systems. By correlating airborne inoculum levels with environmental conditions, it is possible to predict the onset and progression of disease outbreaks, thereby enabling proactive management strategies. These systems allow for the establishment of threshold inoculum levels required for infection, development of early warning systems for farmers, and optimization of the timing and application of control measures. Such predictive approaches are central to Integrated Pest Management (IPM), which emphasizes the judicious use of control strategies to minimize economic losses while reducing environmental impact.

2.5.1 Disease Thresholds and Forecasting Models

The establishment of threshold inoculum levels is a critical component of aerobiological research, as it enables the quantitative relationship between airborne pathogen concentration and disease risk to be defined. Such thresholds provide a scientific basis for predicting the onset and severity of plant diseases. For instance, in the case of *Botrytis squamosa*, an airborne spore concentration of approximately 10-15 spores m^{-3} has been correlated with the development of about one lesion per leaf, indicating a threshold level for infection (Carisse *et al.,* 2005). Similarly, for *Phytophthora infestans*, the causal agent of potato late blight, infection onset has been associated with airborne concentrations of 10-25 sporangia m^{-3}, highlighting the importance of monitoring sporangial density in forecasting disease outbreaks (Fall *et al.,* 2015).

Modern disease forecasting systems integrate multiple parameters to improve predictive accuracy and support timely disease management decisions. These systems incorporate airborne spore concentration, which reflects the availability of inoculum; meteorological parameters, such as temperature, relative humidity, rainfall, and wind patterns, which influence pathogen survival and infection; crop growth stage, which determines host susceptibility; and pathogen virulence, which affects infection efficiency and disease progression.

Advanced atmospheric dispersion models, such as the HYSPLIT (Hybrid Single-Particle Lagrangian Integrated Trajectory) model, are increasingly utilized to simulate and predict the long-distance transport of airborne pathogens. These models integrate meteorological data with particle movement dynamics to trace the origin, trajectory, and deposition patterns of spores, thereby enhancing our understanding of transboundary disease spread and aiding in the development of regional and global disease warning systems.

3. Practical Applications

Aerobiological studies have wide-ranging applications in plant disease management and agricultural planning. Continuous monitoring of airborne spores facilitates the surveillance of important diseases such as rusts, powdery mildews, and leaf spot pathogens, enabling timely intervention. Analysis of seasonal and temporal dynamics of pathogens provides insights into disease cycles and epidemic development. Aerobiological data are also used to determine safe isolation distances in crop production systems, particularly in seed certification programs. Furthermore, pollen monitoring contributes to crop yield prediction and breeding programs, while aerobiological assessments aid in evaluating the potential spread of genetically modified organisms (GMOs). Together, these applications highlight the critical role of aerobiology in enhancing disease management strategies and supporting sustainable agriculture.

3.1 Aerobiological Studies in Major Agricultural Crop Systems

3.1.1 Cereals

Rice

Aerobiological investigations in rice ecosystems have demonstrated that several airborne fungal pathogens, including *Pyricularia oryzae*, *Helminthosporium oryzae*, and *Ustilaginoidea virens*, play a significant role in disease development and yield loss (Chetia and Baruah, 1964). Detailed studies have revealed that spore release of these pathogens exhibits distinct diurnal periodicity, with peak concentrations occurring during nocturnal hours, particularly around 2:00 AM. This periodicity is strongly influenced by environmental factors such as high relative humidity, rainfall events, and prolonged dew formation, which create favorable conditions for spore liberation, survival, and infection (Irabanta Singh and Munanthoi Singh, 2000). Such temporal patterns are critical for understanding infection windows and improving disease forecasting models.

Maize

In maize cropping systems, aerobiological monitoring has identified a diverse spectrum of airborne pathogens, including species of *Helminthosporium*, *Cercospora*, and *Puccinia*. These pathogens are associated with diseases such as leaf blight, leaf spot, and rust. Notably, aerobiological studies have consistently shown that airborne spores can be detected prior to the visible disease symptoms, underscoring their importance as early indicators of impending disease outbreaks (Irabanta Singh and Dorycanta, 1992). This predictive capability is particularly valuable for timely disease management interventions.

3.1.2 Pulses

Aerobiological studies in pulse crops such as pea, broad bean, and black gram have highlighted the presence of multiple airborne pathogens, including *Peronospora pisi*, *Erysiphe polygoni*, and *Uromyces fabae*, which exhibit marked seasonal variation in spore incidence (Irabanta Singh, 1987). These seasonal patterns are closely associated with changes in environmental conditions and crop phenology.

In black gram, major diseases caused by *Colletotrichum*, *Curvularia*, and *Fusarium* species show distinct temporal trends, with peak spore concentrations and disease incidence typically occurring between July and September, coinciding with favorable climatic conditions for pathogen development (Irabanta Singh and Kundala Devi, 1995). Such information is crucial for identifying high-risk periods and implementing timely control measures.

3.1.3 Vegetables

In vegetable crops, aerobiological monitoring has provided valuable insights into the epidemiology of major foliar diseases. In tomato, pathogens such as *Alternaria solani* (early blight) and *Phytophthora infestans* (late blight) are frequently detected in airborne samples, with their occurrence closely linked to environmental conditions and crop growth stages. Similarly, in cabbage, *Alternaria brassicicola* and *Peronospora parasitica* dominate the airspora during winter months, reflecting their adaptation to cooler and humid conditions. In potato, aerobiological studies have demonstrated that spore detection often precedes the onset of visible disease symptoms, and that spore concentration is strongly correlated with environmental parameters such as temperature and humidity, thereby reinforcing the importance of aerobiology in disease forecasting (Bijaya Devi and Irabanta Singh, 2015).

3.1.4 Cash Crops

In sugarcane, airborne pathogens such as *Colletotrichum falcatum* (red rot pathogen) and *Ustilago scitaminea* (smut pathogen) exhibit peak spore concentrations during the vegetative growth stage, indicating a high risk of early infection. Aerobiological studies conducted in lemon orchards have identified a diverse assemblage of airborne fungal spores, with their abundance showing a strong correlation with meteorological parameters such as humidity, temperature, and rainfall. These findings are particularly useful for developing localized disease forecasting and advisory systems (Nimyaola and Irabanta Singh, 2016).

4. Challenges and Future Prospects

4.1 Challenges

Despite of significant advancements, aerobiological research in plant pathology continues to face several critical challenges. One of the primary limitations is the morphological similarity of spores, which complicates accurate identification using conventional microscopy, particularly among closely related taxa. Additionally, there is limited knowledge regarding spore viability and infectivity after atmospheric transport, making it difficult to directly relate spore presence to actual disease risk.

The complexity of pathogen life cycles, especially in fungi with multiple spore stages and hosts, further complicates interpretation of aerobiological data. Moreover, there remains an incomplete understanding of long-distance dispersal mechanisms, including the factors governing survival and deposition of spores over continental scales. These uncertainties hinder the development of fully reliable predictive models and limit the precision of disease forecasting systems.

4.2 Future Directions

Future research in aerobiology is expected to be driven by technological and analytical innovations. The integration of advanced molecular diagnostics, including polymerase chain reaction (PCR), loop-mediated isothermal amplification (LAMP), and high-throughput sequencing (HTS), will significantly improve the sensitivity, specificity, and speed of pathogen detection.

The development of automated, real-time monitoring systems capable of continuous air sampling and rapid pathogen identification will enhance surveillance capabilities and reduce reliance on labor-intensive methods. In parallel, the application of artificial intelligence (AI) and machine learning algorithms in disease forecasting is expected to improve predictive accuracy by integrating large datasets encompassing aerobiological, meteorological, and agronomic variables. The establishment of global aerobiological surveillance networks will facilitate large-scale monitoring of airborne pathogens and support early warning systems across regions and continents. Furthermore, the advent of portable sequencing technologies, such as the Oxford Nanopore Technologies (ONT) MinION platform, offers the potential for on-site, real-time genomic analysis of airborne inoculum, enabling rapid decision-making in the field.

Importantly, climate change is anticipated to have profound effects on aerobiological processes and plant disease epidemiology. Alterations in temperature, precipitation patterns, and atmospheric dynamics are likely to shift pathogen distribution ranges, increase the frequency and severity of epidemics, and extend cropping seasons, thereby creating new challenges for disease management (Van der Heyden *et al.,* 2020). These emerging scenarios underscore the need for adaptive, technology-driven approaches to sustainable plant health management.

Conclusion

Aerobiology constitutes a fundamental component of plant pathology, offering critical insights into the dispersal, survival, and epidemiological significance of airborne pathogens. By enabling the detection and quantification of airborne inoculum, it plays a pivotal role in disease monitoring, forecasting, and the development of integrated disease management strategies.

Aerobiological approaches bridge the gap between pathogen presence and disease occurrence by linking atmospheric inoculum dynamics with environmental conditions and host susceptibility. Recent advancements in molecular diagnostics, meteorological modeling, and automated surveillance technologies have substantially enhanced the accuracy, sensitivity, and temporal resolution of aerobiological studies. Techniques such as real-time pathogen detection, coupled with predictive models integrating weather and crop data, have improved the reliability of early warning systems. Looking forward, the integration of real-time aerobiological data, artificial intelligence, and global surveillance networks is expected to revolutionize plant disease prediction and management. These innovations will facilitate rapid decision-making, optimize control measures, and reduce crop losses. Ultimately, such advancements will contribute significantly to sustainable agriculture and global food security, particularly under changing climatic conditions and increasing demands on agricultural systems.

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GENETICALLY MODIFIED CROPS: ADVANCES, APPLICATIONS, BIOSAFETY, AND FUTURE PROSPECTS

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Abstract

Genetically modified (GM) crops have emerged as a cornerstone of modern agricultural biotechnology, offering innovative solutions to global challenges such as food insecurity, climate change, and declining agricultural productivity. By introducing specific genes into plant genomes through recombinant DNA technology and advanced genome-editing tools, GM crops exhibit enhanced traits including pest resistance, herbicide tolerance, improved nutritional quality, and adaptability to environmental stress. Since their commercialization in the 1990s, GM crops have been widely adopted across both developed and developing nations. Despite their numerous advantages, concerns regarding biosafety, environmental risks, human health implications, and socio-economic impacts continue to generate debate. This chapter provides a comprehensive and critical overview of the development, classification, applications, benefits, risks, regulatory frameworks, and future perspectives of genetically modified crops, supported by current scientific literature and global assessments.

Keywords: Genetically Modified Crops, Transgenic Plants, Agricultural Biotechnology, CRISPR-Cas9, Biosafety, Food Security, Genome Editing.

1. Introduction

Agriculture has undergone significant transformations over the past century, driven by the need to meet the demands of a rapidly growing global population. According to projections, the world population is expected to surpass 9 billion by 2050, necessitating a substantial increase in food production (FAO, 2003). However, conventional agricultural practices face numerous challenges, including limited arable land, climate variability, pest infestations, and declining soil fertility.

Genetic engineering has emerged as a revolutionary approach to crop improvement, enabling the direct manipulation of plant genomes to introduce desirable traits. Unlike traditional breeding methods, which rely on the selection of naturally occurring genetic variations, genetic modification allows precise and targeted insertion of genes from diverse organisms (Gelvin, 2003). This technology has led to the development of genetically modified crops capable of addressing critical agricultural constraints.

Since the introduction of the first commercial GM crops in the mid-1990s, their cultivation has expanded significantly worldwide. Countries such as the United States, Brazil, India, and China have adopted GM crops extensively, particularly for crops like soybean, maize, cotton, and canola (Briefs, 2017). The widespread adoption of GM crops underscores their potential to enhance agricultural productivity and sustainability.

2. Historical Development of Genetically Modified Crops

The historical development of genetically modified (GM) crops is rooted in the remarkable progress of molecular biology and genetics during the 20th century. The discovery of the double-helical structure of DNA by Watson and Crick in 1953 marked a turning point in biological sciences, providing the fundamental understanding of genetic information storage and transmission. This was followed by the development of recombinant DNA technology in the early 1970s, which enabled scientists to manipulate genetic material and transfer genes across species barriers (Cohen *et al.,* 1973).

The first successful genetic transformation of plants was achieved in 1983 using *Agrobacterium tumefaciens*, a soil bacterium capable of naturally transferring DNA into plant genomes. This breakthrough demonstrated the feasibility of introducing foreign genes into plants and laid the foundation for plant genetic engineering (Fraley *et al.,* 1983; Gelvin, 2003).

The commercialization of genetically modified crops began in 1994 with the introduction of the Flavr Savr tomato, engineered for delayed ripening and extended shelf life. Although its market success was limited, it represented a major milestone in agricultural biotechnology (Bruening & Lyons, 2000).

During the late 1990s, the development and widespread adoption of herbicide-tolerant crops (e.g., glyphosate-resistant soybean) and insect-resistant crops (e.g., Bt cotton and Bt maize) revolutionized agriculture. These crops significantly reduced pesticide usage and improved yields (James, 2005; Shelton *et al.,* 2002).

In recent years, advancements in genome-editing technologies such as CRISPR-Cas systems have further transformed genetic engineering by enabling precise and targeted modifications without the need for transgene insertion (Jinek *et al.,* 2012). These developments represent a shift toward more efficient, safe, and acceptable approaches to crop improvement.

3. Techniques Used in Genetic Modification

3.1 Recombinant DNA Technology

Recombinant DNA (rDNA) technology is the foundation of genetic engineering. It involves the isolation of a gene of interest, its insertion into a suitable vector (such as a plasmid), and its integration into the host plant genome. This process allows the expression of new traits in plants that are not achievable through conventional breeding (Gelvin, 2003).

3.2 *Agrobacterium*-Mediated Transformation

Agrobacterium tumefaciens has the natural ability to transfer a segment of its DNA (T-DNA) into plant cells. Scientists exploit this mechanism by replacing the tumor-inducing genes with genes of interest. This method is widely used due to its high efficiency, stable gene integration, and relatively low cost (Gelvin, 2003).

3.3 Biolistic (Gene Gun) Method

The biolistic method involves the delivery of DNA-coated microscopic particles (usually gold or tungsten) into plant tissues using high-velocity propulsion. This technique is particularly useful for monocot plants such as maize and rice, which are less susceptible to *Agrobacterium*-mediated transformation (Sanford, 1990).

3.4 CRISPR-Cas9 and Genome Editing

CRISPR-Cas9 technology enables precise editing of specific DNA sequences within plant genomes. Unlike traditional transgenic approaches, CRISPR allows gene knockout, insertion, or modification without introducing foreign DNA, thereby reducing regulatory concerns and off-target effects (Jinek *et al.,* 2012; Doudna & Charpentier, 2014).

4. Classification of Genetically Modified Crops

4.1 Insect-Resistant Crops

Insect-resistant crops, particularly Bt crops, contain genes from *Bacillus thuringiensis* that produce insecticidal proteins targeting specific pests. These crops have significantly reduced the need for chemical insecticides and increased crop yields (Shelton *et al.,* 2002).

4.2 Herbicide-Tolerant Crops

Herbicide-tolerant crops are engineered to survive applications of broad-spectrum herbicides such as glyphosate. This allows effective weed management and promotes conservation tillage practices, reducing soil erosion (Duke & Powles, 2008).

4.3 Nutritionally Enhanced Crops

Biofortified GM crops are designed to improve nutritional quality. Golden Rice, enriched with β-carotene, is a prominent example aimed at combating vitamin A deficiency in developing countries (Paine *et al.,* 2005).

4.4 Abiotic Stress-Tolerant Crops

These crops are engineered to withstand environmental stresses such as drought, salinity, and extreme temperatures. Such traits are increasingly important in the context of climate change (Zhu, 2016).

5. Applications of Genetically Modified Crops

5.1 Enhancing Food Security

GM crops contribute significantly to global food security by increasing yields and reducing crop losses. A meta-analysis by Klümper and Qaim (2014) reported an average yield increase of 22% in GM crops.

5.2 Environmental Sustainability

GM crops have reduced pesticide use and promoted conservation agriculture. This leads to lower greenhouse gas emissions and improved soil health (Brookes & Barfoot, 2020).

5.3 Industrial Applications

Genetically modified crops are used in the production of biofuels, industrial enzymes, and biodegradable plastics, contributing to sustainable industrial practices (Ma *et al.,* 2005).

5.4 Pharmaceutical Applications

"Molecular farming" involves using plants as bioreactors to produce vaccines, antibodies, and therapeutic proteins, offering cost-effective alternatives to traditional production systems (Ma *et al.,* 2005).

6. Advantages of Genetically Modified Crops

6.1 Increased Agricultural Productivity

Enhanced resistance to pests and environmental stresses leads to higher crop yields and improved food availability (Klümper & Qaim, 2014).

6.2 Reduction in Chemical Usage

Bt crops have significantly reduced the use of chemical pesticides, minimizing environmental pollution and health risks (Brookes & Barfoot, 2020).

6.3 Improved Nutritional Quality

Biofortified crops help address micronutrient deficiencies, particularly in developing countries (Paine *et al.,* 2005).

6.4 Economic Benefits

Farmers benefit economically through increased yields and reduced input costs, although the extent of benefits varies regionally (Klümper & Qaim, 2014).

7. Risks and Challenges

7.1 Human Health Concerns

Potential risks include allergenicity and toxicity; however, extensive evaluations have shown that approved GM foods are safe for consumption (WHO, 2005; Nicolia *et al.,* 2014).

7.2 Environmental Concerns

Concerns include gene flow to wild relatives, development of resistant pests, and effects on non-target organisms. These risks require continuous monitoring (Snow *et al.,* 2005).

7.3 Resistance Development

Prolonged use of Bt crops may lead to insect resistance, necessitating strategies such as refuge planting to delay resistance evolution (Tabashnik *et al.,* 2013).

7.4 Socio-Economic Issues

Intellectual property rights, seed patents, and corporate control raise concerns about farmer autonomy and equitable access to technology.

8. Biosafety and Regulatory Framework

Biosafety ensures that GM crops do not pose risks to human health or the environment. International frameworks such as the Cartagena Protocol on Biosafety regulate the safe handling and movement of genetically modified organisms (FAO, 2003).

Regulatory systems involve rigorous risk assessment, including toxicity, allergenicity, environmental impact, and gene stability. Countries adopt different regulatory approaches based on scientific, socio-economic, and political factors.

9. Ethical and Social Considerations

The adoption of GM crops is influenced by ethical considerations, public perception, and cultural values. Concerns about "tampering with nature," corporate control of seeds, and transparency in labeling continue to shape public debates.

Effective science communication, stakeholder engagement, and policy transparency are essential for improving public acceptance and informed decision-making.

10. Future Prospects

The future of GM crops is being shaped by advanced genome-editing technologies such as CRISPR-Cas systems, which allow precise and efficient genetic modifications (Doudna & Charpentier, 2014).

Emerging innovations include:

- Climate-resilient crops capable of withstanding extreme conditions
- Nitrogen-efficient crops reducing fertilizer dependence
- Enhanced photosynthetic efficiency for higher productivity
- Integration with artificial intelligence and precision agriculture

These advancements are expected to play a crucial role in achieving sustainable agricultural development and global food security.

Conclusion

Genetically modified (GM) crops have significantly reshaped modern agricultural practices by offering effective solutions to major global challenges such as food insecurity, environmental degradation, and climate change. The large-scale adoption of GM crops has resulted in improved crop productivity, enhanced resistance to pests and diseases, and better resource-use efficiency. Several studies have demonstrated that GM crops can increase yields while reducing pesticide inputs, thereby contributing to both economic and environmental sustainability (Klümper & Qaim, 2014; Brookes & Barfoot, 2020).

In addition to increasing agricultural productivity, GM crops have shown considerable promise in improving nutritional quality through biofortification. A well-known example is Golden Rice, which has been engineered to produce β-carotene to combat vitamin A deficiency, particularly in developing countries (Paine *et al.,* 2005). Furthermore, GM crop adoption has facilitated conservation agriculture practices, such as reduced tillage, which help improve soil health and lower greenhouse gas emissions (Brookes & Barfoot, 2020).

Despite these benefits, concerns regarding biosafety, ecological impacts, and socio-economic implications remain significant. Environmental risks, including gene flow to wild relatives, the evolution of resistant pests, and potential effects on non-target organisms, require continuous monitoring and appropriate management strategies (Snow *et al.,* 2005; Tabashnik *et al.,* 2013). Additionally, issues related to intellectual property rights and the control of seed markets raise concerns about equitable access and farmer dependency on biotechnology companies.

From a human health perspective, extensive scientific evaluations over the past decades have consistently indicated that approved GM foods are as safe as their conventional counterparts (WHO, 2005; Nicolia *et al.,* 2014). However, maintaining public trust requires transparent regulatory systems, rigorous safety assessments, and effective science communication.

Looking forward, emerging genome-editing technologies such as CRISPR-Cas systems offer unprecedented precision and efficiency in crop improvement. These technologies have the potential to overcome many limitations associated with traditional genetic modification and may lead to greater public acceptance (Doudna & Charpentier, 2014). Moreover, the integration of GM technology with precision agriculture and climate-smart farming approaches is expected to further enhance agricultural sustainability and resilience.

In conclusion, genetically modified crops represent a powerful tool for addressing the complex challenges of global agriculture. Their successful and responsible implementation depends on a balanced approach that integrates scientific innovation with regulatory oversight, ethical considerations, and public engagement. Continued research, policy support, and global collaboration will be essential to maximize the benefits of GM crops while minimizing potential risks, thereby ensuring a sustainable and resilient food system.

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