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Life Science: A Renaissance Approach

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PREFACE

The book Life Science: A Renaissance Approach has been conceptualized to provide readers with a holistic and multidisciplinary understanding of life sciences in the modern era. The term 'Renaissance' signifies revival, reawakening, and transformation. In this context, the book revisits fundamental biological concepts through the lens of current innovations and applications, reflecting a renaissance in life science education and research.

In recent decades, the life sciences have undergone a paradigm shift, integrating molecular biology, genetics, biotechnology, ecology, and computational sciences to address global challenges. This integration has catalyzed groundbreaking discoveries, from decoding genomes to developing targeted therapeutics, environmental remediation strategies, and sustainable food systems. Recognizing this shift, the chapters in this volume encompass diverse themes, aiming to bridge classical knowledge with contemporary advancements.

The book brings together contributions from researchers and academicians across various sub-disciplines, offering insights into emerging research trends, methodologies, and applications. It caters to undergraduate and postgraduate students, researchers, and educators seeking updated perspectives to enrich their academic pursuits and teaching practices. Each chapter is structured to provide conceptual clarity, recent developments, and practical relevance, fostering curiosity and critical thinking.

Our aim is to rekindle the spirit of inquiry in learners, encouraging them to view life sciences not merely as isolated subjects but as an integrated domain essential for addressing health, environmental, and societal issues. This renaissance approach nurtures interdisciplinary learning and empowers readers to explore innovative solutions to global problems such as climate change, biodiversity loss, and emerging diseases.

We extend our sincere gratitude to all authors and reviewers for their scholarly contributions and valuable suggestions. We also thank the editorial team and publishers for their dedicated efforts in bringing this book to fruition. We hope Life Science: A Renaissance Approach serves as a valuable resource, inspiring readers to engage deeply with the dynamic world of life sciences and contribute meaningfully to its ever-expanding horizons.

- Editors

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FACILITATE TO DAIRY FARM THROUGH VENTILATION FOR HEAT STRESS REDUCTION

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Introduction:

Efficient ventilation is a critical component of dairy farm management, directly impacting animal health, productivity, and overall farm hygiene. Proper airflow helps regulate temperature, humidity, and gas concentrations within housing facilities, creating a comfortable environment for dairy cattle and reducing the risk of respiratory diseases and other health issues. Ventilation is a critical component of dairy farm management that ensures a healthy and comfortable environment for dairy cattle [5]. Proper ventilation involves the circulation of fresh air within the housing facilities to remove excess moisture, heat, odor, dust, and harmful gases such as ammonia and carbon dioxide.

Effective ventilation helps maintain optimal temperature and humidity levels, reducing stress and promoting better health, feed intake, and milk production in dairy animals [7]. It also minimizes the risk of respiratory diseases and other health problems associated with poor air quality.

In dairy farm design, ventilation systems can be natural, mechanical, or a combination of both, tailored to the specific climatic conditions and housing structures. Implementing appropriate ventilation strategies is essential for improving animal welfare, productivity, and overall farm sustainability.

Importance of Ventilation in Dairy Housing Ventilation in dairy housing is essential for maintaining a healthy, comfortable, and productive environment for dairy cows [9]. Its importance includes:

- **Maintaining Air Quality:** Proper ventilation reduces the buildup of harmful gases such as ammonia, carbon dioxide, and methane, which can cause respiratory issues and discomfort.
- **Temperature Regulation:** Adequate airflow helps control indoor temperatures, preventing heat stress during hot weather and maintaining comfort year-round.
- **Moisture Control:** Ventilation reduces humidity levels, preventing the growth of mold and bacteria, which can lead to infections and udder health problems.
- **Odor Management:** Good airflow minimizes unpleasant odors, improving the well-being of both animals and farm workers.

- **Disease Prevention:** Proper ventilation decreases the risk of airborne diseases by reducing pathogen load in the environment.
- **Enhanced Animal Productivity:** Comfortable, well-ventilated housing leads to better feed intake, milk production, and overall health of dairy cows.
- **Animal Welfare:** Ensuring proper airflow aligns with animal welfare standards by providing a clean, comfortable living space.
- **Waste Management:** Proper air circulation aids in the removal of manure odors and moisture, preventing the buildup of harmful bacteria and pests [6].

Types of Ventilation Systems

In dairy housing, proper ventilation is essential for maintaining animal health, comfort, and productivity. There are several types of ventilation systems commonly used, each suitable for different farm designs, climate conditions, and management goals. The main types include:

Natural Ventilation

Natural ventilation systems in dairy housing are essential for maintaining a healthy, comfortable environment for dairy cattle while minimizing energy costs. These systems utilize natural forces such as wind and temperature differences to promote airflow without relying on mechanical fans or ventilation equipment [1].

Key Components of Natural Ventilation in Dairy Housing:

- **Vents and Openings:** Strategically placed sidewall and ridge vents allow fresh air to enter and warm, stale air to escape.
- **Sidewall Openings:** These facilitate cross-ventilation, especially when wind direction is favorable.
- **Ridge Vents or Roof Openings:** Located at the top of the roof to allow hot, stale air to rise and exit.
- **Curtains or Adjustable Partitions:** Can be used to control airflow and optimize ventilation during different weather conditions.
- **Design Principles for Effective Natural Ventilation:**

Figure 1: Natural Ventilation

- **Proper Orientation:** Aligning the building to maximize wind flow, often east-west or north-south.
- **Building Height and Shape:** Taller structures promote better airflow; the shape influences how air moves within.

- **Openings Size and Placement:** Sufficient size and strategic placement ensure effective air exchange.
- **Use of Wind Breaks:** Trees or fences can influence airflow patterns positively or negatively, so their placement should be considered.

Advantages: Reduced energy costs, Improved air quality, Lower maintenance requirements, environmentally friendly.

Limitations: Less control over airflow compared to mechanical systems, Effectiveness depends on local climate and wind conditions, may require supplementary systems in extreme weather.

In Summary: Natural ventilation in dairy housing offers a sustainable and cost-effective way to maintain optimal conditions for dairy cattle, especially in moderate climates. Proper design and placement are crucial to maximize airflow and ensure the health and productivity of the animals.

Description: Utilizes natural airflow driven by wind and temperature differences.

Methods: Sidewall openings, ridge vents, windows, and adjustable curtains.

Advantages: Low cost, minimal energy use.

Limitations: Less control over airflow; effectiveness depends on weather conditions.

Mechanical Ventilation

Description: Uses fans and other mechanical devices to circulate air.

Mechanical Ventilation

Mechanical ventilation systems are essential in dairy housing to maintain optimal environmental conditions, ensuring the health, comfort, and productivity of dairy cattle. Proper ventilation helps control temperature, humidity, air quality, and the removal of odors and harmful gases like ammonia and methane.

- **Positive Pressure Ventilation:** Fans blow air into the barn, creating a positive pressure that pushes stale air out through exhaust vents.
- **Negative Pressure Ventilation:** Exhaust fans remove air from the barn, creating a negative pressure that pulls fresh air in through inlets.
- **Mixed-Flow Ventilation:** Combines both positive and negative pressure methods for optimized airflow.

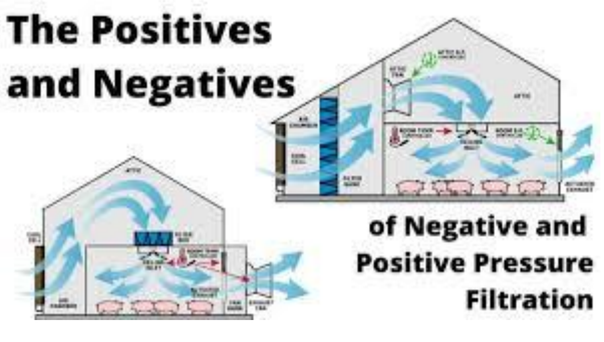

Figure 2: Positive and Negative Pressure Ventilation

Advantages: Greater control over air quality and temperature.

Limitations: Higher energy costs and maintenance.

Tunnel Ventilation

Tunnel ventilation systems are a popular and effective method for managing air quality and temperature in dairy housing. They are designed to provide a continuous flow of fresh air through long, narrow barns, helping to control heat stress, humidity, and airborne contaminants, thereby promoting the health and productivity of dairy cattle [4].

Description: Long, narrow barns with large inlet openings at one or both ends and exhaust fans at the other end.

Operation: Air is drawn through the barn by exhaust fans, providing effective cooling especially in hot climates.

Advantages: Effective in hot weather, suitable for large herds.

Figure 3: Tunnel Ventilation

Limitations: Less effective in cold weather without additional heating.

Cross Ventilation

Cross ventilation systems are an essential component in dairy housing designed to promote healthy airflow, regulate temperature, and improve air quality for dairy cattle. Proper ventilation helps reduce humidity, remove harmful gases like ammonia, and prevent the buildup of heat, thereby enhancing animal comfort and productivity [2].

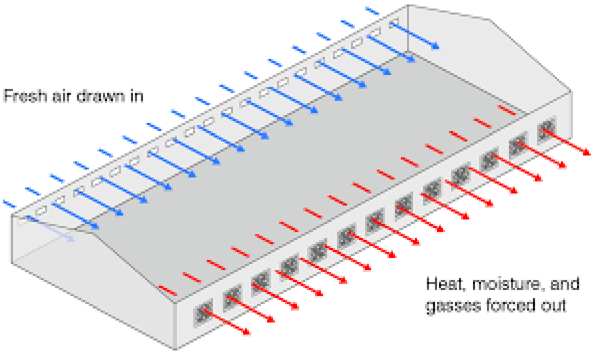

Figure 4: Cross Ventilation

Description: Air enters through openings on one side and exits on the opposite side, creating cross-flow.

Advantages: Good for moderate climates.

Limitations: Less effective in high humidity or extreme weather conditions.

Combination Systems

Combination ventilation systems in dairy housing integrate multiple ventilation strategies to optimize air quality, temperature regulation, humidity control, and animal comfort [3]. By leveraging the strengths of different systems, dairy farmers can create a healthier environment that promotes animal well-being and productivity [8].

Description: Integrates natural and mechanical ventilation to optimize airflow depending on weather conditions.

Each system can be customized based on climate, barn design, herd size, and management practices to ensure optimal air quality, temperature regulation, and humidity control in dairy housing.

Design Considerations for Ventilation

Building Orientation: Positioning to maximize airflow and minimize heat gain.

Vent Placement: Ridge vents, sidewall openings, and exhaust fans should be strategically located.

Air Exchange Rate: Sufficient turnover to maintain air quality; typically, 4-8 air changes per hour for dairy facilities.

Size of Openings: Based on barn size, number of animals, and prevailing weather conditions.

Insulation and Materials: To prevent heat loss or gain, depending on climate.

Factors Influencing Ventilation Effectiveness

Climate Conditions: Hot, humid climates require enhanced cooling strategies.

Barn Design: Open or closed sides, ceiling height, and roof design influence airflow.

Stocking Density: Higher densities necessitate better ventilation to prevent overcrowding.

Manure Management: Regular cleaning reduces odors and improves air quality.

Animal Age and Production Stage: Calves and dry cows may have different ventilation needs compared to lactating cows.

Practical Ventilation Strategies

Natural Ventilation Enhancements:

- Use of adjustable sidewall openings.
- Installing roof vents or ridge openings.
- Ensuring unobstructed airflow paths.

Mechanical Ventilation Optimization:

- Employing adequate exhaust fans with appropriate capacity.
- Using fans in combination with natural ventilation for hybrid systems.
- Incorporating air filtration where necessary.

Environmental Monitoring:

- Using thermometers, hygrometers, and gas detectors.
- Adjusting ventilation based on real-time measurements.
- Monitoring and Maintenance
- Regular inspection of vents, fans, and filters.
- Cleaning and servicing mechanical systems periodically.
- Monitoring environmental parameters to ensure standards are maintained.
- Training staff on ventilation management protocols.

Conclusion:

Effective ventilation is essential for maintaining a healthy, productive dairy herd. Combining proper design, strategic implementation, and regular maintenance of ventilation systems can significantly improve animal welfare and farm efficiency. As climate conditions evolve, adopting adaptable ventilation strategies will become increasingly important for sustainable dairy farming.

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HUMAN HEALTH RISKS: IMPACT OF PESTICIDE APPLICATION

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Abstract:

Pesticides are applied to eliminate the pests and insects that damage crops and negatively affect them. Various types of pesticides have been utilized for safeguarding crops for centuries. Pesticides aid in crop production; nevertheless, they also have a significant detrimental effect on the environment. Overusing pesticides can result in the loss of biodiversity. Numerous birds, aquatic species, and animals face dangers to their existence due to toxic pesticides. Pesticides pose a risk to environmental sustainability and global stability. This chapter aims to explore pesticides, their categories, benefits, and the environmental issues associated with them. The chapter also addresses pollution due to excessive pesticide use and the lasting effects of pesticides on the environment. As the chapter approaches its conclusion, it examines strategies for eliminating pesticide use and ultimately envisions the future consequences of pesticide elimination on the world.

Keywords: Pesticides, Pollution, Human Health, Environment.

Introduction:

The category of chemicals referred to as pesticides includes materials used as, fungicides, herbicides, insecticides, rodenticides, and nematicides [1]. Pesticides are widely recognized as crucial for agricultural advancement, as they help decrease losses in crop yields and enhance the affordability and quality of food [2,3,4]. Due to boost food production and manage insect-transmitted diseases, the development of pesticides surged during World War II (1939-1945). Furthermore, starting in the 1940s, the greater application of synthetic agricultural chemicals allowed for an additional rise in food output [1]. Additionally, global pesticide production rose at an annual rate of roughly 11%, growing from 0.2 million tons during the 1950s to over 5 million tons by the year 2000 [5]. Every year, three billion kilograms of pesticides are applied globally [6], yet merely 1% of these pesticides are successfully utilized for managing insect pests on specific plants [1]. The significant quantities of leftover pesticides infiltrate or contact non-target plants and environmental mediums. Pesticide contamination has, as a result, contaminated the environment and adversely affected human health [1,7].

This literature review initially offers fundamental scientific details regarding the agricultural development process, the historical context of pesticide application, common categories of pesticides in use, and the function of pesticides in agriculture. Attention is specifically directed towards pesticide behavior in the environment, climate change-related influences on pesticide usage, and its negative impacts on the natural surroundings. Ultimately, this research offers a novel approach to the use and regulation of pesticides.

Process of Agricultural Advancement

Agricultural advancement has a rich history in numerous regions across the globe. Farming activities commenced around 10,000 years ago in the Fertile Crescent located in Mesopotamia, which roughly aligns with present-day Iraq, Turkey, Syria, and Jordan [8]. Individuals residing in these regions gathered edible seeds using methods like fire-stick farming and forest gardening. As the population settled more and resided on farms, significant quantities of wheat, barley, peas, lentils, chickpeas, bitter vetch, and flax were grown [9]. Approximately 7500 years ago, rice and sorghum were cultivated in Africa's region [10]. Davies (1968) also points out that certain local crops were domesticated independently in West Africa, New Guinea, and Ethiopia approximately 7500 years ago. In China, rice and millet underwent domestication [11]. America independently cultivated corn, potatoes, and sunflowers [12]. Crops cultivated on farms frequently face issues with pests, weeds, and diseases that may lead to significant reductions in yield. Without pesticides, the decrease in fruits, vegetables, and cereals due to pests and diseases could reach 78%, 54%, and 32%, respectively [13]. Consequently, there is a pressing necessity for researchers and the general public to seek solutions to the issues created by pests and diseases.

Types of Pesticide in Use

Classification of Pesticides using various terms such as, functional groups, chemical categories mechanisms of action, and toxicity levels [14]. Pesticides are primarily classified according to the specific pests they address, including fungicides, insecticides, and herbicides. For example, fungicides are aimed at fungi, insecticides focus on insects, and herbicides are directed at weeds [15,16]. Pesticides are classified into two elements such as organic and inorganic elements according to their chemical classifications. Inorganic pesticides include copper sulfate, ferrous sulfate, lime, sulfur, and copper. The elements of organic pesticides are more complex [17]. Organic pesticides can be classified according to their chemical structure, comprising chlorohydrocarbon insecticides, organophosphate insecticides, carbamate insecticides, synthetic pyrethroid insecticides, herbicides that mimic metabolites and hormones, synthetic urea herbicides. Figure 1 presents an overview of the agricultural usage of each type of pesticide in China [18].

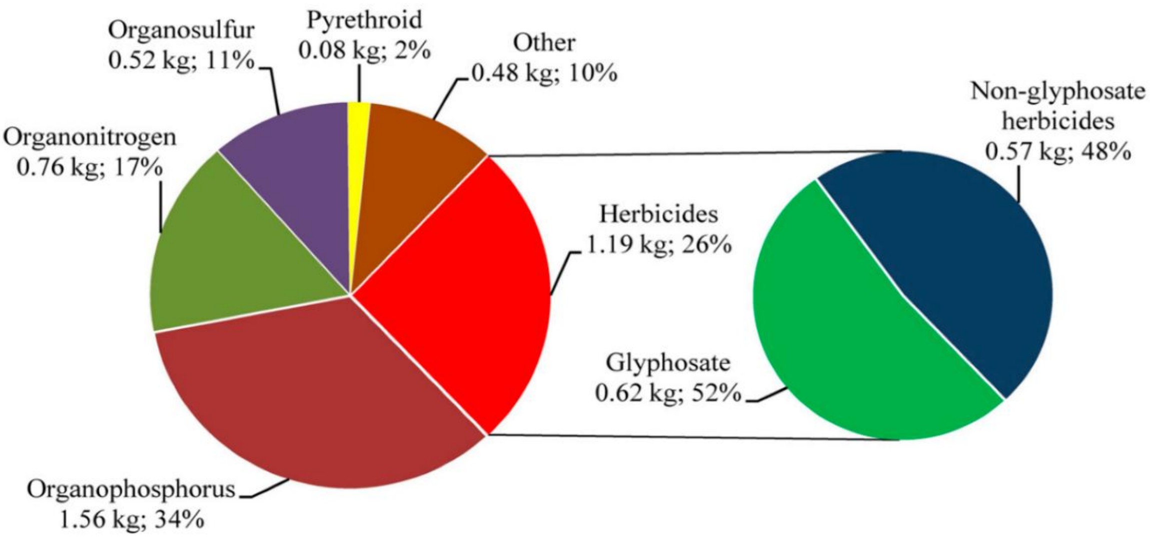

Figure 1: Summary of agricultural use of each class of pesticide in China [18]

Pesticide Behavior in the Environment

When pesticides are used on a specific plant or discarded, they can potentially enter the environment. Upon entering the environment, pesticides may experience processes like transfer (or movement) and degradation [20,21,22]. The breakdown of pesticides in the environment generates new substances [23]. Pesticides move from the intended location to other environmental media or unintended plants through transfer mechanisms such as adsorption, leaching, volatilization, spray drift, and runoff (Figure 2) [24]. The various kinds of chemicals reflect their distinct environmental behaviors. For instance, organochlorine substances like DDT exhibit low immediate toxicity yet demonstrate a notable capacity to build up in tissues and continue causing long-term harm. Their sale has been prohibited in many nations, yet their residues persist in the environment for an extended period due to their characteristics. Although organophosphate pesticides are not very persistent, they exhibit significant acute toxicity in mammals [17,25].

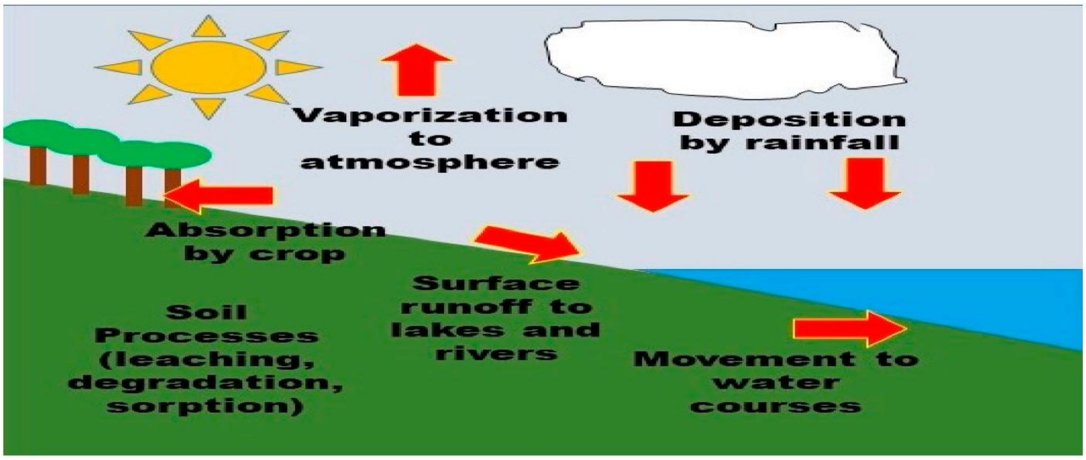

Figure 2: Pesticide behavior in the natural environment

Impact of Climate Change-Related Factors on Pesticide Use

The adoption of synthetic pesticides has surged dramatically after World War II (1939–1945) to avert, lessen, or exterminate pests, decrease agricultural production losses, and enhance cost-effective yields and food quality [25]. The application of pesticides is affected by various elements, including socioeconomic conditions, environmental factors like soil quality, crop development, the presence of pests, weeds, and diseases, as well as how pesticides react in the environment (Figure 3). These elements are primarily affected by climate change (Figure 4)

Figure 3: Influencing factors for pesticide use

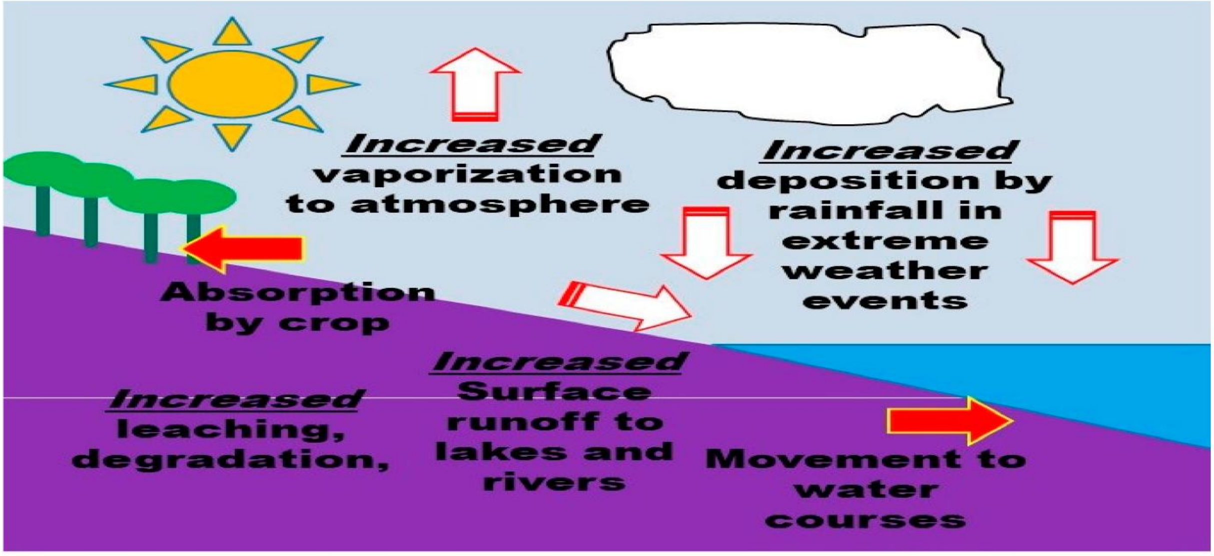

Figure 4: Climatic factors affect the environmental behavior of pesticides

Pesticide Contamination and Its Adverse Effects on the Water

Numerous chemicals, such as certain pesticides, have been found in both surface water and groundwater [20,26]. It is commonly acknowledged that pesticides reach both surface water and groundwater through direct application for managing aquatic weeds and insects, runoff and percolation from agricultural fields, drift from agro-industrial wastewater, discharge from equipment used for the formulation and application of pesticides, atmospheric deposition, and air/water interaction. Groundwater becomes polluted when pesticides leak from agricultural fields, mixing zones, or waste disposal locations [29]. Surface water systems, including rivers, lakes, streams, reservoirs, and estuaries, are especially prone to accumulating pesticides and other materials [27] since they function as small, enclosed receptacles for the by-products of human activity. Additionally, pesticides present in surface water can transfer to groundwater via soil infiltration. They also enter the atmosphere through evaporation and transpiration [30]. Atmospheric water and groundwater can also restore surface waters. The transport of pesticides within water results in the pollution of water sources by pesticides [20,31]. The contamination of groundwater and surface water from pesticides presents considerable dangers to freshwater and coastal ecosystems worldwide [19,28,32]. Moreover, due to high expenses and considerable technological requirements, addressing polluted surface water, particularly contaminated groundwater, presents difficulties [19,33]

Numerous reports exist regarding pesticide pollution in both surface water and groundwater globally [34,35,36,37,38,39]. For instance, the United States Geological Survey (USGS) detected various pesticides in over 90% of water and fish samples gathered from streams in the US [40]. Research findings showed that pesticide pollution was observed in surface water in China's Bohai Sea and Yong-ding River, with varying levels of contamination across different seasons. One report suggested that an increased level of glyphosate in dry seasons could result from decreased dilution from rainfall [41,42,43]. Pesticide contamination in water directly affects the quality of local drinking water and indirectly influences other species by moving through the soil and food chain [44].

Conclusions:

Agricultural progress has an extensive history in various regions across the globe. Considerable benefits have been achieved by utilizing pesticides in different areas, including agriculture and public health. Pesticides applied daily for public health to eradicate pests like mosquitoes, rats, ticks, and mice in residences, workplaces, shopping malls, and along roadways Consequently, the significant load of illnesses attributed to these vectors has been greatly diminished or eradicated. Farmers have utilized them to manage weeds and pests in farming, and significant rises in crop yields have been noted due to pesticide application. When applying pesticides to plants, one must consider the behavior of pesticides in the environment, including their transfer and degradation. Inadequate pesticide application and management, along with pesticide interactions in the environment, result in environmental contamination, which encompasses soil pollution, water pollution, air pollution, and food contamination.

Consequently, it is essential to manage pesticide pollution and its adverse effects on the environment and other non-target species. Additional research should emphasize both workplace and environmental exposures along with the associated health risk assessment of pesticides to enhance the understanding of pesticide usage and management going forward. To lessen the detrimental impact of pesticide pollution on the environment and non-target organisms, innovative scientific approaches and technologies, along with effective strategies like integrated pest management (IPM), regulations that ban high-risk pesticides, and the creation of a national implementation plan (NIP), must be adopted to mitigate the adverse effects of pesticides. Additionally, it is essential to communicate the scientific results of exposure and occupational and environmental health risk evaluations to impart scientific training for pesticide use, prevent negative health impacts from pesticide application, and enhance safety for both applicators and communities to foster sustainable development. Biopesticides must be created in conjunction with chemical pesticides to reduce pesticide pollution.

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A NEW RENAISSANCE FOR CREATIVITY IN TECHNOLOGY AND THE ARTS IN THE CONTEXT OF VIRTUAL WORLDS

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Abstract:

The genesis of new ideas—ranging from immediately applicable innovations to visionary "blue sky" concepts whose value may only be recognized generations later—remains a critical question in research and development. The evolution of computing and digital media offers a compelling case study: while some early visions of technology have endured, others have faded into obsolescence. These raises pressing questions about how we might leverage historical patterns to guide contemporary and future research. In an era where one "Internet year" compresses seven calendar years of progress, virtual worlds emerge as potent accelerators for ideation, prototyping, and evaluation. The diverse ecosystem of digital media—encompassing sensors, interactive games, social platforms, IoT devices, and more—serves as a dynamic testbed for innovation. Yet, as disciplines increasingly adopt virtual environments for collaboration, their effectiveness in bridging methodological divides remains underexplored. This paper argues that traditional disciplinary silos have reached their limits, advocating instead for interdisciplinary collaboration as the path forward. We evaluate current enablers of such collaborations and propose a new Renaissance at the intersection of technology and the arts, where creative processes and technical execution mutually inform breakthroughs.

Keywords: Creative Processes, Virtual Design, Virtual Exhibition, Cyberworlds, Social Media Interactions, Paradigm Shift, Interdisciplinary Collaboration.

1. Introduction:

In the early 21st century, humanity is witnessing a profound cultural and technological transformation—a new renaissance that echoes the creative upheaval of the 15th century, but in a digitally mediated form. At the heart of this transformation lies the convergence of advanced technologies such as artificial intelligence (AI), virtual reality (VR), augmented reality (AR), and blockchain, which are fundamentally redefining the boundaries of artistic expression and technological innovation. Virtual worlds—immersive, persistent, and often decentralized digital environments—have emerged as fertile ground for this creative reawakening.

These virtual spaces, from metaverse platforms to interactive digital galleries and AI-generated environments, offer artists, designers, and technologists unprecedented opportunities for collaboration, storytelling, and experimentation. They dissolve traditional barriers between creator and audience, reality and simulation, and art and code. As a result, new genres of digital performance, immersive art installations, and interactive media are flourishing in ways previously unimaginable.

More than just tools or mediums, virtual worlds are becoming cultural ecosystems where imagination and technology coalesce. In this context, the relationship between art and technology is no longer merely utilitarian; it is symbiotic and generative. This new renaissance challenges conventional notions of authorship, ownership, and aesthetic experience, while simultaneously empowering diverse voices to engage with global audiences in transformative ways.

This paper explores how virtual worlds are catalyzing a resurgence of creativity in both technology and the arts, examining their implications for artistic practice, cultural identity, education, and the future of human expression in an increasingly digital society.

2. Communication

Creation and communication have been fundamental human activities since the dawn of civilisation. Cave paintings, as some of the earliest artefacts, embody both these aspects. They not only conveyed the ideas and experiences of their creators but also reflected the cultural context and available resources of the time. In this sense, creation and communication are bidirectional: they express the internal thoughts of the creator to others and simultaneously reflect back to the creator a sense of what has been brought into being.

Moreover, every created work carries the potential to communicate beyond its original context—to future observers who were not part of its time or culture. It tells a story about the past, though that story may be interpreted in multiple ways depending on the viewer's perspective.

As raw materials and cultural contexts evolve, so too do the forms and meanings of artefacts. The ideas of creators—being dynamic and influenced by their surroundings—also change over time. This synchronicity between creator, context, and creation forms a continuous narrative that not only documents but reshapes cultural meaning. What was once a reflection of one era may become the foundation for new interpretations in another.

Over generations, the meaning of a created work can ripple outward, influencing new cultural understandings—just like a stone cast into a pond sends ripples far and wide.

3. Changes Produced by Tools and Interaction

Another important dimension of creative work lies in its potential to alter the attitudes and perspectives of both the observer and the creator. A powerful image or text can provoke responses ranging from cultural inspiration to geopolitical conflict. For instance, nations may go to war over a visual representation deemed offensive, or conversely, be moved toward reconciliation through the influence of a symbolic image or a compelling piece of writing. In this sense, the impact of creative works can be profound and far-reaching.

Isaac Newton's third law of motion—stating that for every action there is an equal and opposite reaction—though grounded in the physical sciences, can be metaphorically extended to the domains of art, creativity, and culture. Creative expressions may generate responses that ripple through social, emotional, or political domains, producing effects as powerful as any physical force.

The evolution of human creativity has always been shaped by the tools available. From early visual imagery to the development of written language, from two-dimensional drawings to three-dimensional sculptures, tools have enabled creators to give form to abstract thought. The work of Michelangelo, for example—spanning drawings, paintings, and sculptures—embodied his interpretations of religious and philosophical themes, each medium shaped by the tools and materials of his time.

The nature of the tool not only influences the form and outcome of the artwork but also reflects the broader cultural and temporal context. A recreated artwork using modern tools may yield a completely different result, shaped by both technological affordances and contemporary cultural conditions. Thus, the tool is not merely an extension of the creator's hand—it is embedded within the creative environment itself.

Traditionally, artworks—whether visual, textual, or sculptural—have been regarded as immutable. Artistic and literary traditions have long upheld the sanctity of the original work, protecting it through notions of authorship and copyright. These cultural norms positioned the creator as the sole authority, and the audience as passive recipients.

However, contemporary practices increasingly invite participation and reinterpretation. Modern artists may intentionally design interactive installations or exhibitions that allow audiences to contribute, alter, or co-create. In such cases, the original work becomes dynamic—an evolving artefact that incorporates not only the artist's vision but also the collective creativity of those who engage with it. Over time, such participatory works may transform into entirely new forms, reflecting the cumulative dialogue between artist, audience, and context.

4. The Origin of New Ideas

The genesis of a new idea—particularly in the context of creative work—is a complex and often elusive process. Where, indeed, does a new idea originate? Does it emerge from the mind of the creator as a spontaneous insight? Is it sparked by the careful observation of the natural world, as exemplified by the earliest cave paintings that likely mirrored the lived experiences and surroundings of early humans? Could it be catalyzed by the advent of a new tool or medium, offering novel possibilities for expression? Or is it shaped by the broader socio-cultural environment in which the creator is embedded?

In reality, the origin of new ideas often lies in a confluence of these elements. Creative inspiration frequently arises from an intricate blend of internal cognition, external observation, environmental stimulus, cultural conditioning, and technological affordance. It is neither wholly internal nor purely external, but situated within the dynamic interplay between the individual and their world.

This moment of creative genesis is commonly symbolized by the image of a lightbulb—an emblem of sudden insight or illumination. Beyond its visual metaphor, "illumination" in this context captures the essence of cognitive clarity: the moment when disparate elements coalesce into a novel concept or vision. It reflects not just the emergence of something new, but the moment of realization that something new *can* be formed.

New ideas are, thus, not isolated flashes of brilliance, but are often the result of prior experiences, accumulated knowledge, and the creator's interaction with their tools, communities, and surroundings. Whether intuitive or deliberate, the emergence of creative thought is a dynamic and contextually embedded process.

Figure 1: A picture of a lightbulb is associated with someone having an idea, a sign of creativity

5. Does Technology Produce a Paradigm Shift?

The illustration in Figure 1 itself is a product of technological mediation, exemplifying how deeply digital tools have permeated contemporary creative processes. In today's world, technology must be acknowledged as a fundamental component of the creative toolkit. Among these, digital technologies—ranging from image editing software to machine learning algorithms—are increasingly shaping how artists, designers, engineers, and scientists generate and interpret creative outputs.

For example, the renowned artist David Hockney used an iPad to create a series of digital landscape artworks, many of which were showcased in prominent national and international exhibitions. This case exemplifies how technology can serve as an artistic medium. Yet, it also raises critical questions: Is technology merely a neutral enhancer of human creativity, or does it shape and constrain the creative process in subtle, perhaps unintended ways? Could it be that the convenience and power of digital tools obscure or even limit aspects of deep, reflective creativity?

To address these questions, it is necessary to explore the multifaceted roles that technology plays in creative practice.

5.1 Technology as Computation

Digital technology enables algorithmic generation of artistic content through computational design. Computers can execute algorithms that manipulate color, form, and geometry to generate visual outputs that are then rendered via screens or printers. While such works are often displayed alongside traditional artworks, they pose a fundamental question of authorship: Who is the true creator—the machine or the human?

In reality, the computer remains a tool—albeit a powerful one—operating based on human-defined algorithms. The creative impulse still originates from the human designer. This relationship is analogous to Hockney's use of the iPad: while the medium is digital, the artistry remains human. It is worth noting that the acceptance of such tools is often influenced by the status of the creator. Pioneering artists play a critical role in normalizing new tools, thereby expanding the boundaries of what is considered legitimate creative practice.

5.2 Technology as Synthesizer

One of the most powerful aspects of digital technology is its capacity to synthesize disparate data sources into unified creative expressions. Whether combining external inputs (e.g., sensors, video, voice) or internally generated data (e.g., simulations, procedural models), digital systems can produce novel artworks or immersive virtual environments.

Such environments may replicate aspects of the natural world or represent entirely imagined spaces. Here, the technology serves as a canvas for the human imagination—a medium through which abstract concepts can be rendered tangible.

5.3 Technology as Interactor

Beyond synthesis, technology also enables interactive creativity. In architecture, for instance, virtual models allow designers to dynamically alter elements of a structure in real-time, assessing usability, aesthetics, or structural integrity. These systems not only enhance user agency but also embed feedback loops into the design process.

Interactive digital platforms democratize creation by enabling users to manipulate, adapt, and respond to evolving designs. This interactive aspect blurs the lines between creator and user, making creativity a collaborative, iterative act.

5.4 Technology as Integrator

Digital platforms facilitate the integration of multiple forms of media—text, image, sound, and video—into cohesive experiences. Through this multimodal integration, creators are empowered to communicate across diverse expressive registers, making their works more immersive, accessible, and resonant.

The convergence of media through technology allows interdisciplinary narratives to flourish—where, for instance, storytelling can incorporate animation, geospatial data, and voice, creating compelling hybrid forms of expression.

5.5 Technology as Automaton

Finally, technology can operate autonomously when programmed with a defined set of instructions, as in the case of industrial robots or autonomous systems. While these systems lack intentionality or creativity in a human sense, they can perform tasks with high precision and efficiency.

However, these automated processes still originate from human design. The instructions, decision trees, or neural networks are all human-conceived—even if their execution becomes detached from moment-to-moment human oversight. The factory robot, for instance, exemplifies *automation*, not *autonomy*, and is best understood as an extension of the human designer's logic.

5.6 A Paradigm Shift in Creativity through Digital Environments

The emergence of digital environments poses an important question: does the integration of new technology represent a paradigm shift in creative processes? A synthetic or digital world—being artificial yet interactive—offers novel avenues for exploration and innovation. These environments stimulate ideas and support creative practices that might not have been conceivable within the constraints of the physical world. Their potential appears to be limited only by the imagination of those engaging with them.

The use of new tools and approaches often attracts a dedicated community of practitioners who drive innovation and extend its applications. Such developments would not have occurred without the advent of digital technology, marking a clear departure from traditional creative pathways. Moreover, the scale of information involved in these environments is vast—far exceeding that of natural settings. In this sense, digital media shares transformative potential with historical milestones such as the invention of the printing press, which revolutionized communication and knowledge dissemination in the fifteenth century.

This phenomenon can be contextualized using Thomas Kuhn’s concept of a paradigm shift—originally formulated to describe the seismic changes brought about by the Scientific and Industrial Revolutions during the Age of Enlightenment. These shifts redefined humanity’s understanding of nature and introduced efficiencies in manufacturing, communication, and transport. Similarly, digital technologies are reshaping our comprehension of complex phenomena, not necessarily at the macro level, but at more granular levels through disciplines such as genetics, quantum physics, and cosmology.

The key enablers of this digital transformation are the computer, which provides the computational power to construct virtual worlds, and the Internet, which enables global connectivity and collaboration. These tools have facilitated the real-time processing and visualization of massive datasets (often termed *Big Data*), enabling interdisciplinary teams across international research centres to generate insights previously unattainable.

While the shift from the medieval to the scientific era marked one kind of revolution, the current digital transformation may, in retrospect, be recognized as a new Renaissance. Its full impact on society and creative expression may only become fully apparent with time.

Among the numerous changes driven by the digital revolution, connectivity and communication emerge as the most crucial elements affecting both creativity and society at large. These aspects warrant deeper exploration to understand the evolving landscape of human innovation and interaction.

6. Exploring Creativity in the Digital Age

Creativity can be broadly defined as the use of imagination to innovate and produce something new. It involves the generation of original ideas that lead to novel approaches, artworks, or inventions. In many cases—especially in domains like digital environments—creativity may rely heavily on expertise, where technical skill is essential. Beyond skill, it also depends on motivation and opportunity. For instance, the creation of a significant piece of art might require months of dedication, experimentation, and iteration. In emerging areas such as virtual worlds, creativity is often fueled by access to the right tools and environments.

The value of creativity is multifaceted and context-dependent. In the arts, for example, the value of a painting or sculpture may be judged based on its aesthetic appeal. In literature, the worth of a book might vary depending on the genre and its ability to engage readers. When it comes to virtual environments, creative value may lie in the functionality, form, and usability of the digital space.

Communicating the processes of creativity can occur in several ways. Most directly, a created work—such as a painting, sculpture, or digital artifact—can stand alone as a unique expression of the creator's vision. These works are often open to multiple interpretations, both at the time of creation and in later periods. In some cases, the creator may also articulate their intent through descriptive narratives or visual documentation that accompanies the development process. Moreover, a finished creative work may gain aesthetic value and significance that extend far beyond its original context or inspiration.

7. Virtual Worlds and Creativity

Virtual worlds offer dynamic environments where creators and collaborators can come together—regardless of their physical locations—to engage in joint creative tasks or projects. These environments can also include public participants, either as passive viewers or active interactors. In some cases, the audience may even contribute directly to the creative process by proposing modifications to the work, which the original creators may incorporate.

A virtual world can function as an immersive, walk-in environment, such as that illustrated in Figure 2. In such cases, real-time sensor technology embedded in the physical setting (e.g., the CAVE—Cave Automatic Virtual Environment) provides data to computers generating the virtual content. As users move through the physical space, the corresponding virtual experience adjusts in real time, enabling a highly responsive and intuitive interaction.

Additionally, users may be equipped with hand-held devices connected to the system, allowing them to interact directly with virtual objects. These interactions might involve navigation, editing, or modification of the environment. For instance, if the virtual world contains an artwork, the user-as-artist can immediately alter aspects such as shape or colour. For this interaction to be effective, however, the device and interface must be well aligned with the artist's creative preferences and working style, so as to facilitate rather than hinder the creative process.

Interestingly, the term "CAVE" may intentionally allude to Plato's famous Allegory of the Cave from *The Republic*. In Plato's narrative, individuals chained inside a cave perceive only the shadows of reality projected on a wall—suggesting a world of illusion and limited perception. Similarly, in a virtual world, users navigate a constructed reality, where the boundaries between perception, reality, and imagination become fluid and interpretable. This philosophical parallel reinforces the idea that virtual environments can both challenge and expand the boundaries of human creativity and understanding.

Figure 2: A cave digital world

A walk-in virtual environment—such as the Cave system depicted in Fig. 2—illustrates how real-time sensory input from the physical world is processed to simulate an immersive, interactive experience. As users move, their perspective within the virtual space changes accordingly. Equipped with hand-held input devices, users can interact with and even alter virtual elements—such as modifying the color or shape of a digital artwork—on the fly.

However, for such interactions to enhance creativity, the interface must align with the artist's workflow rather than disrupt it.

The Cave system may symbolically reference Plato's *Allegory of the Cave* from *The Republic*, where chained prisoners interpret reality based only on shadows projected on a wall, unaware of the true forms behind them. In contrast, today's virtual environments are not mere philosophical constructs or allegories. Though artificial, they are computationally constructed and simulate real-world experiences, enabling users to explore and interact meaningfully within a modeled 3D space.

Immersive virtual environments have proven particularly effective in architectural design. Research suggests that designers perceive spatial relationships and volumes more effectively in 3D virtual worlds than in traditional 2D blueprints [2]. These environments employ depth cues to simulate three-dimensionality, enhancing exploration and decision-making. This can significantly improve design efficiency and reduce costs.

Virtual worlds also support simulation, exemplified by flight simulators used in pilot training. These simulators replicate the visual and physical conditions of flying with high accuracy and allow for safe practice of both routine and emergency maneuvers. In many ways, such simulations exceed the capabilities of real-world scenarios by enabling safe experimentation and extended training.

Similarly, virtual environments can enhance creative processes, enabling content generation, modification, and exploration at a pace and scale not feasible in the physical world. In this sense, they echo Plato's Cave by enabling users to engage with alternate realities—though here, the realities are constructed, interactive, and editable, often powered by artificial intelligence.

8. Human Creativity

The integration of digital technologies into the creation and dissemination of artistic works has prompted a renewed examination of the cognitive and emotional processes underlying human creativity. This parallels developments in virtual learning environments, which have deepened our understanding of how humans learn in real-world contexts. Similar comparisons are drawn with the application of artificial intelligence (AI), raising critical questions: Do AI systems replicate human cognitive processes, merely at a faster pace and with greater capacity for interaction? Or do they introduce fundamentally different, perhaps even superior, modes of creative production? These questions remain at the forefront of ongoing scholarly debate [7–10].

Digital environments offer artists and content creators a broader spectrum of tools and options than traditional manual methods. This expanded creative landscape allows individuals to experiment with multiple possibilities before selecting their preferred outcome, potentially fostering greater innovation. However, the impact of these tools on creativity is not universal—it may vary according to individual circumstances and the nature of the content being produced.

Looking ahead, the evolution of digital and virtual environments is expected to unlock even more powerful creative capabilities. As with many emerging technologies, the full scope of their potential is difficult to foresee, and there is a tendency to underestimate the transformative effects they may ultimately have [11].

9. Enhancing Creativity

Collaborative initiatives that integrate the expertise of artists, scientists, and social media practitioners have demonstrated significant creative potential, as evidenced by the studies of Liggett *et al.* [12] and Earnshaw *et al.* [13]. These projects, characterized by varying degrees of interdisciplinary collaboration, consistently show that such partnerships contribute substantial added value. This underscores the importance of cross-disciplinary engagement as a catalyst for creative advancement.

Furthermore, the interplay between design rationale and creativity can be highly synergistic [14]. The introduction of novel design approaches often stimulates new perspectives, unlocking unforeseen avenues for innovation and conceptual development.

Digital environments are poised to further extend the boundaries of creative practice. They may give rise to entirely new forms of content that transcend current human capabilities and conceptual frameworks—ushering in a paradigm shift in artistic production and expression [15, 16].

10. Interaction with Audiences

Online art exhibitions—such as the one illustrated in Figure 3—are increasingly being designed with the objective of fostering interaction with their audiences. These interactions are not only immediate but can also inform and shape future content, resulting in dynamic exhibitions that evolve beyond their original scope. The digital nature of these exhibitions enables global access, thereby transcending geographic, national, and cultural boundaries [17, 18]. A noteworthy example of this hybrid model is the Art Expo hosted by Wrexham Glyndwr University, which combines both physical and virtual elements [19, 20].

The growing availability of online resources broadens access and serves the diverse interests of a wide user base [21]. This democratization of exhibition spaces can foster accelerated innovation through audience participation—much like how crowdfunding aggregates support for shared goals. The Internet, now deeply embedded in everyday life, plays a pivotal role in these developments. Clark [22] famously suggested that one Internet year equates to seven traditional calendar years, emphasizing the rapid pace of progress in the digital domain. As a result, online engagement and the integration of digital content can significantly enhance the pace and scope of creative and cultural development [23].

Social media platforms further amplify this effect by enabling rapid dissemination, feedback, and collaboration [24, 25]. When leveraged effectively, the collective power of large, digitally connected audiences can drive substantial and meaningful change in relatively short periods of time [26–30].

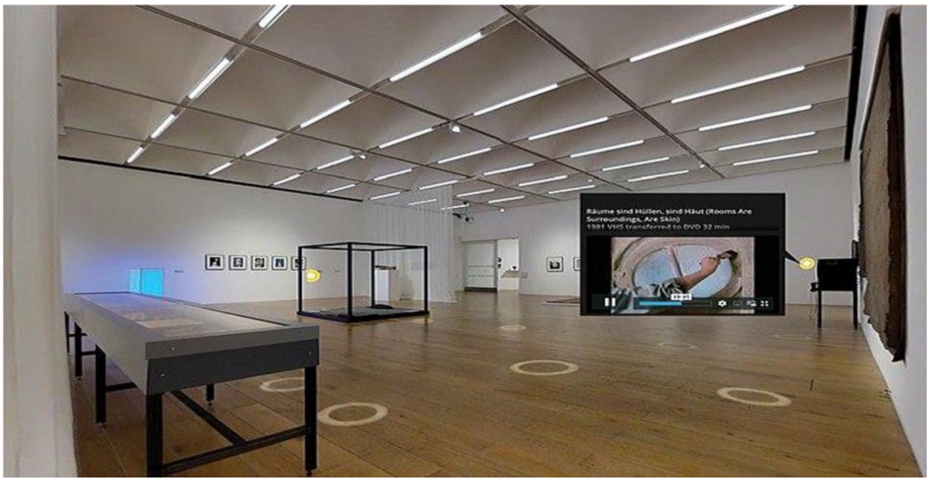

Figure 3: Virtual exhibition produced by V21 Artspace, The house of fame, convened by linder at nottingham contemporary

11. Intrinsic and Extrinsic Creativity

Creativity is an innate human capability, though its development is largely influenced by exposure, experience, and opportunities for exploration. While every individual possesses some degree of intrinsic creativity, its expression often depends on external factors such as the environment, resources, and support systems. Engaging with new information offers individuals the opportunity to respond creatively, building upon and reinterpreting ideas in novel ways [31]. However, not everyone may have equitable access to these opportunities, which can limit the realization of their creative potential.

12. Can Creativity Be Quantitatively Assessed?

Assessing creativity poses a significant challenge due to its subjective and multifaceted nature. Nonetheless, various parameters have been proposed to measure creative output, including aesthetic appeal, originality, cultural or public reception, and long-term commercial value. Early work by Guilford [32] introduced psychometric approaches to assess creativity, laying the groundwork for subsequent research. Scholars have since identified measurable attributes such as uniqueness, complexity, risk-taking, and the diversity of creative outcomes [33, 34]. Although these criteria offer a framework for assessment, they cannot capture the full essence of creative expression, particularly in dynamic, interactive, or interdisciplinary contexts.

13. Organisational Aspects of Creativity

Creativity within organisations is significantly influenced by their structure, culture, and adaptability. Flexible organisations often adopt team-based approaches that encourage interdisciplinary collaboration. When a specific challenge arises, temporary teams are assembled to address the problem, after which they disband and may regroup for new objectives. This dynamic model builds a reservoir of diverse expertise and fosters innovation by avoiding rigid hierarchies and static roles.

In contrast, traditional, historically-rooted structures may be less conducive to innovation, as they resist change and limit cross-functional exchange. Creative organisations actively promote structures that support experimentation and idea generation, although success cannot be guaranteed in every instance [35]. Amabile [36] identified six organisational practices conducive to fostering creativity: support, encouragement, challenge, freedom, adequate resources, and collaborative group work.

Furthermore, organisational environments today are often hybrid—encompassing both physical and digital dimensions. This hybridity introduces new complexities in terms of management, cultural dynamics, and ethical considerations [37–39]. Effective management of such environments requires sensitivity to both technological and human elements.

Conclusions:

The intrinsic link between creativity and communication has been a defining feature of human expression since antiquity. Artworks across time have not only conveyed narratives but have also served as reflections of the cultural and contextual circumstances surrounding their creation. The tools employed in creative production have evolved—from primitive instruments to today's sophisticated digital technologies—each transition enabling new modes of expression and interaction.

In the contemporary digital era, cyberworlds have emerged as platforms where creators and audiences converge. These environments allow for interactive engagement, collaborative content modification, and global dissemination. The integration of computation, interactivity, synthesis, and automation signifies a paradigm shift in creative processes, positioning technology not merely as an enabler but as a co-creator.

The question of how creativity can be evaluated remains complex, particularly in networked digital spaces where audiences also contribute to content evolution. In such contexts, crowd participation may itself be viewed as a dynamic form of creative input.

Looking ahead, technologies such as artificial intelligence hold promise for automating routine processes and generating previously unimagined forms of content. Additionally, augmented reality can enhance user engagement by introducing immersive, multisensory experiences. These innovations are poised to reshape how creativity is expressed, shared, and understood within cyberworlds.

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ROLE OF COW DUNG AND URINE IN AGRICULTURE — A PATHWAY TO SUSTAINABLE FARMING

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Introduction:

Ancient Wisdom for Modern Challenges

Cow dung and cow urine have been cornerstones of traditional Indian agriculture for centuries. These natural by-products, often overlooked in industrial farming, are re-emerging as key resources in the journey toward sustainable, eco-friendly agriculture. This chapter explores their multifaceted roles, scientific relevance, and future potential in enhancing soil health, crop productivity, and environmental sustainability. Cow dung and urine enhance soil fertility and crop productivity, supporting sustainable farming by reducing chemical fertilizer use. It seems likely that they improve soil structure, water retention, and microbial activity, promoting eco-friendly practices. The evidence leans toward their role as natural pest repellents and organic fertilizers, though practices may vary by region and crop type.

Cow Dung: The Living Fertilizer

Cow dung is more than organic waste—it is a biologically rich material teeming with beneficial microorganisms. Mixed with straw or ash for field application. For nutrient supply cow dung is rich in organic matter and essential nutrients like nitrogen, phosphorus, and potassium, acting as a slow-release fertilizer. Cow urine, high in nitrogen and minerals, complements this by boosting soil nutrient levels, potentially increasing crop yields by 20-30% in some studies, such as for maize and wheat.

Soil and Plant Health

Both materials enhance soil structure and water retention, with cow dung improving organic carbon levels (e.g., from 1.33% to 3.21% in potato fields) and cow urine supporting microbial activity. They contain plant growth-promoting bacteria like Azotobacter and Bacillus, aiding nutrient uptake and plant growth, which can transform fallow lands into productive areas.

Pest and Disease Control

Cow urine has natural insecticidal properties, helping control pests like aphids and diseases like bacterial blight in rice, reducing reliance on chemical pesticides. Cow dung also supports antagonistic microorganisms against pathogens, offering a sustainable alternative.

Environmental Impact:

Using cow dung and urine reduces environmental pollution by minimizing chemical inputs, supporting a circular economy by recycling agricultural waste. This aligns with sustainable farming goals, promoting biodiversity and soil health survey note detailed analysis of cow dung and urine in sustainable agriculture cow dung and urine have been integral to agricultural practices, particularly in regions like India, where traditional farming systems have long utilized these byproducts for their nutrient-rich properties. This survey note explores their roles in promoting sustainable farming, drawing from recent research and practical applications, and aims to provide a comprehensive overview for stakeholders in agriculture.

Composition and Nutrient Content:

Cow dung is a complex mixture of undigested plant material, primarily consisting of lignin, cellulose, and hemicelluloses, and is rich in essential nutrients such as nitrogen (N), phosphorus (P), potassium (K), calcium, and magnesium. It also harbours a diverse group of microorganisms, including beneficial bacteria like Azotobacter, Rhizobium, and Bacillus, which contribute to soil health. Cow urine, on the other hand, is composed of approximately 95% water, 2.5% urea, and 2.5% a mixture of minerals, salts, hormones, and enzymes, making it high in nitrogen, potassium, and trace elements such as copper, iron, and zinc. These compositions make both materials valuable as organic fertilizers, providing a slow-release nutrient supply that enhances soil fertility.

Soil Fertility and Structure:

The application of cow dung and urine significantly improves soil fertility by enhancing soil structure, water retention, and nutrient cycling. Cow dung acts as a soil conditioner, increasing organic carbon levels, as evidenced by studies showing an improvement from 1.33% to 3.21% when combined with NPK fertilizers in potato fields. Cow urine further boosts microbial activity, with research indicating increased populations of bacteria (47.0 × 10^5 cfu/g), fungi (34.6×10^4 cfu/g), and actinomycetes (40.0×10^3 cfu/g) when applied with farmyard manure. This microbial enhancement supports nutrient breakdown and availability, crucial for sustainable soil management.

Plant Growth Promotion:

Both cow dung and urine contain plant growth-promoting bacteria (PGPB) that enhance nutrient uptake and protect plants from pathogens. Cow dung supports bacteria like Bacillus subtilis, which solubilize insoluble phosphorus, aiding plant uptake, especially in tropical climates (42–45°C). Cow urine, rich in nitrogen and potassium, accelerates growth in crops like maize, rice, and mustard, with studies showing yield increases of 20-30% for maize and significant improvements in vegetative parameters for gladiolus at 5-10% concentration. These effects are attributed to the presence of growth hormones like auxins, cytokinins, and gibberellins, fostering robust plant development.

Pest and Disease Control:

Cow urine serves as a natural pest repellent and disinfectant, containing compounds like urea, uric acid, and ammonia that deter insects such as aphids, mites, and whiteflies. It is a key component of organic formulations like Panchagavya, which boosts crop health. Research highlights its effectiveness against bacterial blight in rice, with cow dung extracts showing antagonistic effects against pathogens like Rhizoctonia bataticola, often outperforming antibiotics like Penicillin and Streptomycin. Additionally, 219 bacterial strains from cow dung were tested, with 17 killing over 90% of Caenorhabditis elegans within 1 hour, and 14 inhibiting Meloidogyne incognita, demonstrating nematicidal activity.

Organic Fertilizer and Composting:

Cow dung and urine are central to organic farming, reducing reliance on synthetic fertilizers. Cow dung, when mixed with palm oil biomass in a 1:3 ratio, improves compost quality, enhancing pH, electrical conductivity, and the carbon-to-nitrogen (C:N) ratio. Integrated Soil Fertility Management (ISFM) practices, such as applying 3 t/ha cow dung with 100 kg/ha NPK, have increased potato tuber yields from 1.8 t/ha to 8.9 t/ha, showcasing their potential in sustainable agriculture. Cow urine, applied at rates like 34300 l/ha with FYM, increases available nitrogen (272.4 kg/ha), phosphorus (23.5 kg/ha), and potassium (199.9 kg/ha), further supporting soil fertility.

Transformation to Natural Farming and Fallow Land Revitalization:

The use of cow dung and urine facilitates the transition from chemical to natural farming by reducing environmental pollution and promoting biodiversity. They are used in composting with other organic materials (leaves, grass, food waste) to restore nutrient balance and microbial activity in fallow lands, transforming them into productive agricultural areas. This aligns with sustainable practices, as evidenced by a farmer in Zaheerabad, India, who tripled yields on 15 acres using cow dung and urine, demonstrating practical success.

Environmental and Economic Benefits:

Environmentally, cow dung and urine reduce soil degradation, water pollution, and the need for synthetic inputs, supporting a circular economy. Economically, they are low-cost and abundant, particularly in livestock-dependent regions, making them viable for smallholder farmers. Their use minimizes greenhouse gas emissions compared to chemical fertilizers and supports renewable energy production, such as biogas from cow dung, contributing to sustainable agricultural systems. Historical and Cultural Context Historically, cow dung and urine have been used since the Vedic period in India for medicinal and agricultural purposes, reflecting their deep cultural significance. Recent research, driven by fertilizer crises, is reviving these practices, with studies confirming their effectiveness in modern sustainable agriculture. This historical continuity underscores their relevance in contemporary farming systems.

Supporting Evidence and Studies:

Research from various sources, such as "Revitalizing Agriculture: Role of Cow Dung and Urine in Promoting Sustainability" (2024, Bhartiya Krishi Anusandhan Patrika), highlights their role in transforming fallow lands and promoting sustainable practices. The article "Current status of cow dung as a bioresource for sustainable development" (2016, Bioresources and Bioprocessing) details microbial benefits, while "Cow dung and urine are the real crop boosters" (The Hindu, 2018) provides practical examples of yield tripling. Additional studies, such as those on nematicidal activity (219 strains tested, 17 effective), reinforce their scientific backing.

Cow Dung: The Living Fertilizer:

Cow dung is more than organic waste—it is a biologically rich material teeming with beneficial microorganisms. It contains essential nutrients like nitrogen, phosphorus, potassium, and trace elements.

Benefits:

- Improves soil structure and aeration.
- Increases microbial activity in the rhizosphere.
- Enhances water retention capacity.
- Supports slow and sustained nutrient release.

Traditional Uses:

- As a base material for composting.
- In preparation of Farmyard Manure (FYM).
- Mixed with straw or ash for field application.

Cow Urine: A Liquid Bio-Booster

Cow urine (gomutra) is rich in nitrogen, sulfur, sodium, and hormones that stimulate plant growth. When diluted and applied correctly, it serves as a potent bio-enhancer.

Benefits:

- Natural pesticide and fungicide.
- Foliar spray to improve plant immunity.
- Soil drench to boost microbial life.
- Used in bioformulations like Panchagavya, Jeevamrut, and Amritpani.

Panchagavya and Jeevamrut: Traditional Elixirs of Life

These are traditional formulations containing cow dung, cow urine, milk, curd, and ghee, sometimes mixed with jaggery, besan (gram flour), and soil.

Biological Role:

- Acts as a microbial inoculant.

- Supplies enzymes and micronutrients.
- Enhances photosynthesis and root development.
- Field Applications, Seed treatment, Foliar spray.
- Soil conditioner and compost activator.

Scientific Validation and Microbial Profile

Research from agricultural universities and ICAR institutes has shown the presence of beneficial microbes like Azotobacter, Rhizobium, Phosphobacteria.

- Reduction in pest and disease incidence.
- Improvement in soil pH and organic carbon.
- Increased yield and crop quality in cereals, pulses, and vegetables.
- Environmental and Economic Impact.

Environmental Benefits:

- Reduces dependence on chemical fertilizers and pesticides.
- Minimizes soil and water pollution.
- Enhances carbon sequestration through organic matter.

Economic Benefits:

- Low-cost and locally available input.
- Increases income through organic certification.
- Encourages on-farm input generation.

Aspect	Details	Exact Numbers (Examples)
Nutrient Content	Cow dung: N, P, K, Ca, Mg; Cow urine: 95% water, 2.5% urea, 2.5% minerals, hormones, enzymes	95%, 2.5%, 2.5%
Soil Organic Carbon Improvement	Cow dung with NPK increases from 1.33% to 3.21%	1.33% to 3.21%
Crop Yield Increase	Potato yield from 1.8 t/ha to 8.9 t/ha with 3 t/ha cow dung + 100 kg/ha NPK	1.8 t/ha to 8.9 t/ha
Microbial Population	Cow urine with FYM: Bacteria 47.0 × 10^5 cfu/g, Fungi 34.6×10^4 cfu/g, Actinomycetes 40.0×10^3 cfu/g	47.0 × 10^5, 34.6×10^4, 40.0×10^3 cfu/g
Nematicidal Strains	219 strains tested, 17 killed >90% C. elegans within 1 hour, 14 inhibited M. incognita	219, 17, 14 strains

Conclusion:

Cow dung and urine are pivotal in sustainable agriculture, offering a holistic approach to soil health, crop productivity, and environmental stewardship. Their nutrient-rich profiles, microbial enhancements, and pest control properties make them indispensable for eco-friendly farming, supported by both traditional knowledge and modern research. Cow dung and urine offer not just fertility, but a philosophy—a way to reconnect agriculture with nature's cycles. Reviving their use scientifically and ethically bridges ancient wisdom with future sustainability. They hold the promise of a resilient, low-cost, eco-centric agriculture rooted in both biology and tradition

Future Prospects in Sustainable Agriculture:

- **Agro-ecological Models:** Integrating cow-based farming in Natural Farming, Zero Budget Natural Farming (ZBNF) and Integrated Organic Farming Systems.
- **Policy Support:** Incentives for cow-based farming under Paramparagat Krishi Vikas Yojana (PKVY) and National Mission on Sustainable Agriculture (NMSA).

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GINGER (*ZINGIBER OFFICINALE* ROSC.) – A POTENTIAL PLANT OF ASSAM: A REVIEW

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Abstract:

India is one of the largest producers of ginger throughout the globe. This is solely due to the suitable agro-climatic conditions perfect for growth of the plant especially throughout Assam which harbors various indigenous cultivars of this herbaceous plant. Ginger belonging to Karbi-anglong district of Assam has also been recognized worldwide with the prestigious Geographical Indication (GI) tag. The medicinal utility of Ginger was identified significantly in Indian, Chinese, Arabian and Tibetan systems of medicine since ages. Various indigenous communities of the state utilize the various parts of this plant for food, food adjunct and medicinal purposes. Keeping the economic and ethno-medicinal importance of the plant in mind, the following chapter highlights various morphological, ethnobotanical and biochemical details of the crop that can be utilized for identification of the cultivars, establishment of superiority among the cultivars and as selection criteria for further plant improvement programmes.

Keywords: Assam, *Zingiber officinale*, Medicinal, Rhizome, Biochemical, Ginger.

1. Introduction and Historical Background:

Zingiber officinale Rosc. commonly known as ginger belongs to the family Zingiberaceae (Srinivasan *et al.,* 2008) is one of the most widely cultivated perennial herbs in tropical and sub-tropical regions of the world, especially found most in Indo-Malayasian region. Some of the tropical and subtropical countries where abundant Ginger cultivation occurs are India, China, Nepal, Nigeria, Thailand. These 5 countries are infact the first five ginger producing countries (Hazarika & Kakoti., 2013). India and China are presently leading in ginger cultivation. The States in India with most ginger production rate are Andhra Pradesh, Kerala, Himachal Pradesh, Assam, Meghalaya, Mizoram, Arunachal Pradesh, Nagaland, Manipur, Sikkim, Tripura, Orissa and Madhya Pradesh (Hazarika & Kakoti., 2013; Rahman *et al.,* 2009; Srinivasan *et al.,* 2008). The term (generic name) Zingiber is taken from the greek Zingiberis, that is derived from the sanskrit name of the spice, Singabera. Some synonyms of ginger are Adrak (hindi), Ada (Assamese, Bengali, Oriya), Ignee (tamil), Allam (telegu) and Alha (marathi)

The First known documentation work on ginger was done by Van Rhedde (1692) in a Book called 'Hortus Indicus Malabaricus', the initial record of plants presents in Malabar coast of India. The Latin generic name 'Zingiber' has been derived from the Greek word 'Zingiberi' which was in turn derived from the Historic Indian language Sanskrit word 'Sringavera' (Rosengarten, 1969). The primary center of origin for ginger is considered to be from South-East Asia, most probably in India (Burkill, 1966). It was an important export material from India to the Roman Empire over 2000 years ago where it was sought medicinally. The medicinal utility of Ginger was identified significantly in Indian, Chinese, Arabian and Tibetian systems of medicine since ages (Atman & Marcussen, 2001).

Ginger (*Zingiber officinale* Rosc.) comes under the taxonomic family Zingiberaceae. The order is Zingiberales corresponding to the Tribe Zingibereae (Holtum, 1950). The taxonomic family Zingiberaceae, a largely tropical and sub-tropical family is considered as a large monocotyledonous family under the order Zingiberales. This family has more than 1200 species and 53 genera under it (Kress, 1990). More than 70 cultivars of ginger are found throughout India and each of these are identified based on their local names. (Sasikumar *et al.,* 1999). These cultivars vary in their Morphological, cytological, Agronomical, Biochemical and other features as well (Rana & Korla, 2007; Lincy et al.,2008).

2. Ginger Cultivation in North-East India with special reference to Assam

Ginger is one of the main crops grown in NE region of India which actually comprises of approx. 49% of India's area under ginger cultivation and approx. 72% of India's ginger production. The North-Eastern Region of India is thus often projected as "India's Organic Ginger Hub" (Rahman *et al.,* 2009). Organic Ginger is widely cultivated as an economically important plant in Assam. The districts of Assam which have the most production rate of Ginger are: Karbi Anglong, Golaghat, Sivsagar, Tinsukia and Udalguri, Darrang, NC Hills, Sonitpur, Barpeta, Kamrup, Nagaon and Dibrugarh (Hazarika & Kakoti, 2013).

Karbi-Anglong, the largest district in Assam (area-wise) covering an area of 10,434 sq. kms is one of the most crucial ginger producing districts of Assam which supplies organic ginger to North Bengal, New Delhi, etc. and even exports ginger abroad. (Rahman *et al.,* 2009). Ginger of Assam and NE India has higher oil and oleo-resin content as compared to rest of India. Among the states of NE India, Assam has the highest area under ginger cultivation as well as highest production. (Karuppaiyan *et al.,* 2009). In India, Assam is no. 1 in ginger production (122.3 thousand MT) followed by Karnataka (Gogoi, 2020)

Assam and rest of NE India are crucial ginger growing regions solely because of the Agro-climatic conditions that enhance ginger cultivation characterized by warm, humid summers with abundant rainfall and cool winters. (Hazarika & Kakoti, 2013; Das, 2018). Some of the indigenous ginger cultivars present in Assam are: 'Amada', 'Jati ada' (also known as 'jatia ada'), 'Zeng ada' and 'Moran ada' (Hazarika & Kakoti, 2013). The indigenously available cultivars are either named on the basis of the Locality (or area) of its cultivation or may also be based on its certain unique characteristic features. A very prominent example is "Moran ada" as it is popular and is widely cultivated in Moranhat area under Charaideo district of Assam (Rahman *et al.,* 2009). 'Moran ada' is an important and popular source of medicine among various ethnic people throughout Assam. In Mizoram, the popular indigenous cultivar of ginger are 'Thingpuidum' and 'Thingria'. 'Naga Shing' is a popular indigenous ginger cultivar in Manipur. Likewise, Meghalaya has its own indigenous cultivar called as 'Shing Bhukir' which has striking morphological similarities to 'Moran ada' of Assam and is also used medicinally. 'Bhaise' is an important, popular and high yielding indigenous ginger cultivar of Sikkim.

One of the major challenges towards ginger cultivation in Assam and NE India is the Rhizome Rot disease of ginger causing yield losses. This is an issue that needs to be addressed so that the state can maintain a standard production rate of ginger (Dohroo, 2005; Stirling *et al.,* 2009). In Assam, the highest and most destructive crop loss was reported to be significant (Borboruah *et al.,* 2025). Rahman *et al.,* 2009 reported wilt to be another major challenge alongwith Rhizome rot for Ginger cultivation in Assam and NE India.

The plant has an underground stem called rhizome which has a buff colour, Aromatic odour and Pungent taste. The Stalk is erect and 50-90 cm tall and has leaves which are dark green in colour. The leaves are 6-12 inches long with long, narrow lamina, lanceolate and have a pointed apex. Flowers are small sized, cone-like and pale yellow in colour. Calyx is tri-lobed. Corolla is cylindrical. Anthers are double, long, thin and horn shaped. Ovary is ellipsoidal having 3 cells and each cell has many ovules. Stamens are short than corolla, dark purple in colour. Stigma is funnel-shaped (Nazeem *et al.,* 1996)

There are some very unique anatomical features of Ginger (*Zingiber officinale* Rosc.) which are: a complete devoid of Periderm, Cambium is very short lived and the vessels of xylem (of rhizome) consist of unique scalariform thickenings. (Ravindran *et al.,* 1998)

Warm and Humid climate is a pre-requisite for smooth growth of ginger. Moderate rainfall is essential during sowing till sprouting. Well drained soils such as Sandy-loam, Clay-loam are best for ginger. The plant is propagated by rhizome cuttings and harvesting is done by digging and picking rhizomes from underground, washing and sundrying. (Sharma, 2017). Ginger yield varies based on cultivar, plantation season and stage of maturity attained during harvest (Peter *et al.,* 2005).

3. Biochemical Characterization and Ethno-Medicinal Importance of Ginger

Chemical estimations and analysis show that ginger has over 300 varying compounds. The crucial constituents in ginger rhizomes are carbohydrates, Proteins, Lipids, terpene compounds, resins and Phenolics. Some important phenolics in ginger are shogaol, gingerol and paradol. Terpene compounds such as zingiberene, farnescene, Bisabolene and curcumene are crucial in ginger. Amino acids such as leucine are abundant in ginger. Vitamins such as vitamin A, B3, B6 and C are present in ginger. In addition to these, Crude fiber and Minerals are also present. (Prasad & Tyagi, 2015). The essential metals such as Ca, Mg, Fe, Zn, Cu, Co, Cr, Mn and Ni are found in ginger. The toxic metal Pb is absent whereas Cd is present in very trace amounts. (Wagesho & Chandravanshi, 2015). The pungent taste of ginger is solely due to oleoresin gingerol's alcoholic group. Aromatic odour of ginger is due to some volatile oils which are mainly zingiberene and zingiberol. (Sharma, 2017). The Rhizome of ginger is one of the most emerging food sources containing proteolytic enzymes (Ahmad *et al.,* 2013). Proteolytic enzymes are synthesized naturally within our alimentary canal which by the process of proteolysis breaks complex proteinaceous food into amino acids that can be further digested and absorbed by the cells. Intake of proteolytic enzymes can increase our digestive ability as well as our disease resistance capacity. (Taussig & Batkin, 1988). Ginger proteases belong to cysteine type and because of high thermostability, broad pH and plasma-clotting activity, the cysteine proteases is having special interest and plant containing such proteases is being a promising commercial source (Gaur *et al.,* 2010; Ahmad et. al., 2013). Early-stage research also suggested that proteases may have anti-cancer properties (Pillai *et al.,* 2013). Ginger shows sialagogue mechanism enhancing saliva generation resulting in faster and smooth swallowing. (Mardani, 2017).

Fresh and dried ginger rhizomes are popular worldwide as a spice and the extract of ginger is used commonly in food items, beverages, baking and confectionary industries to produce some very economically important products such as pickles, chutney, ginger wine and beer, biscuits and other bakery items, (Mishra, 2009). Oleoresin and essential oil are used as a flavouring agent and medicine. Europeans maintained ginger as a essential component in many pharmaceutical preparations (Parthasarathy *et al.,* 2012).

It has anti-inflammatory, anti-cholestrolemic, anti-viral, anti-bacterial, anti-oxidant, analgesic, Antifungal, Antihelmintic, Antidiabetic, Immune-supportive and Thermoregulatory properties. (Sharma, 2017). Some widely known and common items in the market having ginger as a crucial constituent are Hajmola, Garam-masala, Chaat-masala, Aloo Bhujia, Paneer masala, etc. (Sharma, 2017).

In one of the pioneer works on the Biochemical characterization of ginger, it was found that the rhizome of ginger actually contains a plethora of chemical constituents such as curcumin, bisaboline, 6-gingerol i.e., (5-hydroxy-1-4-hydroxy-3-methoxy phenyl), zingiberene, 6-shogoals, and several other types of lipids that make ginger a medicinally important plant. (Yoshikawa *et al.,* 1993; Mascolo *et al.,* 1989; Bliddal *et al.,* 2000). Ginger has been reported to have various properties such as analgesic, antiulcer, antipyretic, antiemetic, etc. (Mascolo *et al.,* 1989; Phillips *et al.,* 1993; Jana *et al.,* 1999; Adanlawo *et al.,* 2007).There has been detailed analysis of Biochemical contents in ginger rhizome from time to time and it has been reported that Ginger rhizomes contain carbohydrates (approx. 70%), Proteins (small amount), Lipids (approx. 8%), resins, mineral elements, terpenes, phenolics, amino acids, crude fiber and also vitamins (Nicotinic acid & Vitamin A) (Prasad & Tyagi, 2015; Wagesho & Chandravanshi, 2015). It has been reported that the unique odor and flavor of ginger exist due to presence of specific pungent compounds such as Shogaols and Gingerols. (Prasad & Tyagi, 2015). Aromatic odour of ginger is due to some volatile oils which are mainly zingiberene and zingiberol (Sharma, 2017). Gingerols donot have prolonged thermal stability and get transformed to Shogaol under high temperature. (Mishra, 2009). More Pungency is conferred by Shogaol as compared to gingerols. (Jolad *et al.,* 2004).

Parthasarathy *et al.* (2008) gave a very important conclusion that the presence and concentration of various Biochemical constituents in Ginger may vary with cultivar, Influence of environmental conditions and the stage of development attained at the time of harvesting. Variation in presence and abundance of Phytochemical constituents among various cultivars of ginger collected from different geographical locations was also reported by Ravindran & Babu (2004)

Patnaik *et al.* (2016) characterized 20 accessions of Ginger germplasmat HARS, Pottangi considering specific Biochemical contents (Protein, Phenol and Fibre) as one of the important criteria. He observed that Total Protein content & Crude Fibre content approx. matched standard literature but Total phenolic content was found to be very high. Phenolics has been previously reported to show anti-oxidant i.e They can perform neutralization of harmful Free-radicals (Mishra *et al.,* 2011). According to the findings of Patnaik *et al.* (2016) the presence of high amount of Phenolics in Ginger indicate its potential use as an anti-oxidant and also for the treatment of various diseases.

Peter & Kandiannan (1999) conducted phytochemical screening of dry ginger and found out that dry ginger (per 100 gm) contains 10.9% moisture, 1.8% Volatile oil, 6.5% Oleo-resin, 53.0% Starch, 7.2% Crude Fibre, 12.4% Crude Protein and 6.6% Total ash. Latona *et al.* (2012) found some different results. According to Latona *et al.* (2012) ginger contains a high moisture content of about 76.53% followed by crude protein 9.13%, crude fibre 3.07%, fat content 5.09% and ash 2.64%. Approximately similar quantities of the same parameters were reported by Okolo *et al.* (2012) on Dry basis.

Natarajan *et al.* (1972) reported a comparatively high content of crude fibre in Ginger on dry basis. He found the range of crude fibre to be 4.8 to 9.0 %. Muralidharan (1973) also reported large variation of crude fibre content in different varieties of ginger. Low fibre content is one of the most sought attributes of ginger from processing point of view. It has also been reported that high content of dietary fibre can be medicinally important as it can cure hypertension, reduce cholesterol level and also cure constipation (Ishida *et al.,* 2000). Wood & Fox (1965) reported that the fibre content in rhizome was directly proportional to maturity stage of the rhizome. Latona *et al.* (2012) examined the presence of various mineral elements in Ginger Rhizome and found out that that ginger has a high amount calcium 280.0 mg/100g, Iron 279.7 mg/100g, Zinc 64.0 mg/100g, Manganese 5.90 mg/100g and Copper 8.80 mg/100g which are important essential elements. All these essential mineral element compositions indicate that

Ginger rhizome has the property to be used as a medicine for various disorders. Contrary to this, Ajayi *et al.* (2013) found out Potassium to be the most abundant mineral element in Gnger rhizome. His study also showed considerable abundance of calcium, magnesium, sodium, phosphorous, manganese, iron, zinc, and copper. Adanlawo *et al.* (2007) found a different order corresponding to mineral abundance. He found Sodium to be the most abundant mineral element and the order of abundance as Na > K > Ca > P > Mn > Zn > Fe > Cu. Similar results were found by Adeyeye & Fagbohun (2005); Wagesho & Chandravanshi (2015) found the presence of toxic metal Pb in Ginger in very trace amounts. Ash content tells us the mineral content in a particular biological system as Ash consists of all the minerals in it. 'Moran ada', an indigenous ginger cultivar of Assam has been reported to have a highest Ash content among all other indigenous cultivars of ginger in Assam such as 'Bhola ada', 'Amada' and 'Jatia ada'. There is an exception to this result, 'Moran ada' showed high concentrations of all mineral elements except Potassium whereas 'Jatia ada' showed high Potassium amount. Jung (2008) gave an important conclusion regarding the mineral element uptake in plants which can cause difference in their concentration. According to his findings, Mineral uptake by the plant roots may be directly influenced by various conditions or factors such as: soil pH, mineral concentration in soils, Organic matter content, type and variety of plant and also a plant's stage of maturity during harvest.

Ginger essential oil has been found to have varying chemical compositions (Singh *et al.,* 2008). The unique ginger flavor and taste of ginger is dependent on its essential oils. Essential oil content is responsible for the determination of the accurate quality and international market value (price) of ginger (Sekiwa-Iijima *et al.,* 2001). Ginger essential oil has been reported to contain oxygenated monoterpene hydrocarbons such as Z-Citral and Geranial. Singh *et al.* (2008) gave a very unique result. He found that Geranial (25.9%) is also a crucial constituent in ginger oil. Alpha- Pinene, Camphene, 1,8- Cineole, Linalool, Borneol, Zingiberene, Ar-Curcumene etc were also reported to be present from time to time. In addition to all these, sesquiterpene were also identified to be there in very trace amounts. 'Moran ada', an indigenous ginger cultivar of Assam has been reported to have a highest essential oil content except compounds such as Linalool and Geranial among all other indigenous cultivars of ginger in Assam such as 'Bhola ada', 'Amada' and 'Jatia ada'.

Adanlawo *et al.* (2007) found glutamic acid to be the most abundant amino acid and glycine to be the least abundant one. Ajayi *et al.* (2013) conducted analysis of Food value of Ginger in Nigeria and found out Leucine and Glutamic acid as the most abundant amino acids in Ginger rhizomes. Other amino acids reported are Lys, His, Arg, Asp, Met, Thre, Ser, Ala, Cys, Val, Ile, Leu, Tyr, Phe (Ajayi *et al.,* 2013). According to the findings of Adanlawo *et al.* (2007), ginger don't fall under the category of plants with high protein content. He stated that the low value of proteins maybe due to the soil conditions, management and other environmental factors. Several workers stated that spices may not be major protein sources but in case of Ginger, the protein content has some specific importance. They stated that in ginger, an important constituent amino acid termed as phenylalanine is regarded to be the starting component in the gradual biosynthesis of Gingerol which is responsible for the pungency of ginger. Apart from phenylalanine, Leucine another important constituent amino acid has a vital role in the biosynthesis of isopentenyl pyrophosphate, the widely considered compound involved in the formation of mono and sesquiterpene, an aromatic compound (Luckner, 1990).

Famurewa *et al.* (2011) stated that one of the crucial factors behind the high market value of ginger is its high Oleo-resin content. Oleo-resin is actually the addition of overall aromatic and pungent principles of ginger. According to Balachandran *et al.* (2006); one of the reasons behind the highly sought anti-oxidant property of ginger is the high number of Oleo-resins present in it. Some of the other medicinally important features of ginger such as antimicrobial, anti-inflammatory, anticoagulant, anti-hypercholesterolemic, anti-hypertensive, anti-hyperglycemic, antispasmodic and vasodilatory properties are also linked with the presence of Oleo-resins in it. (Bradley, 1992). According to the findings of Ratnambal *et al.* (1987); the Oleo-resin content in *Zingiber officinale* rosc. varied between 3% to 11%.

They also stated that these variations were due to the individual genotypic constitution, extraction methodology, laboratory conditions, the nature of rhizome during extraction, Location of origin and season of Harvesting as well. Significant varying results during analysis of Oleo-resin content was reported by Lewis *et al.* (1972). According to the findings of Onyenekwe & Hashimoto (1999), Concentration of oleoresin in the dry rhizome of ginger ranges from 1.5 to 3%.

A widely accepted range of Oleo-resin content in ginger rhizome of 4.0-7.5 % was given by Balachandran *et al.* (2006). Similar results were shown by Eleazu *et al.* (2012). He also pointed out prominent relation between Oleo-resin content and potassium content in Ginger and suggested that Oleo-resins may be responsible for Potassium content but this needs more research to be done. Eleazu *et al.* (2012) also reported that Ginger has a low quantity of reducing sugars in it. Spices have prominent anti-oxidant activity (Sebranek, 2005). One of the most common protocols applied by workers to determine the anti-oxidant activity in various biological samples is the DPPH (1,1-Diphenyl-2-picrylhydrazyl) free radical scavenging method. DPPH (1,1-Diphenyl-2-picrylhydrazyl) is used as a stable free radical to find out the antioxidant activity (Ozturk *et al.,* 2007). Suhaj (2006) stated that the scavenging activity shown by the biological samples and standard antioxidants on the sable free radical DPPH (1,1-Diphenyl-2-picrylhydrazyl) is taken as a valid and easy assay to determine antioxidant activity in various biological samples. Ginger showed considerable antioxidant activities due to the various Biochemical constituents present in it. ‘Moran ada’ extract, an indigenous ginger cultivar of Assam has been reported to have a highest antioxidant activity among all other indigenous cultivars of ginger in Assam such as ‘Bhola ada’, ‘Amada’ and ‘Jatia ada’. ‘Moran ada’ extract showed highest DPPH radical scavenging activity (94% at 80µg/ml), which is immediately followed by 'Jatia Ada' and 'Bhola Ada'. Polyphenolic compounds are directly involved with antioxidant activities (Yen *et al.,* 1993). Similarly, Phenolic compounds are crucial anti-oxidants (Duh *et al.,* 1999). Flavonoid (a crucial known anti-oxidant) comes under a Polyphenolic compound. 'Moran ada' extract, an indigenous ginger cultivar of Assam has been reported to have a highest Polyphenolic content among all other indigenous cultivars of ginger in Assam such as 'Bhola ada', 'Amada' and 'Jatia ada' which is thus responsible for its high antioxidant activity. Choudhari & Kareppa (2013) conducted a comparative analysis of Biochemical contents between Healthy and Infected Ginger rhizomes and found some prominent differences with respect to the contents. They reported that the crude fibre, gingerols & shagaols, oleoresin, volatile oil, total ash, water soluble ash and acid insoluble ash content of infected plant showed prominent decrease due to infection. However, starch content showed increase in the infected plant as compared to healthy plant.

Motawi *et al.* (2011) conducted analysis of ginger as a nutraceutical. On examination of Ethanolic extract of Ginger, He concluded that there occurs a high amount of carbohydrates in ginger. He also found out that Ginger contains considerable number of tannins and Flavonoids. Another important revelation from his study was that he found a moderate amount of Alkaloids, sterols and terpenes to be present in Ginger. Some important phenolics in ginger are shogaol, gingerol and paradol. Terpene compounds such as zingiberene, farnescene, Bisabolene and curcumene are crucial in ginger. (Prasad & Tyagi, 2015).

It was stated by various workers from time to time that the abundance and concentration of various chemical compounds in ginger which maybe volatile or non-volatile are significantly dependent on the environmental conditions and also on the nature or state of the rhizome (Wohlmuth *et al.,* 2006).

Sharma *et al.* (2016) gave another important addition towards the understanding of Biochemical contents in Ginger rhizome. He concluded that the nature and content of volatile present in and extracted from ginger may differ based on various factors such as Geographical location and origin, post-harvest procedures and Temperature as well. He applies GC-MS technique for accurate characterization of volatile oils and obtained high percentage of sesquiterpenes (66.66%), monoterpenes (17.28%) and aliphatic compounds (13.58%). Among essential oil, he identified Zingiberene as the most abundant component.

Sharma *et al.* (2016) also gave another prominent milestone and showed that volatile oils obtained from ginger showed considerable anti-microbial properties. The oils were tested against bacteria as well as fungi: Bacillus subtilis, Staphylococcus aureus, Escherichia coli, Pseudomonas aeruginosa, Candida albicans and Aspergillus niger. Ahmad *et al.* (2013) stated that Ginger is one of the most emerging sources of proteolytic enzymes. Proteolytic enzymes are certain lytic enzymes that are formed within our alimentary canal and through their lytic action, the breakdown highly complex protein foods into simpler amino acids which can be directly absorbed by the body cells. Proteolytic enzymes increase our digestion ability as well as our disease resistance capacity (Taussig *et al.,* 1988). Rhizome of Ginger contains protease along with various other phytochemical constituents.

Ginger proteases belong to Cysteine type of ptoteases (Huang *et al.,* 2011) and because of high thermostability, broad pH and plasma clotting activity, the cysteine proteases are having special interest and plant containing cysteine protease is being a promising commercial source. (Zhang *et al.,* 2015). Early-stage research also suggested that proteases may have anti-cancer properties (Pillai *et al.,* 2013). Large numbers of Ginger cultivars which are very good source of proteolytic enzymes are widely cultivated in Assam. Various works have been done on isolation, purification and characterization of proteolytic enzymes at both qualitative and quantitative level by different researchers from time to time (Nafi *et al.,* 2013).

Conclusion and Future Prospect:

The indigenous cultivars of Ginger in our country are widely known by their place/locality of cultivation or origin. The distinction and accurate characterization of these cultivars becomes very challenging due to the absence or insufficiency of any prominently visible morphological differences. Thus, Biochemical and molecular markers prove to be a crucial tool for the characterization of various cultivars and also to deduce some inter-relatedness among them in association with cytological and Phylogenetic studies. According to our Literature evidence base, we can see that various Biochemical analysis works have been done on Zingiber species from time to time, but very little is known about the Phytochemical constituents of the indigenous ginger cultivars of Assam. Keeping this fact in mind, A detailed Biochemical study and Characterization of the indigenous ginger cultivars of Assam can increase our range of knowledge on the overall genetic diversity existing within the various indigenous cultivars of *Zingiber officinale* in one of the most crucial ginger producing states of India i.e. Assam. The data obtained can be utilized for identification of the cultivars, establishment of Superiority among the cultivars and as selection criteria for further plant improvement programme. Biochemical analysis on a qualitative as well as quantitative level can provide authentic data on the unexplored indigenous cultivars of Assam**.** Ploidy level study of all the cultivars can be correlated to their various Biochemical characteristics to find out if there is any kind of correlation between ploidy level and Biochemical contents that can be a crucial step towards characterization of the indigenous ginger cultivars of Assam.

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RHIZOSPHERIC ACTINOBACTERIA: A REVIEW

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Abstract:

Rhizosphere is the home for many microorganisms and Actinobacteria are the gram positive filamentous bacteria which, in soil, water and plant tissues. They are also present in rhizosphere of different plants and are beneficial for plant growth and development as they produce plant growth factors including different types of enzymes like amylase, catalase, urease, nitrate reductase again they are able to produce HCN, H_2S and chitinase enzymes which help host plant to defense against different plant pathogen however, could produce siderophore which is a iron chelating compound and produce growth hormone indole acetic acid which is helpful for plant growth and development. They are reported to produce other plant probiotics like phosphate solubilizing and zinc solubilizing compounds. *Streptomyces* is the common atinobacteria found mostly in rhizospheric soil which is reported to produce 60 % of total microbial antibiotic. As per report 78% of natural antibiotics are produced by acinobacteria.

Keywords: Actinobacteria, Antibiotic, Rhizosphere, PGP, *Streptomyces*

Introduction:

The rhizosphere, which is the interface between plant roots and soil, is composed of various chemical compounds and is colonized by diverse range of microorganism. These include fungi, bacteria, archaea, Protozoa, invertebrate, and other organisms, all of which interact with one another and their host plants. These microorganisms assist host plants in defending against pathogen and provide essential nutrients to the plants. (Chepsergon and Moleleki 2023). The phylum Actinobacteria, a group of filamentous, high G+C content, gram positive bacteria, represents one of the largest taxonomic units among the 18 lineages within the domain Bacteria. It comprises of six classes, 25 orders, 52 families, and 232 genera (Stackebrandt and Schumann, 2000). Members of this phylum can be unicellular, motile, nonmotile, filamentous, aerobic, anaerobic, and exhibit a variety of morphological forms such as coccoid (*Micrococcus*), rod (*Arthobacter*), fragmenting hyphal (Nocardia), or branched mycelium (*Streptomyces*) (Salwan and Sharma 2020; Shivlata and Satyanarayana 2015). Actinobacteria have significant agricultural and medicinal value, as they produce organic acids, fix atmospheric nitrogen, contribute to the carbon cycle, and produce antibiotics, enzymes, antiviral, antioxidants, anticancer, and secondary metabolites (Jain *et al.,* 2022). They are also responsible for characteristic earthy smell of soil after rain, which is due to Geosmin, a neutral oil containing carbon and hydrogen produce by *Streptomyces greceus* (Gerber and Lechevalier 1965). Actinobacteria are present in both bulk soil and rhizospheric soil, and can be thermophilic. They inhabit various plant parts, both inside (as endophyte) and on the surface (as epiphyte) of several host plants, including tomato, barley, wheat, rice, soybean, cowpea, chickpea, banana and medicinal plants with dominating genera *Streptomyces,* they also include *Micromonospora, Nocardia, Microbispora, Nonomurea, Mycobacteria, Frankia, Actinoplanes,* and *Saccharopolyspora* (Shaharokhi *et al.,* 2005; Martinez-Hidalgo *et al.,* 2014; Vijaybharathi *et al.,* 2016). *Streptomyces* is the most abundant soil microbe, constituting approximately 10% of total soil microbial community, and is the most extensively studied genus within Actinobacteria due to its beneficial properties and versatile structural adaptations (Janssen 2006; Viaene *et al.,* 2016). In addition to its beneficial aspects, the phylum Actinobacteria also includes pathogenic species such as those in the genera *Mycobacterium, Nocardia,* and *Tropheryma* that affect humans, as well as *Streptomyces scabiei* (which cause scabies in potatoes) and *Corynebacterium* and *Mycobacterium* species that impact animals for (Menendez and Carro, 2019). According to the FAO/WHO Experts Consultation Report are defined as "live microorganism which, when administrated in adequate amounts, confer a health benefit on the host'' (Hill *et al.,* 2014). Within this context, the genus *Frankia* is considered one of the most studied plant probiotic actinobacteria due to its long standing research on nitrogen fixation and its symbiotic relationship with plants (Beijerinck 1901; Carro *et al.,* 2015). However other plant probiotic actinobacteria, such as *Streptomyces,* which enhances plant growth and provide pathogens defense, *Micromonospora,* which engages in symbiosis with rhizobium, and *Arthobacter,* which contributes to iron tolerance, are also significant (Menendez and Carro, 2019) (Fig 1).

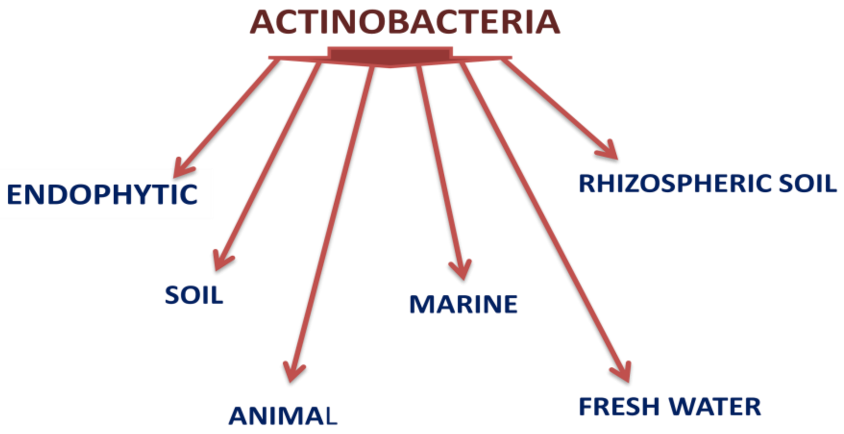

Figure 1: Actinobacteria diversity

Rhizospheric Actinobacteria

Actinobacteria are found in both rhizospheric soil and as endophytes in plant tissues. However the actinobacterial populations in the rhizosphere differ from those in plant tissues due to presence of root exudates and other microbes in the rhizosphere (Rani *et al.,* 2018). These bateria are notable for their ability to hydrolyze chitin, cellulose, starch and other complex carbohydrates by secreting various hydrolytic enzymes in the rhizosphere (Vurukonda *et al.,* 2018). Additionally, actinobacteria actinobacteria produce siderophores, lytic enzymes, indole acetic acid, hydrogen cyanide, ammonia and can solubilize inorganic phosphate (Jog *et al.,* 2012;

Damam *et al.,* 2016). They exhibit enzymatic activities such as the production of protease, lipase, and cellulase (Aditi and Anupma 2015). In recent years researchers are attracted to isolation of from rhizospheric soil from various regions. Actinobacteria can be isolated from the rhizospheres of soil different crop plants including rice, wheat, corn, cotton, pea, tomato, chili, and sugarcane (Ningthoujam *et al.,* 2016; Oskay *et al.,* 2004; Rassem *et al.,* 2018; Anwar *et al.,* 2016; Jalaluldeen *et al.,* 2014; Rodrigues 2018) as well as medicinal plants such as *Aloe indica*, *Curcuma* sp, black paper, and basil (Ramakrishnan *et al.,* 2009; Anusree and Bhai 2017; Elshafie *et al.,* 2023). For examples hundreds of actinobacterial isolates have been identified from the rice rhizosphere in Thailand, with a dominance of the genera *Streptomyces*, which exhibits antagonistic activity against phytopathogen *Pyricularia* sp. Many *Streptomyces* spp produce hydrogen cyanide (HCN), which helps suppress diseases and contribute to mineral mobilization and phosphate release (Passari *et al.,* 2015; Rajavec and Lapanje, 2016) (Table 1, Fig 2).

Table 1: Isolation of actinobacteria from rhizospere soil of different plants

Plant	Genus	References
Medicinal plants	*Streptomyces* sp, *Nocardia, Micromonospora, Actinomadura, Nonomurea* sp	Khamna *et al.,* 2009
Mangrove	*Actinomadura sp*	Ara *et al.,* 2008
Cephalotaxus fortunei	*Actinopolymorpha sp*	Yuan *et al.,* 2010
Yam	*Streptomyces* sp, *Kitasatospora* sp	Palaniyandi *et al.* 2012
Bamboo	*Streptomyces gramineus*	Lee *et al.,* 2012
Pinus sp, prunus sp	*Nocardiopsis spp, Streptomyces spp*	Aouar *et al.,* 2012
Mangrove	*Streptomyces* sp	Mohana *et al.* 2014
Oil palm	*Streptomyces* Spp, Kitasatospora sp	Pithakkit *et al.,* 2015
Leguminous plants	*Streptomyces, Micromonospora, Nocardia, Saccharopolyspora, Actinopolyspora.*	Kaur *et al.,* 2015
Pisum sativum	*Streptomyces spp*	Rassem *et al.,* 2018
Alpinia galanga	*Streptomyces* sp	Rani *et al.* 2016
Rice	*Amycolatopsis* sp	Ningthoujam *et al.,* 2016
Wheat and Tomato	*Streptomyces* spp	Anwar *et al.,* 2016
Black paper	*Streptomyces* spp	Anusree and Bhai 2017
Phoenix dactylifera	*Nocardiopsis spp, Streptomyces spp*	AbdElgawad *et al.,* 2019
Rice	*Streptomyces spp, Amycolatopsis sp*	Rattanakavil *et al.,* 2020
Juniperus excela	*Actinomycetia* sp	Tistechok *et al.,* 2023
Rosemary, Olive	*Streptomyces* spp	Elshafie *et al.,* 2023
Soybean	*Streptomyces sp*	Fatmawati *et al.,* 2023

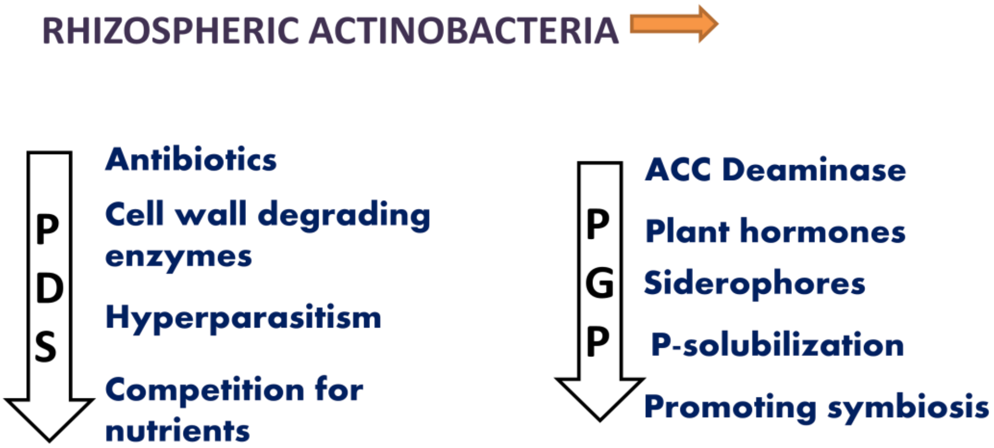

Figure 2: Activities of rhizospheric actinobacteria

Plant Growth Promoting Trait of Actinobacteria

Plant growth promotion by actinobacteria is comparable to that by other bacteria. This plant growth promotion can be direct, through mechanisms such as the production of indole acetic acid, cytokinin, siderophore, nitrogen fixation, and mineral solubilization, or indirect, through biocontrol and stress mitigation (Sathya *et al.,* 2017; Taj *et al.,* 2016; Palaniyandi *et al.,* 2013). Due to these beneficial traits, actinobacteria protect the plants from environmental stresses and various pathogens. Plant growth promoting (PGP) *Streptomyces* spp which also serve as biocontrol agents, are an alternative method for improving rice plant growth (Ngalimat *et al.,* 2021). *Streptomyces* sp is the most abundant genera in rhizospheric soil, alongside *Nocardia* and *Micromonospora*, among plant growth promoting actinobacteria (Bian *et al.,* 2012; Zhang *et al.,* 2016; Raut and Kulkarni *et al.,* 2018). Additionally, tea rhizospheric actinobacteria, such as *Tsukamurella tyrosinosolvens,* have been found to act as organic acid chelating agents (Zhang *et al.,* 2021). Actinobacterial isolates like *Micromonospora, Nocardiodata* and *Frankia* possess genes that code for antagonism, siderophore production, and pyoverdine phytohormone regulation in maize flowering (Oyedoh *et al.* 2023).

Siderophore Production by Actinobacteria

Siderophores are iron chelating secondary metabolites produced by various microorganisms to make iron available for the plants. Iron in soil typically in an insoluble (Fe^{3+}) form but actinobacteria and other microbes can make it soluble (Fe^{2+}) for plant absorbtion. Additionally, siderophore producing actinobacteria protect help plants protect from invasion of pathogen or insects. Several actinobacteria known for their siderophore activity include *Streptomyces* spp, *Rhodococcus, Nocardia, Saccharopolyspora erythraea,* and *Ciricoccus* (Sathya *et al.,* 2017; Swarnalakshmi *et al.,* 2016; Wang *et al.,* 2014)

Indole Acetic Acid (IAA) Production by Actinobacteria

Phytohormones play a crucial role in growth and nodulation (Solans, 2011). Indole acetic acid, a precursor to the plant hormone auxin, is essential for cell elongation, cell division, and other cellular activities. Tokala *et al.* (2002) identified *Streptomyces olivaceoviridis, S. rimosus,* *S. rochei* and other *Streptomyces* species in the tomato rhizosphere that produce indole acetic acid (IAA). Additionally various species of *Streptomyces* and *Nocardiopsis* are capable of producing indole acetic acid (IAA) (Sathya *et al.,* 2017).

Enzymatic Activities by Actinobacteria

Actinobacteria secrete a wide range of hydrolytic enzymes including amylases, cellulases, chitinases, glucanases, hemicellulases, keratinases, ligninases, lipase, pectinases, and protinases (Jain *et al.,* 2022).

Table 2: Inhibitory effects of lytic enzymes produce by actinobacteria

Enzyme	Actinobacteria	Comments	References
Chitinase, Glucanase, Protease, cellulose, lipase	*Strepomyces* sp 9P	Inhibits *Alternia brassicae*, Colletotrichun gloeosporoids,	Shanthi *et al.,* 2021
Chitinases	*S. plymuthica* C48 *S. violaceusniger* XL-2	Inhibit spore germination of Botrytis cinerea and suppresses wood rotting fungi	Sharma *et al.,* 2018
Protenases	*Streptomyces* sp	Manages anthracnose on tomato fruits and inhibits *Fusarium udum.*	Sharma *et al.,* 2018
Chitinase and Glucanase	*S. cavourensis* SY224	Manages anthracnose in pepper	Sharma *et al.,* 2018
Keratinase	*Nocardiopsis* sp SD5	Degrade poultry chicken feather	Anandan *et al.,* 2016
L-asparaginase	*Nocardia sp, Streptomyces karnatatakensis, S. albidoflavous* and *S. grisesus*	-	Anandan *et al.,* 2016
Β-1,3, β-1,4 and β-1,6-glucanases	*Actinoplanes philippinensis, A. campanulatus, Microbispora rosea, Micromonospora chalcea, S. griseoloalbus* and *S. spiralis*	Inhibit *Pythium aphanidermatum* and Phytophthora fragariae, casual agent of damping-off disease in seedlings of cucumber and raspberry.	Shanthi *et al.,* 2021; Sharma *et al.,* 2018

These enzymes play an active role in decomposing lignolytic-cellulose and other organic materials. Beyond decomposition, these enzymes also contribute to biocontrol by fungal cell wall, bacterial membrane, protein membrane, and extracellular virulence. Enzymes such as chitinase, glucanse, protease, and phospholipase, produced by antagonistic actinobacteria, are used as biocontrol agents (Palaniyandi *et al.,* 2013). *Streptomyces* species are particularly noted for their biocontrol properties due to their production of chitinase, glucanase (Lee at al 2012) and protease (Froes *et al.,* 2012). *Actinoplanes campanulatus* secrets β-glucanse, while *Micrmonospora carbonacea* produces β-glucanase, chitinase and cellulose (El-Tarabily *et al.,* 2009; 2000; 1996). Additionally *Amycolatopsis* species have been found to secrete enzymes protease, glucanase and pectinase (Alekhya and Gopalakrishnan, 2016) (Table 2).

Actinobacteria Fixes Nitrogen

Nitrogen is a crucial element for plant productivity and development, but plants are unable to utilize stable nitrogen present in the atmosphere, which constitutes 78% of the air. Nitrogen fixation is a process by which atmospheric nitrogen is converted to ammonia, facilitated by the enzyme nitrogenase. *Frankia* species play a significant role in nitrogen fixation both in leguminous and non leguminous plants by converting atmospheric nitrogen into nitrate or ammonium ions (Oyedoh *et al.,* 2023). *Frankia* infected actinorhizal plants exhibit a similar nitrogen fixation rate to that of legume symbioses (Hibbs and Cromack, 1990). *Frankia* infect host plant root cell through both intercellular and intracellular invasion (Benson and silvester 1993). Actinorhizal actinobacteria, such as *Frankia,* grow continuously, with new cells forming at the apex. Other rhizospheric actinobacteria reported to have nitrogen fixing capabilities include *Arthobacter, Agromyces, Corynebacteria, Mycobacterium, Micromonospora, Propionibacteria,* and *Streptomyces* (Cacciari *et al.,* 1971; Berndt *et al.,* 1989; Biabani *et al.,* 2012; Gtari *et al.,* 2012). The application of *Streptomyces* inoculants in field condition has been shown to improve soil conditions and enhance nodulation in chickpea plant (Gopalkrishnan *et al.,* 2015).

1- Aminocyclopropane-1-Carboxylic Acid (ACC) Deaminase

Ethylene is a plant hormone and associated with ageing and is released in response to stress. Various plant growths promoting actinobacteria produce the enzyme 1-aminocyclopropane-1-carboxylic acid deaminase which hydrolyzes 1 aminocyclo propane-1-carboxylic acid (ACC), immediate precursor of ethytene in plant tissue. This enzyme converts ACC into alpha keto butyrate, methionine and ammonia, thereby regulating ethylene production (Honma and Shimomura, 1978; Glick *et al.,* 1999). Plant inoculated with ACC deaminase producing bacteria show enhanced root elongation and improved shoot growth (Onofre-Lemus *et al.,* 2009). El-Tarabily (2008) isolated *Streptomyces* sp with ACC deaminase activity that promoted tomato plant growth. Additionally, some halophilic actinobacteria, such as *Corynebacterium varabile, Micrococcus yunnanensis and Arthrobacter nicotianae,* have been found to possess ACC deaminase activity, which supports growth in Canola plant under salt stress (Siddikee *et al.,* 2010). Other actinobacteria reported to have ACC deaminase activity include, *Streptomyces, Athrobacter, Mycobacterium, Agreia, Rhodococcus, Actinoplanes, Austwickia, Brevibacterium, Nocardiodaceae* and various other members of the phylum Actinobacteria (Boukhatem *et al.,* 2022).

Actinobacteria Promoting the Mycorrhizal Activity

These organisms are known to fascilitate symbiosis between plant and nitrogen fixing bacteria, as well as enhance mycorrhizal association (Schrey and Tarkka 2008). They contribute to the growth of mycorrhizal fungal hyphae elongation and this association found in roots of clover and sorghum with *Streptomyces coelicolor* and *Streptomyces* sp MCR9 and MCR24 (Sathya *et al.,* 2017). *Streotomyces* along with other bacteria found to promote mycorrhiza development (Frey-Klett *et al.,* 2007) *Streptomyces* associated mycorrhiza are found to produce secondary metabolites like antibiotic cyclohexamide and actiphenol are shown activity against phytopathogenic bacteria and fungi (Schrey *et al.,* 2012). Some members of actinobacteria such as *Streptomyces* MM40, *Actinoplanes* ME3 and *Micromonospora* MM18 found to improve arbuscular mycorrhiza (AM) in clover plants (Solans 2007).

Solubilization of Inorganic Phosphate by Actinobacteria

Phosphate solubilizing microbes including bacteria, fungi and actinobacteria are very common in rhizosphere of plants which enhance the nutrient accessibility to the plants (Frioni 2006). Phosphorus present in the soil are in insoluble form which plants can not taken up but actinobacteria including other microbes can make it available by solubilizing it. Actinobacteria like *Micromonospora, Micrococcus, Streptomyces, Thermobifida, Kitasatospora, Gordonia, Arthobacter* can produce extracellular phytases enzyme which degrades phytate and make an acidic environment in the rhizosphere by secreting acids like malic, oxalic, gluconic, succinic and propanoic that solubilize phosphorous present in the surrounding environment (Shanthi, 2021; Sathya *et al.,* 2017; Yadav and Yadav 2019; Sharma *et al.,* 2013).

Antimicrobial Activities

Antimicrobial biocontrol agents are widely used against plant pathogens. Rhizpspheric actinobacteria can produce bioactive secondary metabolite that protects plants. *Streptomyces* spp (500 species) produces 70-80% of secondary metabolites while other genera like *Micromonospora, Saccharopolyspora, Actinoplanes, Amycolatopsis* has less contribution (Berdy 2005). Isolates with hydrogen cyanide (HCN) production activity has effect against phytopathogen as they hamper the electron transport system of the pathogen. *Streptomyces* sp producing HCN found to active against pathogen *Fusarium oxysporum* (Gifford *et al.,* 2019). Many researchers observed production of enzymes that could hydrolyze fungal pathogen cell wall or produce other anti fungal compounds (Goodfellow and William, 1983). Antagonistic activity of actinobacteria against pathogenic fungi has been reported from many genera and El sayed *et al.* (2023) reported *Nocardiopsis alba* with antifungal activity against phytopathogen *Fusarium oxysporum, Rhizoctonia solani* and *Alternaria brassicicola.* In china *Streptomyces* sp was used against soil born pathogen in cotton plants (Valois *et al.,* 1996). Kim and Nguyen (2015) isolated *Streptomyces fabae* from soybean rhizosphere with antimicrobial activities. Among rhizospheric actinobacteria *Streptomyces* sp is most commonly found genera to provide protection against soil born pathogen like *Fusarium oxysporum* (Mariastuti *et al.,* 2018; Sari *et al.,* 2021), *Rhizoctonia solani* (Ebrahimi-Zarandi *et al.,* 2021), *Aspergillus niger, Phytophtora* *infestans, Penicillum* spp *Endosporium* sp (Belgacem *et al.,* 2023) and *Verticillium dahlia* (Xue *et al.,* 2013). They are also found to active against bacterial pathogen *like Escherishia coli, Bacillus subtilis, Listeria momocytogenes, Klebsiella pneumonie, Acinetobacter boumanie, Pseudomonas aeruginosa* (Belgacem *et al.,* 2023) isolated from *Acacia* rhizosphere. Many rice actinobacteria with antimibrocial activities reported to active against phytopathogens like *Magnaporthe grisea, Rhizoctonia solani, Xanthomonas oryzae pv oryzae and fusarium moniliformae* (Tian *et al.,* 2004) (Table 4).

Worlds two third of antibiotics are produced by *Streptomyces* spp and first antibiotic obtained from actinobacteria was streptothricin in 1942 and later in 1944 streptomycin (Anandan *et al.,* 2016). *Streptomyces violaceusniger* YCED9 can secrets three kinds of antibiotic together are nigerrecine, geldanamycin and guanidyl fingine. Several antibiotics are produced by many actinobacterial isolate viz streptomycin, polyketide, naphthoquinone, mildiomycin, kasugamycin, germicidin and hypnosin, nocathiacins, thiopeptide antibiotic, purpuromycins and microbiaeratin secrets by *Streptomyces, Streptomyces, Streptomyces, Streptoverticillium rimofaciens, S. kasugaensis, S. alboniger, Nocardia, Nocardiopis, Actinoplanes* and *Microbispora* respectively (Swarnalakshmi *et al.,* 2016) (Table 3).

Table 3: Antibiotic produce by some *Streptomyces* spp (Jain *et al.,* 2022)

Antibiotic	Actinobacteria	Role	References
Polyoxin B Polyoxin D	*Streptomyces cacoi var*	Inhibit fungal cell wall formation and, chitin synthase enzyme and rice sheath cause by *Rhizoctonia solani*	Sharma *et al.,* 2018
Avermectins	*S.avermitilis*	Protect host from nematodes	Shanthi *et al.,* 2016
Germicidin and hypnosin	*S. alboniger*	Inhibit spore germination	Swarnalakshmi *et al.,* 2016
Geldanamycin Elixophyllin	*s. hygroscopicus*	Inhibit *Rhizoctonia* root rot of pea	Swarnalakshmi *et al.,* 2016
Kasugamycin	*s. kasugaensis*	Inhibit rice blast and antagonist against fungal pathogen	Kasuga *et al.,* 2017
Mildiomycin	*Streptoverticillium rimofacin*	Inhibit powdery mildew on crops	Sharma *et al.,* 2014
Streptomycin	Streptomyces sp	*Erwinia amylovora*	Doolotkeldieva *et al.,* 2016

Table 4: Example of antimicrobial activities of rhizospheric actiinobacteria against pathogens

Plant	**Genus**	**Pathogen**	**References**
Maize	*Streptomyces* spp	*Cephalosporium maydis*	El. Mehalawy *et al.,* 2004
Corn, cotton	*Streptomyces* sp	*Erwinia sp, Pseudomonas*	Oskay *et al.,* 2004
Pandanus amaryllifolius	*Streptomyces* sp	*Alternaria brassicicola, Colletotricum gloeosporiods, Fusarium oxysporum, Penicillium digitatum, sclerotium rolfsii*	Khamna *et al.,* 2009
Cotton	*Streptomyces sp*	*Verticillium dahlia*	Xue *et al.,* 2013
Mangrove	*Micromonospora, Catellalospora, Nonomuraea, Microbispora*	*Fusarium sp*	Ara *et al.,* 2013
Chili	*Streptomyces sp*	*Fusarium sp*	Jalaluldeen *et al.,* 2014
Onosis angustisstm Lam	*Streptomyces sp*	*Fusarium oxysorum*	Mouloud *et al.,* 2015
Caesalpinia pyramidalis Tul.	*Streptomyces sp*	*Fusarium moniliformis, staphylococcus, candida, bacillus subtilies*	Lacerda *et al.,* 2016
Black rice	*Streptomyces sp*	*Pyricularia oryzae, Rhizoctonia oryzae sativae*	Ningthoujam *et al.,* 2016
sugarcane	*Streptomyces sp*	*Fusarium moniliforme*	Rodrigues 2018
Crinum latifolium	*Streptomyces sp*	*Fusarium sp.*	Tam *et al.,* 2019
Basil	*Streptpmyces sp*	*Monilinia fructigena, Rhizoctonia solani, penicillium spp*	Elshafie *et al.,* 2023
Atriplex halimus L	*Streptomyces sp*	*F. oxysporum, alternia alternarnata*	Boukelloul *et al.,* 2023

Antibiotic Resistances

Microorganisms competing with each other for their survival, space and nutrition and for this they produce antimicrobial compound which create antibiotic resistance mechanism against antimicrobial agents (Bafghi *et al.,* 2019). Vast quantity of resistance genes are produced from antibioting producing microbes like *Streptomyces* sp (Jiang *et al.,* 2017). Abundance of soil *Streptomyces* spp reported to have resistance to considerable number of antibiotics and lead to believe that these are in the environment (Nikaido 2009). Among actinobacteria *Actinoplanes, Collinsella aerofaciens* and *Corynebacterium ulcerans* reported to have multiple resistance genes *marR* gene, *marA* gene and *marR2* gene respectively (Bafghi *et al.,* 2019). Penicillin binding proteins are described in *Corynebaterium resistens, Mycobacterium tuberculosis* and in *Leucobacter chironomi* and β galactamase genes are reported in many species of *Streptomyces* and in other actinobacteria. Vancomycin, first glycopeptides isolated from *Amycolatopsis orientalis* in 1950 (McCormick 1956). Actinobacteria like several species of *Streptomyces* spp, *Nocardiopsis* sp (Zhang *et al.,* 2018), *Nonomurea* sp (Binda *et al.,* 2018) among others were reported to have Vancomycin resistance genes. Chloramphanical was first reported in 1947 from *Streptomyces venezuale* and resistance gene (*cat A-5* gene) for this antibiotic was reported from *Streptomyces satonii* (Zhang *et al.,* 2018).

Beneficial Effect of Actinobacteria on the Nodulation and Growth of Legumes

Inoculation of nodulation plant with actinobacteria increases the number of nodules. Actinorhizal plants are dicotyledonous angiospermic plants that have the ability to fix symbiosis with nitrogen fixing actinobacteria (eg: *Frankia*) and leads to nitrogen fixing root nodules. The mature cell of nodule filled with active filaments of bacteria that fix atmospheric nitrogen (Brunda and Roopam 2023). Legumes i.e Fabales is the one family and 80% of legumes are symbiotic. *Frankia* found to associate with Fagales (Berry *et al.,* 2011*). Frankia* able to secret different types of auxins which help in cell division and nodule formation in actinorhizal symbiosis (Berry *et al.,* 1989; Hammad *et al.,* 2003). In legume plant like *Pisum sativum* L, *Streptomyces* species found to promote nodulation, height and shoot weight (Tokala *et al.,* 2002). However, *Streptomyces* co inoculated with *Bradyrhizobium japonicum* in another legume Soybean plant found to improve root nodulation, seed weight and nitrogen content in soil (Gregor *et al.,* 2003). Again soybean when inoculated with *Nocardia, Streptomyces, Nonomurea* and *Actinomadura* resulted in increase in nodulation, plant growth, dry weight and mineral composition (Nimnoi *et al.,* 2014).

Distribution and Diversity of Actionobacteria in Soil and Plants

Actinobacteria predominantly present in the soil in dormant spore form but favorable conditions like humidity, nutrient availability, temperature, physiological interaction with other microbes make them form mycelia from the spores (Vobies 1992). They make up of 30% of microorganism in the soil and their population 10^6-10^9 bacteria per gram of soil (Bouizgarne and Aouamar, 2014). *Streptomyces* is the most abundant genus of actinobacteria in the soil and many studies suggest this genus as 95% of all isolated soil actinobacteria (Yadav *et al.,* 2018). Besides *Streptomyces* other common genera present in soil are *Streptosporanium, Nocardia, Micromonospora, Actinoplanes* among others (Anandan *et al.,* 2016). Endophytic actinobacteria are biotechnologically very important group of microbes and they are non-pathogenic group of microbes colonize internal tissue of plants from root to aerial part of the plants for their partial or entire life cycle (Santos *et al.,* 2018). Different endophytic actinobacteria reported by researchers from different plant parts (wheat, barley, rice, soybean, banana, tomato, cowpea, chickpea, sugarcane, among them) are *Actinoplanes, Actinomadura, Micrococcus, Streptomyces, Microbispora, Micromonospora, Dietzia, Glycomyces, Kineosporia, Leifsonia, Nocardia, Nocardioids, Pseudonocardia, Saccharopolyspora, Streptosporangium,* along with (Shimizu 2011; Lobo *et al.,* 2019).

Application of Actinobacteria in Crops

Actinobacterial genuses have vast and accepted biotechnological application. The phylum actinobacteria have been studied extensively for its agricultural use. They are mainly use as biocontrol agents, suppression of disease and as a plant growth promoter (Ganapathy and Natesan 2018; Singh and Dubey 2018). *Streptomyces* sp isolated from chickpea rhizosphere with enzymatic activity and IAA, HCN, siderophore activities found to increase plant biomass and seed yield in chickpea. Again khan *et al.,* (2021) reported halotolerant *Arthobacter* from rhizospheric soil with IAA, ABA, siderphore activities were able to increase length of plant and biomass and higher level of cholophyll in soybean plant. However *Arthobacter* from burned Holm oak rhizosphere have IAA, enzymatic and siderophore activities were active in increase plant biomass in Alfalfa and pepper plant (Fernandez-Gonzalez *et al.,* 2017). *Streptomyces* and *Micromonospora* with antimicrobial, p-solubilization, and IAA and siderophore activity have the ability to increase dry weight of Wheat plant infected with *Pythium* (Hamdali *et al.,* 2008). Different Streptomyces species isolated from rhizophere and root endosphere showed different activities like phosphate solubilization, siderophore, IAA, organic acid and antifungal metabolites and also can produce phytase and chitinase (Jog *et al.,* 2014). Several species of *Spreptomyces* found to participate in crop improvement in field condition. *Streptomyces* inoculated to wheat plants in lab chamber found to have increased plant biomass, lateral roots and branch and nutritional contents as compare to uninoculated plant (Jog *et al.,* 2014).

Actinobacteria Tolerance to Different Stresses

Actinobacteria have the ability to survive in different abiotic and biotic stress condition of environment like extreme temperature, drought, pathogen, salinity, acidity, floods etc but use of actinobacteria has received very less importance regarding stress tolerance to plants (Sathya *et al.,* 2017; Adegboye and Babalola, 2015; Passari *et al.,* 2015). Chukwuneme *et al.,* (2020) have reported two actinobacterial genera namely *Streptomyces pseudovenezuelae* and *Arthobacter arilaitensis* which promote growth to maize plant in drought stress condition. *Streptomyces* sp found to enhances growth of Maize and Wheat in saline condition. Siderophore and other PGP trait make them tolerant to heavy metal toxicity. *Streptomyces* sp with ACC deaminase activity make rice to survive in saline condition by producing high level of calcium and potassium (Shanthi, 2021).

Actinobacteria as Agent of Bioremediation/Biodegradation

Bioremediation is an effective and efficient process to transform an environment to its original state by the use of microorganism and its enzymes. Actinobacteria are prospective source for degradation of resistant inorganic and organic contaminants from soil. They can degrade pesticides like carbamate, organophosphorous, organochlorine, urea; pyrethroids etc. Common genera involve are *Arthobacter, Streptomyces, Janibacter, Kokuria, Rhodococcus, Mycobacterium, Nocardia, Frankia* etc (Alvarez *et al.,* 2017). *Streptomyces* spp are found to have detoxifying activity against pesticides like aldrin. DDT, chlordecone, heptachlor, dieldrin etc; *Streptomyces* spp from marine environment of Tamil Nadu had high Zinc biobsorbtion activity (Jain *et al.,* 2022). Lead is a neurotoxic substance and mercury is a hazardous heavy metal which can damage kidney and cardiovascular system and Sanjenbam *et al.,* (2012) describe *Streptomyces* sp can help in biosorbtion of lead and mercury which can spread both in soft and hard tissue. Chromium has carcinogenic and mutagenic effect on organisms and Das and Chandra (1990) were the first to report reduction of chromium by *Streptomyces* sp. Other genera like *Micromonospora, Arthobacter* and *Amycolatopsis* are also found to active in Chromium bioremediation (Amoroso *et al.,* 2013; Camargo *et al.,* 2004).

Conclusion:

Applications of actinobacteria as plant probiotic are still in their beginning stage as compared to other plant growth promoting microorganism or PGP bacteria. Again several numbers of isolates of actinobacteria are isolated from different source like soil, rhizosphere, plant tissue and marine or aquatic environment and relationship with other microbes and plants described. In addition, the rise of antibiotic resistance to effective antibiotics suggested need to search new prominent antibiotic and actinobacteria is a promising producer of secondary metabolites like biocontrol agents for which researchers showing interest in screening and isolation of novel actinobacteria for natural products which can be use in agriculture. It is important to study genetic roles and interaction between plants and microbes or microbes to microbes for which new technologies should be develop and use in agriculture. Application of actinobacteria is limited in agricultural field. Use of microbial product can decrease uses of pesticides and chemical fertilizer in many agricultural fields of the world as an alternative which can encourage use of probiotic actinobacteria in real crop production.

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ROLE OF BRASSINOSTEROIDS AND SALICYCLIC ACID IN PRODUCTIVITY OF FRUIT CROPS

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Abstract:

Plant hormones play a pivotal role in integrating developmental activities, and the utilization of growth regulators has become an integral component of agro-technical procedures for numerous cultivated plants, particularly fruit crops. In this context, exogenous application of plant growth regulators has been shown to mitigate excessive fruit drop in fruit crops (Suman *et al.,* 2017). Brassinosteroids (BRs), a novel class of plant hormones, are gaining prominence as potential catalysts for agricultural development worldwide. Application of exogenous BRs influences various aspects of growth and development in fruit plants, including vegetative growth, flowering, fruit set, growth, ripening, storage, and tolerance to biotic and abiotic stresses. Notably, BRs possess the capacity to counteract genotoxicity and pesticidal residues in horticultural crops, thereby facilitating the production of consumer-friendly fruits. A significant advantage of BRs application lies in its ability to modulate plant responses to abiotic and biotic stresses through modifications in gene expressions and physiological processes (Sharma, S.K., 2021). Salicylic acid (SA), a plant-derived chemical, plays a crucial role in disease resistance and plant defence mechanisms. Post-harvest application of SA in horticultural crops has been demonstrated to reduce fruit rot, maintain quality, and enhance antioxidant activity. Furthermore, SA influences the quality attributes of organic products, including appearance, flavor, astringency, and bitterness. SA also exhibits potential in reducing fruit respiration, ethylene biosynthesis, water loss, microbiological contamination, and maintaining fruit firmness during storage and shelf life (Kapoor *et al.,* 2022).

Keywords: Brassinosteroids, Salicyclic Acid, Genotoxicity, Abiotic Stress, Biotic stress

Introduction:

Plant Growth Regulators (PGRs)

The majority of physiological activities and growth processes in plants are modulated by the action and interaction of endogenous chemical substances, referred to as phytohormones, as well as certain naturally occurring inhibitors such as phenols, flavonols, and abscisic acid. To differentiate these substances from animal hormones, they are designated as phytohormones. According to Thimann (1948), a plant hormone is defined as "an organic substance produced naturally in higher plants, controlling growth or other physiological functions at a site remote from its place of production, and active in minute amounts." Phytohormones have been variably termed as growth hormones, growth-promoting substances, growth substances, growth factors, and growth regulators by different researchers, with corresponding definitions. Auxins were the first naturally occurring hormones to be discovered in plants. In addition to auxins, two other pivotal groups of chemical substances exerting profound influences on the regulation of growth and development in plants have been identified, namely gibberellins and cytokinins. Furthermore, ethylene, abscisic acid (ABA), and more recently, brassinosteroids, have also attained recognition as natural plant growth hormones.

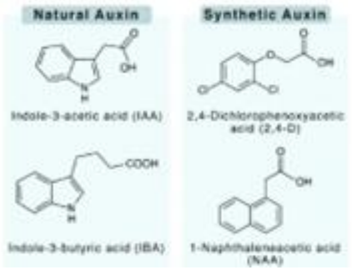

Figure 1: Structure of Auxin

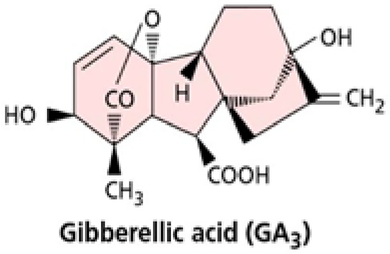

Figure 2: Structure of Gibberellin

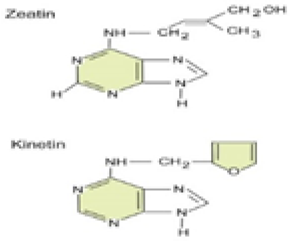

Figure 3: Structure of Cytokinin

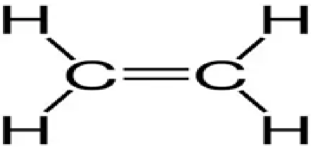

Figure 4: Structure of Ethylene

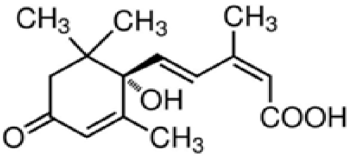

Figure 5: Structure of ABA

Novel Plant growth regulators (PGR) have properties like:

- Sustainable and eco-friendly growth elicitors
- Natural polysaccharides
- Antimicrobial
- Non-toxic
- Biocompatible
- Cheaper

Examples of Novel PGRs

1. Chitosan

Chitin:

1. [(1,4)-2-acetamido-2-deoxy-β-D-glucan]
2. It is the second most abundant molecule in nature.
3. Found primarily in cruslacean shells, insects and fungi

4. Chitosan can suppress the expression level of the genes encoding for chlorophyllase resulting in increased photopigment content.

2. Carrageenan

1. A polysaccharides mainly found in the cell walls of various red algae.

2. They involved in-

- Antimicrobial activity
- Photosynthesis
- N metabolism
- Cell division
- Cell signaling
- Mineral uptake
- Secondary metabolism

3. Melatonin

- An animal hormone.
- It was first reported in plants during 1995 by Suman et al.
- Melatonin Possesses resemblances with auxin as both have common precursors-tryptophan
- Role in reproductive development, circadian rhythm, cell protection, vegetative development as well as responses to both biotic and abiotic stresses.

4. Serotonin

- Biotic and abiotic stresses as well as plant growth and development processes.
- Discovered as animal hormone.

5. Harzianolide

- Discovered from cultures of the fungus Trichoderma harzianum.
- It has role in both plant growth promotion and systemic resistance induction.

6. Strigolactone

- It was found to be distributed in Striga host i.e. sorghum, maize, proso millet.

7. Karrikins

- The first butanolide compound discovered in smoke water and its analogs were name as “karrikins” or KARs.

8. Sodium alginate

- SA has the potential to enhance
  - ✓ Plant height
  - ✓ Bomass
  - ✓ Number of tillers

- ✓ Leaves
- ✓ Leaf area
- ✓ Improve overall vegetative growth in different crops.

9. **Koninginin (a novel metabolite)**
   - The compound inhibited the growth of etiolated wheat coleoptiles by 100% at 10-3 M

The New Generation of Phytohormones

Apart from these, there are PGRs whose efficacy and efficiency are known to us but due to technological gap they are not yet been harnessed at grass root level. These includes Brassinosteroids (BR), Jasmonate (JA) and Salicylic acid (SA).

Brassinosteroids (BRs)

Brassinosteroids (BRs) are poly-hydroxylated steroids and plant hormones that play a pivotal role in signalling during plant growth by regulating a diverse array of physiological processes. These include cell division, development and fertility, senescence, as well as tolerance responses to both biotic and abiotic stress (Oh and Clouse, 2020). Initially, the growth-promoting activity of lipid extracts from pollen grains of rapeseed, *Brassica napus*, was observed in the 1970 bioassay utilizing the bean second internode. Subsequently, the structural elucidation of this distinct class of plant hormones was first established in 1979 in the same plant species (Nolan *et al.,* 2020). Numerous steroid hormones have since been discovered in plants and categorized under the BR class. To date, over seventy BR-class hormones have been reported in plants, and these hormones fulfill many critical functions. BRs are generally distributed uniformly throughout the plant body, where they orchestrate proper growth and development, including pollen tube formation, root growth, cell differentiation, vascular tissue formation, senescence, seed germination, and other processes. Additionally, BRs actively modulate stress responses (both biotic and abiotic) in plants through various mechanisms (Saini *et al.,* 2015). Loss-of-function mutations in different genes have facilitated a deeper understanding of the biosynthesis and signalling events mediated by BRs. In plants, DET2 encodes a functional homolog of mammalian 5α-reductase, catalyzing steroid reductions. Loss-of-function mutations in det2 have underscored the significant roles of BRs in plant steroid biosynthesis (Li and Chory, 1999). Numerous other BR mutants have been reported in Arabidopsis mutant lines, and analyses of these mutants have demonstrated BR perception and signal transduction in plants (Nolan *et al.,* 2020).

Occurrence

Brassinosteroids, specifically Brassinolide (BL) and castasterone (CS) are ubiquitous in the plant kingdom. The presence of Brassinosteroids (BS) has been demonstrated in virtually every part of plants, including pollen, flower buds, fruits, seeds, vascular cambium, leaves, shoots, and roots. These steroidal compounds occur in both free form and conjugated to sugars and fatty acids. To date, approximately 69 BS have been isolated from plants (Bajguz, A. 2011). BS are also present in insect and crown galls, such as those of *Castanea crenata*, *Distylium racemosum*, and *Catharanthus roseus*. Notably, these plants exhibit higher levels of BS compared to normal tissues. Furthermore, young, growing tissues contain higher levels of BS than mature tissues. Pollen and immature seeds are the richest sources of BS, with concentrations ranging from 1-100 μg kg^{-1} of fresh weight, whereas shoots and leaves typically contain lower amounts (0.01-0.1 μg kg^{-1} fresh weight). Since the discovery of BL in 1979, 69 BRs have been isolated from 64 plant species. This includes 53 angiosperms (12 monocotyledons and 41 dicotyledons), 6 gymnosperms, 1 pteridophyte (*Equisetum arvense*), 1 bryophyte (*Marchantia polymorpha*), and 3 algae (*Chlorella vulgaris*, *Cystoseira myrica*, and *Hydrodictyon reticulatum*).

Structure (Zullo *and* Adam, 2003)

Plant sterols, convertible to brassinolide (BL) via teasterone, typhasterol, and castasterone, are synthesized through an isoprenoid biosynthetic pathway involving acetyl CoA, mevalonate, isopentenyl pyrophosphate, geranyl pyrophosphate, and farnesyl pyrophosphate (Symons *et al.,* 2008). Brassinosteroids are polyhydroxy steroid lactones with a structure akin to brassinolide (BS), sharing the same carbon skeleton as animal steroids like cholestane, ergostane, and stigmastane. Chemists and plant physiologists have adopted an approach where brassinolide (BL), the most active and first identified representative of this compound class, serves as the basis structure for the system. Considerable diversity exists in the basic structure at both the cyclic and side chains, facilitating important metabolic transformations to yield two other highly active BS analogues: 24-Epibrassinolide (EBL) and 28-Homobrassinolide (HBL). Moreover, BS are nontoxic (Esposito *et al.,* 2011) and environmentally friendly hormones (Kang and Guo, 2011).

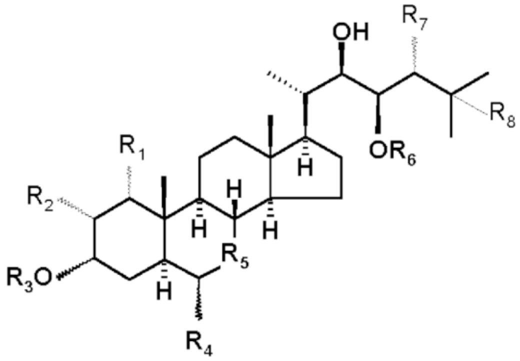

Figure 6: Structure of Brassinosteroids

Biosynthesis of Brassinosteroids

Brassinosteroids are polyhydroxy steroids and are considered the sixth class of hormones in plants. It has been demonstrated that brassinosteroids are synthesized from different sterol components depending on their types. Broadly, depending on the C-24 alkyl group BRs are classified into three major groups i.e., C-27, C-28, and C-29 steroid. The biosynthesis of these three major BRs has followed two lines of conversions. The biosynthesis of all BRs is initially started with the popular Acetyl Co-A which after multiple reactions gives rise to 4α methyl fecosterol. After this reaction, the pathway split into two distinct branches depending on the methylation pattern. The 24-methylene phenol leads to campesterol formation; whereas, 24-ethylidene iophenol produces sitosterols. The most prevalent plant brassinosteroids are a group of C-28 BRs, such as castasterone (CS) and brassinolide (BL) are produced from campesterol. On the other hand, C-27 and C-29 BRs are produced from cholesterol and sitosterol precursors (Wei and Li, 2020).

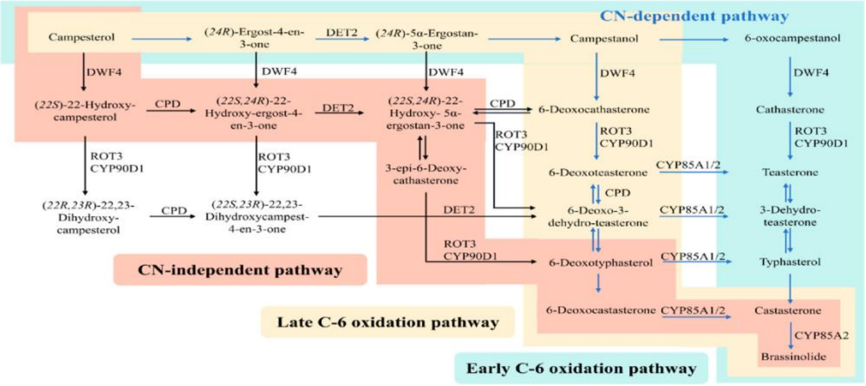

Figure 7: Brassinosteroid Biosynthetic Pathway

Brassinosteroid Signalling Pathway (Basit *et al.,* 2021)

The receptors of the brassinosteroid (BR) signaling pathway are localized on the plasma membrane. The primary receptor is BRI1 (BRASSINOSTEROID INSENSITIVE), a serine-threonine kinase comprising an extracellular domain, a transmembrane domain, and a cytoplasmic domain. For BRI1 to become functional, it requires the presence of BAK1 (BRI1 Associated Receptor Kinase 1), with which it forms a heterodimer. An inhibitory protein, BKI1 (BRI1 Kinase Inhibitor), is associated with the cytoplasmic domain of BRI1, preventing dimerization between BRI1 and BAK1. Binding of BR to the extracellular domain of BRI1 induces dissociation of BKI1 from BRI1. The resulting phosphorylated heterodimer complex initiates BR signaling. Multiple proteins or transcription factors may serve as targets of BR signaling; one such transcription factor is BZR1. In its phosphorylated state, BZR1 is sequestered in the cytoplasm, whereas in its dephosphorylated state, it translocates to the nucleus. Upon entering the nucleus, BZR1 binds to target sites in the promoter regions of BR-sensitive genes, thereby initiating transcription.

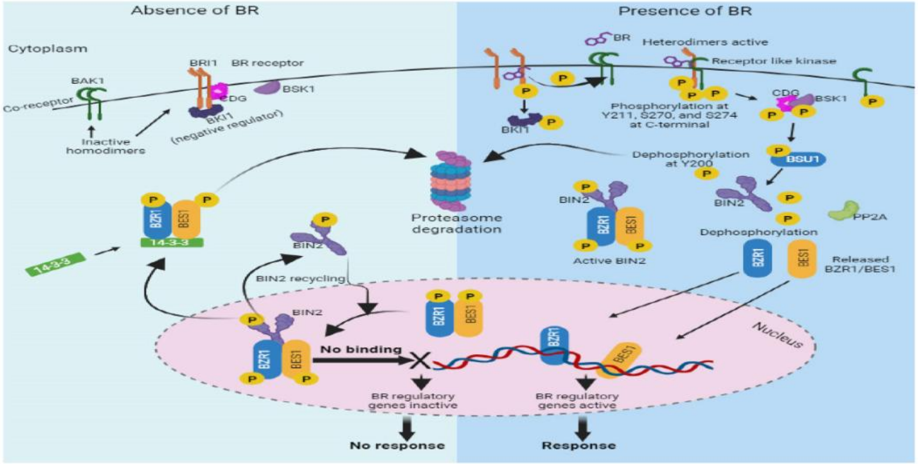

Figure 8: Brassinosteroid signalling pathway

Physiological effects of BRs in plants

Functions of BRs in Plants BRs are involved in various important events in plants which can be broadly classified into three types,

- Functions involved in physiology, growth, and developments;
- Functions involved in cellular and biochemical modulations; and
- Functions involved in stress tolerance (saini *et al.,* 2015; wei and li, 2020).
- The outlined functions of BR under those categories are described below.

i) Functions Involved in Physiology, Growth, and Developments

- Involved in photomorphogenesis.
- Root development and growth regulation.
- Regulation of cell wall chemistry.
- Instigation of seed germination.
- Stomatal movement regulation.
- Growth and development of pollen tubes.
- Regulation of photosynthetic efficacy.
- Hormonal crosstalk.
- Regulation of shoot elongation.
- Enhancement of ethylene biosynthesis and physiology related to ethylene function.
- Promote epinasty.
- Increases yield of vegetable crops.
- Induces male sterility.

ii) Functions Involved in Cellular and Biochemical Modulations

- Vascular differentiation.
- Cell expansion and elongation.
- Promotes cell division.

- Modulates membrane potential.
- Altered redox potentials at the cellular milieu.
- Regulates osmolytes (proline, betaine, sugars, polyols, etc.) and hence acts as osmo-protectants.
- Induces synthesis of phytochemicals.
- Reduces oxidative stress, lipid peroxidation and enhances antioxidant systems for reactive oxygen species (ROS) detoxification.
- Intracellular signal transduction and gene expression.
- Increases DNA and RNA polymerase activity.
- Enhance proton (H+) pump activities.

iii) Functions Involved in Stress Tolerance

- Combats biotic interventions by inducing hormonal systems and stress regulatory gene expressions.
- Osmotic stress.
- Drought tolerance.
- Heat and chilling stress.
- Salinity tolerance.
- Heavy metal stress.

Agricultural Application: Potentiality and Challenges

More than 20 years have passed since the discovery of brassinolide, the inaugural member of the brassinosteroid (BR) class of plant hormones. Not only has this been a period of rapid expansion for the BR class with an increasing number of members, but numerous captivating functions of this hormone class have also emerged. Due to their ability to modulate plant growth and development in diverse ways, coupled with their stress tolerance capabilities, BRs exert substantial effects on agricultural crops. In addition to their endogenous effects, BRs also exhibit effects when applied exogenously to plants. Exogenous application can alter the yield and quality of food grains. Furthermore, BRs are capable of modulating stress responses in plants. While exogenous BR application positively regulates agricultural traits in many crops under laboratory conditions, field trials have often failed dramatically in most cases. The instability of BRs in natural solutions during formulation preparation may account for this failure. Another contributing factor is the inability of exogenously applied BRs to be adequately absorbed deep within plant tissues. External light conditions also significantly impact BR function, interacting with phytochrome signaling cascades in many instances (Kamuro and Takatsuto, 1991). Despite these constraints, ongoing efforts have aimed to standardize BR application methods in agricultural fields, particularly for ameliorating abiotic stress and enhancing post-harvest storage efficiency. Although genomic studies have been conducted to elucidate the functions of this steroid hormone in plants, the precise cell-specific functions of BRs remain elusive. As hormones typically operate in a coordinated manner, investigating the interplay of BRs with other hormonal pathways may provide further insight. Continued research in this field will likely uncover missing pieces of the BR signaling puzzle in the future.

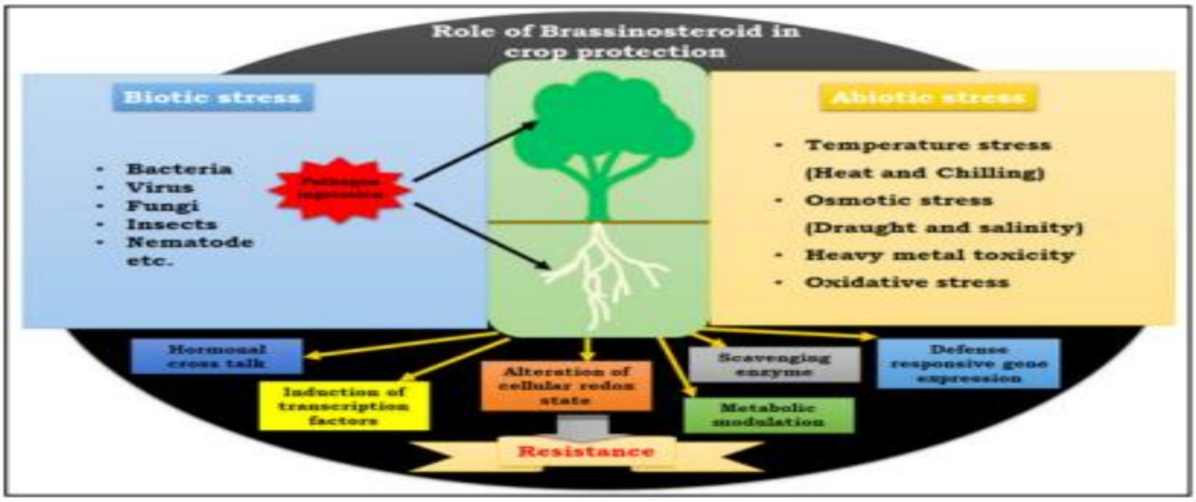

Figure 9: Agricultural Application: Potentiality and Challenges

Salicyclic acid

Salicylic acid and its derivatives, a class of plant hormones produced by plants, belong to the phenolic acids group and consist of a ring structure attached to hydroxyl and carboxyl groups. Salicylic acid is ubiquitously distributed throughout the plant kingdom (Raskin *et al.,* 1990) and is regarded as a potent plant hormone that plays diverse regulatory roles in plant metabolism (Raskin, 1992). Given its pivotal role in photosynthesis, plant water relations, various enzyme activities, and its impact on plants exposed to biotic and abiotic stresses, exogenous application of salicylic acid has been shown to benefit crop growth and biological productivity under fluctuating environmental conditions (Senaratna *et al.,* 2000; Horvath *et al.,* 2007; Hayat *et al.,* 2010). Salicylic acid has garnered significant attention recently due to its regulation of various modalities in plant responses to biological activities (Malamy *et al.,* 1992; Ryals *et al.,* 1996; Shah *et al.,* 2005) and abiotic stressors (Hayat *et al.,* 2010; Ding *et al.,* 2003).

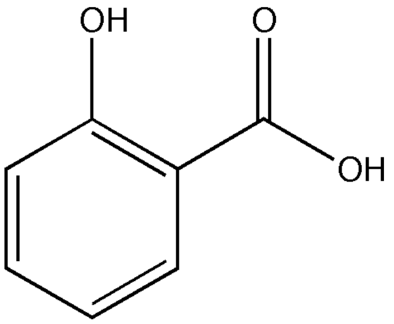

Figure 10: Structure of Salicyclic Acid

Properties of Salicyclic Acid

- An odorless, crystalline solid substance
- Has a sweetish taste
- Used externally for treatment of skin disease
- It has a remote action absorption
- Causes marked irritation of gastric mucous membrane

Physiological role of salicyclic acid

- Plant growth, thermogenesis, flower induction and uptake of ions
- Ethylene biosynthesis, stomatal movement and also reverses the effects of ABA on leaf abscission
- Enhancement of chlorophyll and carotenoid pigments, photosynthetic rate
- Resistance to pathogens by inducing the production of pathogenesis related proteins
- Systemic acquired resistance (SAR)
- Endogenous signalling, mediating in plant defense against pathogens

SA Biosynthesis In higher plants (Hu *et al.,* 2022)

Salicylic acid (SA) is synthesized from chorismate via two distinct metabolic pathways, each comprising multiple steps: the isochorismate synthase (ICS)-derived pathway and the phenylalanine ammonia-lyase (PAL)-derived pathway. Different plant species utilize varying branches for SA biosynthesis. In soybeans, pathogen infections result in equal contributions from the ICS and PAL pathways to the total SA pool. In Arabidopsis, the majority of pathogen-induced SA is derived from the ICS branch via plastid-localized ICS1 (also designated as SA deficient 2, SID2). Arabidopsis possesses two isochorismate synthase genes, ICS1 and ICS2; however, only ICS1 is induced by pathogens. ics1 mutants exhibit 90-95% reduced SA accumulation post-pathogen infection compared to wild-type plants. Only the ics1/ics2 double mutant substantially impairs SA accumulation, indicating that ICS1 generates most SA via isochorismate during pathogen defense. Several Arabidopsis mutants with altered SA accumulation result from mutations in genes encoding ICS pathway components. Recent studies indicate that bacteria utilize the Isochorismate Pyruvate Lyase (IPL) enzyme to directly convert isochorismate to SA, whereas Arabidopsis requires both AvrPphB-susceptible 3 (PBS3) and Enhanced Pseudomonas Susceptibility 1 (EPS1). The amidotransferase PBS3 catalyzes conjugation of isochorismate to glutamate, yielding isochorismate-9-glutamate (IC-9-Glu). Subsequently, IC-9-Glu either spontaneously decays into SA or is converted to SA by EPS1. PBS3 and EPS1 are localized in the cytosol, whereas ICS resides in chloroplasts. Thus, transport of isochorismate from plastids to the cytosol is essential for SA production. EDS5 (Enhanced Disease Susceptibility 5) was initially thought to function as an SA transporter on the chloroplast envelope during pathogen-induced SA accumulation. However, in eds5-3 mutants, coexpression of ICS1 and engineered chloroplast-targeted PBS3 restores SA biosynthesis, suggesting EDS5 participates in isochorismate transport to the cytosol during SA biosynthesis. A minimal amount of SA accumulation is induced by pathogens in the ics1/ics2 double mutant, blocked by the ICS pathway. Arabidopsis contains four PAL genes, and studies utilizing mutants or PAL-specific inhibitors suggest the PAL pathway also contributes to SA biosynthesis. Nonetheless, PAL quadruple mutants retain approximately 25% of wild-type basal SA levels and roughly 50% of induced SA levels following pathogen infection. The PAL pathway involves synthesis of trans-cinnamic acid from phenylalanine, subsequently converted to SA via benzoic acid.

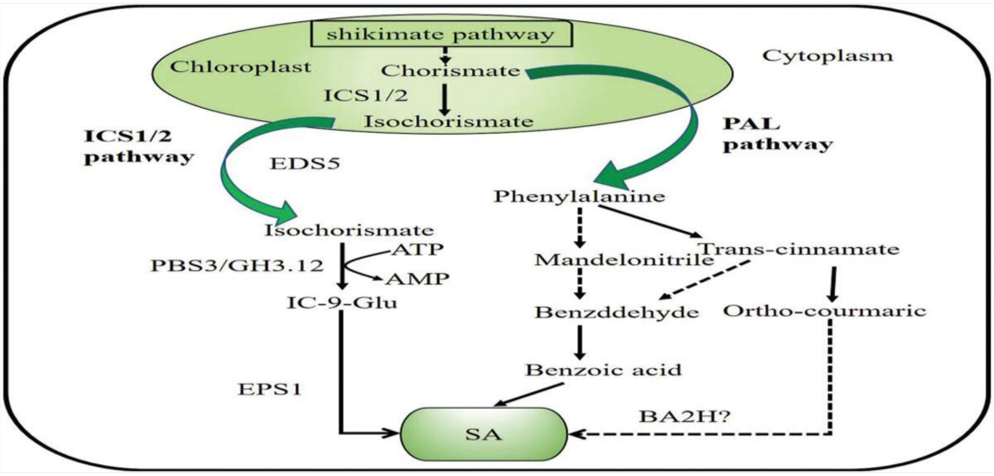

Figure 11: Biosynthesis of Salicyclic acid

SA Signaling Components (Sharma *et al.*, 2023)

The salicylic acid (SA) signaling pathway in Arabidopsis thaliana is activated by two receptor classes: Nonexpressor of Pathogenesis-Related Genes (NPR1) and NPR1-Like Protein 3/4 (NPR3/4). This activation stimulates the expression of defense-related genes and immunity. Neither NPR1 nor NPR3/NPR4 possess DNA-binding domains; thus, they interact with transcription factors such as TGA2/5/6 for signal transduction. NPR1 was identified through genetic analysis of SA-insensitive mutants. NPR1 functions as a transcriptional coactivator essential for the expression of pathogenesis-related (PR) genes and broad-spectrum disease resistance. In contrast to NPR1, NPR3 and NPR4 negatively regulate plant defense; npr3/npr4 mutants exhibit enhanced PR gene expression and basal resistance. NPR3 and NPR4 were identified as SA receptors based on their high affinities for SA. NPR4 possesses an SA-binding core domain that undergoes refolding upon SA binding, forming a helical fold that encapsulates SA within its hydrophobic core. The interaction between NPR1 and NPR4 is disrupted by SA-induced conformational changes in the NPR4 core. SA binding by NPR1 has also been reported, although results vary between studies. Analogous to their negative association with SA signaling, NPR3 and NPR4 function as CRL3 substrate receptors for NPR1 polyubiquitination and degradation. SA-mediated gene expression is controlled by NPR3 and NPR4 through modulation of NPR1 stability. NIM1-Interacting 1 (NIMIN1), a negative regulator of SA signaling, is strongly induced by SA in addition to NPR3 and NPR4. NIMIN1 negatively regulates NPR1-mediated immune responses by interacting with NPR1. The nimin1 mutant exhibits enhanced SA-induced PR1 expression, whereas NIMIN1 overexpression results in phenotypes similar to npr1 mutants, including reduced PR1 expression post-SA induction, compromised systemic acquired resistance (SAR), and SA intolerance. SAR depends on the activation of NPR1 and inhibition of NPR3/NPR4 by SA, both contributing to pattern-triggered immunity (PTI) and effector-triggered immunity (ETI).

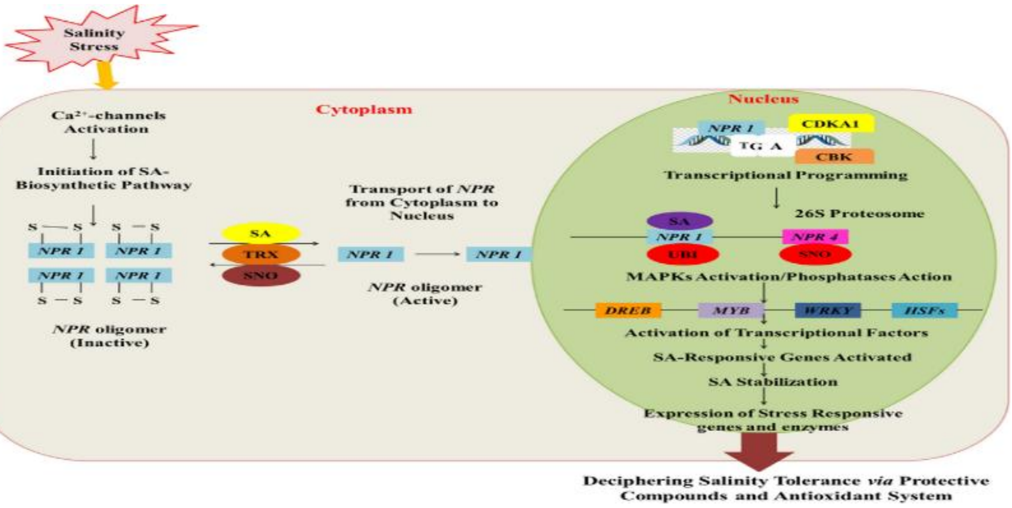

Figure 12: Mode of action of Salicyclic acid

Future Perspectives:

Over the past two decades, substantial progress has been made in elucidating the mechanisms involved in brassinosteroid (BR) signaling and transduction in plant systems. The majority of findings are based on studies conducted on model plant species like Arabidopsis. However, the relevance of these findings may deviate when considering higher woody species. Although BRs have been found to influence several developmental and physiological processes in higher plants, few studies illustrate the molecular mechanisms involved in regulating the biological processes of woody perennials. Advancements in research along these lines will improve understanding of genetic determinants of BR biosynthesis at the molecular level and further explore possibilities of BR uses for targeted horticultural applications. More emphasis is also required on elucidating the role of BRs in tolerance to different types of stresses faced by fruit orchards. In-depth studies on hormonal cross-talk with other hormones like abscisic acid, jasmonic acid, auxins, gibberellins, etc., will facilitate the use of these hormones for enhanced horticultural output and extending the shelf or storage life of climacteric and non-climacteric fruits. Fruit crop-specific scientific studies are needed for optimizing the concentration and standardizing the stage and mode of BR application for cost-effective orchard management. Salicylic acid is perhaps the only compound on Earth's surface to mediate such diverse functions as curing various human ailments, protecting plants from various biotic and abiotic stresses, and affecting various physiological and biochemical processes of plants (Popova *et al.* 2012). In the future, biochemical and physiological changes in plants induced by salicylic acid may be explored as biochemical markers, which may further be transformed into genetic markers and utilized in genetic engineering of plants for making them tolerant to various stresses. Future studies should focus on the mechanisms of action of salicylic acid in systemic resistance of fruits using molecular, proteomic, and metabolic approaches and identify the molecular events involved in the signalling of salicylic acid-induced disease resistance in fruits.

Conclusion:

More than four decades after the discovery of brassinosteroids, it is widely acknowledged that these molecules play a role in numerous critical physiological processes, ranging from cell division and growth to responses to changing environmental conditions. Conversely, the absence of BRs leads to malformations at the leaf level and limited growth development. Although numerous examples over the years have demonstrated that BR use in post-harvest can yield substantial benefits, many studies have not been classified as presented in this review. Firstly, information was provided on the use of BRs in the post-harvest of fruits and vegetables, catalogued by family (with Solanaceae and Rosaceae being the most studied to date), and the mechanism of action of these substances was also included in a simplified form. Secondly, questions were posed regarding the use of BRs in post-harvest stages of marketing, seeking to clarify information that is not yet clear, including the feasibility of using endogenous BR inhibitors when justified.

Finally, new challenges await researchers using BRs in post-harvest, namely:

1) finding simple and profitable application methods;
2) promoting and conducting studies on the influence of the developmental state of certain horticultural products on the action of these hormonal regulators;
3) considering the use of synthetic BRs with enhanced effectiveness based on new chemical structures and knowledge of their structure-function relationship;
4) guaranteeing the safety of these new substances, including BR inhibitors.

In horticultural crops, ascorbic acid (AA) and salicylic acid (SA) have had a considerable impact beyond the scope of this analysis, which focused on a limited number of AA and SA features. Numerous opportunities exist for combining them with current technology to provide consumers with high-quality horticultural output while reducing post-harvest losses, particularly for perishable fruits, vegetables, and ornamentals. The scientific community can utilize AA and SA to investigate biochemical and physiological reactions of horticultural produce. Further research is needed to understand diverse responses within different horticultural crops to enable safe usage of the technology.

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PHYSIOTHERAPY ASSESSMENT IN SCHOOL HEALTH PROGRAMS: ESTABLISHING THE NEED FOR ROUTINE SCREENING IN HEALTHY CHILDREN

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Abstract:

Current school health assessments largely concentrate on vision, hearing, and basic anthropometric indicators like height and weight. However, essential physiotherapy-focused parameters such as muscular strength, posture, flexibility, endurance, coordination, nutritional status, and quality of life are often overlooked in these screenings (World Health Organization, 1997; MoHFW India, 2023). Emerging literature emphasizes the significance of incorporating these functional and psychosocial domains. Ferrari *et al.* (2019) established that handgrip strength, measured using a dynamometer, not only reflects physical fitness but is also linked to cognitive functioning. The 9-Hole Peg Test, with normative values published by Xu *et al.* (2017), is effective in assessing fine motor abilities across age groups. For evaluating endurance and strength in children, Sun *et al.* (2020) recommended field-friendly tests like sit-ups and standing broad jumps. Likewise, Longmuir *et al.* (2017) validated the Canadian Agility and Movement Skill Assessment (CAMSA) for its efficiency in capturing both motor skills and speed. Further, studies such as Souza *et al.* (2024) observed that flexibility tends to decline in less physically active children. Research by Alghamdi *et al.* (2020) revealed compromised balance and mobility in obese school-aged populations, while Villarreal *et al.* (2018) reported that higher absolute strength in these children is often accompanied by reduced endurance and agility. Jandial *et al.* (2010) advocated for pGALS, a quick screening protocol for identifying musculoskeletal anomalies in school settings. Additionally, quality of life assessments like the PedsQL and functional nutritional evaluations (e.g., MUAC, BIA, grip strength correlations) help detect hidden psychosocial or metabolic risks that conventional screenings miss. This chapter proposes a structured, domain-specific screening model led by physiotherapists to enable early detection, timely referral, and improved long-term physical, nutritional, and psychosocial outcomes in school-going children.

Keywords: Physiotherapy, School Screening, Functional Assessment, Grip Strength, Motor Development, pGALS, CAMSA.

1. Introduction:

1.1 Overview of School Health Programs

School health programs are structured public health initiatives aimed at promoting and maintaining the health of school-going children through organized services including health education, screenings, and access to care. They serve as a primary touchpoint for children, especially in underserved and rural areas, where regular medical access may be limited. The World Health Organization has long emphasized that comprehensive school health services are a crucial component of child health strategies, enabling not only the identification of health problems but also fostering lifelong health-seeking behavior and promoting school attendance and academic success [1].

In India, school health initiatives like the School Health Programme under Ayushman Bharat aim to address basic health needs including vision, dental, hearing, and nutritional assessments [2]. However, these programs often fall short in addressing physical functionality, movement disorders, and musculoskeletal health, which are equally important for holistic development.

1.2 Role of Physiotherapy in Pediatric Public Health

Physiotherapy in pediatric health plays a preventive and promotive role, especially in identifying and managing developmental delays, postural anomalies, and movement-related dysfunctions. Despite its proven benefits, physiotherapy remains underutilized in school-based settings, often due to a lack of awareness or policy-level integration [3]. Physiotherapists are uniquely positioned to assess physical development markers such as strength, flexibility, coordination, and posture—areas not typically covered in general health check-ups.

Studies have shown that including physiotherapy screening in early childhood settings can aid in detecting motor impairments, balance issues, and asymmetries that may impact participation in physical activity or even academic performance [4]. A proactive physiotherapy approach helps not only in preventing disability but also in promoting motor competence and physical literacy among children.

1.3 Importance of Early Detection and Prevention

The early school years represent a critical window for physical and neurological development. Undetected musculoskeletal issues, poor posture, or coordination deficits in this phase can lead to cumulative biomechanical stress, early fatigue, decreased participation in physical education, and later-life orthopedic or lifestyle diseases [5]. Emerging research suggests a strong link between physical fitness in childhood and cognitive outcomes, emotional well-being, and future health behaviors [6].

Routine physiotherapy screenings can help identify risk factors such as flat feet, scoliosis, hypermobility, or muscle imbalances before they become clinically significant. Moreover, early therapeutic interventions are not only more effective but also more cost-efficient in preventing long-term morbidity [7]. Despite this, structured physiotherapy assessments are rarely part of routine school health programs, highlighting a significant gap in current child health policies.

This chapter aims to address that gap by proposing a structured, evidence-based physiotherapy assessment framework tailored for school settings. It outlines standardized assessment tools, age-appropriate screening strategies, and pathways for early referral and management—thus offering a scalable model for integration into existing school health systems.

2. Growth and Development in School-Aged Children

2.1 Normal Physical Development Milestones

During the school years (6–12 years), children show continuous maturation in their motor abilities, neuromuscular coordination, and postural control. Key gross motor milestones include refined gait patterns, skipping, hopping, catching, and balance skills, while fine motor milestones encompass handwriting and tool use. These skills are not only vital for academic success but also for social integration and self-esteem development [8].

According to the National Institute for Research in Reproductive and Child Health (NIRRCH), the physical growth of Indian children in this age group shows significant inter-individual variability, influenced by socioeconomic status, nutritional factors, and regional disparities [9]. In Indian school settings, disparities in physical development due to malnutrition, anemia, and lack of physical activity opportunities are not uncommon and must be considered while assessing developmental progress.

2.2 Common Developmental Deviations and Postural Issues

Indian school children frequently present with postural problems such as forward head posture, increased thoracic kyphosis, scoliosis, and flat feet—often linked to poorly designed classroom furniture, heavy school bags, and a lack of awareness about posture [10]. A cross-sectional study conducted in Maharashtra found a high prevalence of abnormal postural alignments in children aged 6–12 years, with nearly 40% exhibiting some form of musculoskeletal deviation, particularly in urban schools [11].

Additionally, conditions like Developmental Coordination Disorder (DCD) often remain undiagnosed in India due to the limited integration of physiotherapists in school health setups. Teachers and parents may misinterpret poor motor performance as laziness or disinterest, resulting in under-referral for proper evaluation [12]. Such issues, if not addressed early, may persist into adolescence and adulthood, affecting long-term physical and mental health outcomes.

2.3 Impact of Sedentary Lifestyle and Screen Time

Indian children, especially in urban and semi-urban settings, are increasingly adopting sedentary behaviors due to academic pressures and digital exposure. According to a 2019 Indian Council of Medical Research (ICMR) report, over 70% of school-aged children in urban India exceed the recommended 2 hours/day screen time, often at the cost of physical play [13]. This is strongly associated with reduced muscle strength, poor endurance, postural abnormalities, and rising trends of childhood obesity.

An Indian study by Arora *et al.* (2021) from Delhi NCR schools revealed a significant correlation between screen time and the prevalence of musculoskeletal discomfort, particularly neck and low back pain, even among children as young as 8 years [14]. These findings are consistent with international data [15] but highlight a more urgent public health challenge due to the dual burden of inactivity and undernutrition seen in India.

Physiotherapists, therefore, can play a transformative role by educating schools and parents about balancing academic demands with physical activity and by implementing movement-based interventions within the curriculum.

3. Rationale for Routine Physiotherapy Screening

3.1 Burden of Undiagnosed Musculoskeletal and Postural Issues

High Prevalence, Low Detection: Studies from both rural and urban schools across India report that 1 in 3 children show signs of postural or musculoskeletal dysfunctions that are rarely addressed due to lack of formal screening systems [16, 25].

Hidden Academic Barriers: Poor posture, joint hypermobility, or core instability can manifest as fatigue, difficulty in sitting or writing for long periods, and reduced classroom performance—often misattributed to behavioral issues or learning difficulties [26].

Underrepresentation in National Programs: The School Health Programme (Ayushman Bharat) continues to exclude physiotherapy from its core screening framework, despite increasing data supporting its inclusion as a primary preventive service [17, 27].

Gender & Growth Considerations: Adolescent girls are at higher risk of musculoskeletal issues due to hormonal changes and societal restrictions on physical activity. Yet, gender-specific screening is almost absent in most school programs [28].

3.2 Evidence-Based Need for Early Identification

Improved Health Trajectories: Evidence shows that children who undergo regular physical screening and motor assessments are more likely to engage in physical activity and less likely to develop chronic pain syndromes as adults [19, 29].

Window of Plasticity: The early school years are characterized by high neuromuscular plasticity, making them ideal for interventions to correct faulty movement patterns and prevent compensatory musculoskeletal adaptations [30].

Cost-Effective Intervention: School-based physiotherapy screenings are low-cost and high-impact, especially in resource-limited settings. Early detection avoids expensive interventions later, including surgeries or long-term rehabilitation [20, 31].

Evidence from School-Based Models: Pilot initiatives in Indian states like Maharashtra, Kerala, and Telangana have shown that routine physical screening by physiotherapists significantly improves early detection of scoliosis, pes planus, hypermobility, and poor motor coordination, with good compliance by schools and parents [20, 32].

3.3 Long-Term Implications of Undetected Physical Impairments

Chronic Pain Syndromes: Childhood spinal asymmetries and joint instabilities, if uncorrected, can lead to adolescent back pain, temporomandibular dysfunction, and even early onset of osteoarthritis [22, 33].

Reduced Participation and Physical Literacy: Children with undiagnosed physical limitations often avoid sports and physical activity, contributing to obesity, low confidence, and social withdrawal—creating a negative movement cycle [34].

Educational Impact: Poor posture, visual-motor coordination issues, or muscle fatigue can interfere with handwriting, classroom posture, and task persistence—factors directly correlated with academic outcomes [26, 35].

Mental Health Risks: Children who cannot participate in age-appropriate physical activity due to physical impairments may experience low self-esteem, anxiety, or bullying, impacting emotional development [36].

Public Health Burden: From a systems perspective, failure to detect physical impairments during school age contributes to the rising national burden of lifestyle diseases, orthopedic complications, and workplace productivity loss in adulthood. [24, 37].

4. Target Domains for Screening

A physiotherapy-based school screening model must incorporate a multidimensional approach that goes beyond conventional health metrics. The following domains reflect the critical areas of child development that should be assessed routinely to support early detection of neuromuscular, musculoskeletal, and functional deficits.

4. Target Domains for Screening:

Domain	Assessment Tool / Method	Purpose / Key Insights	Reference
4.1 Grip Strength	Handheld dynamometer (e.g., Jamar)	Measures strength, neuromotor maturity, and cognitive performance. Predicts handwriting skill and function.	[38, 39, 40]
4.2 Fine Motor Dexterity	9-Hole Peg Test (9HPT)	Assesses fine motor speed and coordination. Detects DCD and academic skill deficits.	[41]

4.3 Muscular Endurance & Strength	Sit-ups (1 min), Standing Broad Jump	Evaluates core strength, posture control, and stamina in classroom activities.	[42]
4.4 Agility & Coordination	CAMSA (Canadian Agility and Movement Skill Assessment)	Assesses agility, motor planning, and object control skills. Screens for DCD.	[43]
4.5 Flexibility	Sit-and-Reach Test	Assesses hamstring/lower back flexibility. Linked to posture and sedentary behavior.	[44]
4.6 Postural Alignment & Balance	Visual check, Single-leg stance, Star Excursion Balance Test	Identifies scoliosis, motor deficits, and participation barriers.	[45]
4.7 Obesity & Movement Risks	BMI (Body Mass Index), Gait/posture analysis	Links excess fat with poor balance, coordination, and movement quality.	[46]
4.8 Normal Weight Obesity (NWO)	Grip strength, Sit-ups, Jump tests	Detects children with normal BMI but high body fat. Risk of poor coordination and strength.	[40, 47]
4.9 Quality of Life (QoL)	PedsQL Questionnaire	Screens psychosocial and school engagement issues. Supports referrals.	[48]
4.10 Nutritional Assessment	BMI, MUAC (Mid-Upper Arm Circumference), 24-hour recall, BIA (Bioelectrical Impedance Analysis)	Detects subclinical malnutrition and muscle mass deficits. Flags intervention needs.	[38, 39, 49, 50]

5. Challenges and Barriers

Despite the growing evidence supporting early functional screening in schools, several challenges impede its effective implementation.

5.1 Lack of Awareness among Educators and Parents

Most educators and parents are unaware of the early signs of musculoskeletal or neuromotor dysfunctions unless overt or disruptive. There is a tendency to equate "healthy appearance" with normal development, overlooking subtle delays in posture, motor coordination, or endurance [51]. Teachers may not be trained to recognize signs of conditions like developmental coordination disorder (DCD), and parents may not seek assessments unless academic performance suffers. This lack of awareness delays early intervention, increasing the burden of untreated functional limitations.

5.2 Resource and Manpower Constraints

In many public schools, particularly in low-resource settings, there is a lack of infrastructure, physiotherapy personnel, and assessment tools. Budget allocations for school health programs prioritize immunizations and nutrition, with little inclusion of developmental screening or physiotherapy services [52]. Even when physiotherapists are available, caseloads and travel between schools can be prohibitive, reducing the feasibility of regular and comprehensive assessments.

5.3 Inconsistent Policies and Fragmented Implementation

India's school health initiatives (e.g., the Rashtriya Bal Swasthya Karyakram – RBSK) primarily focus on detecting congenital and overt structural conditions but lack integration of functional assessments and physiotherapy-led screening [53]. There is also a gap in linking assessment findings with structured referrals or rehabilitation pathways, resulting in missed opportunities for early intervention.

6. Recommendations for Practice

To strengthen physiotherapy's role in school health programs, the following strategies are recommended.

6.1 Screening Frequency and Age-Specific Guidelines

Screening should be age-appropriate and periodic—ideally at key developmental stages such as entry to primary school (5–6 years), mid-primary (8–9 years), early adolescence (12–13 years), and late adolescence (16–17 years). These windows capture motor milestones, pubertal changes, and ergonomic transitions like backpack use and extended sitting [54]. Normative values for tests such as grip strength, sit-ups, and CAMSA should be tailored to Indian children and updated regularly.

6.2 Creating Referral Pathways and Follow-Up Systems

Screening must not end with evaluation. Physiotherapists should establish school-to-clinic referral systems involving parents, pediatricians, and multidisciplinary teams. Simple referral templates and digital records can support longitudinal monitoring. In schools with in-house health staff, physiotherapists can collaborate with counselors, special educators, or nurses to implement and monitor interventions [55].

6.3 Capacity Building of Physiotherapists for Pediatric Screening

Undergraduate and postgraduate physiotherapy curricula should include structured modules on school-based pediatric assessments. In-service training and continuous professional development workshops can improve competence in using tools like the 9-HPT, SEBT, and

CAMSA. Partnerships with education boards can open avenues for physiotherapists to be formally included in school health programs [56].

School-Based Physiotherapy Screening Framework

- **Pre-Screening Preparation**
    - Obtain informed parental consent
    - Distribute student screening questionnaires
    - Review academic, behavioral, and medical history
- **Basic Health Screening**
    - Record height, weight, and BMI
    - Observe fatigue, asymmetry, or unusual movement patterns
- **Physiotherapy Screening – Key Domains**
    - **Muscle Strength & Endurance:** Grip strength, sit-to-stand, plank
    - **Dexterity & Coordination:** 9-Hole Peg Test, balance tests
    - **Posture & Flexibility:** Wall test, toe-touch, shoulder flexibility
    - **Agility & Motor Control:** Timed Up and Go, shuttle run
    - **Functional Mobility & Gait:** Observational analysis, step tests
- **Scoring & Risk Stratification**
    - Use cutoff values to categorize into low, moderate, or high risk
- **Referral & Parental Notification**
    - Issue reports with findings and recommended interventions
- **Follow-Up & Reassessment**
    - Plan periodic reevaluation for high-risk students
- **Feedback Loop**
    - Share outcomes with school, parents, and health teams

7. Global Comparison of School-Based Health and Physiotherapy Screening Policies: Insights for Indian Implementation

Countries like Canada, Australia, the US, and the UK have school health programs with integrated physiotherapy services supported by national departments. Frameworks like Canada's Comprehensive School Health and Australia's Health Promoting Schools incorporate screenings for posture, balance, and motor skills through collaboration with physiotherapists, OTs, and nurses [57, 58]. In India, however, programs like RBSK under the NHM focus on medical/developmental issues but overlook functional musculoskeletal or neuromotor concerns unless severe [59]. Developed nations use standardized tools (CAPL, BOT-2, and CAMSA), while Indian schools often depend on periodic camps with limited follow-up [60]. Individualized education plans in these countries include physiotherapy, unlike India where integration is minimal and awareness among school staff is low. Policy gaps, lack of trained professionals, and poor implementation widen this disparity. India's health programs must adapt international evidence-based frameworks to include physiotherapy-led school screenings.

8. Integrating Physiotherapy into School Health Framework

The increased awareness of developmental and postural issues, physiotherapists are vital to school health systems. Current services in India are limited to medical and psychological checks, missing physical impairments that affect learning and activity participation. Physiotherapists bring expertise in movement, posture, ergonomics, and rehabilitation, offering individualized screenings and ergonomic guidance (e.g., posture, backpack use). Their integration supports inclusive education, especially for children with special needs. Given the rising sedentary lifestyle and undetected dysfunctions, physiotherapy is essential—not optional—for preventive child health and holistic development.

Conclusion:

Schools offer a unique opportunity for early physical health interventions. While India's school screenings address basic health, functional issues are often missed. This chapter promotes physiotherapy-led assessments—posture, coordination, endurance—as part of routine health checks. A multidisciplinary model including physiotherapists ensures early detection, effective referral, and long-term health improvement. Global models show these approaches boost academic outcomes, reduce healthcare costs, and support inclusive growth. Physiotherapy must be embedded in national school health policies to foster healthier, more active generations.

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SAFEGUARDING HONEY BEES:
PILLARS OF POLLINATION AND ECOSYSTEM HEALTH

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Honey bees (*Apis mellifera*) are among the most vital pollinators in global ecosystems, contributing to the pollination of approximately 70% of the world's crops, including fruits, vegetables, and nuts (Klein *et al.,* 2007). Their role in agriculture and biodiversity is indispensable, supporting food security and ecosystem stability. However, honey bee populations face unprecedented threats from habitat loss, pesticides, climate change, and diseases. This chapter explores the importance of honey bee conservation, the challenges they face, and actionable strategies to ensure their survival. The Ecological and Economic Importance of Honey Bees Honey bees are keystone species, meaning their presence significantly influences the health of entire ecosystems. Through pollination, they enable the reproduction of numerous plant species, which in turn support diverse wildlife. Economically, honey bees contribute billions of dollars annually to global agriculture. In the United States alone, their pollination services are valued at over $15 billion annually (Calderone, 2012). Beyond crops, honey bees produce honey, beeswax, and other products, supporting livelihoods worldwide. Threats to honey Bee Populations. Honey bees face a multitude of threats, which have led to alarming declines in their populations. The phenomenon known as Colony Collapse Disorder (CCD), where worker bees abruptly disappear, has been a significant concern since the early 2000s (van Engels dorp *et al.,* 2009). Key threats include: Habitat Loss: Urbanization, monoculture agriculture, and deforestation reduce the availability of diverse forage plants essential for bee nutrition, decline nutritional value for bees, leading to malnutrition and weakened colonies (Naug, 2009).

Climate change, driven by human activities such as industrialization and deforestation, is rapidly altering global ecosystems. These changes in temperature, precipitation patterns, and habitat conditions pose significant threats to biodiversity, particularly to pollinators like honeybees (Apis spp.). As essential agents of pollination for over 35% of global crops, honeybees face a myriad of climate-induced challenges, including disrupted foraging behaviours, habitat degradation, and heightened susceptibility to pests and diseases. This paper examines how climate change affects honeybee behaviour, physiology, distribution, and interactions with pathogens. It also explores their critical ecological and economic roles, particularly within the

Indian agricultural landscape. Finally, it highlights strategic conservation approaches, such as habitat restoration, climate-smart farming, and national policy initiatives like India's "Sweet Kranti" Honey Mission, as pathways to safeguard these indispensable pollinators and ensure long-term food security.

Honey bees (*Apis mellifera*) are among nature's most industrious architects, weaving intricate connections between plants, ecosystems, and human livelihoods through their pollination services. These small insects are responsible for pollinating approximately 70% of global crop species, supporting the production of fruits, vegetables, nuts, and seeds that form the backbone of human diets (Klein *et al.,* 2007). Beyond agriculture, honey bees contribute to biodiversity by enabling the reproduction of countless wild plants, which sustain wildlife and maintain ecosystem balance. Yet, honey bee populations are in decline, threatened by a complex web of environmental, chemical, and biological challenges. This chapter delves into the critical role of honey bees, the threats endangering their survival, and the innovative strategies needed to ensure their conservation for future generations. The Vital Role of Honey Bees Honey bees are keystone species, meaning their presence has a disproportionate impact on their ecosystems. Their pollination services facilitate the reproduction of flowering plants, which provide food and habitat for other species, from birds to mammals. In agricultural systems, honey bees are indispensable, contributing to the yield of crops such as apples, almonds, blueberries, and cucumbers. The economic value of their pollination services is staggering, estimated at $15–20 billion annually in the United States alone and over $150 billion globally (Calderone, 2012; Gallai *et al.,* 2009). Beyond crops, honey bees produce honey, beeswax, propolis, and royal jelly, supporting beekeeping industries and cultural traditions worldwide. Honey bees also play a cultural and symbolic role. In many societies, they represent diligence, community, and harmony with nature. Their intricate social structures—where workers, drones, and queens cooperate seamlessly—offer lessons in resilience and collaboration. However, the alarming decline in honey bee populations threatens these ecological, economic, and cultural contributions, necessitating urgent conservation efforts.

Honeybee Diversity and Ecological Significance

- **Species Richness**

Honeybees belong to the Apoidea superfamily under the Apiformes clade and are distinguished by their plumose hairs and pollen-carrying adaptations. Worldwide, there are over 17,500 bee species across seven families, with India hosting 633 native species. Prominent among these are:

- **Role in Pollination**

Honeybees are responsible for pollinating 80% of all insect-pollinated crops and are particularly effective due to their floral fidelity—consistent foraging on a single plant species per trip (Waser, 1986). Key crops such as apples, almonds, coffee, and sunflowers benefit from bee pollination, resulting in up to 43% higher yields and improved crop quality (Khalifa *et al.,* 2021). In India, smallholder farms depend heavily on both wild and managed bees to maintain sustainable yields with minimal chemical input (Garibaldi *et al.,* 2019).

- **Climate Change Impacts on Honeybee Populations**

- **Disruption of Floral Scents**

Rising temperatures and water stress prompt plants to produce altered volatile organic compounds, disrupting the scent cues bees rely on for foraging (Burger, 1982). Impaired navigation and reduced nectar detection lead to nutritional stress and eventual colony decline (Gullan & Cranston, 2010).

- **Phenological Mismatches**

Climate-induced shifts in flowering seasons can desynchronize bee emergence and floral bloom. Such mismatches reduce food availability for bees and hinder effective plant pollination, threatening reproductive cycles of both plants and insects (Visser *et al.,* 2004).

- **Habitat Contraction**

Bee habitats, particularly in North America and Europe, have shifted or shrunk by up to 200 miles due to changing climate and land-use patterns (Kerr *et al.,* 2015). Native bees, especially bumblebees, exhibit less adaptability compared to other insects, making them highly vulnerable (Rosenkranz, 2010).

- **Disease Vulnerability**

Diseases and Parasites: The Varroa mite (Varroa destructor), Nosema fungi, and viral infections weaken colonies and increase mortality rates. Diseases and Parasites: The Varroa mite (Varroa destructor) is a devastating parasite that feeds on bee hemolymph and transmits viruses, such as Deformed Wing Virus. Left unchecked, Varroa infestations can decimate colonies within months. Nosema, a fungal pathogen, and bacterial diseases like American foulbrood further threaten bee health, particularly in stressed colonies (Higes *et al.,* 2008).

- **Native Bee Endangerment**

Less studied solitary and native bees—like the yellow carpet bee—are facing extinction risks due to loss of ecological niches. These species are crucial for biodiversity and often perform specialized pollination functions (Goulson, 2018).

- **Pesticides effect**

Neonicotinoids and other chemical pesticides impair bee navigation, reproduction, and immune systems (Goulson *et al.,* 2015). Pesticides and Chemical Exposure: Neonicotinoids, a class of systemic insecticides, are particularly harmful, impairing bee navigation, memory, and immune function (Goulson *et al.,* 2015). Sublethal doses can disrupt foraging behavior and reproduction, weakening colonies over time.

Other chemicals, such as fungicides and herbicides, exacerbate these effects by reducing food sources and altering gut microbiomes (Mullin *et al.,* 2010).

Strategies for Honeybee Conservation in a Changing Climate:

- **Agri-Environment Programs**

In the UK, conservation practices such as beetle banks, hedgerows, and conservation headlands have improved bee habitats (Goulson, 2003). India can adopt similar models by integrating wildflower strips and organic buffer zones into farming systems.

- **Urban Green Infrastructure**

Green roofs, parks, and community gardens in cities support pollinator communities while moderating urban heat islands (Braaker *et al.,* 2017). With increasing urbanization, integrating pollinator-friendly design in city planning becomes essential (Tanda, 2023).

- **Bee-Friendly Agriculture**

Transitioning from pesticide-heavy farming to organic or integrated pest management (IPM) can reduce bee mortality. Practices like planting cover crops and providing nesting sites in soil or wooden tunnels support both managed and wild bees (Dar *et al.,* 2017).

- **Policy Interventions**

India's "Sweet Kranti" Honey Mission (2017) aims to promote beekeeping for livelihood and conservation, projecting a 4.43% annual growth in apiculture by 2025 (National Bee Board, 2023). State-level schemes such as the Mukhyamantri Madhu Vikas Yojana in Himachal Pradesh and tribal support programs in Tamil Nadu illustrate region-specific approaches to strengthening pollinator resilience.

- **Technological and Scientific Solutions**

The World Bee Project uses AI and IoT technologies for real-time monitoring of bee health and behavior. Simultaneously, breeding programs for disease-resistant bees and research on climate-resilient forage crops are essential to future-proof apiculture.

- **Supporting Beekeepers**

Providing subsidies for sustainable beekeeping practices and research into disease-resistant bee strains can bolster colony resilience.

Training programs for beekeepers on Varroa mite management and organic practices are critical.

- **Public Awareness and Education**

Community initiatives, such as school programs and citizen science projects, can raise awareness about the importance of bees and encourage conservation efforts.

Labelling products as "bee-friendly" incentivizes consumer support for sustainable agriculture.

- **Policy and Research**

Governments should enforce policies protecting pollinator habitats and fund research into CCD and other threats.

International collaboration, such as the Convention on Biological Diversity, can promote global conservation standards.

Conclusion:

Climate change poses a profound threat to global honeybee populations, disrupting floral cues, seasonal timing, habitats, and increasing exposure to diseases. In a country like India, where pollination services are vital to agriculture, these challenges are especially critical. Although honeybees possess adaptive potential, escalating climate pressures may outpace their resilience. Loss of wildflower meadows and hedgerows further limits forage, forcing bees to travel longer distances, expending energy and increasing their vulnerability.

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LIFE SCIENCES AND ENVIRONMENTAL SUSTAINABILITY

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Abstract:

The urgent need for environmental sustainability has emerged from escalating global crises such as climate change, biodiversity loss and resource depletion. Life sciences, encompassing biology, biotechnology, microbiology and ecology, provide innovative and sustainable solutions to these challenges. This chapter explores the critical role of life sciences in environmental sustainability through approaches such as bioremediation, renewable energy development, sustainable agriculture and industrial innovation. It also addresses ethical concerns, technological progress and future directions while emphasizing the importance of an integrated, Renaissance-inspired perspective that combines scientific advancement with ecological responsibility.

Keywords: Life Sciences, Environmental Sustainability, Bioremediation, Bioenergy, Climate Change.

Introduction:

Environmental sustainability, defined as meeting present needs without compromising the ability of future generations to meet theirs, is now a global priority (Brundtland Commission, 1987). The acceleration of industrialization and population growth has contributed to severe ecological challenges including climate change, habitat destruction and biodiversity decline (Pretty, 2018). To mitigate these issues, life sciences have emerged as key contributors by providing strategies that promote sustainability and resource efficiency (Singh *et al.,* 2016).

A Renaissance-inspired approach to life sciences advocates for multidisciplinarity, integrating traditional biological sciences with modern technologies such as artificial intelligence, nanotechnology and synthetic biology (Verma *et al.,* 2019). This approach not only advances scientific discovery but also ensures that technological innovations harmonize with environmental ethics.

Life Sciences and Environmental Sustainability: A Holistic View

The application of life sciences spans diverse fields, all converging toward the common goal of sustainability. Biotechnology has revolutionized waste management, enabling the degradation of persistent pollutants through biological processes. For example, *Ideonella sakaiensis*, a bacterium discovered in 2016, produces PETase enzymes capable of degrading polyethylene terephthalate, a widely used plastic (Yoshida *et al.,* 2016). Similarly, enzyme-based wastewater treatment methods have minimized the reliance on hazardous chemicals, promoting greener industrial practices (Ahuja *et al.,* 2018).

Bioremediation represents another cornerstone of environmental biotechnology. Microorganisms such as *Pseudomonas putida* have been successfully employed to degrade hydrocarbons in oil-contaminated sites (Das & Chandran, 2011). In addition, fungi like *Aspergillus niger* absorb heavy metals and remediate polluted soils (Gadd, 2004). Complementary to this is phytoremediation, a process wherein plants such as *Brassica juncea* accumulate heavy metals like arsenic and cadmium from soil, offering an economical and eco-friendly remediation strategy (Ali *et al.,* 2013).

Conservation Biology and Biodiversity Protection

Biodiversity is the foundation of ecosystem resilience and its conservation is crucial for sustainable development. Life sciences contribute significantly through genetic techniques such as DNA barcoding, which facilitates species identification and monitoring (Hebert *et al.,* 2003). Assisted reproductive technologies, including in vitro fertilization and cryopreservation, are employed to rescue endangered species from extinction (Holt *et al.,* 2004). These interventions, combined with microbial inoculants for habitat restoration, ensure ecosystem recovery and species survival.

Sustainable Agriculture and Food Security

Agriculture, a primary driver of human sustenance, has also been a major source of environmental degradation due to intensive chemical input. Life sciences present sustainable alternatives through the use of biofertilizers and biopesticides. Nitrogen-fixing bacteria like *Rhizobium* and *Azospirillum* enhance soil fertility naturally, reducing the dependency on synthetic fertilizers (Bhattacharyya & Jha, 2012). Microbial pesticides such as *Bacillus thuringiensis* provide effective pest control without harming beneficial organisms (Sanahuja *et al.,* 2011).

The advent of CRISPR-Cas gene-editing technology has further transformed agricultural sustainability. This tool enables the precise development of crops that are drought-tolerant, pest-resistant and nutritionally enhanced, ensuring resilience against climate change (Chen *et al.,* 2019).

Bioenergy and Industrial Sustainability

Transitioning to renewable energy sources is critical for reducing greenhouse gas emissions. Biofuels such as ethanol and biodiesel, derived from plant biomass and microalgae respectively, exemplify sustainable energy alternatives (Ragauskas *et al.,* 2014). Anaerobic digestion of organic waste into biogas not only generates energy but also addresses the issue of waste disposal (Khan *et al.,* 2016).

Industries have also embraced biocatalysis, using enzymes to replace hazardous chemicals in manufacturing processes (Sheldon & Woodley, 2018). Additionally, the development of bioplastics like polyhydroxyalkanoates (PHA) reduces the environmental burden of conventional petroleum-based plastics (Chen, 2010).

Climate Change Mitigation through Life Sciences

Life sciences significantly contribute to mitigating climate change impacts. Algal systems for carbon sequestration provide an effective method for capturing atmospheric CO_2 (Wang *et al.,* 2008). Similarly, phytoplankton in marine ecosystems play a critical role in global carbon cycling, reinforcing the need for ocean biodiversity conservation (Field *et al.,* 1998).

Ethical Concerns and Challenges

Despite their promise, biotechnological interventions raise ethical and ecological concerns. The release of genetically modified organisms (GMOs) into natural ecosystems may disrupt ecological balance (Snow *et al.,* 2005). Synthetic biology, while revolutionary, also poses biosecurity risks that demand stringent governance frameworks (Kuiken, 2015). Balancing innovation with ethical responsibility remains a fundamental challenge.

Future Directions

The future of environmental sustainability lies in integrating life sciences with advanced technologies and systemic thinking. The concept of a circular bioeconomy envisions resource cycles where waste is converted into valuable products (Dahiya *et al.,* 2020). Synthetic biology promises engineered organisms capable of detoxifying pollutants and generating renewable energy (Cameron *et al.,* 2014). Artificial intelligence will further complement these efforts by enabling predictive environmental modeling and optimizing agricultural practices (Rolnick *et al.,* 2022).

Conclusion:

Life sciences have become indispensable in addressing global environmental challenges. By embracing a Renaissance-inspired approach that unites biology, technology and ethics, humanity can chart a path toward a sustainable future. The convergence of scientific innovation with ecological stewardship ensures that progress does not come at the cost of planetary health.

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AYURGENOMICS AND THE SCIENCE OF REBALANCE: A RENAISSANCE FUSION OF ANCIENT AND MODERN HEALTH PARADIGMS

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Abstract:

The resurgence of integrative paradigms in life sciences marks a modern renaissance in healthcare, blending traditional knowledge systems with contemporary biomedical science. Ayurgenomics, a synthesis of Ayurveda and genomics exemplifies this shift by aligning the ancient concept of *Prakriti* with modern genetic frameworks to enable personalized and preventive health interventions. By mapping individual constitutional types (Vata, Pitta, Kapha) to genomic markers, Ayurgenomics supports the development of precision medicine strategies for chronic, lifestyle and non-communicable diseases. This approach aligns with global transitions in healthcare toward predictive, preventive and personalized models. Core Ayurvedic principles such as *Dinacharya*, *Ritucharya* and *Ahara-Vihara* find scientific relevance in circadian biology, lifestyle medicine and personalized nutrition. When combined with genomic tools like pharmacogenomics (the study of how genes affect a person's response to drugs), single nucleotide polymorphisms (SNPs) and gene environment interaction studies, Ayurgenomics provides an evidence-informed framework for individualized care, drug response prediction, and early disease risk stratification. Despite its promise, integration faces challenges, including standardization of *Prakriti* assessment, ethical use of genetic data and the need for interdisciplinary research and training. Initiatives like the Prakriti Assessment Scale (PAS) and advances in bioinformatics and machine learning have improved classification accuracy and clinical applicability. Ayurgenomics represents a transformative healthcare model that merges ancient insights with molecular science. Its successful implementation depends on regulatory support, robust clinical evidence and collaborative frameworks that respect both scientific rigor and cultural heritage. As such, Ayurgenomics holds the potential to revolutionize 21st-century medicine by offering a holistic, individualized and sustainable approach to health and disease.

Keywords: Ayurgenomics, Prakriti, Personalized Medicine, Pharmacogenomics, Preventive Healthcare.

Introduction:

The concept of a "renaissance" in life sciences signifies a resurgence of interest in holistic paradigms that blend traditional knowledge systems with modern scientific innovations. This paradigm shift promotes a more integrative view of health and disease, merging ancient wisdom with contemporary biomedical insights. Ayurgenomics exemplifies this renaissance by integrating the Ayurvedic concept of *Prakriti*—the individual's constitutional type based on the balance of three *Doshas* (Vata, Pitta, Kapha)—with genomics to create individualized healthcare solutions (Ranade, 2024; Madgulwar & Shewalkar, 2025). This approach holds significant relevance for addressing complex, chronic, and lifestyle-related diseases that demand multifactorial and personalized strategies.

By aligning genomic data with *Prakriti*-based assessments, Ayurgenomics provides a framework for precision medicine—tailoring diet, lifestyle, and treatments according to individual profiles (Huang *et al.,* 2022; Singh *et al.,* 2019). This integration also supports cost-effective screening and early intervention, especially in populations at risk of non-communicable diseases (Mukerji, 2023). Globally, the healthcare system is transitioning toward predictive, preventive, and personalized care, and Ayurgenomics complements this shift by incorporating preventive strategies rooted in traditional diagnostics (Mukerji, 2023).

While promising, the integration of Ayurveda with genomics poses challenges, including the need for scientific validation and interdisciplinary collaboration. The development of effective frameworks and practitioner training is essential to ensure safe, evidence-based implementation. Nonetheless, Ayurgenomics offers a compelling model for transforming healthcare through a synergistic blend of ancient and modern health paradigms.

Ayurveda and the Philosophy of Rebalance

The table 1 outlines the foundational Ayurvedic concepts that form the basis of holistic health.

Table 1: Core Principles of Ayurveda in the Philosophy of Rebalance

Ayurvedic Principle	Description	Scientific Relevance	References
Tridosha	Vata, Pitta, and Kapha regulate physiological processes; imbalance leads to disease.	Foundation for personalized diagnosis and treatment.	Sen *et al.,* 2024; Lata, 2024
Prakriti	Individual constitution determined by dominant dosha(s).	Basis for individualized dietary and lifestyle recommendations.	Thakur *et al.,* 2024; Lata, 2024
Dinacharya	Daily routine aligned with natural cycles.	Promotes circadian health and homeostasis.	Singh & Zambare, 2024
Ritucharya	Seasonal regimen for diet and lifestyle.	Helps mitigate environmental impact on health.	Jamdade *et al.,* 2024
Ahara & Vihara	Diet and lifestyle practices customized to Prakriti.	Supports preventive healthcare and immunity.	Priyanshu *et al.,* 2024; Sen *et al.,* 2024

Each principle like Tridosha, Prakriti, Dinacharya and Ahara—offers an individualized and preventive approach to wellness. The scientific relevance is drawn from their alignment with emerging ideas in circadian biology, personalized nutrition, and lifestyle medicine.

Genomics and Personalized Medicine

Table 2 highlights the essential elements of modern genomics, such as gene-environment interactions and pharmacogenomics. It illustrates how technological advances are used for disease risk prediction, targeted therapy, and precision health management.

Table 2: Components of Genomics and Personalized Medicine

Component	Function/Description	Applications in Medicine	References
Genomics	Study of entire DNA and gene variants.	Identifying disease-linked mutations.	Hays, 2021; Hasanzad *et al.,* 2021
Epigenetics	Regulation of gene expression without DNA change.	Explains gene-environment interactions and disease onset.	Langevin & Kelsey, 2020; Farooqui *et al.,* 2024
Gene–Environment Interaction	Interplay of genes with external factors like toxins or food.	Risk stratification and personalized prevention.	Langevin & Kelsey, 2020
SNPs & GWAS	Genetic variations studied via genome-wide association studies.	Biomarker discovery and drug response prediction.	Hays, 2021
Precision & Personalized Medicine	Use of genomics for tailored treatment.	Drug efficacy, reduced side effects, and early diagnosis.	Meyersfeld, 2021; Qian *et al.,* 2024; Pandey & Gupta, 2024

Ayurgenomics: The Integrative Bridge

Table 3 bridges traditional Ayurvedic Prakriti classification with modern genetic markers. It illustrates how Ayurgenomics offers an integrative model combining ancient diagnostic systems with genomic tools to improve personalized healthcare outcomes.

Table 3: Key Features and Applications of Ayurgenomics

Aspect	Description	Application	References
Prakriti Typing	Constitution classification (Vata, Pitta, Kapha).	Individualized diet, lifestyle, and treatment plans.	Madgulwar & Shewalkar, 2025
Genetic Mapping	Linking Prakriti with genes like HLA, CYP2C19.	Predicting disease susceptibility and drug metabolism.	Sharma & Prajapati, 2020; Huang *et al.,* 2022
Pharmacogenomics	Prakriti-based drug response prediction.	Personalized medicine and safe dosing.	Sharma & Prajapati, 2020
Metabolic Disorders	Disease risk varies by Prakriti.	Targeted intervention for diabetes and obesity.	Huang *et al.,* 2022
Immunological Insights	Prakriti influences immune reactivity.	Tailored approaches to inflammation and immunity.	Madgulwar & Shewalkar, 2025

Renaissance Potential in Modern Healthcare

The integration of Ayurgenomics into modern healthcare signifies a renaissance of ancient wisdom within the framework of contemporary science. By uniting the Ayurvedic concept of *Prakriti* with genomic insights, this approach offers personalized, holistic solutions to pressing global health challenges, including non-communicable diseases (NCDs), antibiotic resistance, and mental health concerns (Wallace, 2020; Kalra *et al.,* 2024; Bagga *et al.,* 2024).

In managing NCDs, Ayurgenomics facilitates tailored lifestyle and dietary interventions by considering individual genetic profiles and *Prakriti*, thereby enabling preventive strategies (Mukerji, 2023; Wallace, 2020). Its emphasis on boosting natural immunity through diet and lifestyle may reduce overdependence on antibiotics, contributing to antibiotic resistance mitigation (Asif & Sahithi, 2024; Kalra *et al.,* 2024). Furthermore, by incorporating traditional mind-body practices, Ayurgenomics enriches modern approaches to mental health care (Bagga *et al.,* 2024; Wallace, 2020).

From a health system perspective, the preventive and low-cost nature of Ayurveda presents an affordable model suitable for widespread adoption (Gupta, 2024). Its cultural relevance enhances community acceptance, fostering inclusive healthcare delivery (Sharma *et al.,* 2023).

However, integration demands critical attention to ethical and socio-cultural dimensions. Challenges include scientific validation, standardization, and bridging knowledge systems while overcoming biases (Kalra *et al.,* 2024). Patient empowerment through education is vital to uphold ethical standards (Bagga *et al.,* 2024). Moreover, safeguarding and documenting traditional knowledge is essential for its responsible incorporation into future healthcare paradigms (Sharma *et al.,* 2023).

By addressing these challenges, Ayurgenomics can help shape a sustainable, culturally sensitive, and patient-centered healthcare future.

Challenges and Future Prospects

The integration of Ayurveda with modern genomics, termed Ayurgenomics, presents a promising avenue for personalized medicine, yet it faces several challenges. Central to this integration is the standardization of *Prakriti* assessment—a foundational Ayurvedic concept—into reproducible, scientifically valid frameworks. The development of a validated Prakriti Assessment Scale (PAS), featuring 91 predictors across 30 domains, marks progress toward this goal (Singh *et al.,* 2022). However, the lack of standardized drug testing and certification continues to hinder global acceptance (Saini & Tripathi, 2024).

Large-scale genomic-Ayurvedic databases are essential to validate genetic correlates of *Prakriti* and to strengthen evidence-based personalized healthcare (Madgulwar & Shewalkar, 2025; Sharma & Prajapati, 2020). Yet, the absence of comprehensive health policies and ethical regulatory frameworks remains a critical barrier to integration (Srikanth, 2021; Saini & Tripathi, 2024).

Interdisciplinary training is crucial. Initiatives by institutions like the All-India Institute of Ayurveda support capacity-building in bioinformatics and Ayurveda (Goel *et al.,* 2024). Collaborative research between traditional practitioners and modern scientists is needed to generate evidence-based data, ensuring safety and efficacy (Saini & Tripathi, 2024).

The convergence of Ayurveda with bioinformatics, including the use of machine learning models for *Prakriti* prediction, demonstrates high accuracy and potential for developing personalized treatment protocols (Bhosale *et al.,* 2024; Goel *et al.,* 2024).

While the prospects are vast, realizing the full potential of Ayurgenomics will require robust data infrastructure, regulatory clarity and a collaborative ecosystem bridging traditional wisdom with scientific innovation.

Conclusion:

Ayurgenomics represents a scientific renaissance in integrative medicine, merging the ancient wisdom of Ayurveda with the precision of modern genomics to offer personalized health solutions. Rooted in the Ayurvedic concept of *Prakriti*—akin to an individual's genetic constitution—Ayurgenomics provides a framework for tailoring interventions based on physiological and molecular profiles (Madgulwar & Shewalkar, 2025; Ranade, 2024). This approach aligns with the goals of personalized medicine, emphasizing early diagnosis, prevention, and individualized treatment.

By incorporating holistic health principles with genomic science, Ayurgenomics fosters a comprehensive understanding of disease and wellness, promoting customized lifestyle and dietary regimens (Wallace, 2020). Scientific advancements in genomics and proteomics further support the validation of Ayurvedic practices, enabling the identification of molecular mechanisms and disease biomarkers (Saini & Tripathi, 2024).

Future research must focus on interdisciplinary collaboration between traditional practitioners and biomedical scientists to develop evidence-based models that strengthen this integrative approach (Saini & Tripathi, 2024). Leveraging high-throughput technologies and machine learning tools can elucidate therapeutic pathways, aid drug repurposing, and identify novel targets (Mukerji, 2023). Rigorous clinical trials are essential to establish safety and efficacy in real-world settings (Ranade, 2024).

Policy and education must evolve accordingly. Integrating Ayurgenomics into academic curricula can equip future healthcare professionals with holistic perspectives (Rao, 2022), while dedicated policy frameworks should support cross-disciplinary collaboration and informed referrals (Mukerji, 2023). Ethical guidelines must also govern the responsible use of genetic data in personalized care (Saini & Tripathi, 2024).

Ayurgenomics thus holds transformative potential for 21st-century healthcare—uniting ancient insights and cutting-edge science to create a truly personalized, preventive, and patient-centric medical paradigm.

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BIFURCATION THEORY AND ITS APPLICATION IN CELL CYCLE

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Abstract:

Bifurcation theory, a branch of mathematics rooted in nonlinear dynamical systems, explores how slight variations in parameters lead to significant qualitative changes in system behavior. In biological contexts, this theory provides insight into network dynamics, such as the regulatory switches of the eukaryotic cell cycle—a critical process whose disruption can result in cancer. Mathematical models, particularly those using ordinary differential equations, simulate protein dynamics in cells as deterministic systems. Recent research has developed a generic model of the eukaryotic cell cycle adaptable across organisms, highlighting conserved mechanisms and attributing variability to differences in protein concentrations and affinities.

Keywords: Bifurcation, Cell Cycle, Protein Concentration

Introduction:

Biological applications of bifurcation theory provide a framework for understanding the behavior of biological networks modelled as dynamical systems. In the context of a biological system, bifurcation theory describes how small changes in an input parameter can cause a bifurcation or qualitative change in the behavior of the system. The ability to make dramatic change in system output is often essential to organism function, and bifurcations are therefore ubiquitous in biological networks such as the switches of the cell cycle. The eukaryotic cell cycle is very complex and is one of the most studied topics, since its misregulation leads to cancers It is possibly a good example of a mathematical model as it deals with simple calculus but gives valid results. Two research groups have produced several models of the cell cycle simulating several organisms. They have recently produced a generic eukaryotic cell cycle model which can represent a particular eukaryote depending on the values of the parameters, demonstrating that the idiosyncrasies of the individual cell cycles are due to different protein concentrations and affinities, while the underlying mechanisms are conserved (Csikasz-Nagy *et al.,* 2006). By means of a system of ordinary differential equations these models show the change in time (dynamical system) of the protein inside a single typical cell; this type of model is called a deterministic process (whereas a model describing a statistical distribution of protein concentrations in a population of cells is called a stochastic process.

Bifurcation theory is a field of mathematics that studies qualitative changes in the behavior of a system as a parameter is varied. It originates in the study of nonlinear dynamical systems. A bifurcation occurs when a small, smooth change in a system parameter causes a sudden qualitative change in its long-term behavior. Mathematically, bifurcations are studied using ordinary differential equations (ODEs), discrete dynamical systems, and partial differential equations (PDEs).

It is the study of qualitative changes in the behavior of dynamical systems, finds significant application in understanding the cell cycle and cell division. It helps model how small changes in cellular parameters can lead to abrupt shifts in cell behavior, such as transitions between different phases of the cell cycle or the initiation of cell division.

Bifurcation Theory and the Cell Cycle:

Bifurcation theory in the context of cell biology helps us understand how cells transition between different states — particularly, cell cycle phases — in response to internal and external signals. The cell cycle is a tightly regulated sequence of events that leads to cell division. It consists of:

- G_1 phase (growth)
- S phase (DNA synthesis)
- G_2 phase (preparation for mitosis)
- M phase (mitosis/cell division)

The transitions between these phases are controlled by regulatory networks, mainly involving cyclins, cyclin-dependent kinases (CDKs), and their inhibitors.

Why Use Bifurcation Theory in Cell Cycle Studies?

The cell cycle behaves like a dynamical system:

- It has stable steady states like G_1, G_2.
- Transitions between states are often switch-like and irreversible.
- Small changes in certain parameters (e.g., growth factors, cyclin levels) can lead to dramatic changes in behavior.

Bifurcation theory explains:

- How and when transitions occur
- The on/off switching mechanism of cell cycle checkpoints
- The emergence of oscillations or cycles in protein concentrations (e.g., Cyclin/CDK)

Bifurcation theory is used in cell cycle studies to understand how cells make critical decisions — such as whether to divide, pause, or die — in response to small changes in intracellular signals or external conditions. Here's why it's important:

1. Cell Cycle is a Dynamical System

- The cell cycle is governed by a network of nonlinear biochemical reactions, particularly involving cyclins, CDKs, and inhibitors.
- These molecular interactions can be described using ordinary differential equations (ODEs), making them ideal for analysis through bifurcation theory.

The cell cycle—the series of stages a cell goes through to grow and divide—is not just a sequence of events. It is a dynamical system, meaning its behavior evolves continuously over time in response to internal and external signals. This time-dependent progression is governed by nonlinear interactions among proteins, especially cyclins, cyclin-dependent kinases (CDKs), and their regulators. Why Is the Cell Cycle a Dynamical System? It is because of the following reasons:

Continuous Changes in Molecular Concentrations:

One of the defining features of the cell cycle as a dynamical system is the continuous, time-dependent changes in molecular concentrations of regulatory proteins. These fluctuations are not abrupt or stepwise, but rather evolve smoothly over time due to underlying biochemical interactions and feedback mechanisms. Key proteins like cyclins are synthesized and degraded over time. Their interactions with CDKs lead to time-varying activities that govern transitions between cell cycle phases.

The most important regulators of the cell cycle include in the table 1:

Table 1: Important regulators of the cell cycle involved

Molecule	Function
Cyclins (A, B, D, E)	Regulatory subunits that activate CDKs
CDKs (e.g., CDK1, CDK2)	Kinases that drive progression through cell cycle phases
CDK inhibitors (e.g., p21, p27)	Block CDK activity during stress or DNA damage
Wee1 kinase	Inhibits CDKs by phosphorylation
Cdc25 phosphatase	Activates CDKs by removing inhibitory phosphate
APC/C complex	Degrades cyclins to reset the cycle

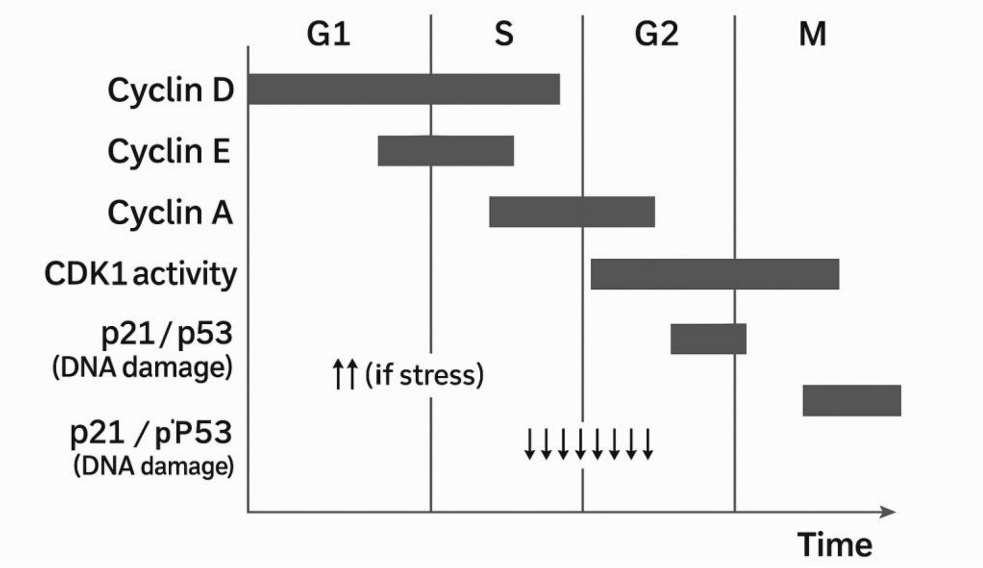
The Concentrations Changes in the following ways such as:

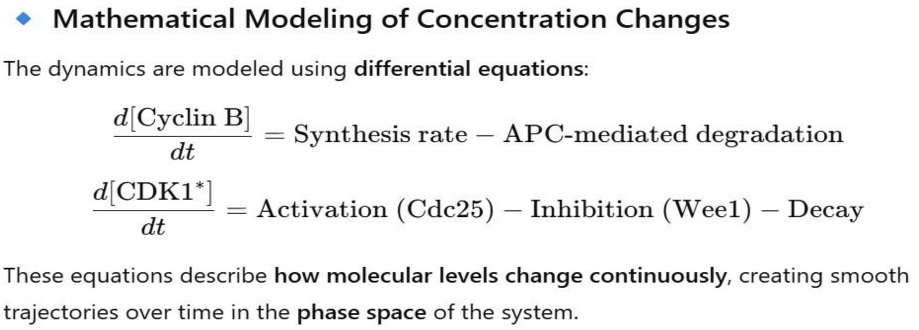
- Cyclin Synthesis and Degradation Cyclins are synthesized in a phase-specific manner:
- Cyclin D increases during G_1 Cyclin E peaks at G_1/S transitionCyclin A during S and G_2
- Cyclin B accumulates during G_2 and peaks at M They are degraded by ubiquitinmediated proteolysis (for example by APC/C), ensuring their timely removal.
- CDK activity follows cyclin levels CDK levels are relatively constant.CDK activity, however, depends on binding to cyclins and post-translational modifications. This activity rises and falls with cyclin concentration.

- Checkpoint Proteins Respond dynamically; Proteins like p21 and p53 increase in response to DNA damage and inhibit CDKs, causing delays in the cycle. Their levels also change continuously depending on cellular stress and repair signals.
- Feedback Loops Modulate Timing: Positive feedback (e.g., CDK1 → Cdc25 → CDK1) makes transitions sharper. Negative feedback (e.g., CDK1 → APC → Cyclin B degradation) creates oscillations.

Visualization: Cyclin and CDK Activity Over Time

Imagine a time axis spanning one full cell cycle. Here's a simplified description of molecular changes: (Sha *et al.,* 2003)





◆ **Mathematical Modeling of Concentration Changes**

The dynamics are modeled using **differential equations**:

$$\frac{d[\text{Cyclin B}]}{dt} = \text{Synthesis rate} - \text{APC-mediated degradation}$$

$$\frac{d[\text{CDK1}^*]}{dt} = \text{Activation (Cdc25)} - \text{Inhibition (Wee1)} - \text{Decay}$$

These equations describe **how molecular levels change continuously**, creating smooth trajectories over time in the **phase space** of the system.

(Source: Battogtokh & Tyson ,2004)

Table 2: The major biological implications are shown in the following table

Biological Implications Process	**Molecular Behavior**
Phase transitions	Triggered by cyclin accumulation crossing a threshold
Checkpoint arrest	Caused by increased levels of inhibitors like p21
Mitosis entry and exit	Sharp rise and fall in Cyclin B-CDK1 activity
Cell cycle synchronization	Coordination of many molecules through timed dynamics

Thus we can summarize that Continuous molecular concentration changes are the driving force behind smooth yet precisely timed transitions in the cell cycle. These changes are tightly regulated by synthesis, degradation, and feedback loops. Mathematical models and bifurcation theory help explain how gradual molecular changes can lead to sudden, irreversible cellular decisions like entering mitosis.

2. Phase Transitions as Dynamic Switches

- Transitions between G1 → S or G2 → M are not gradual—they're sharp, switch-like changes.
- These result from nonlinear feedback loops, which are hallmarks of dynamical systems.

Transitions in the Cell Cycle as Dynamic Switches

One of the most fascinating features of the cell cycle is that its phase transitions—like G_1 to S or G_2 to M—occur not gradually, but in an all-or-none (switch-like) manner. These transitions are governed by underlying nonlinear biochemical interactions that behave like dynamic switches. A dynamic switch is a behavior in a dynamical system where a small, continuous change in input or a system parameter causes a sudden, discrete shift in system state. In the context of the cell cycle, this means The cell either remains in the current phase or commits irreversibly to the next phase. Transitions are sharp, not gradual. Bifurcation theory (especially saddle-node bifurcations and bistability) explains the underlying mechanics.

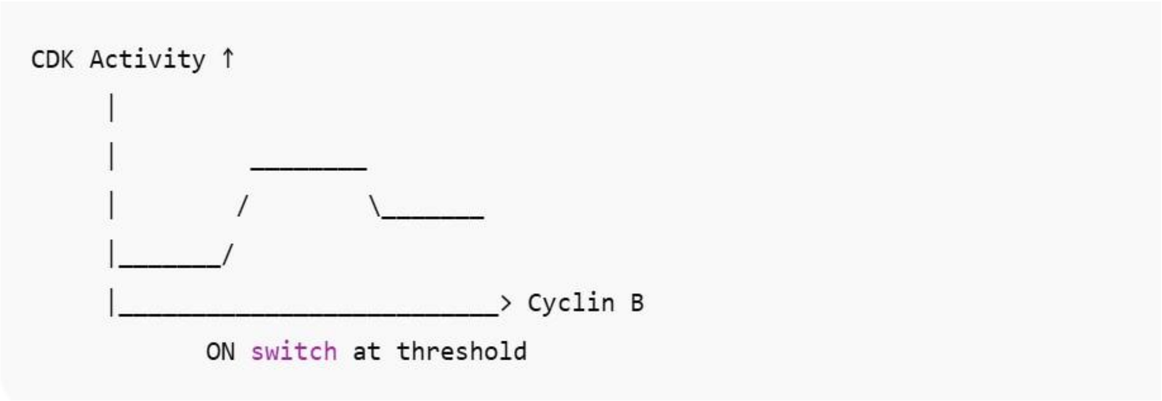
Some biological examples of switch-like transitions

- **Example 1: G_1/S Transition (Restriction Point):** Once a cell passes the restriction point, it commits to DNA replication and division, even if growth factors are removed. And it is driven by a positive feedback loop**:** Cyclin E-CDK2 inhibits Rb, which release E2F, which increases cyclin E expression → reinforces CDK2 activation. The result is bistability and an irreversible switch into S phase.
- **Example 2: G_2/M Transition (Entry into Mitosis):** It is Regulated by Cyclin B-CDK1**.**Active CDK1activates Cdc25 (which removes inhibitory phosphate) and inhibits Wee1 (which adds inhibitory phosphate) These positive feedback loops ensure the sudden, switch-like activation of CDK1. Once it is activated, the cell enters mitosis irreversibly.

The major mechanism behind switch behavior are bistability, positive feedback, hysteresis etc.

- **Bistability-** The system can rest in two stable states**:** During Low CDK activity → G1 or G2 (inactive state) where as High CDK activity → S or M phase (active state) Thus a threshold of cyclin/CDK or growth signal must be crossed to switch states.
- **Positive Feedback**—It ensures that once a transition starts, it accelerates itself and reduces the chance of partial or failed transitions.

- **Hysteresis** -The system **remembers its previous state**. We can't revert to the previous phase by simply reversing the trigger for e.g., reducing cyclin levels.This prevents the cell from "changing its mind" mid-transition.



```
CDK Activity ↑
     |
     |         _______
     |       /        \______
     |______/
     |__________________________> Cyclin B
            ON switch at threshold
```

A model of bifurcation diagram of CDK1 activity vs. cyclin concentration (Sha *et al.,* 2003)

The biological importance of dynamic switches is the cell cycle commitment which prevents back tracking once the division is decided. The check point fidelity ensures to caught such as DNA damage. The DNA replication and Mitosis tightly coordinates the timing precision and the malfunctioning switches lead to uncontrolled division, hence it is biologically very important in cancer prevention. Thus, the Phase transitions in the cell cycle act as dynamic switches — driven by feedback loops, bistability, and nonlinear kinetics. These switches guarantee precision, irreversibility, and robustness of cell division. Bifurcation theory provides the mathematical framework to analyze and understand these transitions. Thus, the key biological concepts related to bifurcations are:

- **CDK-Cyclin Complexes:** Drive the cell through different phases. Their activation/inhibition is nonlinear and can lead to bistable behavior.
- **Checkpoints: G_1**/S and G_2/M transitions are decision points regulated through feedback loops. Bifurcation theory helps model threshold behavior at these checkpoints.
- **Feedback Loops: Positive feedback** sharpens transitions (e.g., rapid Cyclin B-CDK1 activation). **Negative feedback** can lead to oscillations (e.g., mitotic oscillator in early embryos).

3. Mitosis as a Bifurcation Event

Mitosis, the process of cell division, can be viewed as a bifurcation where the cell transitions from a single state (the parent cell) to two daughter cells.

Mitosis—the final step in the cell cycle where a parent cell divides into two genetically identical daughter cells—can be interpreted through the lens of bifurcation theory. In this view, mitosis is not merely a mechanical event, but a dynamical transition**, or** bifurcation**,** in the cell's regulatory system that results in a qualitative change in the system's state. In dynamical systems theory**,** a bifurcation refers to a point where a small change in a system parameter causes a sudden, qualitative shift in its behavior. In mitosis the parent cell represents a single, stable state. The decision to divide is triggered by changes in key molecular signals (especially CDK1-Cyclin B). Once these signals reach a critical threshold level the cell undergoes a dramatic transition suddenly entering mitosis. After division, the system evolves to a new configuration that is two distinct daughter cells.

The biological basis of mitosis as a bifurcation are as follows-

i. **1-Triggering the Bifurcation:** CDK1-Cyclin B activation The G_2/M transition is governed by Cyclin B-CDK1 complex formation. This complex is kept inactive by inhibitory phosphorylation (via Wee1) and activated by Cdc25 phosphatase. Positive feedback loops in this network create a bistable switch. At low Cyclin B levels → CDK1 is OFF at G_2 phase where as at high Cyclin B levels → CDK1 turns ON sharply and entry into M phase. This is a saddle-node bifurcation, where the system jumps from G_2 to M state.

ii. **Irreversibility:** which ensures the commitment to division That is once the mitotic threshold is passed, The system cannot return to G_2 by simply reducing Cyclin B levels. This irreversibility is due to hysteresis—a hallmark of bifurcation behavior. It ensures that the cell does not partially enter mitosis or revert back mid-process.

So the outcome of the bifurcation is the system splits into two i.e after successful mitosis: The regulatory system resets in each daughter cell. The Cyclins are degraded (e.g., via APC/C activation) to bring the system back to G_1. In a dynamical sense, the single trajectory (parent cell path) bifurcates into two new, reset trajectories (daughter cells).

Simple equation showing a bistable switch near Mitosis can be represented Mathematically as :-

$$\frac{d[\text{CDK1}^*]}{dt} = \frac{k \cdot [\text{Cyclin B}]^n}{K^n + [\text{Cyclin B}]^n} - \text{degradation}$$

(Source: Battogtokh & Tyson ,2004)

The above model exhibits the following features such as: Threshold behavior Switch-like activation Stable high activity once threshold is crossed (M phase entry)Thus a bifurcation diagram (Cyclin B vs. CDK1 activity) would show a sharp jump—a hallmark of a bifurcation.

The biological Implications of viewing mitosis as a bifurcation are ensures mitosis only occurs when all conditions are met **(**Sharp, irreversible transitions)**,** transition is tightly regulated by DNA integrity, spindle assembly, etc.(Checkpoint control**)** ,splitting into two daughter cells corresponds to a system split or branch**(** Robust division outcome) and post-mitosis degradation of Cyclins resets system for next cycle (Reset of the system) Thus Mitosis, when seen through bifurcation theory, is more than cell division—it's a system-level state transition**:** It is driven by nonlinear molecular feedback. It exhibits threshold behavior**,** irreversibility**,** and qualitative change**.** This view provides a powerful, predictive framework to study cell cycle regulation**,** disease progression (e.g., cancer)**,** and synthetic control of cellular behavior.

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THE ROLE OF BIOINFORMATICS IN ADVANCING PLANT BREEDING

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Abstract:

The integration of bioinformatics into plant breeding has revolutionized the development of sustainable and resilient crops to address global agricultural challenges. Bioinformatics leverages computational tools and omics technologies, such as genomics, transcriptomics, proteomics and metabolomics, to accelerate the identification and selection of desirable traits in crops. It facilitates genome sequencing, gene annotation and the discovery of quantitative trait loci (QTLs), enabling precision in marker-assisted selection (MAS) and genomic selection (GS). Transcriptomics sheds light on gene expression and regulatory networks, while proteomics and metabolomics offer insights into the biochemical and physiological pathways underlying stress tolerance, growth and nutritional quality. The integration of multi-omics data, powered by advanced bioinformatics algorithms, provides a holistic understanding of plant systems, crucial for developing climate-resilient and high-yielding varieties. Artificial intelligence (AI) and machine learning further amplify the impact of bioinformatics by analyzing complex datasets, predicting trait performance and optimizing breeding strategies. These technologies, combined with genome editing tools like CRISPR-Cas9, enable precision breeding for specific traits, such as pest resistance and enhanced nutritional profiles. Additionally, bioinformatics plays a vital role in digital phenotyping, germplasm conservation and biodiversity management, ensuring the availability of genetic resources for future breeding programs. Despite its transformative potential, bioinformatics in plant breeding faces challenges, including data management, skill gaps and the integration of diverse datasets. Addressing these challenges through interdisciplinary collaboration, open-source platforms and investment in infrastructure is essential for maximizing its benefits. The future prospects of bioinformatics in plant breeding are vast, encompassing real-time crop monitoring, synthetic crop development and sustainable farming practices.

Keywords: Bioinformatics, Plant Breeding, Genomics, Transcriptomics, Precision Agriculture, Multi-Omics Integration.

Introduction:

Bioinformatics has emerged as a transformative force in modern agriculture, particularly in the realm of plant breeding (Vassilev *et al.,* 2005) (King, 2004). As global populations continue to rise and environmental challenges such as climate change intensify, the need for sustainable and efficient agricultural practices has never been more pressing. Conventional plant breeding methods, while foundational, are often time-consuming and imprecise (Breseghello & Coelho, 2013). To address these challenges, bioinformatics offers a robust and innovative approach to accelerate crop improvement, enhance productivity and develop resilience against biotic and abiotic stresses.

At its core, bioinformatics is the interdisciplinary fusion of biology, computer science and statistics (Luscombe *et al.,* 2001). By leveraging computational tools and algorithms, it enables the analysis and interpretation of vast amounts of biological data generated through advanced technologies like high-throughput genome sequencing, transcriptomics and proteomics. For plant breeders, these insights are invaluable (Christoper *et al.,* 2003). They allow for the precise identification of genes and genetic markers associated with desirable traits such as drought tolerance, pest resistance and improved nutritional content (ElSayed & Rafudeen, 2012). Unlike traditional phenotypic selection, which relies on observable characteristics, bioinformatics delves deep into the molecular mechanisms governing these traits, offering unprecedented accuracy and efficiency. One of the most significant contributions of bioinformatics to plant breeding is its role in genomics. Whole-genome sequencing and genome-wide association studies (GWAS) have revolutionized the identification of quantitative trait loci (QTLs), which are crucial for understanding the genetic basis of complex traits. Marker-assisted selection (MAS) and genomic selection (GS), powered by bioinformatics (Francia *et al.,* 2005), have further streamlined the breeding process by enabling early and precise screening of breeding lines. These approaches not only save time but also significantly reduce the resources required for developing new crop varieties.

Moreover, bioinformatics extends beyond genomics to encompass transcriptomics, proteomics, and metabolomics (Moolhuijzen, 2011). Transcriptomics offers insights into gene expression patterns, illuminating how plants respond to environmental stresses and developmental cues. Proteomics and metabolomics (Feussner & Polle, 2015), on the other hand, delve into the functional and biochemical aspects of plant physiology. Together, these omics approaches provide a comprehensive understanding of plant systems, which is crucial for designing crops tailored to specific agro-ecological conditions.

In the era of big data, bioinformatics has embraced cutting-edge technologies such as artificial intelligence (AI) and machine learning (Kashyap *et al.,* 2016; Gagneur *et al.,* 2017; Greene *et al.,* 2014). These Bioinformatics tools are adept at analyzing complex datasets, predicting trait performance and identifying novel genetic variants. For instance, AI-driven bioinformatics tools have been instrumental in guiding precision breeding efforts using technologies like CRISPR-Cas9 for genome editing. Such advancements underscore the role of bioinformatics as a cornerstone of next-generation plant breeding strategies (Jayashree & Hoisington, 2010; Littlejohn, 2001; Ougham & Huang, 2004), enabling researchers to enhance crop resilience and yield while minimizing environmental impact. The integration of these technologies not only accelerates the breeding process but also fosters a more sustainable agricultural future by allowing for targeted interventions that address specific challenges posed by climate change and pest pressures.(Badjakov *et al.,* 2017) (Parry *et al.,* 2012)(Taranto *et al.,* 2018) This transformative approach empowers scientists to create crops that are not only high-yielding but also better equipped to thrive in diverse and changing environments, ultimately contributing to global food security..

By harnessing the power of data-driven approaches, bioinformatics has the potential to address some of the most pressing agricultural challenges of our time. From ensuring food security to mitigating the impacts of climate change, its applications are as diverse as they are impactful (Iquebal *et al.,* 2015). As research and technological innovation continue to advance, the synergy between bioinformatics and plant breeding will undoubtedly shape the future of sustainable agriculture.

Applications of Bioinformatics in Plant Breeding

Bioinformatics has significantly transformed the landscape of plant breeding by offering powerful tools and methodologies to analyze and interpret complex biological data. Below are some key applications:

1. Genome Sequencing and Assembly

- Bioinformatics enables the sequencing and assembly of plant genomes, providing a comprehensive understanding of the genetic makeup of crops (King, 2004).
- Tools like genome-wide association studies (GWAS) and quantitative trait loci (QTL) mapping help identify genetic regions linked to important agronomic traits such as drought tolerance, disease resistance and higher yield (Kadirvel *et al.,* 2015; Rafalski, 2002).

2. Marker-Assisted Selection (MAS)

- Molecular markers linked to desirable traits can be identified using bioinformatics, allowing for precise screening in breeding programs (Langridge & Chalmers, 2004).
- MAS reduces reliance on traditional phenotypic selection, accelerating the breeding process and improving accuracy.

3. Genomic Selection

- Bioinformatics facilitates genomic selection, where statistical models are used to predict the performance of breeding lines based on genetic data (Vassilev *et al.,* 2005)

- This method is particularly useful for complex traits controlled by multiple genes, such as yield and stress tolerance.

4. Transcriptomics in Gene Expression Analysis

- By studying RNA sequences, bioinformatics tools provide insights into gene expression patterns during plant development or under stress conditions (Tripathi *et al.,* 2015).
- This information helps breeders understand the regulatory networks influencing key traits and select candidate genes for crop improvement.

5. Proteomics and Metabolomics

- Bioinformatics is crucial in analyzing proteomic data to understand protein functions and their roles in stress responses, growth and development (Kumar & Mann, 2009).
- Metabolomics, supported by bioinformatics, identifies metabolic pathways associated with traits like nutritional quality, flavor and stress tolerance.

6. Multi-Omics Integration

- A systems biology approach integrates genomics, transcriptomics, proteomics and metabolomics data for a holistic view of plant systems (Zheng *et al.,* 2014).
- This enables the development of crops that are resilient to multiple environmental stresses, such as drought and salinity.

7. Precision Breeding with CRISPR-Cas9

- Bioinformatics guides genome editing by identifying target genes for CRISPR-Cas9-based modifications (Alkhnbashi *et al.,* 2020).
- This precision technology allows for the development of crops with enhanced traits, such as pest resistance or improved nutritional profiles.

8. Artificial Intelligence and Machine Learning

- AI and machine learning algorithms analyze vast datasets generated through high-throughput sequencing and omics studies.
- These tools predict trait performance, optimize breeding strategies and uncover novel genetic variants.

9. Digital Phenotyping

- Combining bioinformatics (Berger *et al.,* 2013) techniques with digital imaging technologies allows for the analysis of phenotypic traits such as plant height, leaf area and flowering time.
- Digital phenotyping offers non-invasive methods to assess the performance of breeding lines under different environmental conditions (Yol *et al.,* 2015; Walter *et al.,* 2015).

10. Conservation of Genetic Resources

- Bioinformatics aids in the characterization and management of genetic diversity in germplasm collections.
- It helps identify and conserve rare alleles that can be used to breed climate-resilient crop varieties.

Bioinformatics Tools and Their Applications in Plant Breeding

A wide range of bioinformatics tools has been developed to analyze biological data and aid in plant breeding (Ougham & Huang, 2004; Vassilev *et al.,* 2005; Littlejohn, 2001). These tools cater to various aspects of genomics, transcriptomics, proteomics, metabolomics and computational modeling. Below is an overview of some key tools and their applications in plant breeding:

1. Tools for Genomic Analysis (Chen *et al.,* 2009)

- **BLAST (Basic Local Alignment Search Tool):**
    - *Application:* Compares nucleotide or protein sequences against databases to identify similarities. Used for gene annotation and locating homologous genes associated with important traits.
- **MAKER:**
    - *Application:* A genome annotation pipeline that integrates evidence from multiple sources, helping annotate plant genomes accurately.
- **GATK (Genome Analysis Toolkit):**
    - *Application:* Identifies and analyzes genetic variants such as single nucleotide polymorphisms (SNPs) and insertions/deletions (indels), which are critical for QTL mapping and marker-assisted selection.
- **PLINK:**
    - *Application:* Used for GWAS and population genetics studies, enabling the identification of genetic loci associated with desired agronomic traits.

2. Tools for Transcriptomics (Battke, 2012)

- **TopHat and HISAT2:**
    - *Application:* Align RNA-Seq reads to reference genomes, enabling the analysis of gene expression and identification of splice variants.
- **Cufflinks:**
    - *Application:* Quantifies transcript abundance and assembles novel transcripts, aiding in the discovery of stress-responsive genes.
- **DESeq2 and edgeR:**
    - *Application:* Tools for differential gene expression analysis, helping researchers study how plants respond to environmental changes.

3. Tools for Proteomics (Palagi *et al.,* 2006)

- **Mascot:**
    - *Application:* Identifies proteins by matching experimental mass spectrometry data to protein databases. Useful for studying proteins involved in stress tolerance and growth.

- **ProteinPilot:**
    - *Application:* Analyzes protein modifications and interactions, revealing functional pathways associated with key traits.
- **Cytoscape:**
    - *Application:* Visualizes molecular interaction networks, aiding in understanding protein-protein interactions in plant systems.

4. Tools for Metabolomics (Lazar *et al.,* 2015)

- **MetaboAnalyst:**
    - *Application:* Performs statistical analysis of metabolomic data to identify metabolic pathways linked to stress tolerance, yield enhancement, or nutritional quality.
- **KEGG (Kyoto Encyclopedia of Genes and Genomes):**
    - *Application:* Provides pathway maps for metabolic networks, helping identify key metabolic routes for crop improvement.

5. Multi-Omics Integration Tools (Meng *et al.,* 2014)

- **iCluster:**
    - *Application:* Integrates data from genomics, transcriptomics, proteomics and metabolomics for holistic analysis of plant systems.
- **MixOmics:**
    - *Application:* Facilitates the integration and visualization of multi-omics datasets, offering insights into complex trait regulation.
- **Galaxy:**
    - *Application:* A platform for reproducible bioinformatics workflows that incorporates various omics tools in a user-friendly environment.

6. Tools for Breeding Predictions (Unemi, 2003) (Estaghvirou *et al.,* 2013)

- **TASSEL (Trait Analysis by Association, Evolution and Linkage):**
    - *Application:* Performs association mapping and linkage disequilibrium analysis to link genetic markers with phenotypic traits.
- **GenSel:**
    - *Application:* Implements genomic selection models to predict breeding values based on genotype and phenotype data.
- **Breeding API (BrAPI):**
    - *Application:* Provides a framework for data exchange and analysis in plant breeding programs.

7. Artificial Intelligence and Machine Learning Tools

- **DeepVariant:**
    - *Application:* Employs AI to call genetic variants with high accuracy, aiding precision breeding efforts.

  - *Application:* A machine learning platform that predicts trait performance based on genotype and environmental data.
- **TensorFlow and PyTorch:**
  - *Application:* Enable custom machine learning models for analyzing large-scale omics data in plant breeding.

Challenges of Bioinformatics in Plant Breeding

While bioinformatics has revolutionized the field of plant breeding, it is not without its challenges (Ambrosino *et al.,* 2018; Ong *et al.,* 2016). Addressing these hurdles is crucial to fully realizing its potential in advancing agriculture. Below are some key challenges:

1. Data Overload and Management

- **Challenge:** High-throughput technologies generate massive amounts of data, including genomic, transcriptomic, proteomic and metabolomic datasets.
- **Implication:** Efficient storage, processing and management of this data require robust computational infrastructure and expertise.

2. Integration of Multi-Omics Data

- **Challenge:** Combining data from various omics platforms to gain a holistic understanding of plant systems is complex.
- **Implication:** The lack of standardized protocols and software for multi-omics integration limits the usability of such data.

3. Computational Power and Cost

- **Challenge:** Bioinformatics analyses, especially genome assembly and machine learning models, demand significant computational resources.
- **Implication:** High-performance computing facilities may not be accessible to researchers in developing regions, creating a disparity in technological adoption.

4. Skill Gap and Expertise

- **Challenge:** A multidisciplinary approach involving biology, computer science and statistics is essential in bioinformatics, but experts proficient in all three areas are rare.
- **Implication:** The lack of trained bioinformaticians hinders the implementation of advanced tools in plant breeding programs.

5. Data Accuracy and Quality

- **Challenge:** Errors in sequencing, annotation, or alignment can compromise the reliability of bioinformatics analyses.
- **Implication:** Poor-quality data can lead to inaccurate conclusions, affecting breeding decisions and downstream applications.

6. Interoperability of Tools

- **Challenge:** The wide variety of bioinformatics tools available often lacks interoperability, making it difficult to integrate results from multiple platforms.

- **Implication:** Researchers spend additional time and resources resolving compatibility issues, slowing progress.

7. Ethical and Legal Considerations

- **Challenge:** The use of genetic data raises ethical concerns regarding privacy, ownership and benefit-sharing, particularly in international collaborations.
- **Implication:** Unresolved legal frameworks can deter data sharing and hinder collaborative research.

8. Scalability for Real-World Applications

- **Challenge:** Many bioinformatics tools and models are developed in controlled environments and may not scale effectively for large, diverse breeding programs.
- **Implication:** Bridging the gap between research outputs and practical implementation is critical.

9. Accessibility and Democratization

- **Challenge:** Subscription-based software, expensive licenses and limited open-source alternatives restrict access to bioinformatics tools for resource-limited institutions.
- **Implication:** This creates an uneven playing field in global research efforts.

10. Keeping Pace with Rapid Technological Advancements

- **Challenge:** The rapid evolution of sequencing technologies, algorithms and databases necessitates continuous learning and updates.
- **Implication:** Researchers may struggle to keep up, leading to the underutilization of the latest advancements.

Future Prospects of Bioinformatics in Plant Breeding

The future of bioinformatics in plant breeding holds immense promise, driven by advances in computational biology, omics technologies and artificial intelligence. Here are some of the most exciting prospects (Saha *et al.,* 2023), (Cruz, 2022) (Ougham & Huang, 2004):

1. Enhanced Precision Breeding

- Emerging technologies like CRISPR-Cas systems, combined with bioinformatics, will enable more precise gene editing to develop crops with specific traits such as enhanced yield, improved nutritional content and climate resilience.
- Predictive models using machine learning will allow breeders to foresee trait performance under various environmental conditions, optimizing breeding strategies.

2. Real-Time Crop Monitoring

- Integration of bioinformatics with Internet of Things (IoT) devices and remote sensing technologies will facilitate real-time monitoring of crop health, growth patterns and environmental interactions.
- This will enable timely interventions in agricultural practices, improving productivity and resource efficiency.

3. Multi-Omics Data Integration

- Future advancements will focus on integrating data from genomics, transcriptomics, proteomics and metabolomics to provide a comprehensive understanding of plant systems.
- Such holistic insights will enable the development of crops that can withstand multiple stresses, such as drought, salinity and heat.

4. Development of Synthetic Crops

- Synthetic biology, powered by bioinformatics, will pave the way for designing entirely new plant species or modifying existing ones to meet specific agricultural needs.
- These synthetic crops could be tailored for bioenergy production, pharmaceutical applications, or novel food sources.

5. Climate-Resilient Agriculture

- Bioinformatics will play a crucial role in identifying and incorporating genes responsible for climate resilience, ensuring food security in the face of global warming and unpredictable weather patterns.
- By simulating stress conditions using computational tools, researchers can design crops that thrive under extreme environments.

6. AI-Driven Innovations

- Artificial intelligence and deep learning models will become integral in analyzing complex datasets, uncovering hidden patterns and accelerating the discovery of key genes and pathways.
- AI will also revolutionize phenotyping, automating the assessment of plant traits through image recognition and data analytics.

7. Biodiversity and Conservation

- Bioinformatics will aid in characterizing and conserving genetic resources from wild relatives of crops, ensuring that valuable alleles are preserved for future breeding efforts.
- Efforts in bioprospecting will identify untapped genetic diversity that can be used to address emerging agricultural challenges.

8. Accessible and Open-Source Platforms

- The development of user-friendly and open-source bioinformatics tools will democratize access to cutting-edge technologies, enabling researchers from resource-limited regions to contribute to global agricultural innovation.
- Cloud computing and collaborative platforms will make data analysis more accessible and scalable.

9. Predictive Breeding for Global Challenges

- Predictive models will enable breeders to anticipate future agricultural challenges, such as emerging diseases or shifting climatic zones, allowing proactive development of resistant crop varieties.
- This holistic approach will not only enhance agricultural productivity but also promote biodiversity and resilience within ecosystems, ensuring that farming can adapt to the challenges posed by climate change and population growth.s will incorporate real-world data to ensure the practical applicability of research outcomes.

10. Sustainable and Personalized Farming

- Bioinformatics will support the development of region-specific crop varieties tailored to local environmental and socio-economic conditions.
- Integration with sustainable farming practices will lead to reduced resource usage, minimized environmental impact and increased food security.

Conclusion:

Bioinformatics has established itself as a cornerstone in the advancement of modern plant breeding, offering unparalleled precision, efficiency and innovation. By harnessing the power of computational biology and omics technologies, researchers are addressing critical challenges in agriculture, including climate change, food security and sustainability. From genome sequencing and marker-assisted selection to transcriptomics, proteomics and machine learning-driven predictions, bioinformatics provides tools and methodologies that significantly accelerate the development of resilient, high-yielding and resource-efficient crops. While the field faces challenges such as data management, the need for computational expertise and integration of multi-omics data, ongoing advancements in artificial intelligence, open-source platforms and multi-disciplinary collaboration are paving the way for even more impactful contributions. The future prospects are both promising and transformative, with bioinformatics driving innovations in precision breeding, real-time crop monitoring and sustainable agricultural practices.

Ultimately, the synergy between bioinformatics and plant breeding represents a paradigm shift in how we approach crop improvement, ensuring a resilient and productive agricultural future for the growing global population. This interdisciplinary approach holds immense potential to not only meet present-day challenges but also to redefine the boundaries of agricultural science.

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Life Science: A Renaissance Approach

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