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CYTOGENETICS, EVOLUTION, PLANT BREEDING AND BIOSTATISTICS



Edited by
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PREFACE

Cytogenetics, Evolution, Plant Breeding, and Biostatistics represent the intricate tapestry of life, where the threads of genetics weave together the story of living organisms. This comprehensive volume endeavors to unravel the complexities of these interrelated fields, offering readers a holistic understanding of the fundamental processes that govern the evolution and improvement of plant species.

In the realm of Cytogenetics, the study of chromosomes and their variations lays the foundation for comprehending the hereditary mechanisms that underpin life. This book explores the intricacies of chromosomal structures, aberrations, and their implications in the context of genetic diversity and evolution. Readers will embark on a journey through the microscopic world of cells, gaining insights into the marvels of genetic architecture and the dynamic nature of genomes.

Evolution, the driving force behind the diversity of life, is a central theme in this volume. The book delves into the mechanisms of natural selection, adaptation, and speciation, providing a nuanced exploration of the processes that have shaped the myriad forms of life on our planet. From the molecular intricacies of evolutionary changes to the broader ecological context, the chapters within elucidate the profound connections between genetics and the unfolding drama of life's evolution.

Plant Breeding emerges as a critical discipline in the quest to enhance agricultural productivity, improve crop traits, and address global food security challenges. This book navigates the principles and methodologies of plant breeding, offering a comprehensive guide to selecting, crossing, and developing superior plant varieties. Through case studies and practical insights, readers will gain a deep appreciation for the science and art of breeding crops that meet the demands of a growing world population.

This book is designed to serve as a valuable resource for students, researchers, and professionals seeking a comprehensive guide to the intricate tapestry of Cytogenetics, Evolution, Plant Breeding, and Biostatistics. The synthesis of these disciplines offers a panoramic view of the processes that govern life, from the molecular intricacies within cells to the broader patterns of evolution and agricultural innovation.

Embark on this intellectual journey, where the secrets of chromosomes, the forces of evolution, the art of plant breeding, and the precision of biostatistics converge to unveil the captivating story of life on Earth.

(Editor)

CONTENT

S. No.	Chapter	Page
1	Gene Expression Network Analysis (GENA) – A Biostatistical method to unravel intricate relationships between Genes <i>Santhosh Kumar Rajamani</i>	1-13
2	Applications of Biostatistics <i>Talad Khan, Harihar, Samuel Gorden Singh, Priya Yadav</i>	14-40
3	Evolution, Plant Breeding, and Biodiversity: Interconnected Threads in the Tapestry of Life <i>Dr Sarika Yadav</i>	41-50
4	Plant Breeding: Evolution and Recent Trends in Advancing Crop Improvement <i>Dr Sarika Yadav</i>	51-61
5	Bioinformatics In Plant Genomics for Next-Generation Plant Breeding <i>Chethan Kumar Ramniklal, Garima Verma, Ajay Kumar Shukla, Vimal Kumar Yadav, Vishnu Yadav, Vineet Bharti, Kunal Agam, Shailendra Kumar</i>	62-87
6	Plant Breeding History A Review <i>Dr. Sushil Kumar Verma</i>	88-99

7	Research Progress of Plant Cytogenetics <i>Chethan Kumar Ramniklal, Garima Verma, Ajay Kumar Shukla, Vimal Kumar Yadav, Vishnu Yadav, Vineet Bharti, Kunal Agam, Shailendra Kumar</i>	100-117
8	Mutations In Plant Evolution, Crop Domestication, and Breeding <i>Chethan Kumar Ramniklal, Garima Verma, Ajay Kumar Shukla, Vimal Kumar Yadav, Vishnu Yadav, Vineet Bharti, Kunal Agam, Shailendra Kumar</i>	118-127
9	Parthenium Weed: Its Biological Suppression Through Allelopathy <i>Jai Knox</i>	128-138
10	Introduction to Biostatistics : A Brief Overview <i>Ekta Dubey</i>	139-150

CHAPTER - 01

GENE EXPRESSION NETWORK ANALYSIS (GENA) – A BIOSTATISTICAL METHOD TO UNRAVEL INTRICATE RELATIONSHIPS BETWEEN GENES

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Abstract

A deeper understanding of biological processes, disease mechanisms, and prospective therapeutic targets can be attained by Gene Expression Network Analysis (GENA), which offers a potent framework for revealing the intricate regulatory mechanisms controlling gene expression.

GENA is a computational method to understand the intricate interactions and relationships between genes in a biological system. It entails using network theory, statistical analysis, and gene expression data to pinpoint functional modules, regulatory linkages, and important genes or pathways involved in a particular biological process or illness.

This chapter broadly outlines the principles and practices of GENA to a novice reader. It outlines a simple method of performing a GENA using online Rice gene expression datasets available on various websites.

1.1. Introduction

A computational method called gene expression network analysis is used to understand the intricate interactions and relationships between the genes in a biological system. It entails using network theory, statistical analysis, and gene expression data to pinpoint functional modules, regulatory linkages, and important genes or pathways involved in a particular biological process or illness.

1.2. Obtaining gene expression data

Obtaining gene expression data, which can be produced using methods like microarrays or RNA sequencing, is the initial stage in gene expression network analysis. These data reveal the expression levels of thousands of genes across various situations or samples. Next, noise is removed from the gene expression data, experimental biases are adjusted for,

1.3. Co-expression Databases for information

Resources that contain data on the co-expression of genes are called co-expression databases. Co-expression is the occurrence of coordinated gene expression of two or more genes. This can occur when the same transcription factor controls genes or when they are involved in the same biological activity.

The identification of genes that are probably functionally linked can be done using co-expression databases. This can be helpful for a number of things, including:

Co-expression databases can be used to find genes that have not yet been implicated in a given biological process. Co-expression

databases can be used to annotate genes with functional data, including the biological process in which they take part.

- **Identification of illness genes:** Co-expression databases can be used to find genes that are probably implicated in a given disease.
- **Drug target identification:** Genes that may be prospective drug targets can be found using co-expression databases.

Online internet gene information databases like *Coexpedia*, *Ingenuity Pathway*, *GeneFriends*, *COXPRESdb*, and *Analysis DAVID* provide data on gene co-expression in various cell types, tissues, or organisms. They might also keep records of the genes that are linked together in certain disorders or the functional interactions between different genes.

Online co-expression databases represent an invaluable tool for a deeper understanding of gene functionality and regulation. The information is accurate based on experimental or computational data, and expression values are normalized (Zhang & Horvath, 2005).

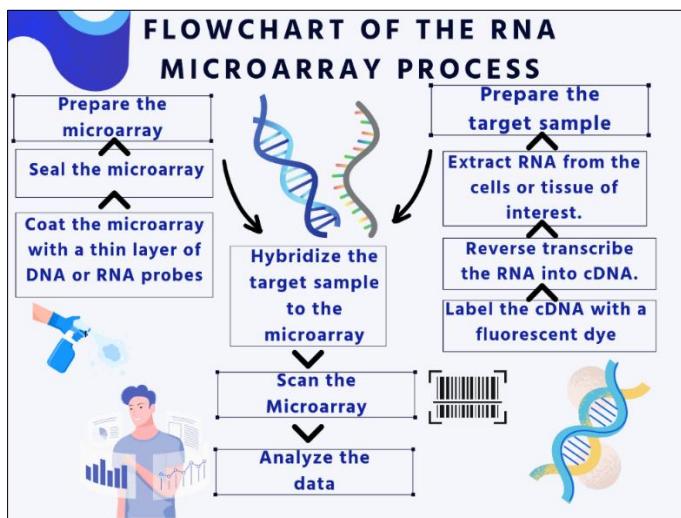
1.4. DNA or RNA microarray

A collection of microscopic DNA or RNA spots adhered to a solid surface is known as a DNA or RNA microarray. DNA or RNA microarrays are used by scientists to genotype different parts of a genome or to evaluate the expression levels of several genes at once. Picomoles (10–12 moles) of a particular DNA or RNA sequence, known as probes (or reporters or oligos), are present in each DNA or RNA location. These can be a brief segment of a gene or other

DNA element that is used to hybridize a target sample of cDNA or cRNA (also known as anti-sense RNA/ complementary RNA) under stringent conditions.

The following is the procedure for using a DNA or RNA microarray:

- a. A thin layer of DNA or RNA probes is placed on top of the microarray.
- b. A fluorescent dye has been used to label the target sample.
- c. The microarray is hybridized with the target sample.
- d. A laser is used to scan the microarray to find the labeled target molecules' fluorescence.
- e. The degree of expression of each gene or DNA region is determined by measuring the fluorescence intensity at each site.



*Fig 1: Flowchart of RNA Microarray process
(original illustration of authors)*

There are numerous uses for DNA or RNA microarrays, including:

- In a single experiment, gene expression profiling measures thousands of genes' expression levels. This can be used to investigate how various therapies affect gene expression or to find genes that are expressed differently in various cell types or tissues.
- Genotype analysis entails detecting whether a certain DNA mutation is present or absent. This can be used to determine who is at risk for contracting particular diseases or to diagnose hereditary diseases.
- In comparative genomic hybridization, the DNA composition of two or more samples is compared. Chromosome abnormalities, such as deletions or duplications, can be found with this method.

Obtaining gene expression data, which can be produced using methods like microarrays or RNA sequencing, is the initial stage in gene expression network analysis. These data reveal the expression levels of thousands of genes across various situations or samples.

Next, noise is removed from the gene expression data, experimental biases are adjusted, and the expression values are normalized.

This helps to ensure that the data is organized properly for more analysis.

After the data has been prepared, network inference algorithms are used to build the gene expression network. Based on gene expression patterns, these algorithms use statistical and computational techniques to infer the regulatory links between genes. Common strategies include model-based strategies like

Bayesian networks or ordinary differential equations as well as correlation-based strategies like Pearson correlation or mutual information (Nacu et al., 2007).

1.5. Network Analysis of Genetic Data

After the network has been constructed, numerous network analysis approaches are used to acquire an understanding of the dynamics and functional architecture of the gene regulatory network. Detecting densely connected gene groups known as modules or clusters and finding critical regulatory genes may be necessary to uncover highly connected genes or "hubs" that provide important functions in the network (Zimmermann et al., 2005).

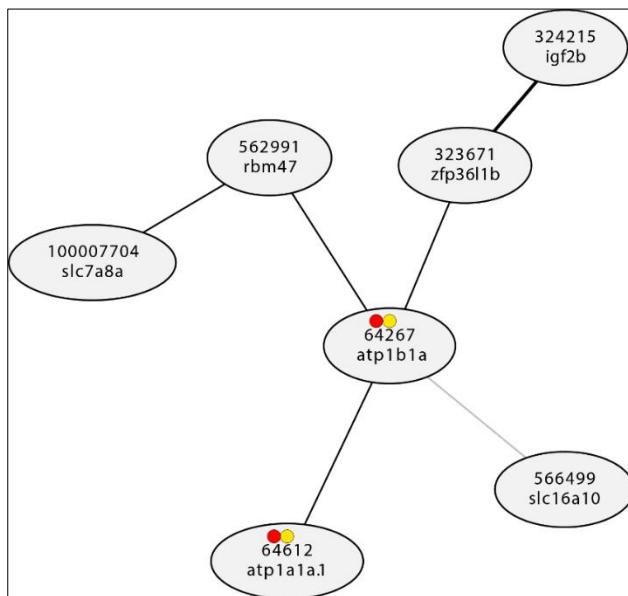


Fig 2: Example of actual Gene Expression network drawn from expression information available at RiceFriend (RiceFREND is a Japanese rice gene coexpression database consisting of a large online collection of microarray Data of rice <https://ricefrend.dna.affrc.go.jp/>) (Edwards, 2007 and Sato et al., 2012))

1.6. Scale-free Gene Interaction Network

When a network is scale-free, its degree distribution has a power-law shape, indicating that only a small number of nodes—known as "hubs" or "high-degree nodes"—have many connections compared to the vast majority of nodes. In contrast to this distribution, the degree distribution in a random network follows a bell-shaped normal distribution.

Scale-free gene interaction network analysis can provide details about biological systems' structure, modularity, and functional characteristics. It can aid in locating key genes essential for preserving a network's stability and resilience. The structure and characteristics of the network can also be studied to discover prospective therapeutic targets, understand disease causes, and forecast the consequences of perturbations or genetic variants on the network and cellular behaviour.

A scale-free network with hubs indicates that a small number of nodes are crucial in tying together different portions of the network. The effectiveness and connectivity of the network can be greatly impacted by removing or interrupting these hubs. Scale-free networks are strengthened against random failures by this characteristic but become more susceptible to deliberate attacks on the high-degree nodes. Scale-free gene interaction networks are analyzed to reveal their biological importance using a variety of computational and statistical techniques, including network creation algorithms, network clustering, centrality measures, and module discovery methods.

Preferential attachment is a common theory to explain how scale-free networks arise. This mechanism states that new nodes entering the network are more likely to link to nodes that already have a large number of connections. As a result, well-connected nodes continue to gain connections over time, causing the power-law degree distribution. This phenomenon is known as the "rich-get-richer" phenomenon (Rajamani & Iyer, 2023a).

The World Wide Web, biological networks, social networks, and many other real-world systems all contain scale-free networks. Due to their special characteristics and implications for network dynamics, information dissemination, and resilience, they have received a great deal of attention in the field of network science (Sato et al., 2012).

The '*barabasi_albert_graph*' function from the Python NetworkX module is used in the code above to create a scale-free network using the Barabasi-Albert model. The 'n' parameter indicates the number of nodes, whereas the 'm' parameter indicates the number of edges to attach from a new node to existing nodes.

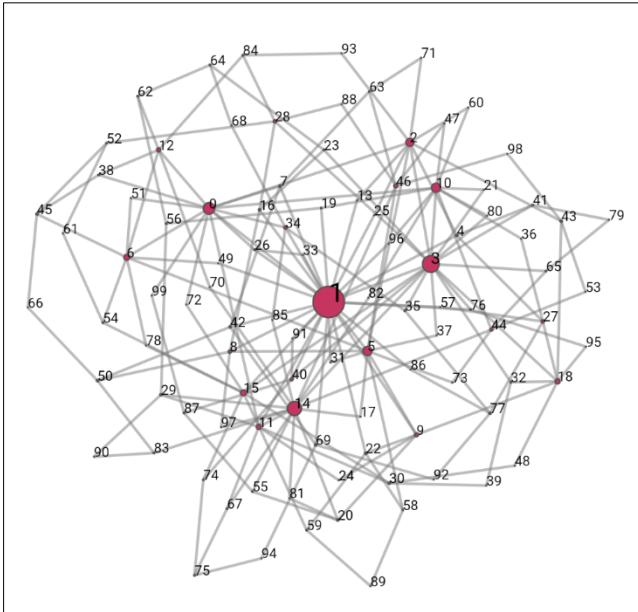


Fig 3. Example of Scale-free network with hubs (large nodes) number 1, 14, 3, 5, 26, 10, 2, and 0. The node size is proportional to the number of edges adjacent to it. This is a scale-free network of 100 nodes. Most nodes have only two edges, and hubs have multiple edges due to “preferential attachment”. (original illustration of authors) (Aslak & Maier, 2019)

1.7. Formation of Scale-free Networks

Hubs and preferential attachment are important ideas in network analysis concerning how scale-free networks are formed and structured.

- **Hubs:** Compared to other nodes in the network, hubs have a disproportionately large number of connections. In other words, they are nodes with lots of connections. Hubs are essential for preserving connectivity and the network's general structure in scale-free networks. They serve as hubs for the network's many nodes, facilitating communication and information exchange. Network connectivity may be

adversely affected by the removal or disruption of hubs, leaving them open to deliberate attacks or malfunctions (Sato et al., 2012).

In gene interaction networks, the edges stand in for interactions or connections between the genes' nodes, representing genes. Protein-protein interactions are an example of a physical interaction. Regulatory interactions include gene regulation and signalling cascades.

- **Preferential attachment:** Preferential attachment is a process that accounts for the expansion of scale-free networks. According to this, new nodes joining a network are more likely to connect to nodes that are already connected to many other nodes. In other words, nodes with more connections and a higher degree are more likely to draw in new connections. The rich-get-richer phenomenon, whereby well-connected nodes tend to assemble even more connections over time, is caused by this preferred attachment mechanism. As a result, a power-law degree distribution is formed, with most nodes having just a small number of connections and a select few nodes (hubs) having a huge number of connections(Sato et al., 2011).

Preferential attachment has been noted in a number of real-world networks, including citation networks, social networks, the World Wide Web, and biological networks. It aids in developing scale-free networks and explains the establishment of hub-like nodes (Rajamani & Iyer, 2023b).

Preferential attachment is a notion that has been extensively researched in the field of network science. It has implications for network resilience, information diffusion, and network growth.

- **Power-law degree distribution:** A certain structural feature of a complex network known as a power-law degree distribution is present in scale-free networks. In computing terminology, the degree distribution of a network is the distribution of the number of connections (edges) that each node in the network possesses.

Given that gene interaction networks are scale-free, it follows that a limited subset of genes (hubs) are essential for tying together various genes or network modules. These hub genes are frequently linked to crucial signalling networks, fundamental cellular processes, or important biological activities. The integrity of the entire network and biological function may be significantly impacted by the disruption or dysfunction of these hub genes (RiceFREN, n.d.).

This allows researchers to locate important transcription factors or regulatory genes that regulate the expression of other genes. Additionally, regulatory patterns and signalling pathways within the network can be found with the aid of network analysis. It can also be used to compare networks between various samples or situations to spot changes in gene regulatory relationships linked to certain biological functions or disease states (Rajamani & Iyer, 2023c). Experimental validation methods like knockouts or overexpression of genes, chromatin immunoprecipitation, or reporter gene assays

can be used to verify the results of gene expression network analysis. This allows researchers to locate important transcription factors or regulatory genes that regulate the expression of other genes. Additionally, regulatory patterns and signalling pathways within the network can be found with the aid of network analysis. Additionally, it can be used to compare networks between various samples or situations in order to spot changes in gene regulatory relationships linked to certain biological functions or disease states. Experimental validation methods like knockdown or overexpression experiments, chromatin immunoprecipitation, or reporter gene assays can be used to verify the results of gene expression network analysis.

1.8. Conclusion

Gene expression network analysis can provide a deeper understanding of biological processes, disease mechanisms, and prospective therapeutic targets, which offers a potent framework for revealing the intricate regulatory mechanisms controlling gene expression.

1.9. References

1. Aslak, U., & Maier, B. (2019). Netwulf: Interactive visualization of networks in Python. *Journal of Open Source Software*, 4(42), 1425. <https://doi.org/10.21105/joss.01425>
2. Edwards, D. (2007). *Plant bioinformatics: methods and protocols*. Humana Press.
3. Nacu, S., Critchley-Thorne, R., Lee, P., & Holmes, S. (2007). Gene expression network analysis and applications to immunology. *Bioinformatics*, 23(7), 850–858. <https://doi.org/10.1093/bioinformatics/btm019>
4. Rajamani, S. K., & Iyer, R. S. (2023a). Machine Learning-Based Mobile Applications Using Python and Scikit-Learn. Advances in Wireless Technologies and Telecommunication Book Series, 282–306. <https://doi.org/10.4018/978-1-6684-8582-8.ch016>

5. Santhosh Kumar Rajamani & Radha Srinivasan Iyer. (2023b). Declining Freshwater Species Biodiversity. In N. K. Chourasia & K. Chahal (Eds.), Perspectives on Global Biodiversity Scenarios and Environmental Services in the 21st Century (pp. 22–56). IGI Global. <https://doi.org/10.4018/978-1-6684-9034-1.ch002>
6. Rajamani, S. K., & Iyer, R. S. (2023c). Methods of Complex Network Analysis to Screen for Cyberbullying (pp. 218–242). CRC Press. <https://doi.org/10.1201/9781003393061-16>
7. RiceFREND. (n.d.). Ricefrend.dna.affrc.go.jp. Retrieved July 8, 2023, from <https://ricefrend.dna.affrc.go.jp/>
8. Sato, Y. S., Antonio, B. A., Nobukazu Namiki, Hinako Takehisa, Minami, H., Kaori Kamatsuki, Sugimoto, K., Shimizu, Y., Hirohiko Hirochika, & Yoshiaki Nagamura. (2011). *RiceXPro: a platform for monitoring gene expression in japonica rice grown under natural field conditions.* 39(Database), D1141–D1148. <https://doi.org/10.1093/nar/gkq1085>
9. Sato, Y. S., Hinako Takehisa, Kaori Kamatsuki, Minami, H., Nobukazu Namiki, Hiroshi Ikawa, Hajime Ohyanagi, Sugimoto, K., Antonio, B. A., & Yoshiaki Nagamura. (2012). *RiceXPro Version 3.0: expanding the informatics resource for rice transcriptome.* 41(D1), D1206–D1213. <https://doi.org/10.1093/nar/gks1125>
10. Sato, Y., Namiki, N., Takehisa, H., Kamatsuki, K., Minami, H., Ikawa, H., Ohyanagi, H., Sugimoto, K., Itoh, J.-I., Antonio, B. A., & Nagamura, Y. (2012). RiceFREND: a platform for retrieving coexpressed gene networks in rice. *Nucleic Acids Research*, 41, D1. <https://doi.org/10.1093/nar/gks1122>
11. Zhang, B., & Horvath, S. (2005). A General Framework for Weighted Gene Co-Expression Network Analysis. *Statistical Applications in Genetics and Molecular Biology*, 4(1). <https://doi.org/10.2202/1544-6115.1128>
12. Zimmermann, P., Hennig, L., & Gruissem, W. (2005). Gene-expression analysis and network discovery using Genevestigator. *Trends in Plant Science*, 10(9), 407–409. <https://doi.org/10.1016/j.tplants.2005.07.003>

CHAPTER -02

APPLICATIONS OF BIOSTATISTICS

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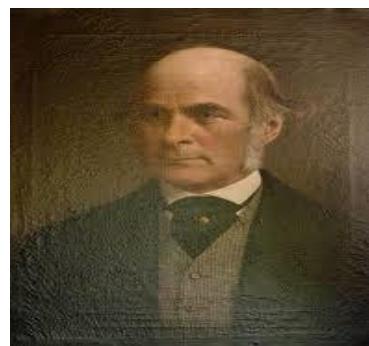
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2.1. Introduction

Biostatistics is the science that collects, classifies, and tabulates numerical facts as the basis for explaining, describing, and comparing phenomena.

It is the branch of applied statistics applied in many areas of Biology, including Epidemiology, Medical sciences, Health Sciences, Pharmaceutical Sciences, and Environmental sciences.

Francis Galton (1822-1911) is called as the father of biostatistics. He created the statistical concept of correlation. Sir Galton used statistical tools to study differences among the human population for the first time. He also invented questionnaires and surveys to collect data on human communities.



Francis Galton (1822-1911)
Father of Biostatistic

W.F.R. Weldom is credited with coining the term biometry. **Karl Pearson (1857-1936)**, regarded as the father of modern statistics,

was greatly motivated by Francis Galton's research. He established a laboratory and started the issue of the Biometrika journal. His major contribution was correlation and regression. Adolphe Quetelet (1796-1874) was the first scientist to introduce biostatistics concepts, combining theory and practical statistics methods in biological and medical applications.

2.2. Categories of Statistics

2.2.1. Pure Statistics

Pure statistics is the basic statistics. It is further classified into four subcategories.

a. Descriptive Statistics

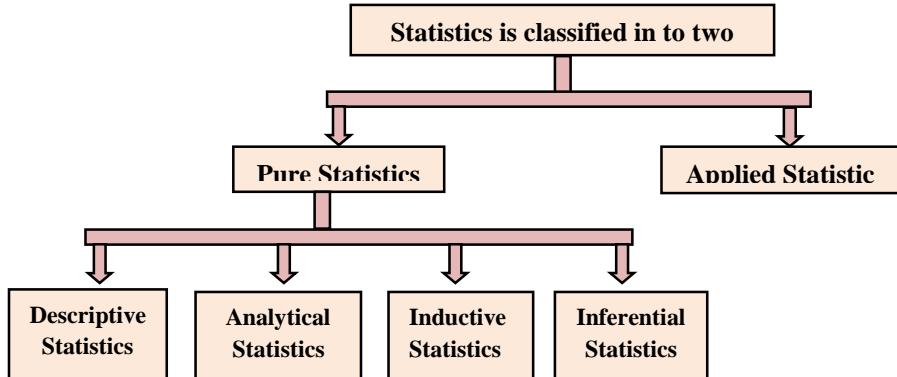
These are the statistical tools and analyses which describe and summarize the main features of the data. Examples: Measure of central tendency (Mean, Median, and Mode), Measure of dispersion (Range, mean deviation, and standard deviation).

b. Analytical Statistics

Analytical statistics deal with all tools in the statistics used to compare different variables and help to establish functional relationships between variables or data. Examples: Correlation and Regression.

c. Inductive Statistics

Inductive statistics is the use of statistical tools to generate conclusions on the basis of random observation.



- d. **Inferential Statistics** is the application of statistics theories to analyze research problems. It includes complex calculations, analysis, and comparisons, such as statistical quality control, index numbers, and vital statistics.

2.2.2. Applied Statistics

Applied statistics is the use of statistical techniques to solve real-world data analysis problems.

2.3. Applications of Biostatistics

a. In Anatomy and Physiology

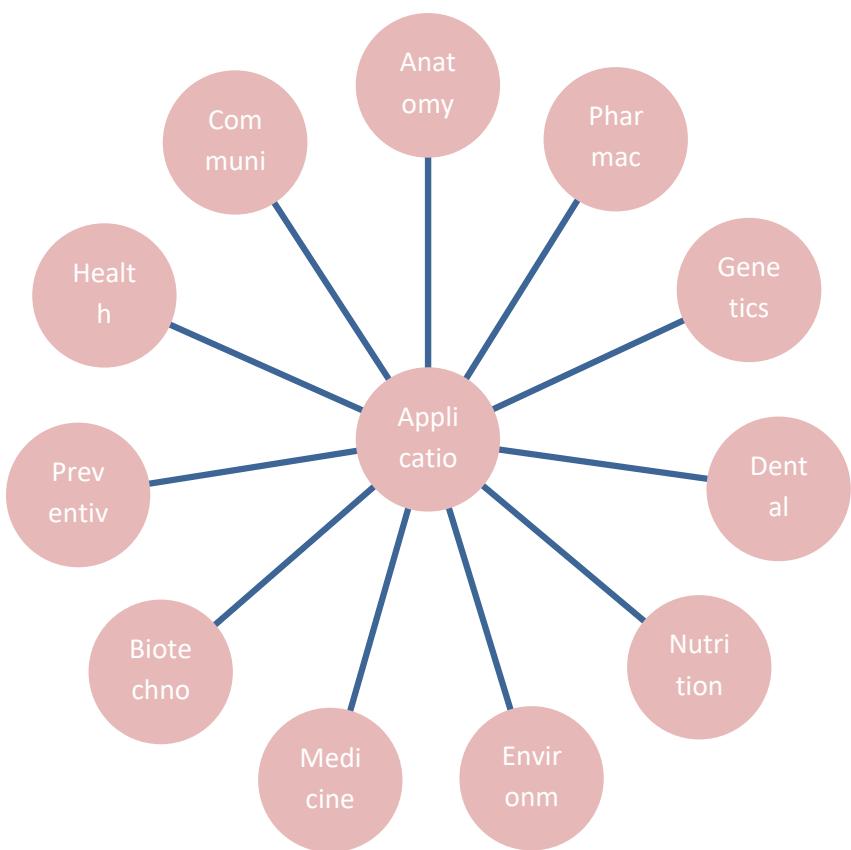
- To define what is normal or healthy in a population.
- To find the limits of normality in variables such as weight, pulse rate, etc., in a population.
- To find the correlation between two variables, such as height and weight, whether weight increases or decreases proportionately with height.

b. *In Pharmacology*

- To find the action of drug – A drug is given to humans to see whether the changes produced are due to the drug or by chance.
- To compare the action of two different drugs or two successive dosages of the same drug.
- To find the relative potency of a new drug with respect to a standard drug.

c. *In Medicine*

- To compare the efficacy of a particular drug, operation or line of treatment, the percentage cured, relieved or died in the experiment and control groups is compared and difference due to chance or otherwise is found by applying statistical techniques.
- To find an association between two attributes: cancer, smoking, filariasis, and social class.
- To identify signs and symptoms of a disease or syndrome.
- Cough in typhoid is found by chance, and fever is found in almost every case.
- To test the usefulness of sera and vaccines in the field- The percentage of attacks or deaths among the vaccinated subjects is compared with that among the unvaccinated ones to find whether the difference observed is statistically significant.



d. *Preventive medicine*

- To provide the magnitude of any health problem in the community.
- To find out the basic factors underlying ill-health.
- To evaluate the health programs that were introduced in the community (success/failure)?
- To introduce and promote health legislation.

e. In Health Planning and Evaluation

- The methods used in dealing with statistics in the fields of medicine, biology, and public health are for planning, conducting, and analyzing data.
- In carrying out a valid and reliable health situation analysis, including in proper summarization and interpretation of data.
- In proper evaluation of the achievements and failures of a health programs.

f. In Biotechnology

Study of genetic modification of plants and animals to gene therapy, medicine and drug manufacturing, reproductive therapy, and even energy production. In all these cases, research is conducted to test whether it has the desired performance.

g. In Community Medicine and Public Health

- To evaluate the efficacy of sera and vaccines in the field..
- To test whether the difference between two populations is real or a chance occurrence.
- To study the correlation between attributes in the same population.
- To measure the morbidity and mortality.
- To evaluate the achievements of public health programs.
- To fix priorities in public health programs.
- It helps in the compilation of data, drawing conclusions and making recommendations.

h. In Genetics

- Some fundamental aspects, in particular, are the concept of Analysis of Variance in Human Genetics, while statistical and probabilistic methods are now central to many aspects of the analysis of questions in human genetics.
- The most common areas where one can find extensive applications of statistical methods in human genetics is Human Genome Project, Linkage Analysis, and Sequencing.

i. In Nutrition

Analysis of DNA, RNA, protein, low-molecular-weight metabolites, and access to bioinformatics databases.

j. In Dental Science

- To find the statistical difference between the means of the two groups. Ex: Mean plaque scores of two groups.
- To assess oral health in the community and determine the availability and utilization of dental care facilities.
- To promote oral health legislation and create administrative standards for oral health care delivery.

k. In Environmental Science

- Baseline studies document the present state of an environment to provide background in case of unknown changes in the future.
- Targeted studies to describe the likely impact of planned changes or accidental occurrences.
- Regular monitoring to attempt to detect changes in the environment.

2.4. Steps in Biostatistics

A biological investigation is carried out through the following sequential steps.

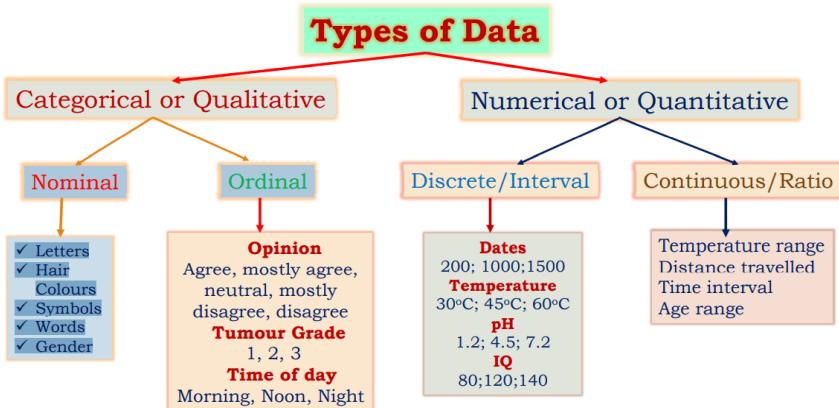
- (1). Collection of variables/data
- (2). Classification of the collected data
- (3). Analysis of data
- (4). Interpretation of data

Data can be defined as a systematic record of a particular quantity. It is the different values of that quantity represented together in a set. It is a collection of facts and figures to be used for a specific purpose, such as a survey or analysis. When arranged in an organized form, it can be called information. The source of data (primary data, secondary data) is also an important factor.

Types of Data - Data may be qualitative or quantitative.

Qualitative Data represent some characteristics or attributes. They depict descriptions that may be observed but cannot be computed or calculated. For example, data on attributes such as intelligence, honesty, wisdom, cleanliness, and creativity collected using the students of your class as a sample would be classified as qualitative.

Quantitative Data can be measured and not simply observed. They can be numerically represented, and calculations can be performed on them. For example, the height of the plant, the yield of the plant, and the number of students playing different sports. This information is numerical and can be classified as quantitative.



2.5. Diagrammatic Representation of Data

Diagrams always help the statistician visualise a numerical complex's meaning at a glance. A large number of diagrams are used in biostatistical analysis. They are as follows.

- Line diagram
- Bar diagram
- Pie diagram
- A **line diagram** is the simplest type of diagram. For diagrammatic representation of data, the discrete variable can be presented by a line diagram. The variable is taken on the X-axis, and the frequencies of the observations are on the Y-axis. For example, the frequency distribution of a discrete variable (chlorophyll mutant) is given in Table 1.

Table 1. Frequency distribution of a discrete variable

Chlorophyll mutant	Frequency
Albina	50
Xantha	44
Chlorinia	36
Viridis	30
Chloro Viridis	16

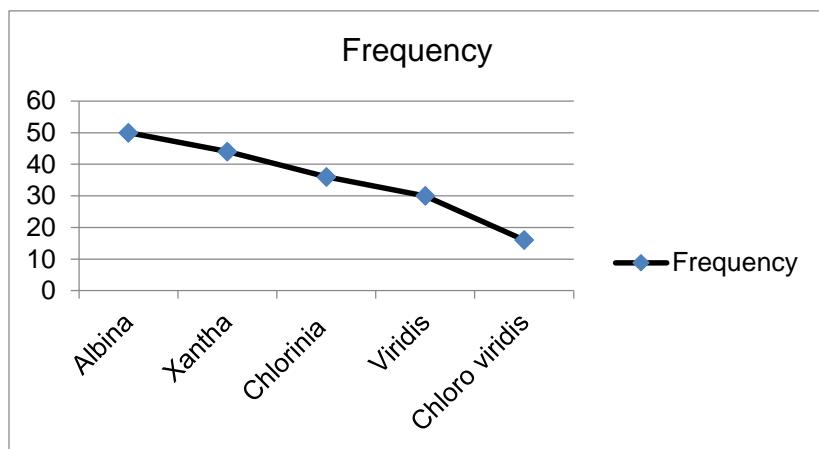


Fig 1. The line diagram represents the data in Table 1.

- b. **Bar Diagram** is commonly used in practice to present statistical data. They are also known as one-dimensional diagrams because the bar's length is important, not the width. For example, various chlorophyll mutant types may be shown by means of a bar diagram. Since these are of the same width, only the length varies.

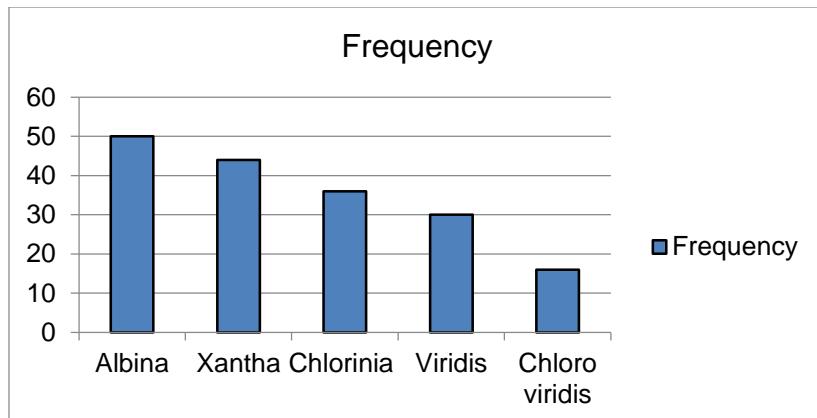


Fig 2. Bar diagram representation of the data in Table 1.

The highest frequency is shown by albino mutant and the lowest by chlоро viridis.

- c. **Pie Diagram** is another way of presenting discrete data of qualitative characteristics such as blood groups, age groups and total area under cultivation for different crops.

Table 2. Percentage of Blood groups

Blood groups	Percentage
A	26.5
B	34.5
O	31.6
AB	7.4

In situations where different components or frequencies are to be shown by means of sectors of a circle, the angles of the sectors are proportional to the respective measurement of the different components and such a diagram is called a pie diagram.

Percentage of Blood groups

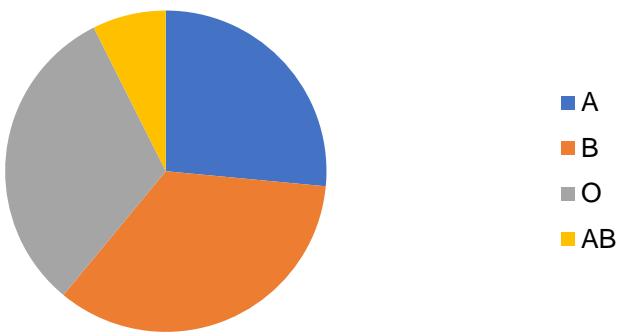


Fig 3. Pie diagram representing the percentage of Blood groups as given in Table 2

2.6. Measure of Central Tendency

Measures of central tendency are sometimes needed to make meaningful interpretations of the data. Generally, it is found that in any distribution, values of the variable tend to congregate around a central value of the distribution. This distribution tendency is known as its central tendency, and the measures devised to consider this tendency are known as measures of central tendency.

When we discuss the distribution of data in biology or agriculture, there are usually three basic measures of the central tendency. These are Arithmetic mean, Median and Mod.

2.7. Arithmetic Mean

It is the most familiar and widely used measure of central tendency. It represents the entire data by one value, which is obtained by adding all the values and dividing this total by the number of observations.

2.7.1 Calculation of Arithmetic Mean

Calculation of arithmetic mean in a series of individual observations: The arithmetic mean of an individual series can be calculated either by direct method or by shortcut method. However, the result of both methods will be the same.

Direct Method: the arithmetic mean is computed by summing up the observation and dividing the sum by the total number of observations.

$$\bar{x} = x_1 + x_2 + x_3 + \dots + x_n \text{ Or } \bar{x} = \frac{\sum x}{n}$$

\bar{x} =arithmetic mean

$\sum x$ =sum of all values of the variable, x i.e. x_1, x_2, x_3

n =number of observation

Example: Calculate the arithmetic mean of the following set of observations: 7, 6, 8, 10, 13, 14.

Solution $\bar{x} = \frac{\sum x}{n}$
 $\sum x = 58$
 $n = 6$
 $\bar{x} = 58 / 6$
 $\bar{x} = 9.67$

Short-cut Method: the short-cut method is used where the number of observations is large to avoid the considerable difficulty in calculating the arithmetic mean. This method is based on an important property: the algebraic sum of the deviations of a series of individual observations from their mean equals zero. For example, the arithmetic mean of 7, 6, 9, 8, 10 is 8. The deviations from the mean are -1, -2, +1, 0, +2. Thus, the total is zero. Therefore,

we can assume an arbitrary mean to find out the deviations from this assumed mean. Here, the total of deviations will not be zero. The total is divided by the number of observations and added to the assumed mean, the actual arithmetic mean. Symbolically;

$$\bar{x} = A + \sum dn$$

\bar{x} =arithmetic mean

A = Assumed mean

D = deviation of items from the assumed mean ($x - A$)

$\sum d$ = sum of deviation

Example: the following example shows the arithmetic mean calculation from the number of spikelets per spike in wheat.

Number of spikelets per spike = 18, 20, 21, 19, 28, 22, 29, 30, 31, 35

Solution: Assumed mean = 24

Spikelets per spike X	Deviation from the assumed mean $D = (x - A)$
18	-6
19	-5
20	-4
21	-3
22	-2
28	4
29	5
30	6
31	7
35	11
$n = 10$	$\sum d = -20 + 33 = 13$

$$\bar{x} = A + \sum dn$$

$$A = 24$$

$$\sum d = 13$$

$$n = 10$$

$$\bar{x} = 24 + \frac{13}{10} = 24 + 1.3 = 25.3$$

$$\bar{x} = 25.3$$

Calculation of arithmetic mean in a discrete series: For computation of arithmetic mean in a discrete series, the values of the variable are multiplied by their respective frequencies. However, the number of observations is equal to the total of the frequencies. The formulae for computing the arithmetic mean by direct and short-cut methods are as follows.

Direct Method: In a discrete series, the frequency of each row is multiplied by its respective value. The total is then divided by the number of frequencies to determine the arithmetic mean.

$$x = \sum fx_n \quad \text{or} \quad \bar{x} = \frac{\sum fx}{\sum f}$$

Where \bar{x} = arithmetic mean

$\sum f$ = sum of frequencies

$\sum fx$ = sum of values of the variable and their corresponding frequencies

Example: The data recorded on the number of chlorophyll-deficient plants in a lentil population is given below. Calculate the arithmetic mean.

Number of chlorophyll-deficient plants	Number of plants
0	34
1	14
2	20
3	24
4	25
5	33

Solution:

Number of chlorophyll-deficient plants X	Number of plants f	Fx
0	34	0
1	14	14
2	20	40
3	24	72
4	25	100
5	33	165
	$\sum f = 150$	$\sum Fx = 391$

$$\bar{x} = \frac{\sum Fx}{\sum f}$$

$$\sum Fx = 391, \quad \sum f = 150$$

$$\bar{x} = \frac{391}{150} = 2.61$$

$$\bar{x} = 2.61$$

Short-cut Method: In this method, the deviations of the items from an assumed mean are multiplied by their respective frequencies and summed up. This total is then divided by the total frequencies and added to the assumed mean. The arithmetic mean is calculated on the basis of this given formula.

$$\bar{x} = A + \frac{\sum fd}{\sum f}$$

Where \bar{x} = arithmetic mean

A = assumed mean

$\sum fd$ = sum of the deviations from the assumed mean and respective frequencies

$\sum f$ = sum of the frequencies

Example: Calculate the arithmetic mean from the data given in the table.

Number of leaves	Number of plants
5	6
10	5
15	9
20	4
25	3
30	6
35	4
40	3

Solution: Assumed mean = 25

Number of leaves (x)	Number of plants(f)	d = (x-25)	Fd
5	6	-20	-120
10	5	-15	-75
15	9	-10	-90
20	4	-5	-20
25	3	0	0
30	6	5	30
35	4	10	40
40	3	15	45

$$\sum f = 40$$

$$\bar{x} = 25 + (-19)40$$

$$25 + (-4.75)$$

$$\bar{x} = 20.25$$

Calculation of arithmetic mean in a continuous series: In a continuous series, the arithmetic mean may be calculated after taking into consideration the mid-points of various classes. Any of the following methods can calculate the mean. The arithmetic mean will be the same in all those methods.

Direct Method: The following formula can be used to calculate the arithmetic mean in a continuous series by direct method.

$$\bar{x} = \frac{\sum fm}{\sum f}$$

Where \bar{x} = arithmetic mean

$\sum fm$ = sum of values of mid-points multiplied by
the respective frequency of each class

$\sum f$ = sum of frequency

f = frequency of each class

m = mid-point of various classes

Mid-point = Lower limit + Upper limit / 2

Example: Calculate the arithmetic mean from the following data

Solution:

Plant height (cm)	0-10	10-20	20-30	30-40	40-50	50-60
Number of varieties	5	10	25	30	20	10

Solution:

Plant height (cm) classes	Number of varieties f	Mid-point M	Fm
0-10	5	5	25
10-20	10	15	150
20-30	25	25	625
30-40	30	35	1050
40-50	20	45	900
50-60	10	55	550
		$\sum f = 100$	$\sum fm = 3300$

$$\bar{x} = \frac{\sum fm}{\sum f}$$

$$\sum fm = 3300$$

$$\sum f = 100$$

$$\bar{x} = \frac{3300}{100} = 33$$

$$\bar{x} = 33$$

2.8. Median

Median data are arranged in ascending and descending series rather than middle items, or an item with an equal number of data on both sides is known as the median. It is thus clear that the median divides the data into two groups. Each item is less than the median one of the groups, whereas the other is more than the median. If the number of data is, then the value of the middle $[N+1]^{th}$ item will be known as the median.

2.8.1. Calculation of Median

Calculation of Median in an individual series

For calculating the median in a series of individual observations, the following steps are taken:

1 Arrange the data in 11 ascending or descending order. The answer will be the same both way

2 median is located by finding the size of $N+12^{\text{th}}$ item

$M = \text{size of the } N+12^{\text{th}} \text{ item}$

$M = \text{median}$

$n = \text{number of observation}$

Example: find out the median from the data recorded on the number of clusters per plant in a pulse crop.

Number of clusters = 10, 18, 17, 19, 10, 15, 11, 17, 12

Solution: Arrange the data either in ascending or descending order

S.No.	Data arranged in ascending order.
1	10
2	10
3	11
4	12
5	15
6	17
7	17
8	18
9	19

Median = size of $N+12^{\text{th}}$ item

Median = size of $9+12^{\text{th}}$ item

Median = size of 5^{th} item = 15

Median = 15

Calculation of median in a discrete series:

For the computation of the median in discrete series, one should take into consideration the following steps

1 Data should be arranged in ascending or descending order of magnitude.

2 Find out the cumulative frequencies.

3 Median = size of $N+12^{\text{th}}$ item

Found out the value of $N+12^{\text{th}}$ item. It can be found by first locating the cumulative frequency equal to $N+12$ or the next higher to this and then determining the value corresponding to it. This will be the value of the median.

Example: find out the value of the median from the following data.

Number of angular seeded plants	12	8	17	10	11	16	18	14	6	7
Number of plants	39	33	42	40	47	42	60	50	22	25

Solution

Angular-seeded plants in ascending order	Number of plants F	Cumulative frequency Cf
6	22	22
7	25	47
8	33	80
10	40	120
11	47	167
12	39	206
14	50	256
16	42	298
17	42	340
18	60	400

Median = size of $N+12^{\text{th}}$ item

Median = size of 400+12 or 200.5th item

Median = size of 200.5 item = 12

Median = 12

Calculation of median in a continuous series:

The following formula is used for determining the exact value of the median.

$$\text{Median} = L + \frac{n}{2} - Cf \times i$$

L = lower limit of the median class

Cf = cumulative frequency of the class preceding the median class

f = frequency of the median class

i = class-interval

however, it should be remembered that instead of the lower limit of the median class, one can take the upper limit of the median class.

In this case, class intervals should be in descending order, and frequencies should be cumulative from top to bottom.

Example: Calculate the value of the median from the data recorded on the number of grains per gearhead on 300 wheat gearheads

Number of grains per gearhead	5-10	10-15	15-20	20-25	25-30	30-35	35-40	40-45
freqencies	2	27	52	118	57	27	13	4

Solution

Number of grains per gearhead Classes	Frequency F	Cumulative frequency Cf
5-10	2	2
10-15	27	29

15-20	52	81
20-25	118	190
25-30	57	256
30-35	27	283
35-40	13	296
40-45	4	300

$$\text{Median} = L + \frac{n_2 - cff}{f} \times i$$

$$\text{Median} = 30 + \frac{35 - 21}{10} \times 10$$

$$\text{Median} = 30 + \frac{14}{10} \times 10$$

$$= 30 + 14 = 44$$

Median = 44

2.9. MODE

In statistical data, the item with the highest frequency is known as mode.

2.9.1. Calculation of mode in an individual series

Example: find the mode of the following data relating to the weights of a sample of 10 experimental animals.

S.No.	1	2	3	4	5	6	7	8	9	10
Weight (kg)	10	11	10	12	12	11	9	8	11	11

Solution

Weight (kgs)	Number of animals
8	1
9	1
10	2
11	4
12	1
13	1

Since item 11 is the maximum number of items, i.e., 4 items, the modal value is 11.

Calculation of mode in continuous series

Mode is calculated by applying the following formula:

$$\text{Mode} = L_1 + \frac{f-f_1}{2f-f_1-f_2} (L_1 - L_2)$$

L_1 = lower frequency of mode = higher frequency of mode

f_1 = frequency of the class before the class of mode

f_2 = frequency of the class next to the class of mode

Example: calculate the mode of frequency in the given table.

Class range	3-6	6-9	9-12	12-15	15-18	18-21	21-24
Frequency	2	5	21	23	10	12	3

Solution The Above table shows that the maximum frequency is 23, which is in the class range 12-15.

Therefore, according to the formula

$$\text{Mode} = L_1 + \frac{f-f_1}{2f-f_1-f_2} (L_1 - L_2)$$

$$L_1 = 12$$

$$L_2 = 15$$

$$f = 23$$

$$f_1 = 21$$

$$f_2 = 10$$

$$\text{Mode} = 12 + \frac{23-21}{2(23)-21-10} (15-12)$$

$$\text{Mode} = 12 + \frac{2}{3} (15-12)$$

$$12 + \frac{2}{3} (15-12) = 12 + 0.6666666666666667 \times 3$$

$$\text{Mode} = 12 + 0.6666666666666667 \times 3$$

2.10. Standard Deviation

Standard deviation is the most commonly used absolute measure of dispersion. The concept of standard deviation was first introduced by Karl Pearson in 1893. Standard deviation is defined as the square root of the variance.

Standard deviation, $(x-\bar{x})^2 n-1$

OR

Standard deviation, $s = \sqrt{\frac{\sum (x - \bar{x})^2}{n-1}}$

Calculation of Standard Deviation:

For example, calculate the standard deviation from the following data

Variables (x) = 10, 13, 17, 22, 27, 30, 31, 32

Solution

Variable x	x^2
10	100
13	169
17	289
22	484
27	729
30	900
31	961
32	1024
$\sum x = 182$	$\sum x^2 = 4656$

$$s = \sqrt{\frac{\sum (x - \bar{x})^2}{n-1}}$$

$$s = \sqrt{4656 - \frac{182^2}{8-1}}$$

$$= \sqrt{4656 - \frac{331248}{7}}$$

$$s = \sqrt{4656 - 4140.5}$$

$$= 515.5 \ 7$$

$$s = 73.64 = 8.58$$

2.11. Review Exercises

1). Calculate the arithmetic mean from the data given in the table.

Number of leaves	5	10	15	20	25	30	35	40
Number of plants	6	5	9	4	3	6	4	3

2). Calculate the arithmetic mean from the following data.

Plant height cms	0-10	10-20	20-30	30-40	40-50	50-60
Number of varieties	5	10	25	30	20	10

3). Calculate the value of the median from the data recorded on the number of grains per earhead on 300 wheat earheads.

Number of grains per gearhead	5-10	10-15	15-20	20-25	25-30	30-35	35-40	40-45
freqencies	2	27	52	118	57	27	13	4

4). Calculate the median from the following data.

Classes	0-10	10-30	30-60	60-80	80-90	90-100
freqencies	5	16	30	12	6	1

5). Calculate the mode from the given data.

8, 10, 10, 9, 12, 7, 11, 11, 10

6). Calculate the mode from the following data.

Variable(x)	2	4	6	8	10	12	14	16	18	20
Frequency(y)	15	20	25	2	730	20	15	21	10	11

7). From the following data of the weight of 125 students, determine the modal weight.

Weight(lbs.)	40-50	50-60	60-70	70-80	80-90	90-100	100-110	110-120
Number of students	8	12	24	31	32	11	5	2

8). Calculate the standard deviation from the following data.

12, 25, 29, 27, 30, 32, 26

CHAPTER – 03

EVOLUTION, PLANT BREEDING, AND BIODIVERSITY: INTERCONNECTED THREADS IN THE TAPESTRY OF LIFE

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Abstract

Evolution, plant breeding, and biodiversity are inextricably linked, forming the intricate tapestry of life. Evolution, the driving force behind the diversification of life on Earth, has shaped the genetic makeup of plants, endowing them with remarkable traits and adaptations. Plant breeding, a human-directed process that harnesses the principles of evolution, has accelerated the development of crop varieties with enhanced yields, improved nutritional value, and resilience to environmental stresses. However, the pursuit of agricultural productivity has often come at the expense of biodiversity, leading to the loss of wild species and the erosion of genetic diversity within crops.

This paper explores the interconnectedness of evolution, plant breeding, and biodiversity, highlighting the delicate balance between maximizing agricultural output and preserving the rich tapestry of plant life. It emphasizes the importance of sustainable breeding practices that conserve genetic diversity and promote the development of ecologically sound agricultural systems.

Keywords: Evolution, plant breeding, biodiversity, crop improvement, genetic diversity, sustainable agriculture

3.1. Introduction

The intricate dance between evolution, plant breeding, and biodiversity weaves a complex tapestry that forms the fabric of life on Earth. Though diverse in their origins and influences, these interconnected threads contribute to ecosystems' resilience, adaptability, and sustainability. Evolution, plant breeding, and biodiversity are inextricably linked, forming the intricate tapestry of life on Earth. Evolution, the driving force behind the diversification of life on Earth, has shaped the genetic makeup of plants, endowing them with remarkable traits and adaptations. Plant breeding, a human-directed process that harnesses the principles of evolution, has accelerated the development of crop varieties with enhanced yields, improved nutritional value, and resilience to environmental stresses. However, the pursuit of agricultural productivity has often come at the expense of biodiversity, leading to the loss of wild species and the erosion of genetic diversity within crops (NCBI, 1989).

3.2. The Role of Evolution in Plant Diversity

Life on Earth emerged billions of years ago from a common ancestor, and through the process of evolution, it has diversified into a staggering array of species, each with its unique characteristics and adaptations. Plants play a crucial role in this tapestry of life, producing oxygen, providing food and shelter for countless organisms, and shaping the very ecosystems that sustain us.

Evolution has endowed plants with an incredible diversity of forms, from towering trees to delicate mosses and vibrantly flowering meadows to sun-drenched deserts. This remarkable diversity is a testament to the power of evolution, which has driven plants to adapt to a wide range of environmental conditions and ecological niches. At the heart of life's diversity lies the process of evolution. Over millions of years, living organisms have adapted and diversified through the relentless forces of natural selection, mutation, and genetic drift. As crucial components of terrestrial ecosystems, plants exemplify the beauty of evolutionary processes, showcasing a remarkable array of adaptations to diverse environmental niches (Nickrent DL et al., 2000; Allard, 2023).

3.3. Plant Breeding: Human-guided Evolution:

With the advent of agriculture, humans became active participants in the evolutionary narrative. Plant breeding emerged as a powerful tool, enabling the intentional selection and manipulation of plant genetic material to enhance desirable traits. From the earliest domestication of crops to modern biotechnological advancements, plant breeding has played a pivotal role in shaping the crops that sustain human populations.

However, this human-guided evolution has not been without consequences. The pursuit of high-yielding crops with specific traits has led to a narrowing of genetic diversity within cultivated species. This reduction in genetic variability raises concerns about the resilience of crops in the face of changing environmental conditions, pests, and diseases (Smýkal, P et al., 2018; Prabhu L. et al., 2012).

3.3.1. The History of Plant Breeding

While evolution has shaped plants over aeons, humans have also played a role in shaping plant diversity through the practice of plant breeding. Plant breeding, the deliberate manipulation of plant genomes to produce desired traits, has been practised for centuries, with early farmers unknowingly engaging in this process by selecting seeds from crops with desirable characteristics.

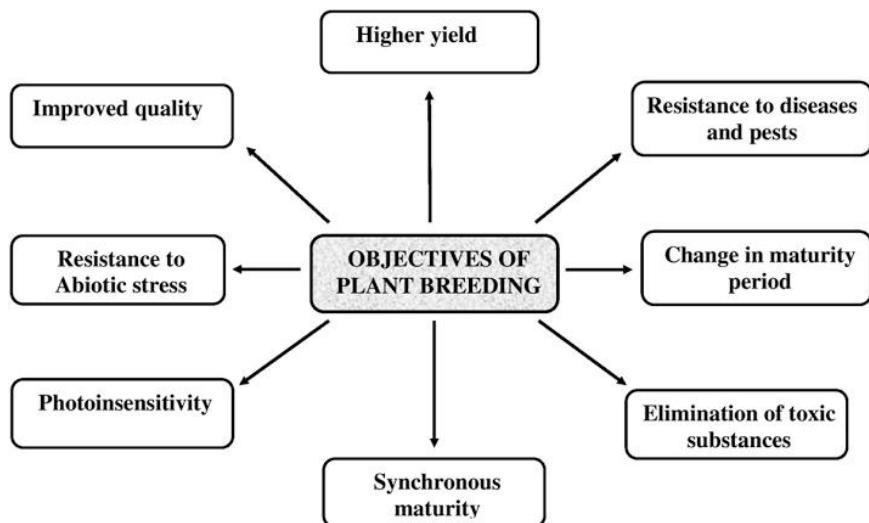
The formalization of plant breeding began in the 19th century with the groundbreaking work of Gregor Mendel, an Austrian monk who discovered the basic principles of inheritance. Mendel's experiments revealed the existence of discrete units of inheritance, now known as genes, which dictate the traits of an organism.

Building upon Mendel's discoveries, plant breeders have developed sophisticated techniques to manipulate plant genomes, including hybridization, selection, and genetic engineering. These techniques have enabled the development of crop varieties with significantly improved yields, enhanced nutritional value, and increased resistance to pests and diseases (Prabhu L. et al., 2012).

3.3.2. The Impact of Plant Breeding on Agriculture

Plant breeding has revolutionized agriculture, developing high-yielding crop varieties that have played a critical role in feeding the world's growing population. The Green Revolution, a period of rapid agricultural growth in the mid-20th century, was largely driven by the introduction of new crop varieties developed through plant breeding.

These advances have undoubtedly contributed to increased food production and improved food security. However, the focus on a few high-yielding crop varieties has also had unintended consequences, leading to the decline of traditional varieties and the loss of wild species. This erosion of genetic diversity has made crops more vulnerable to pests and diseases, threatening the stability of food production systems (Wu, F et al., 2004).



3.4. Biodiversity: A Measure of Life's Richness

Biodiversity, encompassing the variety of life at genetic, species, and ecosystem levels, is both a measure of ecological health and a source of resilience. Plant biodiversity, in particular, is essential for the stability and sustainability of ecosystems. Diverse plant communities contribute to nutrient cycling, soil health, and the provision of ecosystem services, such as pollination and pest control.

3.4.1. The Importance of Conserving Biodiversity

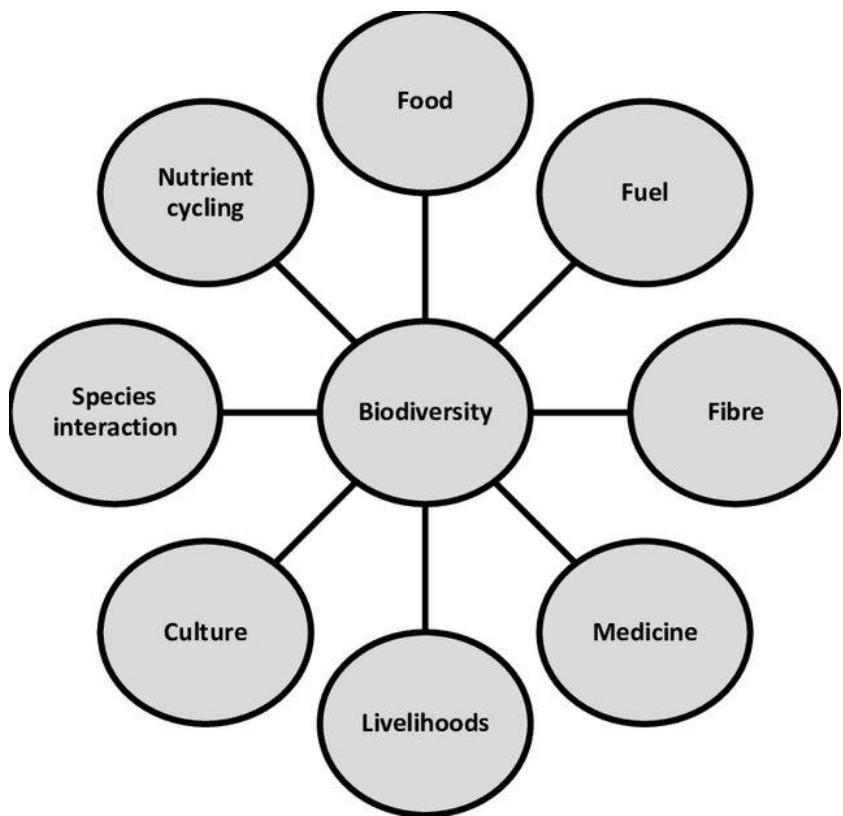
Biodiversity, the variety of life on Earth, is not merely a collection of species; it is the intricate web of life that supports the very foundations of our existence. From the microscopic organisms that cycle nutrients in the soil to the towering trees that filter the air we breathe, biodiversity plays a vital role in maintaining healthy ecosystems and ensuring the long-term sustainability of human society (IISD & FAO).

3.5. Biodiversity provides a multitude of benefits, including:

Ecosystem services: Ecosystems, the complex communities of living organisms and their physical environments provide a range of essential services that are critical for human well-being. These services include clean air and water, pollination of crops, protection from floods and erosion, and regulation of climate.

Genetic resources: Biodiversity is a reservoir of genetic resources that can be used to develop new crops, medicines, and other products. The diversity of genes within species and among species provides a vast pool of potential traits that can be harnessed for human benefit.

Cultural value: Biodiversity has cultural and spiritual significance for many people around the world. Traditional knowledge and practices related to biodiversity are often deeply intertwined with cultural identities and spiritual beliefs.



3.6. The Future of Sustainable Agriculture

Balancing the need for increased food production with the conservation of biodiversity is a critical challenge facing humanity. The future of sustainable agriculture lies in adopting practices that respect the delicate balance of the natural world.

Sustainable breeding practices, such as participatory breeding and conservation breeding, aim to conserve genetic diversity and develop crops that are adapted to local environments and resistant to pests and diseases. Agroecology, an approach to agriculture that mimics the natural processes of ecosystems, emphasizes the use of

diverse cropping systems, integrated pest management, and soil conservation practices. Protecting wild habitats, including forests, wetlands, and grasslands, is essential for conserving biodiversity and maintaining the ecological services that support human society (Bhawana Srivastava et al., 2023).

By adopting sustainable practices, we can ensure that agriculture continues to meet the needs of a growing population while preserving the rich tapestry of life on Earth.

3.7. The Interconnected Web

The intersection of evolution, plant breeding, and biodiversity forms a complex web where each thread influences the others. Human-driven plant breeding can inadvertently impact the genetic diversity of natural plant populations through gene flow and competition. Conversely, the genetic diversity present in natural plant populations serves as a valuable resource for future breeding efforts, offering a wellspring of traits for developing crops resilient to environmental challenges.

3.8. Preserving the Tapestry: Conservation and Sustainable Practices

In light of these interconnected relationships, conservation efforts become paramount. Preserving natural habitats, protecting endangered plant species, and promoting sustainable agricultural practices that consider ecological diversity is essential for maintaining the delicate balance between human needs and the preservation of biodiversity (Hashim Aslam Khan, 2023).

3.9. Conclusion

Evolution, plant breeding, and biodiversity are not isolated concepts but are deeply entwined, shaping the past, present, and future of life on Earth. Recognizing and respecting these interconnected threads in the tapestry of life is essential for fostering a harmonious coexistence between humans and the diverse array of plant life that sustains our planet. The key to sustainable agriculture, thriving ecosystems, and a healthier planet for future generations lies in this awareness.

3.10. References

1. National Research Council (US) Committee on Research Opportunities in Biology. Opportunities in Biology. Washington (DC): National Academies Press (US); 1989. 8, Evolution and Diversity. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK217815/>
2. Nickrent DL, Parkinson CL, Palmer JD, Duff RJ. Multigene phylogeny of land plants with special reference to bryophytes and the earliest land plants. *Mol Biol Evol*. 2000 Dec;17(12):1885-95. doi: 10.1093/oxfordjournals.molbev.a026290. PMID: 11110905.
3. <https://infinitylearn.com/surge/biology/evolution-of-life-on-earth/>
4. Allard, R.W.. "plant breeding". *Encyclopedia Britannica*, 22 May. 2023, <https://www.britannica.com/science/plant-breeding>. Accessed 25 November 2023.
5. Smýkal, P.; Nelson, M.N.; Berger, J.D.; Von Wettberg, E.J.B. The Impact of Genetic Changes during Crop Domestication. *Agronomy* 2018, 8, 119. <https://doi.org/10.3390/agronomy8070119>
6. Prabhu L. Pingali, Green Revolution: Impacts, limits, and the path ahead, Edited by William C. Clark, Harvard University, Cambridge, MA, July 31, 2012, 109 (31) 12302-12308, <https://doi.org/10.1073/pnas.091295310>
7. Wu, F., & P.Butz, W. (2004). The Green Revolution. In The Future of Genetically Modified Crops: Lessons from the Green Revolution (1st ed., pp. 11–38). RAND Corporation. <http://www.jstor.org/stable/10.7249/mg161rc.11>
8. <https://www.iisd.org/articles/deep-dive/biological-diversity-protecting-variety-life-earth>
9. <https://www.fao.org/3/i6583e/i6583e.pdf>
10. Bhawana Srivastava, P.B.Reddy, Recent Advances In Biodiversity Research, September 2023, Publisher: International Multidisciplinary

Research Foundation Ratna Prasad Multidisciplinary Research & Educational Society # 1-90, Near VTPS Main Gate, Ibrahimpatnam, Vijayawada, A.P., India ISBN: ISBN 978-93-90146-61-1

11. Hashim Aslam Khan, 2023, Preserving Life's Tapestry: The Crucial Role of Biodiversity in Ecological Balance, <https://medium.com/@raohashim27/preserving-lifes-tapestry-the-crucial-role-of-biodiversity-in-ecological-balance-b48d06e75f42>

CHAPTER - 04

PLANT BREEDING: EVOLUTION AND RECENT TRENDS IN ADVANCING CROP IMPROVEMENT

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Abstract

As a science and practice, plant breeding has undergone a remarkable evolution over centuries, transforming from traditional, empirical methods to a sophisticated, technology-driven discipline. This paper provides a comprehensive overview of the historical evolution of plant breeding, tracing its roots from early domestication to the advent of modern molecular techniques. This chapter explores emerging trends in plant breeding, such as the utilization of big data and artificial intelligence to analyze vast datasets for genotype-phenotype associations and the incorporation of climate-smart breeding strategies to address the challenges posed by climate change. Collaborative efforts between public and private sectors and international collaborations foster a more inclusive and holistic approach to plant breeding, ensuring the equitable distribution of improved varieties across diverse agroecological zones.

Keywords - Plant Breeding, crop improvement, artificial intelligence, for genotype-phenotype, climate-smart breeding

4.1.Introduction

Plant breeding, an age-old practice, has evolved over centuries into a sophisticated scientific discipline, constantly adapting to address the global demand for enhanced crop traits. From traditional methods of selection to the modern era of molecular precision, the journey of plant breeding is marked by transformative milestones. This paper delves into the historical evolution and recent trends that characterize the dynamic field of plant breeding.

The early roots of plant breeding can be traced back to the dawn of agriculture when humans began consciously selecting and cultivating plants with favourable characteristics. This empirical approach laid the foundation for more systematic breeding methods. The insights of Gregor Mendel in the 19th century introduced a genetic framework, paving the way for a more scientific understanding of heritability in plants. The mid-20th century saw a revolution in agricultural practices known as the Green Revolution, where the integration of modern breeding techniques and the introduction of high-yielding varieties significantly increased global food production (Borlaug, 2007).

In the contemporary era, plant breeding has embraced molecular tools and genomics to expedite the development of crops with desired traits. Marker-assisted selection, genomic selection, and gene editing technologies such as CRISPR-Cas9 have become integral to precision breeding, offering unprecedented control over the plant genome (Jinek et al., 2012; Varshney et al., 2018). These

techniques have been pivotal in addressing challenges such as pest resistance, disease tolerance, and improved nutritional content.

Advancements in data science and artificial intelligence are reshaping the landscape of plant breeding. Big data analytics enable breeders to navigate vast datasets, unravelling complex relationships between genetic markers and phenotypic traits. This integration of technology not only enhances the efficiency of breeding programs but also contributes to a deeper understanding of plant biology (Cobb et al., 2013).

Moreover, the recognition of climate change as a major threat to agriculture has led to the emergence of climate-smart breeding strategies. These strategies aim to develop crops that are resilient to changing environmental conditions, ensuring food security in the face of a warming planet (Tester and Langridge, 2010).

The collaborative efforts between the public and private sectors and international partnerships are crucial for the continued success of plant breeding on a global scale. Shared resources, knowledge, and technologies contribute to a more inclusive and sustainable approach to crop improvement (Kamoun et al., 2019).

As we explore plant breeding evolution and recent trends, it becomes evident that the intersection of tradition and innovation holds the key to addressing contemporary challenges in agriculture. By understanding the historical context and embracing cutting-edge technologies, we position ourselves to propel plant breeding into a future where sustainable and resilient crops contribute to global food security.

4.2. Historical evolution of plant breeding

Plant breeding has undergone a fascinating evolutionary journey, marked by the transition from empirical selection to sophisticated molecular techniques. This overview highlights key milestones in the historical evolution of plant breeding.

a. Early Domestication and Selection

The early stages of plant breeding involved selecting and cultivating plants with desirable traits, contributing to the domestication of crops (Harlan, 1992).

b. Gregor Mendel's Laws of Inheritance

Gregor Mendel's groundbreaking work laid the foundation for understanding the principles of inheritance, providing a theoretical basis for systematic breeding (Mendel, 1865).

c. Emergence of Systematic Breeding

The application of systematic breeding approaches became more prominent, especially with the development of hybrid maize varieties (Duvick, 2005).

d. Green Revolution and Modern Breeding Techniques

The Green Revolution of the mid-20th century marked a transformative period, introducing high-yielding varieties and modern breeding techniques (Borlaug, 2007; Khush, 2001).

e. Genomics and Molecular Tools in Plant Breeding

Advances in genomics revolutionized plant breeding, allowing for a deeper understanding of plant genomes and the development of molecular tools (Varshney et al., 2009).

f. Marker-Assisted Selection (MAS) and Genomic Selection

Marker-assisted selection and genomic selection became essential tools for accelerating the breeding process by targeting specific traits (Collard et al., 2005).

g. CRISPR-Cas9 Technology and Precision Breeding

The advent of CRISPR-Cas9 technology introduced unprecedented precision in modifying the plant genome, enabling targeted improvements (Hsu et al., 2017).

h. Integration of Big Data and Artificial Intelligence

Big data and artificial intelligence have transformed plant breeding by enabling efficient analysis of vast datasets to uncover genotype-phenotype associations (Cobb et al., 2013).

i. Climate-Smart Breeding Strategies

In response to climate change, breeding strategies focus on developing crops that are resilient to evolving environmental conditions (Tester et al., 2010).

j. Global Collaboration in Plant Breeding

International collaboration and partnerships between the public and private sectors play a pivotal role in advancing plant breeding on a global scale (Kamoun et al., 2015).

4.3. Emerging Trends in Plant Breeding: Utilization of Big Data and Artificial Intelligence for Genotype-Phenotype Associations

a. Big Data Analytics in Plant Breeding

Advances in high-throughput technologies generate large-scale datasets, providing a wealth of information on plant genomes and phenotypes. Big data analytics enable breeders to sift through this

information efficiently, uncovering complex relationships between genotypes and phenotypes (Cobb et al., 2013).

b. Artificial Intelligence (AI) in Genomic Selection

AI, particularly deep learning models, is increasingly applied for genomic selection. These models leverage multi-trait, multi-environment datasets to predict plant traits more accurately, facilitating the identification of superior genotypes (Montesinos-López et al., 2017).

c. Integration of Omics Data for Comprehensive Analysis

The integration of various omics data, including genomics, transcriptomics, and metabolomics, enables a comprehensive understanding of plant traits. Advanced analytical methods, including machine learning, extract valuable insights from these multi-dimensional datasets (Tardieu et al., 2017).

d. Predictive Breeding Models

Predictive breeding models utilize machine learning algorithms to forecast how specific genotypes will perform under various conditions, allowing breeders to make informed decisions for disease resistance and other complex traits (Poland et al., 2016).

e. High-Throughput Phenotyping Technologies

The integration of high-throughput phenotyping technologies, such as remote sensing and imaging techniques, provides vast datasets for plant performance in the field. Advanced analytics help uncover genotype-phenotype associations under diverse environmental conditions (Fiorani et al., 2013).

f. Crowdsourced Data and Collaborative Platforms

Crowdsourced data from multiple sources and collaborative platforms allow the pooling of diverse datasets, fostering a more comprehensive understanding of genotype-phenotype associations (Yu et al., 2018).

g. Real-Time Monitoring and Sensor Networks

Real-time monitoring and sensor networks, including advanced imaging techniques, provide continuous data streams. AI algorithms process this real-time information to enhance our understanding of how plants respond to dynamic environmental conditions (Li et al., 2014).

Integrating big data analytics and artificial intelligence into plant breeding practices represents a transformative shift, allowing for more precise and informed decision-making in developing crops with improved traits. These technologies are instrumental in unlocking the potential of large-scale datasets and accelerating plant breeding advancements.

4.4. Incorporation of Climate-Smart Breeding Strategies to Address the Challenges Posed by Climate Change

This review discusses the potential of agricultural biotechnology, including climate-smart breeding, as a tool to enhance crop adaptation and resilience in the face of climate variability (Varshney et al., 2011).

a. Climate-Resilient Crop Varieties

The paper emphasizes the importance of developing climate-resilient crop varieties and discusses statistical models for predicting crop yield responses to climate change (Lobell et al., 2010).

b. Drought Tolerance Breeding

This study focuses on genetic and genomic tools for improving drought tolerance in wheat, showcasing the application of advanced breeding strategies to address water scarcity challenges (Fleury et al., 2010).

c. Heat Stress Mitigation

Examining the impact of night time temperature on wheat, this study highlights the need to consider diurnal temperature variations in breeding strategies to enhance heat stress resilience (Prasad et al., 2008).

d. Multi-Trait Breeding for Climate Resilience

The paper emphasizes the importance of rapid breeding and varietal replacement as critical components in adapting cropping systems to climate change, emphasizing a multi-trait breeding approach (Atlin et al., 2017).

e. Integration of Remote Sensing and Genomic Tools

Exploring the integration of remote sensing with genomic tools, this study highlights the potential of field-based phenomics for accelerating plant genetics research, including climate-smart breeding (White et al., 2012).

f. Global Collaboration for Climate-Resilient Crops

The paper emphasizes the need for global collaboration to raise wheat yield potential and addresses climate change challenges, calling for coordinated efforts in breeding resilient crops (Reynolds et al., 2009).

The incorporation of climate-smart breeding strategies involves a multifaceted approach, considering traits such as drought tolerance, heat stress resilience, and the integration of advanced technologies to address the challenges posed by climate change. These references provide insights into different aspects of climate-smart breeding strategies and their application in the context of a changing climate.

4.5. References

1. Borlaug, N. E. (2007). Sixty-two years of fighting hunger: Personal recollections. *Euphytica*, 157(3), 287-297.
2. Jinek, M., Chylinski, K., Fonfara, I., Hauer, M., Doudna, J. A., & Charpentier, E. (2012). A programmable dual-RNA-guided DNA endonuclease in adaptive bacterial immunity. *Science*, 337(6096), 816-821.
3. Varshney, R. K., Nayak, S. N., May, G. D., & Jackson, S. A. (2018). Next-generation sequencing technologies and their implications for crop genetics and breeding. *Trends in biotechnology*, 26(9), 522-530.
4. Cobb, J. N., Declerck, G., Greenberg, A., Clark, R., & McCouch, S. (2013). Next-generation phenotyping: requirements and strategies for enhancing our understanding of genotype–phenotype relationships and its relevance to crop improvement. *Theoretical and Applied Genetics*, 126(4), 867-887.
5. Tester, M., & Langridge, P. (2010). Breeding technologies to increase crop production in a changing world. *Science*, 327(5967), 818-822.
6. Kamoun, S., Furzer, O., Jones, J. D., Judelson, H. S., Ali, G. S., Dalio, R. J., ... & Jones, R. W. (2019). The top 10 oomycete pathogens in molecular plant pathology. *Molecular Plant Pathology*, 20(6), 809-804.
7. Harlan, J. R. (1992). *Crops and Man*. American Society of Agronomy, Crop Science Society of America, Soil Science Society of America.
8. Mendel, G. (1865). Experiments on plant hybrids. *Verhandlungen des Naturforschenden Vereines in Brünn*, Bd, 4.

9. Duvick, D. N. (2005). The contribution of breeding to yield advances in maize (*Zea mays* L.). *Advances in Agronomy*, 86, 83-145.
10. Borlaug, N. E. (2007). Sixty-two years of fighting hunger: Personal recollections. *Euphytica*, 157(3), 287-297.
11. Khush, G. S. (2001). Green revolution: the way forward. *Nature Reviews Genetics*, 2(10), 815-822.
12. Varshney, R. K., Nayak, S. N., May, G. D., & Jackson, S. A. (2009). Next-generation sequencing technologies and their implications for crop genetics and breeding. *Trends in Biotechnology*, 27(9), 522-530.
13. Collard, B. C., Jahufer, M. Z., Brouwer, J. B., & Pang, E. C. (2005). An introduction to markers, quantitative trait loci (QTL) mapping and marker-assisted selection for crop improvement: The basic concepts. *Euphytica*, 142(1-2), 169-196.
14. Hsu, P. D., Lander, E. S., & Zhang, F. (2014). Development and applications of CRISPR-Cas9 for genome engineering. *Cell*, 157(6), 1262-1278.
15. Cobb, J. N., Declerck, G., Greenberg, A., Clark, R., & McCouch, S. (2013). Next-generation phenotyping: requirements and strategies for enhancing our understanding of genotype–phenotype relationships and its relevance to crop improvement. *Theoretical and Applied Genetics*, 126(4), 867-887.
16. Tester, M., & Langridge, P. (2010). Breeding technologies to increase crop production in a changing world. *Science*, 327(5967), 818-822.
17. Kamoun, S., Furzer, O., Jones, J. D., Judelson, H. S., Ali, G. S., Dalio, R. J., ... & Jones, R. W. (2015). The top 10 oomycete pathogens in molecular plant pathology. *Molecular Plant Pathology*, 16(4), 413-434.
18. Cobb, J. N., Declerck, G., Greenberg, A., Clark, R., & McCouch, S. (2013). Next-generation phenotyping: requirements and strategies for enhancing our understanding of genotype–phenotype relationships and its relevance to crop improvement. *Theoretical and Applied Genetics*, 126(4), 867-887.
19. Montesinos-López, O. A., Montesinos-López, A., Crossa, J., Gianola, D., & Hernández-Suárez, C. M. (2017). Multi-trait, multi-environment deep learning modeling for genomic-enabled prediction of plant traits. *Genes, Genomes, Genetics*, 7(5), 1571-1586.
20. Tardieu, F., Cabrera-Bosquet, L., Pridmore, T., & Bennett, M. (2017). Plant phenomics, from sensors to knowledge. *Current Biology*, 27(15), R770-R783.
21. Poland, J., & Rutkoski, J. (2016). Advances and challenges in genomic selection for disease resistance. *Annual Review of Phytopathology*, 54, 79-98.
22. Fiorani, F., & Schurr, U. (2013). Future scenarios for plant phenotyping. *Annual Review of Plant Biology*, 64, 267-291.
23. Yu, J., & Tiedemann, J. (2018). Integrating high-throughput phenotyping and genetic association analysis to dissect the genetic architecture of

- temporal salinity responses in rice. *G3: Genes, Genomes, Genetics*, 8(9), 2989-3001.
- 24. Li, L., Zhang, Q., Huang, D., & Yang, W. (2014). A review of imaging techniques for plant phenotyping. *Sensors*, 14(11), 20078-20111.
 - 25. Varshney, R. K., Bansal, K. C., Aggarwal, P. K., Datta, S. K., Craufurd, P. Q., & Bouman, B. A. M. (2011). Agricultural biotechnology for crop improvement in a variable climate: hope or hype? *Trends in Plant Science*, 16(7), 363-371.
 - 26. Lobell, D. B., & Burke, M. B. (2010). On the use of statistical models to predict crop yield responses to climate change. *Agricultural and Forest Meteorology*, 150(11), 1443-1452.
 - 27. Fleury, D., Jefferies, S., Kuchel, H., & Langridge, P. (2010). Genetic and genomic tools to improve drought tolerance in wheat. *Journal of Experimental Botany*, 61(12), 3211-3222.
 - 28. Prasad, P. V. V., Pisipati, S. R., Ristic, Z., Bukovnik, U., & Fritz, A. K. (2008). Impact of Nighttime Temperature on Physiology and Growth of Spring Wheat. *Crop Science*, 48(6), 2372-2380.
 - 29. Atlin, G. N., Cairns, J. E., & Das, B. (2017). Rapid breeding and varietal replacement are critical to adaptation of cropping systems in the developing world to climate change. *Global Food Security*, 12, 31-37.
 - 30. White, J. W., Andrade-Sanchez, P., Gore, M. A., Bronson, K. F., Coffelt, T. A., Conley, M. M., ... & Sharda, A. (2012). Field-based phenomics for plant genetics research. *Field Crops Research*, 133, 101-112.
 - 31. Reynolds, M., Foulkes, M. J., Slafer, G. A., Berry, P., Parry, M. A. J., & Snape, J. W. (2009). Raising yield potential in wheat. *Journal of Experimental Botany*, 60(7), 1899-1918.

CHAPTER - 05

BIOINFORMATICS IN PLANT GENOMICS FOR NEXT-GENERATION PLANT BREEDING

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Abstract

Bioinformatics is an interdisciplinary field of study that combines computer science, mathematics, and biology. In the era of remarkable advancements in omics technologies, bioinformatics' crucial position is becoming increasingly significant due to its basic support in characterizing the complex elements of biological capabilities. Moreover, methods powered by bioinformatics improve our understanding of stress responses, adaption mechanisms, and interactions between microbes and plants. Researchers can forecast phenotypic outcomes, decipher gene networks, and enhance breeding strategies for increased resistance,

yield, and nutritional content by utilizing big data analytics and machine learning algorithms. To effectively utilize bioinformatics' potential in plant genomics, it is imperative that breeders, bioinformaticians, and plant biologists work together. A new era of precision breeding with the potential to address global concerns in agriculture, food security, and sustainability is being ushered in by the collaboration between experimental data collection and computer analyses as we traverse the next-generation plant breeding period. The purposes of this chapter are to cover the following points: the application of plant breeding to bioinformatics, a bioinformatics approach to molecular information and plant breeding, agriculture's use of genomics and the significance of the genome after sequencing and tools for Genome Comparison.

Keywords: Bioinformatics, Plant Genomics, breeding strategies, genomic data, phenotypic outcomes, unravelling gene networks, and optimising breeding strategies for increased resilience, yield, and nutritional content.

5.1. Introduction

The word "bioinformatics" has gained popularity during the past few decades in all fields of biological science study. A more structured, computerized system was needed to gather, store, manage, and analyze the enormous amounts of biological data produced in research across all sectors due to the ongoing development and improvement of molecular biology and the resulting explosive expansion of biological information (Gomez-Casati et al., 2018).

Bioinformatics is an effective method for classifying and arranging biological data into databases, a recently developed multidisciplinary topic that has gained popularity in recent years (Zhang et al., 2013). A computer-based scientific subject, "bioinformatics", combines computer science, biology, and mathematics to create a unified discipline for analysing and interpreting datasets related to proteomics and genomics (Tiwari 2020).

Bioinformatics is an interdisciplinary branch of research that brings together computer science, mathematics, and biology. Because bioinformatics is fundamental to defining the intricate components of biological capabilities, its importance is growing in this era of amazing advances in omics technologies. Because of the basic breakthroughs that the multiple omics projects that are blooming internationally are providing in a number of agricultural sciences disciplines, bioinformatics is becoming more and more relevant in these fields of research. In general, bioinformatics is the multidisciplinary study of biological entities (genes, proteins, and physiological indices) through the application of informatics techniques, including statistical methods and a variety of algorithms. Processing physiologically complex data can be done explicitly with computer technologies, a typical practice in specialized databases like protein, nucleic acid, and custom functional databases (Chen et al., 2017).

Bioinformatics tools facilitate research on topics like sustainable agriculture, which reduces the cost of complex studies (Małyska et al., 2017).

The creation of software tools and algorithms as tools for biological data interpretation and the gathering and analysis of databases are Numerous biological fields depend heavily on bioinformatics because of its applications' ability to give a wide range of data, such as protein domains and structures, nucleotide and amino acid sequences, and expression patterns from different organisms (Tiwari 2020). Similarly, bioinformatics, which offers complete genetic information of different plant species to enable effective research into plants as biological resources for humans, has also been utilized by the field of plant biotechnology (Rhee et al., 20006).

Generating new plant varieties is the goal of plant breeding. This lengthy process starts with basic research and takes many years, requiring a substantial outlay of funds (Smith et al., 2022).

Crop breeding extensively uses genomics-assisted breeding since it is cost-effective and efficient. The field of genomics has promise for tracking molecular changes during development under a variety of settings, including variations in plant physiology, pathogen pressure, and environmental factors. It may also aid in understanding the structure and operation of biological systems (Nordin et al., 2022).

According to Esposito et al. (2016), samples for genomics research might be taken from the same or various individuals within the same species or from distinct species.

Furthermore, utilizing sequence conservation between species with tiny genomes that are easier to research and those with vast and complex genomes that include the majority of existing crop species comparative genomics enables the investigation of certain features among related plants.

5.2. Scope of Bioinformatics

During the initial developmental stages, Bioinformatics was considered just a mere tool for comparative and analytical studies; the scope of application of Bioinformatics in various fields was underestimated; only to the surprise of researchers and academicians, Bioinformatics has now become quintessential in every research area including Biotechnology, Evolutionary studies, Crop Improvement, Insect and Pest resistance, to improve nutritional quality, for development of drought-resistant varieties and many others. In fact, Bioinformatics has brought revolutionary changes in the way research is perceived where screening and analysis of thousands of samples is possible with relative ease compared to the traditional research methods, which rely on experimentation trial and error method. Bioinformatics helps analyze and interpret a large amount of data in less time and with improved efficiency and result output.

5.3. Bioinformatics Tools

i) Biological databases

Biological databases are a virtual space where data from various sectors of biological research are processed, arranged in a uniform manner and made available for research

references, functioning as a digital library. Each database contains molecular biology data concerning a particular species of plant or animal that are arranged in different files, containing different records representing the same information (Xiong, 2009). The purpose of the biological database is to create a digital library that is easy to manage, and the information can be retrieved from anywhere in the world besides storing it for a prolonged duration for easy retrieval of data. A user can easily retrieve the information stored in the database by a specific input into the database called ‘Value’. The specific algorithms used in the database help the user to retrieve the information based on his input. The entire process, termed ‘Query,’ displays the stored data in the record.

The database can be classified into primary and secondary databases. The Primary database comprises annotations of DNA, RNA and protein sequence, structure and expression profiles. The secondary database comprises analytical and comparative narration such as variants, mutations, chromosomal aberrations, and different motifs and protein domains that are stored in the primary database (Xiong, 2009). Though the main purpose of the database is data retrieval and accessibility, the information stored in the database also provides a better understanding of evolutionary linkages between different organisms based on their sequence similarities, shared motifs and domains.

Table 1: Classification of databases in the 2004 edition of the Molecular Biology Database Collection

Sr. No	Category	Number of Databases
1	Genomics	164
2	Protein sequences	87
3	Human/Vertebrate genomes	77
4	Human genes and diseases	77
5	Structures	64
6	Nucleotide sequences	59
7	Microarray/Gene expression	39
8	Metabolic and signalling pathways	33
9	RNA sequences	32
10	Proteomics	6
11	Others	6

(Source: D. Vassilev, J. Leunissen, A. Atanassov, A. Nenov & G. Dimov (2005) Application of Bioinformatics in Plant Breeding, Biotechnology & Biotechnological Equipment, 19:sup3, 139-152)

ii) Software and tools

With the development of technology, newer and modified tools have been made available for researchers and academicians to better understand the molecular dynamics of different biological molecules, including deciphering their structure, domains, motifs, and even their expression patterns have shed light into various metabolic pathways where biomolecules interact with other molecules and cause the effect in both plants and animals. Computer programs like BLAST, NCBI, Cluster Analysis tools, and ExPasy provide a platform to understand proteins' basic primary and quaternary structures. Certain other tools that provide a

basic understanding of the protein motifs and structure are provided in Table 2.

Table 2: A brief description of different tools for genome analysis, protein domain and structure prediction, protein-ligand interaction

Name	Method	Description	URL
IntFOLD	A unified interface for Tertiary structure prediction /3D modelling and model quality assessment, Domain prediction , Protein-Ligand binding residue prediction	Automated webserver and downloadable programs	https://www.reading.ac.uk/bioinf/IntFOLD/IntFOLD7_form.html
Phyre and Phyre2	Remote template detection, 3D modelling	Webserver with job manager, genome searching and other facilities	Phyre : http://www.sbg.bio.ic.ac.uk/phyre/html/ Phyre2 : http://www.sbg.bio.ic.ac.uk/phyre2/html/page.cgi?id=index
SWISS-MODEL	Local similarity/ fragment assembly	Automated webserver for protein structure homology-modeling	https://swissmodel.expasy.org/
BHAGEERATH-H	Combination of ab initio folding and homology methods	Protein tertiary structure predictions	http://www.scfbio-iitd.res.in/bhageerath/bhageerath_h.jsp
I-TASSER	Cluster analysis	Predicts protein 3D structure based on threading approach	https://zhanggroup.org/I-TASSER/

SCRATCH	Domain prediction	Protein structure and structural prediction server, provides evolutionary information	https://scratch.proteomics.ics.uci.edu/
PROTINFO	3D modelling tool	De novo protein structure prediction web server	http://protinfo.compbio.buffalo.edu/ppc/
ROBETTA	Protein structure and domain prediction	De novo Automated structure prediction analysis tool used to infer protein structural information	http://robetta.bakerlab.org/
3D-JIGSAW	3D modelling tool	Server to build three-dimensional model	http://bmm.cancerresearchuk.org/djigsaw/
3D-PSSM	3D modelling tool	Threading approach using 1D and 3D profiles coupled with secondary structure.	http://www.sbg.bio.ic.ac.uk/dpssm/index2.html
PSIPRED	Protein motifs analysis, Protein domain comparison	A combination of methods such as sequence alignment with structure based scoring and neural network based jury system to calculate final score for the alignment.	http://bioinf.cs.ucl.ac.uk/psipred/

5.4. Major Research Areas

Apart from the tools mentioned in Table 2 a plethora of information and data has been made available in public domains. The amount of information available in the present day is enriched with every aspect of systems biology, including DNA, RNA, Protein structure, their domains, their motifs, information about SNPs (Single Nucleotide Polymorphism), mutations, expression patterns and information of different small RNA molecules which are involved in the different metabolic pathway for upregulating or downregulating and many times silencing the gene altogether. The onus lies on the researcher/academician/observer to interpret the data and translate it into meaningful information that provides better output; hence, data interpretation is crucial.

The available data can be used in several fields of research and areas, such as sequence analysis.

5.5. Sequence analysis

The major challenge researchers faced was understanding the nucleotide sequence of a given set of genes in an organism. The advent of genome sequencing has provided the needed tool to decipher the hidden genetic code of different organisms, including the entire human genome sequence. The Human Genome Project, which began in the late 90s and advancement in the different sequencing methods throughout the decades has enabled the researcher to decipher the genetic codes and nucleotide sequences of not just humans but also of many other organisms, including model organisms like *Arabidopsis thaliana*, Zebra fish, Mice, Rice.

Moreover, the latest sequencing techniques have empowered researchers worldwide to sequence individual genes of different organisms and publish them in databases for the academic world through online databases like BLAST. The database contains gene sequences, coding sequences, non-coding sequences, mRNA sequences, translations of mRNA, and sequences of chromosomes, which can be used to identify the gene of interest based on individual research interests; it also enables to compare the different coding sequences, check the degree of sequence homology in different organisms and also help in designing probes or primers for molecular techniques such as PCR, DNA fingerprinting and a wide range of other methods used in different fields like Medicine, Pharmaceuticals, Agriculture, Biotechnology, Molecular diagnosis, Disease treatment, Crop improvement. Depending on the type of sequences to compare, there are different programs:

- i. **blastp** compares an amino acid query sequence against a protein sequence database
- ii. **blastn** compares a nucleotide query sequence against a nucleotide sequence database
- iii. **blastx** compares a nucleotide query sequence translated in all reading frames against a protein sequence database
- iv. **tblastn** compares a protein query sequence against a nucleotide sequence database dynamically translated in all reading frames

- v. **tblastx** compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

Sequence annotations include the comparison of mRNA sequences and DNA sequences, including the coding and non-coding sequences, which are important for rDNA technology and plant tissue culture. The database also provides information about junk genes, which constitute a major portion of the genomes of eukaryotic organisms, humans in particular, and their sequences, and it helps to understand their possible role in metabolism and molecular interactions, if any.

5.6. Analysis of Gene Expression

The research areas pertaining to gene expression incorporate several techniques including determining the gene activity by comparing the expression profile of mRNA at different time points using several techniques like microarray, expressed sequence tags (EST), serial analysis of gene expression (SAGE) tag sequencing, Massively parallel signature sequence (MPSS), RNAseq also referred to as Whole Transcriptome Shotgun Sequencing (WTSS) are all high throughput sequence analysis techniques that involve a certain degree of background noise/error which can be effectively handled by creating modified tools using bioinformatics that provide accurate information about the Gene expression profile in organisms.

5.7. Analysis of Gene Regulation

Gene regulation is one of the complex biochemical activities that involves a hormone or a peptide that interacts with a specific receptor on the cell surface and results in a complex cascade of switching on and off a different set of intermediate proteins or biomolecules, which, in turn, determine the extent of gene expression, either by upregulating or downregulating the gene expression. Here, bioinformatic tools can be used to understand the extent of interplay between the different molecules and the different motifs involved in the molecular pathway. For example, the Promoter sequences are of great importance, and the promoter motifs, such as the upstream and downstream regulatory elements, influence the extent of transcription of that particular mRNA; further, the small RNA termed as siRNA, miRNA, picoRNA and many other forms bind to certain motifs in the 3'UTR or 5'UTR of the mRNA and either upregulate or downregulate the protein expression. Bioinformatic tools help illuminate the different types of motifs in these biomolecules. Further comparison of microarray data helps to identify different gene expression profiles in a normal stage and the changes seen in the expression profile during a diseased condition to better understand the motifs or domains involved. Understanding the expression profile in a single cell helps to compare the difference in cell cycle regulation of a healthy cell and one with a diseased condition like cancer. Cluster analysis tools further help to understand the co-expression of different genes and their interactions. Examples of clustering algorithms applied in gene

clustering are k-means clustering, self-organizing maps (SOMs), hierarchical clustering, and consensus clustering methods such as the Bi-CoPaM.

5.8. Analysis of Protein Expression

Previously several techniques encompassing molecular analysis such as the RNA seq, upregulation and downregulation of genes, promoter sequence and motifs all played a central role in understanding the molecular dynamics in organisms, including plants which all come under the Transcriptional/Post-transcriptional events, present-day more importance is being given to Translational modifications, protein-protein interactions and several bioinformatics tools such as the MALDI-TOF, MS, Ion exchange chromatography, microarray have found more significance, since all the metabolic activities inside the cell and in a particular environment are due to proteins that interact with other proteins or biomolecules to bring in the subsequent change. Several tools have enabled us to identify and narrow down to a particular target protein or a gene or, in many cases, to a particular small RNA molecule that drives protein expression regulation, including the protein-protein interaction studies. Bioinformatic tools and databases are very much involved in understanding protein microarray and HT MS data; the former approach faces similar hurdles as those encountered with microarrays targeted at mRNA, while the latter involves the problem of comparing large amounts of mass data against predicted masses from protein sequence databases, besides the complicated

statistical analysis of samples where multiple, but incomplete peptides from each protein have been detected.

5.9. Advanced Image Analysis

Out of the several techniques involved in molecular biology, microscopy and imaging play a crucial role in understanding and documenting the molecular dynamics of a cell. Advanced techniques such as FACS, Fluorescent microscopy, Stereomicroscopes, SEM (Scanning Electron Microscope), and TEM (Transmission Electron Microscope) all find widespread application in Plant and Animal Research. Apart from high throughput screening, these modern-day instruments are upgraded to suit the end user directly by providing the user with a comparative analysis of different sets of genes as well as profiling different organisms through the available data in the databases. Microscopy aids in several studies, including

- high-throughput and high-fidelity quantification and sub-cellular localization (high-content screening, cytohistopathology, Bioimage informatics)
- morphometrics
- clinical image analysis and visualization
- behavioural observations from extended video recordings of laboratory animals
- Infrared measurements for metabolic activity determination
- Inferring clone overlaps in DNA mapping, e.g. the Sulston score

5.10. Application of Bioinformatics in Agriculture

Biological research throughout the world has been generating a huge amount of research data, which is safely stored in databases and can be assessed by individuals based on their research interests. Due to the ever-increasing demand for food grains by the increasing population and non-availability of expanding spaces, there is constant pressure on the researchers in Plant biology and Agriculture to constantly upgrade their knowledge and develop methods to not just raise the nutritional quality of the food grains but at the same time develop varieties for better adaptability in changing climatic conditions, disease resistance, drought tolerance, stress tolerance, salt tolerance, pest resistant, high yielding varieties that can be used for human consumption as well as fodder for farm animals to keep them healthy. This has led to extensive research focusing on developing different varieties through breeding programs that utilize the information available in the database to generate hybrid varieties either by plant breeding or through plant tissue culture and rDNA technology. This is where bioinformatics plays a crucial role, where all the data is stored in different databases that are easily accessible for research purposes.

5.11. Crop database

As already mentioned, databases prove to be vital in sharing information and safekeeping, and are also essential in research for gathering information about the different proteins in different crop plants, their genes, and RNA sequence in order to understand their systems biology and to incorporate a specific gene from one host to

other to develop a better variety. There have been databases exclusively designed for specific crops that serve a model organism, including *Arabidopsis thaliana* (Watercress) and *Oryza sativa* (Rice) (Proost et al. 2009). The database helps in comparative analysis between the model and non-model plants and in developing better quality crops.

Table 3: Examples of genomic databases related to crop improvement

Database Name	Web Link
Brachypodium database	http://www.brachypodium.org/
Brassica rapa genome database	http://brassicadb.org/
DNA Data Bank of Japan (DDBJ)	http://ddbj.sakura.ne.jp/
European bioinformatics institute, EnsEMBL plants	http://plants.ensembl.org/
European Molecular Biology Laboratory (EMBL) nucleotide sequence database	http://www.ebi.ac.uk/embl/
GenBank	http://www.ncbi.nlm.nih.gov/genbank/
Gramene	http://www.gramene.org/
Graingenes	http://wheat.pw.usda.gov/
International Crop Information System (ICIS)	http://www.icis.cgiar.org
International Nucleotide Sequence Database Collaboration (INSDC)	http://www.insdc.org/

Legume Information System (LIS)	http://www.comparative-legumes.org/
MaizeGDB	http://www.maizegdb.org/
Maize sequence database	http://www.maizesequence.org/
Oryzabase	http://www.shigen.nig.ac.jp/rice/oryzabase/
Panzea	http://www.panzea.org/
Phytozome	http://www.phytozome.net/
The Plant Ontology	http://www.plantontology.org/
Plaza	http://bioinformatics.psb.ugent.be/plaza/
Rice Genome Annotation Project	http://rice.plantbiology.msu.edu/
SSR Primer	http://flora.acpfg.com.au/ssrprimer2/
SSR taxonomy tree	http://appliedbioinformatics.com.au/projects/ssrtaxonomy/php/
SOL Genomics Network (SGN)	http://solgenomics.net/
SoyBase	http://soybase.org/
TAGdb	http://flora.acpfg.com.au/tagdb/
The Crop Expressed Sequence Tag database, CR-EST	http://pgrc.ipk-gatersleben.de/cr-est/
The Triticeae Repeat Sequence Database (TREP)	http://wheat.pw.usda.gov/ITMI/Repeats/
Wheat genome information	http://www.wheatgenome.info

(Source: Lai Kaitao, Michał T. Lorenc and David Edwards (2012) Genomic Databases for Crop Improvement, *Agronomy* 2012, 2, 62-73; doi:10.3390/agronomy2010062)

5.12. Pest Resistant Crop Variety

The information about the toxic protein present in *Bacillus thuringiensis*, is due to the gene CryIIB, CryIAC and other similar genes that produce crystal protein an inactive toxin that gets activated in the gut of Lepidoptera insect larvae gut (bulworm, corn worm) has enabled us to genetically engineer the gene in Cotton plants and Corn to create a GM crop Bt-Cotton and Bt-Corn which are resistant to the insect pest. A cluster of similar genes have to be

used to create genetically modified potato and maize that are termed as Bt crops, which can resist their insect pest and improve the farm output in each cycle. This has helped the farmers grow cotton and corn without fearing losing the crop to insect pests. Similarly, siRNA (Silencing RNA) has been found to be particularly effective against the soil nematode *Meloidogyne incognito*, which infests tobacco roots, rendering the crop useless. Yet another example is the characterization of 30 different genes that can be used to create Rice resistant to the bacteria *Xanthomonas oryzae*, which otherwise causes Bacterial blight of Rice.

Table 4: Examples of insect-resistant crops. Most are cry genes from *Bacillus thuringiensis*

Plant/Crop	Gene Introduced	Target Insects
Cotton	cryIA(a) cryIA(b) cryIA(c) cry IIA cryIEC Potato-inhibitor GNA	Lepidoptera Homoptera
Potato/Sweet potato	Cry3Aa Cry1A(c) Cowpea trypsin inhibitor GNA	Coleoptera Lepidoptera
Soybean	CryIA(b) cryIA(c)	Lepidoptera
Rice	cryIA(b) cryIA(c) Pin II cryIC sbk+sck	Lepidoptera
Maize	cry3BbI cryIAb cryI9c	Lepidoptera

Canola	cryIa(c)	Lepidoptera
Chickpea	cryIA(c) cry2Aa cryIA(c) + cryIA(b)	Lepidoptera
Tomato	cryIA (c) cryIA(b)	Lepidoptera
Alfalfa	Cry3a	Coleoptera

5.13. Improving the Nutritional quality of the crop.

Several earlier attempts have been made to constantly improve the nutritional quality of crops through Plant breeding; though successful, it is quite tedious, and all the required qualities may not be present in the improved variety. rDNA technology, on the other hand, has been very successful in improving nutritional quality since it involves directly identifying the gene of interest and inserting it into the host to get the desired results; here again, the database plays a crucial role in order to identify the nucleotide sequence of the desired gene and to amplify it and insert it into desired organisms. This approach has successfully improved nutritional quality; one such example is the Golden Rice. The gene for beta carotene, a precursor for the synthesis of Vitamin A, has been isolated and successfully incorporated in the Rice genome, thereby developing a new variety of rice which supplements the dietary vitamin A requirements and significantly reduces the occurrence of anaemia, night blindness due to deficiency of Vitamin A and iron (Paine et al. 2005). In other similar instances deleting the gene coding for an enzyme called polygalactouronidase responsible for the breakdown of cell wall in tomatoes has helped to

develop a new variety of tomato with an improved shelf life and can be stored for a comparatively longer duration rather than the usual 2-3 days, and yet in another variety insertion of a gene from fungi enables it to stay on the vine for longer duration and remains fresh (Fraser et al. 2009).

5.14. Drought Resistant/Stress tolerant varieties

Considerable progress has been made in developing crop varieties that are resistant to drought as well as tolerant to various degrees of stress, including Salinity, Alkalinity, and Heavy metal toxicity. Some of the crop varieties developed have also shown lower water consumption enabling to increase in the total land area under agricultural production, the land which was otherwise considered unfertile or waste (Wang et al. 2004). Here again, bioinformatics plays a crucial role in understanding the molecular mechanisms underlying the tolerance to various stress and drought conditions. Some of the recent varieties reported by (Gonzales et al. 2019) transgenic wheat transformed with mutated transcription factor (HaHB4) belonging to homeodomain-leucine zipper family (HD-Zip I) from *Helianthus annuus* (sunflower) had increased water use efficiency and yield. Similarly, transgenic wheat carrying a GmDREBI gene from soybean showed drought tolerance (Gao et al. 2005).

Table 5: List of abiotic-stress-tolerant transgenic plants

Target	Host	Gene	Tolerance	Trait improvement
<i>Arabidopsis thaliana</i>	<i>Triticum aestivum</i>	TNHX1, TVP1	Salt, drought	Improved shoot growth
<i>Arabidopsis thaliana</i>	<i>Suaeda salsa</i> , wheat, yeast, cotton	SsNHX1, SsNHX1, TaNHX1, ScNHX1	Salt, drought	High salt tolerance. Better growth
<i>Arabidopsis thaliana</i>	<i>Solanum lycopersicum</i>	LeNHX2	Salt	Better growth and high fresh weight
<i>Brassica juncea</i>	<i>Pennisitum glaucum</i>	pgNHX1	Salt	Normal plant growth at 300mmol/L NaCl
<i>Jatropha</i>	<i>Salicornia brachiata</i>	SbNHX1	Salt	Salt tolerance upto 200mmol/L of NaCl
<i>Madicago sativa</i>	<i>Triticum aestivum</i>	TaNHX2	Salt	High antiporters activity under 200mmol/L NaCl
<i>Nicotiana tabaccum</i>	<i>Gossipium hirsutum</i>	GhNHX1	Salt	About 100% increase in dry weight
<i>Petunia hybrida</i>	<i>Arabidopsis thaliana</i>	AtNHX1	Salt, drought	Improvement in shoot and root length
<i>Zea mays</i>	<i>Oryza sativa</i>	OsNHX1	Salt	Increased biomass production

5.15. Selected Internet resources for Plant Bioinformatics

- Arabidopsis Genome Initiative (AGI)
<http://genome-www.stanford.edu/Arabidopsis/AGI>
- Arabidopsis Genome Data Analysis, Cold Spring Harbor Laboratory

<http://nucleus.cshl.org/protarab>

- Plant Genome and Information Center, USDA

<http://www.nal.usda.gov/pgdic>

- UK Crop Plant Bioinformatics Network

<http://synteny.nott.ac.uk/agr/agr.html>

- The Institute for Genomic Research (TIGR) Database

<http://www.tigr.org>

- Arabidopsis Genome Center at the University of Pennsylvania

<http://genome.bio.upenn.edu/ATGCUP.html>

- The Genome Sequencing Center of Washington University in St Louis

<http://genome.wustl.edu/gsc>

- Grain Genes Database

<http://wheat.pw.usda.gov>

- Maize Genome Database

<http://www.agron.missouri.edu>

- Arabidopsis Internal Coding Exon Finder

<http://clio.cshl.org/genefinder/ARAB/arab.html>

- Net Plant Gene V2.0 Web Prediction Server

<http://www.cbs.dtu.dk/NetPlantGene.html>

5.16. Plant breeding

A crucial area where bioinformatics becomes an indispensable tool is plant breeding. Through breeding, new varieties have been developed with features like better nutritional quality, yield, and disease resistance. Bioinformatics has played a crucial role in all of this. It has been made possible by analysing the genome sequences and comparative studies done with relative ease

compared to the traditional methods, which were rather time-consuming. Omics data, including genomics and proteomics, provide a better understanding of the various plant responses in different conditions and help us develop varieties based on the changing climatic conditions. Here, omics have become an important tool for data comparison and future breeding and management systems for developing crops with better traits (Michelmore H.W 2003).

5.17. Soil Microbe Management

The interplay between different microbes and the plant is important to understand how the crops get affected by the presence or absence of a certain microbe in the soil. The transcriptome and genome analysis, along with the experimental evidence of the effect of microbes on plant growth, become crucial while setting up a crop. Some interactions between the microbe and the plant may not be fruitful, while others may be essential for the healthy development of the plant where the microbe would be crucial to the growth of the plant, such as *Rhizobium leguminosarum* a soil bacterium with the ability to fix atmospheric nitrogen becomes crucial in maintaining the nutrient balance of the soil and thereby its presence becomes essential to grow crops belonging to the family Leguminaceae. The omics data helps us better understand the molecular interactions that are crucial for certain kinds of crops and thereby helps us improve the crop yield by taking appropriate measures (Berg 2009, Schenk 2012).

5.18. Plant disease Management

It has been possible to understand the molecular interplay between the pathogen and the host through different protein-protein interaction studies and take corrective measures to try and eliminate several diseases and pests from the crop. Bioinformatics have many practical applications in current plant disease management with respect to the study of host-pathogen interactions and understanding the disease genetics and pathogenicity factor of a pathogen, which ultimately help in designing the best management options.

5.19. Future prospects

The incorporation of Bioinformatics in Plant and Animal science has gone a long way in order to improve the varieties with specific desired traits; however, one area that remains to be addressed is the constant evolution of lower microorganisms such as bacteria and fungi, which is not taken into account while creating new hybrid varieties which may become irrelevant if the pathogenic microbes evolve at much faster rates. Besides pathogens, the constantly changing climatic conditions are also a real threat, which at present is overseen, and we might face challenges sooner or later.

References

1. Chen C., Huang H., Wu C.H. Protein Bioinformatics Databases and Resources. *Methods Mol. Biol.* 2017;1558:3–39. doi: 10.1007/978-1-4939-6783-4_1.
2. Małyska A., Jacobi J. Plant breeding as the cornerstone of a sustainable bioeconomy. *New Biotechnol.* 2018;40:129–132. doi: 10.1016/j.nbt.2017.06.011.
3. Gomez-Casati DF, Busi MV, Barchiesi J, Peralta DA, Hedin N, Bhaduria V. Applications of bioinformatics to plant biotechnology. *Curr Issues Mol Biol.* 2018;27:89–104. doi: 10.21775/cimb.027.089.

4. Zhang SY, Liu SL. Bioinformatics. In: Maloy S, Hughes K, editors. Brenner's Encyclopedia of Genetics. 2. London: Academic Press; 2013.
5. Tiwari A, Singh P, Kumawat S. Applications of bioinformatics in plant breeding system. *Int J Curr Microbial App Sci*. 2020; 11:2825–2831.
6. Rhee SY, Dickerson J, Xu D. Bioinformatics and its applications in plant biology. *Annu Rev Plant Biol*. 2006; 57:335–360. doi: 10.1146/annurev.arplant.56.032604.144103.
7. Smith A.M. FAO should focus on real not nominal food prices. *Nature*. 2022; 602:33. doi: 10.1038/d41586-022-00221-4.
8. Nordin S.M., Zolkepli I.A., Rizal A.R.A., Tariq R., Mannan S., Ramayah T. Paving the way to paddy food security: A multigroup analysis of agricultural education on Circular Economy Adoption. *J. Clean. Prod.* 2022;375:134089. doi: 10.1016/j.jclepro.2022.134089.
9. Esposito A., Colantuono C., Ruggieri V., Chiusano M.L. Bioinformatics for agriculture in the Next-Generation sequencing era. *Chem. Biol. Technol. Agric.* 2016; 3:9. doi: 10.1186/s40538-016-0054-8.
10. Tiwari A, Singh P, and Kumawat S. Application of Bioinformatics in Plant Breeding System. *Int.J.Curr.Microbiol.App.Sci* (2020) Special Issue-11: 2825-2831
11. Proost S, Van Bel M, Sterck L, Billiau K, Van Parys T, Van de Peer Y, et al. PLAZA (2009). A comparative genomics resource to study gene and genome evolution in plants. *Plant Cell*, 21: 3718-3731.
12. Paine JA, Shipton CA, Chaggar S, Howells RM, Kennedy MJ, Vernon G, et al. (2005). Improving the nutritional value of Golden Rice through increased pro-vitamin A content. *Nat Biotechnol*. 23: 482-487.
13. Fraser PD, Enfissi E, Bramley PM. (2009). Genetic engineering of carotenoid formation in tomato fruit and the potential application of systems and synthetic biology approaches. *Archives of Biochemistry and Biophysics*, 483: 196-204.
14. Wang S, Wan C, Wang Y, Chen H, Zhou Z, Fu H et al. (2004). The characteristics of Na^{⁺, K^{⁺ and free proline distribution in several drought-resistant plants of the Alxa Desert, China. *Journal of arid environments*, 56: 525-539.}}
15. Gonzales F.F., Capella M., Ribichich K.K., Curin F., Giacomelli J.J., Ayala R., Watson G., Otegui M.E., Chan R.L. Field-grown transgenic wheat expressing the sunflower gene HaHB4 significantly outyields the wild type. *J.Exp.Bot*.2019; 1669-1681.
16. Gao.S., Xu H., Cheng X., Chen M., Xu Z., Li L., Ye X., Du L., Hao X., Ma Y. Improvement of wheat drought and salt tolerance by expression of a stress inducible transcription factor GmDREB of soyabean (*Glycine max*) Chin. *Sci. Bull.* 2005 ; 50:2714-2723.
17. Berg G. (2009). Plant-microbe interactions promoting plant growth and health: perspectives for controlled use of microorganisms in agriculture. *Appl Microbiol Biotechnol*, 84: 11-18
18. Michelmore, R. W. (2003). The impact zone: genomics and breeding for durable disease resistance. *Current Opinion in Plant Biology*6:397–404.

CHAPTER – 06

PLANT BREEDING HISTORY A REVIEW

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Abstract

Plant breeding has evolved from the genesis of human agriculture. The farmers did the plant breeding on farmland; with the advent of technologies, many of the methods have been adapted to breed plants in laboratories artificially. The Present paper elaborates on the history of the evolution of plant breeding over the centuries. The new technologies that have come to different countries to increase plant breeding techniques are discussed in the paper. Plant breeding ensures food security and sustainable development for the future years.

Keywords: Plant Breeding, Evolution of plant breeding, Green revolution, Plant Breeding Technologies

6.1. Introduction

The definition of "plant breeding" is "an art and science" that refers to the technology of enhancing a plant's genetic composition for human economic benefit. Plant breeding has developed since the beginning of agricultural humankind. Plant breeding can be divided into the following broad categories based on centuries of evolution:

The earliest known instance of plant breeding happened accidentally during the Early Domestication (Prehistoric Era) period when people moved from nomadic to settled agricultural communities. They chose plants with desired characteristics like bigger seeds or more appetising fruits for cultivation. This unintentional selection established the foundation for the domestication of numerous crops.

Ancient Selective Breeding (3000 BCE–1500 CE): As agriculture developed, people started to choose and cultivate plants for particular qualities deliberately. During this time, fundamental breeding methods like controlled pollination and seed selection from plants with desired traits were developed. The breeding of rice in Asia and wheat and barley in ancient Mesopotamia are two examples.

The Scientific Revolution (16th–18th centuries): An increasing number of people were interested in comprehending inheritance fundamentals during the Renaissance and the Scientific Revolution. Early scientists such as Gregor Mendel established the groundwork for modern genetics with their studies on the inheritance of traits in plants. Mendel's contributions, nevertheless, were not well known until the early 20th century.

The Green Revolution, which took place in the middle of the 20th century, marked a dramatic advancement in plant breeding. Using conventional breeding techniques, scientists like Norman Borlaug created high-yielding cultivars of staple crops like rice and wheat. In many regions of the world, these new cultivars were vital in boosting food production and averting starvation.

Biotechnology Advances (late 20th century to present): Plant breeding has undergone a revolutionary change with the introduction of molecular biology and biotechnology. Genetic engineering and marker-assisted selection are two methods that have made it possible to modify plant features more precisely. Genes from other organisms have been incorporated into genetically modified (GM) crops to improve characteristics like resistance to pests and drought.



Fig 1: Plant Breeding Impact

21st-century Genomic Era: Recent developments in genomics have expedited plant breeding even more. Thanks to advances in high-throughput sequencing technologies and bioinformatics tools, scientists can now analyse whole genomes, pinpoint genes linked to

particular traits, and use genomic selection to speed up the breeding process.

6.2. Review of literature

Lehnert, H., Berner, T., Lang, D., Beier, S., Stein, N., Himmelbach, A., Kilian, B., & Keilwagen, J. (2022) Ever since their wild ancestors were domesticated, breeding has gradually changed the genetic makeup of crop plants. It is hypothesised that elite wheat breeding pools have too little genetic diversity to meet upcoming challenges. On the other hand, wheat plant genetic resources (PGRs) kept in genebanks are important repositories of untapped genetic diversity. Therefore, identifying the useful allelic diversity present in PGRs and transferring it into elite breeding pools is crucial to ensuring breeding progress in the future. Here, an iSelect single nucleotide polymorphism (SNP) chip array and reduced-representation genomic sequencing were used to examine a varied collection of contemporary winter wheat cultivars and genebank accessions. These dataset analyses offered an in-depth understanding of the genetic diversity, population structure, origins of novel allelic diversity, and genomic areas impacted by breeding practices. 57 regions were genomic signatures of selection, and 827 were found to be private alleles linked only to genebank accessions. Initial evidence for putative traits associated with these identified regions came from the presence of large chromosomal modifications (i.e., introgressions from wheat wild relatives), quantitative trait loci, and known functional wheat genes. Ontology enrichment analysis results corroborated these conclusions. The results would

enable the targeted introduction of novel allelic diversity into elite wheat breeding pools, which would encourage future research and breeding. Statement of Significance: In order to meet future challenges and ensure breeding progress, genetic diversity stored in gene banks must be utilised. Here, we offer new insights into the genomic regions targeted by breeding efforts thus far as well as those associated with allelic diversity that are absent from elite wheat. These results provide insights into the genomic signatures of selection and how beneficial alleles can be introduced from plant genetic resources into elite breeding pools.

Ludvíková, M., & Griga, M. (2022). Summarises the pea (*Pisum sativum* L.) transformation's history, significant turning points, present situation, and future prospects as a tool for pea crop breeding. It provides an overview of the evolution of pea transformation, starting with the initial methodological trials and continuing through the full transformation and regeneration of genetically modified (GM) plants, transformation utilising the first genes of interest (GOI), and, most recently, targeted genome editing techniques. We demonstrate how the application of genetic engineering and contemporary biotechnological techniques to pea breeding could facilitate the production of new pea cultivars and expedite the breeding process. The emphasis is on genetic engineering, a great technique to add desirable genes that aren't found in the pea genome naturally to the gene pool. The various GOI that have been used for pea transformation to date, along with different methods of pea transformation, are discussed with the aim

of enhancing the traits of transgenic peas. Among the pea characteristics that have already been altered through genetic engineering are tolerance to herbicides and resistance to viruses, fungi, and insect pests. Utilising genetically modified peas also includes a crucial chapter on the creation of phytopharmaceuticals. We contrast the approaches to transgene introduction in peas and the use of various reporter and selective genes. There is a passing reference to the transformation of other major legumes, such as beans and soybeans. This paper summarises the impact of genetically modified (GM) peas on animal health, including feeding tests and allergenicity. It also assesses the possible advantages and disadvantages of pea modification and compares the current state of technology with the initial expectations of GM peas.

Cortés, A. J., & Du, H. (2023). Therefore, genetic mapping emerges as a crucial stage in the pre-breeding pipeline that finally yields candidate markers and genes for additional marker-guided applications, like parental screening, marker-assisted selection, and gene editing. Genetic mapping also makes the genetic architecture of important traits visible. He was more specific in imagining gene targets for biotic stresses; in particular, he suggested that allelic variation at the R genes, which are eventually prone to gene editing, could harness clubroot control techniques in cruciferous crops. As old as agriculture itself, human-driven plant selection established the groundwork for modern farming and plant breeding.

6.3. Plant Breeding & Technologies Across the Globe

These early breeding techniques resulted in a large yield increase in the United States in the early 20th century. Similar yield increases were not produced elsewhere until after World War II; the Green Revolution increased crop production in the developing world in the 1960s.

Beginning in the late 19th century, successful commercial plant breeding companies were established. John Garton founded Gartons Agricultural Plant Breeders in the 1890s in England. Garton was among the pioneers in commercialising novel cross-pollinated crop varieties. The cultivation of rice has been common in Vietnam ever since. (Khanh,2021)

India's approach to plant breeding has changed, but The Department of Agriculture was established by the Indian government in 1871. In Pusa, Bihar, the Imperial Agricultural Research Institute was founded (1905). Agricultural colleges were founded in Coimbatore, Kanpur, Pune, Sabour, and Llyalpur in 1805. In 1926, the Imperial Council of Agricultural Research was founded. Subsequently, the name was modified to Indian Council Agricultural Research First Agricultural University, which was founded in 1960 at Pantnagar, Nainital, Uttar Pradesh. Project ICAR's initial release of hybrid maize varieties in 1961 marked the start of coordinated efforts to improve the other crops.

Brazil, home to two of the world's most important biomes—the Amazon and the Atlantic Forest—and one of the largest agricultural areas, plays a critical role in global biodiversity and food security.

The study revealed a correlation between root morphology, P deficiency, seedling dry weight and two SNPs tagging the MAPKKK and AGC protein kinase genes. These findings suggest that the kinase proteins are involved in regulating root architecture and responses to P deficiency. In order to control the cotton boll weevil (CBW), Ribeiro et al. used RNA interference-mediated gene silencing to create cotton transgenic lines that expressed double-stranded RNA (dsRNA) for three potential target genes: vitellogenin (I AgVg i), ecdysis-triggering hormone receptor (I AgETHr i), and chitin synthase 2 (I AgCHS2 i). Modern omics techniques and developments in molecular and cell biology have made significant progress possible in plant sciences across the globe, leading to the creation of new instruments and enhanced resolution of already-existing ones. (dos Reis,2023). Over the past 50 years, Brazilian agriculture has expanded significantly. The establishment of EMBRAPA and other research institutes or state companies, with an emphasis on the production of new cultivars, the growth in graduate programmes, which qualified hundreds of professionals, and the adoption of the cultivar protection law, which encourages investments in seed production, are the main causes of this. The main objective of this work was to look back at the events that led the nation to become one of the biggest exporters of grains, fruits, and fibres globally from being an importer of these goods. Using a few agricultural products as examples, this article emphasises the major role that plant breeding has played recently. In addition, there are still many significant obstacles to be solved, and Brazilian

breeders' involvement will be essential to advancing agriculture in the years to come. (Ramalho, 2021).

Artificial intelligence (AI) has become a cutting-edge field that is widely used indoors for plant science and offers a great opportunity to shape modern crop breeding. Developments in crop phenomics, environmental, and other "omics" fields are opening doors to the detailed, intricate biological mechanisms that drive crop responses to environmental stressors. Plant scientists now have precise instruments to assess the crucial agronomic features for larger-sized germplasm at shorter time intervals during the early growth stages thanks to these "omics" approaches. The large amount of data and the intricate relationships it contains, however, make it difficult to comprehend the intricate processes underlying the genes that shape agronomic traits. AI offers enormous computational power as well as a plethora of new tools and breeding techniques. This review covers how artificial intelligence (AI) is being applied to modern breeding practices to help solve problems in high-throughput phenotyping and gene functional analysis. It will also discuss how these developments are opening up new possibilities for breeding in the future and how environmental data can be widely used in breeding.

Furthermore, the best use of high-throughput field phenotyping, genomics, and enviromics is hampered by the enormous challenge of linking genotype to phenotype in today's breeding methods. This review, we go into detail about why artificial intelligence (AI) will be the tool of choice for improving the accuracy of high-throughput

crop phenotyping, genotyping, and environmental typing data. We also look at the emerging strategies and difficulties surrounding the integration of multiomics big computing data. Thus, quick gene identification may be possible with the combination of AI and "omics" technologies, which could ultimately speed up agricultural improvement initiatives. (Khan & others, 2022).

Fig 2: Revolution of Plant Breeding

Four Revolutions of Plant Breeding

Selective Breeding	Mutation Breeding	Transgenic Breeding	Genome Editing
Thousands of years	Since 1920s	Since 1980s	Since 2000s
Desired gene is incorporated along with many other genes, which then have to be bred out	Desired mutation is incorporated along with many other random mutations, which may need to be bred out	Only the desired gene is incorporated, but randomly inserted	Wider range of genetic changes achievable, potentially in all crop species
Random, slow, crossing only works within species	Random, unpredictable, but relatively fast	Random insertion, inserts foreign genes	Precise, fast, leaves no trace

While addressing shortcomings of the Green Revolution, new plant breeding technologies (NPBTs) offer large potential for sustainable agricultural development and food security, including genetically modified and gene-edited crops. This article examines the potential, dangers, and real-world effects of NPBTs. There is also a discussion of regulatory issues. Exciting science and some obvious benefits are already apparent, but excessive regulation and misunderstandings by the general public could prevent NPBTs from being developed and used effectively. While overregulation is most noticeable in

Europe, it also impacts developing nations in Asia and Africa, which stand to gain the most from NPBTs. Reforms to regulations and a public discourse grounded in science are necessary. (Qaim, M., 2020).

6.4. Conclusion

Plant breeding produces a very high return on investment. Such investments remain centrepieces for meeting the challenges in any region. Importance must be given to future breeding priorities for each crop, the actors involved, and the importance of dissemination and farmer adoption mechanisms, and concludes with some policy recommendations. Increasing plant breeding across the nations would ensure food security for the world as the people taking up agriculture, and the non-availability of land are becoming major concerns over the years to come.

6.5. References

1. Khanh, T. D., Duong, V. X., Nguyen, P. C., Xuan, T. D., Trung, N. T., Trung, K. H., Gioi, D. H., et al. (2021). Rice Breeding in Vietnam: Retrospects, Challenges and Prospects. *Agriculture*, 11(5), 397. MDPI AG. Retrieved from <http://dx.doi.org/10.3390/agriculture11050397>
2. Lehnert, H., Berner, T., Lang, D., Beier, S., Stein, N., Himmelbach, A., Kilian, B., & Keilwagen, J. (2022). Insights into breeding history, hotspot regions of selection, and untapped allelic diversity for bread wheat breeding. *Plant Journal*, 112(4), 897–918. <https://doi.org/10.1111/tpj.15952>
3. LUDVÍKOVÁ, M., & GRIGA, M. (2022). Pea transformation: History, current status and challenges. *Czech Journal of Genetics & Plant Breeding*, 58(3), 127–161. <https://doi.org/10.17221/24/2022-CJGPB>
4. Cortés, A. J., & Du, H. (2023). Molecular Genetics Enhances Plant Breeding. *International Journal of Molecular Sciences*, 24(12), 9977. <https://doi.org/10.3390/ijms24129977>
5. dos Reis, P. A. B., Magalhaes, J. V., Miller, R. N. G., & Fontes, E. P. B. (2023). State-of-the-Art Molecular Plant Sciences in Brazil. *International Journal of Molecular Sciences*, 24(10), 8909. <https://doi.org/10.3390/ijms24108909>

6. Qaim, M. (2020). Role of New Plant Breeding Technologies for Food Security and Sustainable Agricultural Development. *Applied Economic Perspectives & Policy*, 42(2), 129–150. <https://doi.org/10.1002/aepp.13044>
7. Morgante M, Salamini F (2003) From plant genomics to breeding practice. *Curr Opin Biotechnol* 14 214–219
8. Ramalho, M. A. P., Marques, T. L., & do Carmo Lemos, R. (2021). Plant breeding in Brazil: Retrospective of the past 50 years. *Crop Breeding & Applied Biotechnology*, 21, 1–11. <https://doi.org/10.1590/1984-70332021v21Sa16>
9. Evenson, R.E., and D. Gollin. 2003. Assessing the Impact of the Green Revolution, 1960–2000. *Science* 300 : 758 – 762
10. Khan, M. H. U., Wang, S., Wang, J., Ahmar, S., Saeed, S., Khan, S. U., Xu, X., et al. (2022). Applications of Artificial Intelligence in Climate-Resilient Smart-Crop Breeding. *International Journal of Molecular Sciences*, 23(19), 11156. MDPI AG. Retrieved from <http://dx.doi.org/10.3390/ijms231911156>
11. Sharma HC, Crouch JH, Sharma KK, Seetharama N, Hash CT (2002) Applications of biotechnology for crop improvement: prospects and constraints. *Plant Sci* 163 381–395

CHAPTER - 07

RESEARCH PROGRESS OF PLANT CYTOGENETICS

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Abstract

Cytogenetic methods are crucial for assessing the initial genetic consequences following mutagenesis therapy in a timely manner. They are time-consuming and labour-intensive but necessary for the studies of genotoxic and cytotoxic effects in mutagenesis and environmental monitoring. Plant genotoxicity standard laboratory testing has historically included conventional cytogenetic studies. The micronucleus test is one technique that is particularly important for studying genotoxicity in plants. Nowadays, chromosomal abnormalities can be detected using cytogenetic techniques that go beyond traditional cytogenetics, and they have received substantial support from the rapid advancement of molecular biology as well as

greatly enhanced techniques for microscopic inspection and assessment. Different methods have made it possible to comprehend the mechanisms behind micronuclei's creation, shape, and genetic activity in recent years. There are a lot of studies on this subject in humans and animals, but there is a dearth of information regarding plants. This article gives an extensive summary of the state of our understanding of plant micronuclei properties. We focus on the impact of recent modern developments on our knowledge of plant cell micronuclei. We discuss the most recent mutagenesis applications of the micronucleus test together with the current advancements and evaluate the environmental situation.

Keywords: chromosome aberrations, cytogenetics, DNA damage, micronuclei, mutagenesis

7.1. Introduction

The field of genetics, cytology, and cell biology, known as cytogenetics, examines nuclear genomes at the chromosome level. In the domains of mutagenesis, genotoxicity investigations, and basic plant cell biology, cytogenetics makes the chromosome a significant target. Conventional cytogenetic techniques were and are widely employed. Plant genome structure, dynamics, and evolution are benefited by modern cytogenetic technologies, which use sophisticated microscopy and imaging techniques to advance the analysis of epigenetic DNA and histone changes as well as DNA damage utilizing fluorescent antibodies. Additionally, they have aided in the thorough assessment of the impacts of certain mutagens, such as micronuclei (MN), on the plant genome that manifests as

chromosome abnormalities. Mutagens alter the DNA molecule's structure, resulting in double-strand breaks (DSBs) that generate MN. There is DNA loss when MN is eliminated. Numerous physical, chemical, and environmental mutagenic conditions can lead to the formation of micronuclei. The widely used micronucleus test is based on an analysis of their frequency. We present a thorough summary of the state of the art regarding MN properties in plants. Critical scientific issues are the main topic of this paper: Is the distribution of DNA damage that resulted in the production of micronuclei random, where do plant micronuclei come from, do epigenetic mechanisms have a role in the development of micronuclei, how could chromatin's genetic activity be involved in the creation of micronuclei.

Plant chromosomal handling, structure, behaviour, and manipulation advanced throughout the years 1996–1997. Protocols for flow sorting, microdissection, and microcloning were improved. A variety of DNA sequences were mapped at a resolution of a few kilobases using fibre FISH. There have been reports of over 400 wheat deletion stocks, and it has been shown that telomeric sequence addition made *de novo* can repair broken chromosomes. Sequences of centromeric DNA were discovered. It was shown how telomeric ends function in pairing. Mitosis may be hampered by chromosomal arms that appear abnormally lengthy. Notable were novel events and the promise of wide hybrids for genomic study (Bikrarn et al., 1998).

The study of the composition and operation of plant chromosomes is the main focus of the field of plant cytogenetics. DNA and proteins combine to form thread-like structures called chromosomes, which house genetic material. Scientists can investigate many facets of plant genetics, evolution, and breeding with the aid of an understanding of plant cytogenetics. The main focuses of plant cytogenetics are as follows:

1. Analyzing the quantity, size, and form of chromosomes in plant cells; this includes looking at karyotypes, which are pictures of every chromosome in a cell.
2. Chromosomal Aberrations: Examining anomalies or modifications to chromosomal structure. This can include changes that affect plants' growth and operation, including deletions, duplications, translocations, and inversions.
3. Polyploidy: the study of plants, or polyploids, that have several sets of chromosomes. Plants frequently exhibit polyploidy, which can substantially impact their appearance, physiology, and adaptation.
3. Genome mapping: identifying the precise positions on chromosomes of genes and other DNA sequences. Knowing this information is essential to comprehending the inheritance and expression of genes.
4. Cytogenetic Techniques: Using a variety of lab methods, including fluorescence in situ hybridization (FISH), karyotyping, and molecular markers, to examine and modify plant chromosomes.
5. Evolutionary Studies: Examining how plant chromosomes and genomes have changed over time. The cytogenetics of several plant species can be compared to assist scientists in determining the evolutionary links among them.
6. Breeding Programs: To create

new varieties with desired features, plant breeding programs make use of cytogenetic expertise. Breeders can choose and develop new plant types more intelligently when they are aware of the chromosomal basis of features.

Our knowledge of plant biology, evolution, and genetics has advanced significantly thanks to the field of plant cytogenetics. Additionally, by assisting in the creation of crops with enhanced qualities like disease resistance, yield, and nutritional content, it has useful uses in agriculture.

7.2. Chromosome Structure and Function

In order to better understand the genetic basis of plant features and to aid in plant breeding and evolutionary research, the area of plant cytogenetics investigates the structure and function of plant chromosomes. Technological developments in cytogenetics are still adding to our understanding of plant genomes and their useful applications in biology and agriculture. Scientists were examining how different plant species' chromosomes are arranged and function.

Developments in molecular methods, such as genomic sequencing and fluorescence in situ hybridization (FISH), were advancing our knowledge of chromosomal shape and function (Daniel Scholes 2012).

7.3. Polyploidy and Genome Evolution

Plant cytogenetics focuses exclusively on the chromosomes of plants. Cytogenetics is the study of chromosomal structure and function. It entails analyzing their quantity, composition, and role as

well as how these elements affect plants' growth, development, and evolution. In plant cytogenetics, methods including karyotyping, fluorescent in situ hybridization (FISH), and molecular markers are frequently employed to examine chromosomal properties. Plants frequently have numerous sets of chromosomes, a condition known as polyploidy. Scientists studying plant cytogenetics were investigating how polyploidy affected the evolution and adaptability of genomes. Comparative cytogenetics allows researchers to track the evolutionary links between various plant species through the analysis of chromosome structure (Pamela S Soltis et al., 2015).

7.4. Molecular Markers and Mapping

Plant cytogenetics and molecular markers are essential tools to comprehend and modify plant genetics for ecological, agricultural, and conservation goals. They expand our knowledge of plant biology generally and in the areas of agricultural improvement and plant breeding. The advent of genetic maps and molecular markers made the identification and mapping of certain genes on plant chromosomes easier. Crop improvement initiatives benefited from the integration of cytogenetic techniques with molecular tools for the fine-scale mapping of significant features (Keith L Adams et al., 2005; Huai-Yang Xiong et al., 2005).

7.5. Genomic Variation and Biodiversity

The biodiversity of living things is greatly influenced by genomic variation. The diversity of species, habitats, and genetic variation within species are all included in the term "biodiversity," which describes the variety of life on Earth. Genomic variation is the term

used to describe variations in DNA sequences between individuals within a population or between populations of the same species. The following are some important links between biodiversity and genetic variation.

7.6. Genetic Diversity within Species

Individuals within a species display genetic variety as a result of variations in their DNA sequences. Processes, including genetic recombination during reproduction, gene transfer between populations, and mutations, give rise to this variety. A population cannot adapt to changing conditions, fend off diseases, or handle other ecological difficulties without genetic diversity (Debbie et al., 2010).

7.7. Adaptation and Evolution

Natural selection and evolution are based on genomic variation. Individuals with qualities beneficial in a changing environment are more likely to be produced by populations with higher genetic diversity. Natural selection gradually affects these differences, resulting in the evolution of populations and species with characteristics that improve their chances of surviving and procreating.

7.8. Ecosystem Functioning

Genetic biodiversity plays a role in the functioning of ecosystems. Within an ecosystem, different species have distinct functions to play, and the species' genetic diversity influences these roles. Ecosystem resilience is also impacted by genetic variety within

species, as it gives populations the adaptability they need to react to changes in their surroundings.

7.9. Conservation

Preserving genetic diversity is essential to the preservation of threatened species. In small populations, a decrease in genetic variety might increase the danger of extinction through inbreeding. In order to secure the long-term survival of populations, conservation efforts frequently concentrate on maintaining not only the species but also the genetic variety within them (Klein, William 2007).

7.10. Human Impact

Climate change, pollution, and habitat degradation are examples of human actions that can have a negative effect on biodiversity and genetic variation. For example, small populations cut off by habitat fragmentation may lose genetic diversity. To lessen the negative effects of human activity on biodiversity, conservation efforts must take into account both the maintenance of genetic diversity and the preservation of habitats. A key element of biodiversity, genomic variation affects populations' and ecosystems' resilience, evolution, and adaptability. The preservation and sustainable management of biological resources on Earth depend on our ability to comprehend and protect genetic diversity.

7.11. Plant cytogenetics and Technological Advances

Technological developments in imaging and computer analysis improved cytogenetic research's effectiveness and precision.

Plant cytogenetics was increasingly using high-throughput sequencing technology, which made it possible to analyze complete plant genomes in detail.

7.12. Chromosome Structure and Function

In cytogenetic studies, the quantity, makeup, and activity of chromosomes in plants are frequently investigated. Knowing the structure of chromosomes is essential to identifying the genetic composition of plants.

7.13. Karyotyping

Chromosomes are arranged and categorized according to their size, shape, and other attributes during karyotyping. Researchers can find chromosomal abnormalities with the aid of this approach.

7.14. Fluorescence in Situ Hybridization (FISH)

A molecular cytogenetic method called FISH is used to see particular DNA sequences on chromosomes. FISH can be used in plant cytogenetics to map genes and detect chromosomal rearrangements.

7.15. Molecular Markers

Plant genes are mapped using molecular markers such as SNPs (single nucleotide polymorphisms) and SSRs (simple sequence repeats). These markers are used to research genetic diversity. These markers facilitate the identification of genes on chromosomes and the study of trait inheritance.

7.16. Technological Advances

a. Next-Generation Sequencing (NGS)

High-throughput sequencing of complete plant genomes, which has transformed genomics, has been made possible by NGS technologies. This has made it easier to identify genes and comprehend how they work.

b. CRISPR-Cas9 Technology

Researchers can precisely alter individual genes in plants and learn more about their roles thanks to the CRISPR-Cas9 system. Genetically modified crops have developed faster because to this technology.

c. Bioinformatics

Large-scale genomic data produced by NGS technology can be handled and analyzed with great help from bioinformatics advances. Tools for bioinformatics help with functional element discovery, comparative genomics, and genome annotation.

d. High-Resolution Imaging

Plant chromosomes and cellular components may be imaged at great resolution thanks to advancements in microscopy techniques. This advances our knowledge of plant cell biology and facilitates in-depth cytogenetic investigations.

e. Omics Technologies

A comprehensive understanding of plant biology is possible through the integration of diverse omics technologies, including transcriptomics, proteomics, and genomes. These methods aid in the deciphering of intricate regulatory networks and the comprehension

of plant reactions to external stimuli. The subject of plant cytogenetics and technology is ever-evolving; therefore, it's vital to remember that progress may have been made since my last update. Scholars persistently investigate novel approaches and innovations to enhance our comprehension of plant genetics and augment agricultural and environmental uses.

7.17. Plant Cytogenetics and Applications in Plant Breeding

Plant cytogenetics, which offers information on genetic diversity, chromosomal rearrangements, and possible sources of resistance to illnesses and environmental pressures, was crucial in the development of plant breeding programs. Because it offers important insights into plants' chromosomal makeup and genetic makeup, cytogenetics plays a critical role in plant breeding. Cytogenetics plays the following important functions in plant breeding:

Chromosome Number and Structure Analysis:

Cytogenetic methods can ascertain the quantity and organization of chromosomes in a plant species. Knowing this information is essential to comprehending various plant species' genetic potential and interplant compatibility.

a. Inducing Polyploidy

Cytogenetics plays a crucial role in the research and induction of polyploidy, which is the state in which an organism possesses more than one pair of chromosomes. Polyploid plants are valuable for plant breeding because they frequently display increased vigour, disease resistance, and other desired features.

b. Chromosomal Aberration Identification

Chromosomal abnormalities, including deletions, duplications, and translocations, can be found via cytogenetic research. Finding these anomalies is essential to comprehending the genetic stability and possible problems in plant breeding initiatives.

c. Mapping Genes and Markers

Molecular markers linked to desired qualities can be identified, and gene mapping is aided by cytogenetics. By using marker-assisted selection, plant breeders can increase the breeding process's efficiency with this information.

d. Genomic in Situ Hybridization (GISH)

It is a cytogenetic method used to examine the genetic makeup of hybrid plants, particularly those with distant relatives. Understanding how particular features from wild relatives are introduced into domesticated species is made possible by this.

e. Karyotype Analysis

Karyotypes are visual representations of an organism's chromosomes that are created with the aid of cytogenetic analysis. A snapshot of the genome's structure is provided by karyotyping, which facilitates the detection of structural rearrangements and chromosomal abnormalities.

f. Choice of Parental Lines

By offering details on chromosomal stability and compatibility, cytogenetics assists in the choice of parental lines for breeding projects. This guarantees that the selected parents have the genetic makeup necessary to produce desired children.

g. Assessment of Genetic Diversity

Research on cytogenetics plays a role in determining how diverse a plant species' genome is. Developing breeding strategies to improve qualities like tolerance to diseases, pests, and environmental stress requires understanding genetic diversity.

h. Hybridization Studies

Cytogenetics is used to investigate the hybridization process to make sure that the generated hybrids have the appropriate chromosomal makeup. This is essential for crossbreeding efforts in plant development to be successful.

7.18. Quality Control in Breeding Programs

Plant varieties established through selective breeding can have their genetic stability and purity guaranteed thanks to the use of cytogenetic methods in quality control procedures. Cytogenetics is a fundamental tool in plant breeding that helps create better, genetically stable cultivars by supplying vital information about the genetic composition of plants.

7.19. Plant Cytogenetics and Conservation and Restoration

Cytogenetic research has been useful in the conservation of endangered plant species by shedding light on their reproductive strategies and genetic diversity.

Understanding plant population cytogenetics in damaged settings helped restore ecology. Check out recent scientific papers, conference proceedings, and reliable internet resources to obtain the most recent information on plant cytogenetics. Updates on the field's advancement are probably going to come from scientists and

organizations working in plant genetics and genomics. Plant cytogenetics contributes significantly to conservation and restoration endeavours by offering essential insights on plant communities' genetic composition, variability, and stability. In these situations, plant cytogenetics plays the following important responsibilities:

1. Genetic Diversity Assessment

Genetic diversity within and between plant populations is evaluated with cytogenetic research. For conservation efforts to be successful, it is crucial to comprehend genetic variety since it sheds light on a species' flexibility and resilience.

2. Identification of Endangered or Threatened Species

Plant species that are endangered or threatened can be identified and described using cytogenetic techniques. This data is essential for setting priorities for conservation initiatives and efficiently allocating resources.

3. Population Dynamics and Structure

Cytogenetic research is useful in understanding the dynamics and structure of plant populations. Having this knowledge is essential for developing conservation plans, particularly when working with isolated or fragmented populations.

4. Introgression and Hybridization

The detection of introgression, or the exchange of genes across species, is aided by cytogenetics. This is crucial to comprehending the possible effects on native species' genetic integrity and directing conservation efforts.

5. Breeding Programs for Restoration

Designing and executing breeding programs with the goal of repairing damaged ecosystems requires an understanding of plant cytogenetics. Breeding programs might aim to enhance characteristics like disease resistance, stress tolerance, and flexibility.

6. Seed Banking

Initiatives related to seed banking can benefit greatly from the use of cytogenetic information. It guarantees the gathering and preservation of seeds that faithfully capture a species' genetic diversity, serving as a resource for upcoming restoration projects.

7. Identification of Polyploidy and Aneuploidy

Cytogenetic methods are useful in distinguishing between polyploidy, which is the multiplication of whole sets of chromosomes, and aneuploidy, which is a fluctuation in the number of chromosomes. Since these occurrences can substantially impact a species' fitness and adaptation, understanding them is essential for protecting and restoring plant populations.

8. Monitoring Genetic Stability

Monitoring Genetic Stability: Especially in small and isolated populations, cytogenetics makes it possible to track changes in genetic stability across time. With the use of this data, conservationists can determine a population's long-term viability and take the necessary action in the event that genetic erosion is discovered.

9. Conservation Planning and Policy

Cytogenetic data aid policy and strategy creation for conservation. Policymakers can use the collected information to inform their decisions on managing and protecting plant species and their ecosystems. Because it offers critical insights into the genetic characteristics of plant populations, directs tactics for their protection, and makes sustainable biodiversity management easier, cytogenetics plays a critical role in directing conservation and restoration efforts for plant species (Klein, William 2007).

7.20. Conclusion

Plant cytogenetics research has advanced significantly throughout time, offering important new perspectives on the complex field of plant genetics. As we commemorate the one-year anniversary of the start of this study, it is clear that the field has experienced significant advancements that have deepened our understanding of the structure, behaviour, and evolution of plant chromosomes. The development and use of sophisticated cytogenetic methods, such as fluorescence in situ hybridization (FISH) and molecular markers, has been one of the major accomplishments. These methods have allowed scientists to examine plant genomes with a level of precision never before possible. These instruments have been essential in deciphering intricate chromosomal rearrangements, pinpointing significant genetic loci, and clarifying plant adaptation and evolution processes. Furthermore, new directions for thorough analysis of plant genomes have been made possible by combining cytogenetic research with other omics techniques such as

transcriptomics, proteomics, and genomics. A more comprehensive knowledge of the functional implications of chromosomal differences has been made possible by this multidisciplinary approach, which has revealed insights into the ways in which these variations affect plant development, stress response, and overall fitness. Plant cytogenetics research has yielded valuable insights that have broadened our understanding of plant genetics and had applications in crop improvement and breeding initiatives. The production of molecular markers for marker-assisted selection has been made easier by the identification of particular chromosomal areas linked to desirable qualities. This has sped up the breeding process for crops with increased nutritional content, pest and disease resistance, and yield. As we take stock of last year's accomplishments, we must also recognize the global research community's cooperative efforts that have advanced our collective understanding of plant cytogenetics. Further significant discoveries could be made in the future as technology develops further and allows scientists to examine the intricacies of plant genomes in greater detail.

Finally, it should be noted that there has been a great deal of progress in plant cytogenetics, which holds promise for applications in agriculture as well as fundamental scientific understanding. Future developments in plant genetics research will surely be shaped by the ongoing cooperation of established cytogenetic approaches with state-of-the-art technology, opening the door to breakthroughs that support sustainable agriculture and global food security.

7.21. References

1. Bikram S. Gill, Bernd Friebe. Plant cytogenetics at the dawn of the 21st century. *Current Opinion in Plant Biology* 1998; 1(2):109-115.
2. Daniel Scholes, Program in Ecology, Evolution, and Conservation Biology, School of Integrative Biology, University of Illinois, Urbana, Illinois 61801. E-mail: scholes2@illinois.edu Published online 12 April 2012 in Wiley Online Library (wileyonlinelibrary.com). DOI: 10.1002/cyto.a.22054.
3. Pamela S Soltis, D Blaine Merchant, Yves Van de Peer and Douglas E Soltis. Polyploidy and genome evolution in plants. *Current Opinion in Genetics & Development* 2015, 35:119–125.
4. Keith L Adams, Jonathan F Wendel. Polyploidy and genome evolution in plants. *Curr Opin Plant Biol.* 2005;8(2):135-41. doi: 10.1016/j.pbi.2005.01.001.
5. Huai-Yang Xiong, Li-Juan Zhao, Li-Jia Li. Cytogenetic maps and their applications in plants. *Yi Chuan.* 2005; 27(4):659-64.
6. Debbie M. Figueroa, Hank W. Bass. A historical and modern perspective on plant cytogenetics. *Briefings in Functional Genomics,* 2010; 9(2):95-102.

CHAPTER – 08

MUTATIONS IN PLANT EVOLUTION, CROP DOMESTICATION, AND BREEDING

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Abstract

The important significance that mutations have had in crop domestication processes, plant evolution, and as crucial variables in modern breeding techniques is examined in this in-depth analysis. Since the dawn of agriculture and continuing to the present, plants have experienced genetic alterations brought about by natural selection, cultural manipulation, and spontaneous mutations. The intricate relationships between human cultivation, natural selection, and scientific breeding techniques have led to the development of crop varieties with enhanced traits, productivity, and adaptability. Mutation breeding is the only straightforward way to enhance seedless crops and cultivars. Many more strong physical and

chemical mutagens have been developed since the first reports of induced mutagenesis using x-rays were made about a century ago. Additionally, techniques for applying these mutagens in seed (self- and cross-pollinated) and vegetatively propagated crops have been devised. The function of mutations in the evolution of plants and crops is examined in this overview, which is followed by a discussion of the options available for mutation breeding programs, including mutagenic chemicals, treatment techniques ranging from cell cultures to whole plants, and some of the successes. The combination of plant molecular methods and mutation techniques offers interesting new avenues for current plant development.

Key words: Mutations in plant evolution, crop domestication, and breeding

8.1. Introduction

Highlighting the influence of mutations on the shift from wild progenitors to domesticated crops with desired agronomic properties, the article looks at the historical background of crop domestication. We examine how mutations, from point mutations to structural changes, arise and contribute to phenotypic variety through the lenses of molecular genetics and genomics. Since important genes linked to desirable features like disease resistance, yield, and nutritional content can now be identified, advances in sequencing technologies have allowed for hitherto unheard-of insights into the genomic landscapes of cultivated plants (Bourgis et al. 2008, Pathirana et al. 2009). Mutations play a crucial role in plant evolution, crop domestication, and breeding.

Here's an overview of how mutations contribute to these processes:

8.2. Plant Evolution

As with all living things, mutations are essential to the evolution of plants. A variety of events, including exposure to radiation, toxins, or mistakes made during DNA replication, can result in mutations, which are haphazard alterations in an organism's DNA sequence. Mutations aid plant evolution in the following ways:

a. Genetic Diversity

Genetic variety is introduced into a population through mutations. A population's capacity to adjust to shifting environmental conditions depends on its diversity. Plants with advantageous mutations that provide benefits in particular conditions have a higher chance of surviving and procreating.

b. Adaptation to Environmental Changes

Mutations can result in characteristics that improve a plant's capacity for environmental survival. A mutation could, for instance, provide tolerance to high temperatures, pest resistance, or the capacity to grow in many types of soil. These beneficial characteristics may spread more widely in a population over time.

c. Selective Pressure

Herbivores, competition from other species, and climate change are examples of environmental variables that exert selective pressure. Future generations are more likely to inherit mutations that offer a reproductive or survival advantage in the face of these stresses.

d. Speciation

Plant species can diverge due to the accumulation of mutations over extended periods of time. If populations endure diverse ecological conditions or are geographically isolated, they may eventually diverge into new species with different sets of mutations.

e. Genetic Drift

Chance and random occurrences can greatly impact which alleles become more or less common in small populations. Over time, mutations may impact this phenomenon, sometimes referred to as genetic drift, which can result in alterations in a population's genetic composition.

f. Domestication

Through artificial selection throughout the domestication process, humans have contributed to the development of plants. Crops with enhanced nutritional value, insect resistance, and higher yields have been developed over many generations as a result of deliberate breeding for desired features.

g. Mutualistic partnerships

Plants and other creatures, such as nitrogen-fixing bacteria or mycorrhizal fungi, frequently develop mutualistic partnerships. Enhancing these interactions through mutations can benefit the plant and its symbiotic partner, which can impact the plant's evolutionary path. It's crucial to remember that many mutations are neutral or even harmful; not all mutations are advantageous. The beneficial mutations are subject to natural selection, which eventually encourages their persistence in a population. Overall, the interplay

between mutation, natural selection, and environmental factors shapes the evolutionary trajectory of plant species.

(Clark and Donoghue 2018; Barker et al. 2016; Pathirana et al. 2011).

8.3. Crop Domestication

Crop domestication has benefited greatly from mutations, which have led to the development of beneficial features that make crops more suited for cultivation and human use. Crop domestication is the process of choosing and breeding plants that have particular traits, like higher yields, better tastes, resistance to pests and diseases, and flexibility in growing environments. A few examples of how mutations have impacted crop domestication:

a. Seed Size and Germination

During domestication, mutations that produced larger seeds and changed the germination process were preferred because they allowed for higher crop yields and more straightforward farming methods.

b. Plant Architecture

To make crops easier to manage, harvest, and nurture in small spaces, mutations favouring more compact growth, less branching, and an upright stature were chosen.

c. Shattering Resistance

To facilitate harvesting, mutations that result in non-shattering types were chosen. This characteristic makes seed loss during harvesting avoidable and facilitates more effective collecting.

d. Less Bitterness and Toxins

To enhance the flavour and safety of crops for human consumption, mutations that lessen bitterness or remove toxins were preferred.

e. Photoperiod Sensitivity

Variations in photoperiod sensitivity enabled crops to be adapted to a greater variety of conditions, offering flexibility in terms of when they might be planted and harvested.

f. Disease Resistance

Mutations resulting in enhanced disease resistance were chosen to protect crops from common diseases and promote overall production and quality.

g. Adaptation to New Environments

The expansion of agriculture throughout various locations largely depended on genetic mutations that adapted crops to various soil types, temperatures, and growth environments. Natural and human-driven selection acting on genetic differences, including mutations, is what drives the process of domestication. Over time, These mutations have helped generate a wide variety of crops vital to humankind's global nutrition (Heslop-Harrison et al., 2007; Meyer et al., 2009).

8.4. Breeding

In the process of breeding and genetic variety, mutations are important. Mutations are frequently used in breeding operations to introduce desired features or remove unwanted ones. The following are important details about breeding-related mutations:

- a. **Natural Mutations:** Genetic variation in populations arises from spontaneous natural mutations. Breeders of plants and animals can recognize and choose individuals who possess naturally occurring mutations that bestow desired characteristics.
- b. **Induced Mutations:** Certain mutations are purposefully brought about by exposure to chemicals or radiation, among other techniques. It is possible to generate genetic diversity by induced mutations, which will aid in the creation of new types.
- c. **Selective Breeding:** Breeders employ selective breeding to spread individuals with certain mutations or qualities. This may eventually result in the emergence of new types with enhanced traits.
- d. **Mutation Breeding:** This method involves exposing plants to mutagenic substances to cause mutations. Following a screening process to identify desirable qualities, the mutant plants are chosen for additional breeding based on which ones exhibit the desired properties.
- e. **Genetic Engineering:** Genetic engineering methods like CRISPR-Cas9 can modify specific genes with precision. With such accuracy, genetic manipulation can be used to insert or remove particular features from an organism.
- f. **Disease Resistance:** Finding or creating mutations that give immunity to pathogens is a common step in breeding for

disease resistance. This is essential in order to maintain the well-being and production of animals and crops.

- g. **Quality Traits:** The quality of agricultural goods can also be impacted by mutations. For instance, mutations may affect a fruit or vegetable's flavour, nutritional value, or shelf life. Although advantageous qualities can result from mutations, there is always a chance of unforeseen repercussions or the introduction of unwanted traits. Regulations and ethical issues influence the application of mutation-based breeding techniques.
- h. **Monitoring and Testing:** In order to guarantee the stability of desired features and identify any unintended effects, modern breeding operations frequently entail stringent testing and monitoring.

All things considered, mutations are an inherent component of the genetic landscape, and by carefully managing their breeding, we can help create more resilient and superior livestock and crops. It is imperative to strike a balance between the possible advantages and ethical and environmental factors (Van Harten et al., 1998; Jagadeesan et al., 2021; Gaur et al., 2008).

8.5. Challenges and considerations

Along with undesirable effects, unintended consequences can also produce positive traits. Strict selection and screening are required to ensure crops' overall safety and quality. Certain breeding techniques and the use of genetic modification raise ethical and environmental

questions. Finding a balance between innovation and responsible application is crucial. In conclusion, mutations are primarily responsible for plant populations' genetic diversity and adaptation. Through the processes of domestication, breeding, and evolution, humans have changed and refined plant features to fit a range of requirements. Modern agriculture still heavily relies on understanding and altering mutations to generate crops with improved and more resilient traits (Khanh et al., 2021; Pathirana, 2021).

8.6. Conclusion

The analysis also clarifies how mutations function in modern breeding programs, highlighting the combination of conventional breeding practices with state-of-the-art molecular tools like CRISPR-Cas9 gene editing. Strategies to hasten the creation of crops with increased resilience to biotic and abiotic challenges are reviewed, including the use of natural genetic variety and the controlled introduction of advantageous mutations. The ethical issues surrounding the application of genetic engineering to crop enhancement are also covered, highlighting the necessity of sustainable and ethical methods.

8.7. References

1. Ranjith Pathirana. Mutations in plant evolution, crop domestication and breeding. Tropical Agricultural Research & Extension 2021; 24 (3): 1-35.
2. Bourgis F, Guyot R, Gherbi H, Tailliez E, Amabile I, Salse J, Lorieux M, Delseny M and Ghesquière A 2008 Characterization of the major fragrance gene from an aromatic japonica rice and analysis of its diversity in Asian cultivated rice. Theoretical and Applied Genetics 117:353-368.

3. Pathirana R 2011 Plant mutation breeding in agriculture. CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources 6:1-20.
4. Pathirana R, Vitiyala T and Gunaratne NS 2009 Use of induced mutations to adapt aromatic rice to low country conditions of Sri Lanka, in Induced plant mutations in the genomics era Proceedings of an International Joint FAO/IAEA Symposium, International Atomic Energy Agency, Vienna, Austria. pp 388-390.
5. Clark JW and Donoghue PCJ 2018 Wholegenome duplication and plant macroevolution. Trends in Plant Science 23:933-945.
6. Barker MS, Li Z, Kidder TI, Reardon CR, Lai Z, Oliveira LO, Scascitelli M and Rieseberg LH 2016 Most Compositae (Asteraceae) are descendants of a paleohexaploid and all share a paleotetraploid ancestor with the Calyceraceae. American Journal of Botany 103:1203-1211.
7. Heslop-Harrison JS and Schwarzacher T 2007 Domestication, genomics and the future for banana. Annals of Botany 100:1073-1084.
8. Meyer RS and Purugganan MD 2013 Evolution of crop species: genetics of domestication and diversification. Nature Reviews Genetics 14:840-852.
9. Purugganan MD and Fuller DQ 2009 The nature of selection during plant domestication. Nature 457:843-848.
10. Van Harten AM 1998 Mutation breeding: theory and practical applications. Cambridge University Press, Cambridge, UK.
11. Jagadeesan S and Thumballi Ramabhatta G 2021 Mutation Breeding in India: Accomplishments and Socio- Economic Impact, International Atomic Energy Agency (IAEA), Vienna. pp 23-25.
12. Gaur PM, Gour VK and Srinivasan S 2008 An induced brachytic mutant of chickpea and its possible use in ideotype breeding. Euphytica 159:35-41.
13. Khanh TD, Duong VX, Nguyen PC, Xuan TD, Trung NT, Trung KH, Gioi DH, Hoang NH, Tran H-D, Trung DM and Huong BTT 2021 Rice breeding in Vietnam: Retrospects, challenges and prospects. Agriculture 11:397

CHAPTER – 09

PARTHENIUM WEED: ITS BIOLOGICAL SUPPRESSION THROUGH ALLELOPATHY

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Weed has been defined in the Oxford dictionary as a small, useless plant growing where it is not wanted. In the absence of natural constraints, such weeds grow out of proportion and become a menace.

Carrot weed, *Parthenium hysterophorus* L. (Asteraceae), is an annual herbaceous plant supposed to have originated in North East Mexico, and during the last hundred years, it has spread to Australia, Africa and Asia. Until 1977, this weed did not find any place in the world's worst weeds (Fig-1).



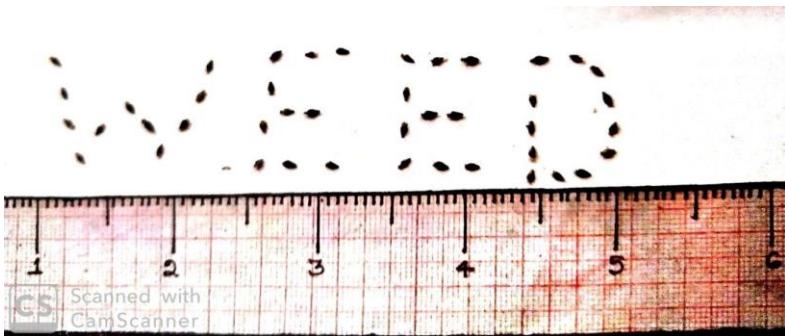
Fig-1. *Parthenium* plant

Within the last 10 years, it has become one of the seven most dangerous weeds in the world. It is an aggressive invader of disturbed and degraded land, rapidly displacing native and planted pastures. In addition to reducing land productivity, the plant causes acute allergic dermatitis and rhinitis in susceptible humans. In Australia, *Parthenium* is a serious problem in perennial grassland in Central Queensland, where it can reduce beef production by as much as AU\$ 16.5 million annually. In India, this weed causes yield losses of up to 40 percent in several crops and is reported to reduce forage production by up to 90 percent. *Parthenium* contains sesquiterpene lactones, which induce several allergic reactions in susceptible, continuously exposed individuals. It has been declared a national health hazard in view of its serious skin allergies to man and animals. In India, 4-7 percent of the human population suffers from recognizable clinical symptoms associated with *Parthenium*, while 42-52 percent are sensitized without showing symptoms.

Although herbicide application and disposal with mechanical devices like flame throwers have considerable merits, being cost-effective and providing immediate solutions to most weed problems, they are not the only or necessarily the best solution because of rising expenses and the need for continued treatment. Besides chemical pollution, enormous cost, danger of toxicity to non-target organisms, treatment in non-agricultural areas, and rapidity of reinvasion of treated areas soon after the effect is

diminished are known drawbacks of chemical control. Since no single agent is able to control this weed, perhaps with such a prolific and aggressive weed (Fig-2), this should come as no surprise. However, It is still considered that the long-term solution will lie in releasing a guild of specific agents to hit as many plant organs as possible, thus gradually reducing the weed vigour over time. In view of the urgency to develop suitable alternatives/supplements to chemical weedicides for control of this obnoxious weed, especially under Indian conditions, where the pesticides are not only non-judiciously and indiscriminately applied but are also expensive, the use of botanic agents could be of great help in effectively suppressing this weed.

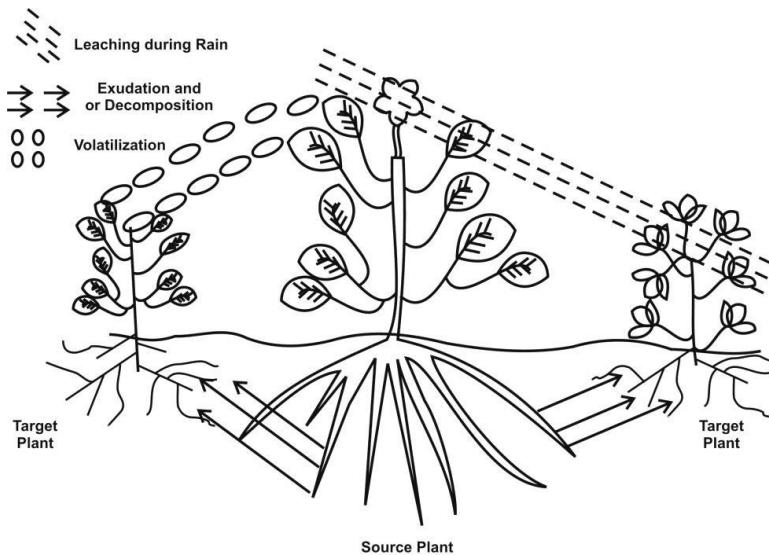
Fig-2. *Parthenium* seeds



Allelopathy has been defined as a beneficial or detrimental effect from a donor plant to the recipient by a chemical pathway (Rice, 1984). The harmful impact of allelopathy can be exploited for pest and weed control (Kohli et al., 1998). Many researchers have documented the potential of allelopathic plants to reduce

pathogens and affect weed emergence. The most common effect of allelochemicals may occur through leaching, volatilization, root exudation and decay of the fallen parts either through biotic or abiotic means (Anaya et al., 1990). In the recent years, creating competition between native and alien species has gained momentum. Numerous plants are reported to possess allelopathic potential, and effort has been made to use them in weed control. The term ‘Allelopathy’ is derived from two Greek words: Alleon means each other, and Pathos means to suffer, i.e. the injurious effect of one upon another.

Fig-3. Schematic Representation of ways allelochemicals enter an enterprise production ecosystem



However, Molisch, 1937 coined this term, which refers to all biochemical interactions (stimulatory and inhibitory) among plants, including micro-organisms. It represents the plant-against-

plant aspect of the broader field of chemical ecology. Some authors have used the term more restrictedly to describe only the harmful effect of one higher plant upon another. Allelochemicals that inhibit the growth of some species at certain concentrations may stimulate the growth of the same or different species at lower concentrations. (Narwal, 1994). Allelopathy is a relatively new branch of science (Lal and Oudhia, 1999). With the help of allelopathy, weed-crop, crop-weed, crop-crop, and weed-weed interactions can easily be explained. The chemical exudates from allelopathic plants are proposed to play a major role in the allelopathy mode of action. Evidence showed that higher plants release a diversity of allelochemicals into the environment, including phenolics, alkaloids, long-chain fatty acids, terpenoids and flavonoids (Rice, 1984). However, these compounds are available in low concentrations in most allelopathic plants.

Positive and negative allelopathic effect of *Parthenium* on many agricultural crops and other plant species has been reported (Oudhia and Tripathi, 1998), and it has been established that *Parthenium* has an inhibitory effect on surrounding herbaceous vegetation (Nath, 1988). Hundreds of secondary metabolites are in the plant kingdom, and many are phytotoxic (Einhellig, 2002). Allelopathic effects of these compounds are often observed to occur early in the life cycle, causing inhibition of seed germination and/or seedling growth. The compounds exhibit a wide range of mechanisms of action, affecting DNA (alkaloids),

photosynthetic and mitochondrial function (quinones), phytohormone activity, ion uptake and water balance (phenolics). Interpretations of action mechanisms are complicated because individual compounds can have multiple phytotoxic effects (Einhellig, 2002). In the course of an extensive survey carried out to assess the distribution of *Parthenium* in India in the years 1987-1990 (Aneja et al., 1991), it was observed that *Parthenium* does not grow in proximity to some plant species. This was suggestive of the natural antagonism of these species to *Parthenium*. The first observation that antagonistic competitor plants could replace *P. hysterophorus* and therefore had potential for biological control appears to have been made by Singh, 1983 who noted that *Cassia uniflora* moved into areas previously occupied by *Parthenium* weed in the Maharashtra State of India. Subsequently, Naithani, 1987 also observed that *C. sericea* had the ability to smoother or overgrow *P. hysterophorus* in North-East India, whilst, in Southern India, it was reported to reduce the vigour of *Parthenium* weed (Mahadevappa and Ramaiah ,1988).

Aqueous foliar leachates of *Azadirachta indica*, *Prosopis juliflora*, *P. cineraria* inhibit seed germination of *Parthenium* by more than 95 percent (Dhawan et al., 1994). Several other plants like *Tephrosea purpurea*, *Amaranthus spinosus*, *Hyptis savolensis*, *Sida cordifolia* and other species of *Cassia* have been found to suppress *Parthenium*. Studies were undertaken to observe the allelopathic potential of all the selected botanic agents

on *Parthenium hysterophorus* both *in vivo* and *in vitro*, and also to find out if any allelopathic component is involved in substantiating the visual observation and, if so, whether the selected botanic agents sufficient enough to replace *Parthenium* in the nature in the long run or it needs further human effort to help from spreading this weed in nature with minimum effort to replace it. The allelopathic properties of plants can be explained successfully as a tool for weed reduction. The chemical exudates from allelopathic plants are proposed to play a major role in the allelopathy mode of action.

Parthenium hysterophorus L., a common problematic weed of wastelands as well as crop fields in India, is well known for its lethal allelopathic effect on many agricultural crops, including chickpea, kodo mustard, linseed etc. (Oudhia and Tripathi, 1998). It also has the potential to disrupt the natural ecosystem and become a curse for biodiversity in many places in India. In order to manage this noxious weed in an ecologically safe and viable manner, there is a trend towards searching for botanic agents plant species which can replace this weed through allelopathic mechanisms. During field surveys, it has been observed that at some sites, *Cassia occidentalis*, *Calotropis procera*, *Chenopodium album*, *Croton bonplandianum*, *Abutilon theophrasti*, *Acacia arabica* have replaced this weed in patches. Mamatha and Mahadevappa(1992), based on their preliminary surveys, have reported that *Cassia sericea*, *C. tora*, *Tephrosia*

purpurea and *Croton bonplandianum* restricted *Parthenium* invasion in many states in India.

Aqueous extracts of root, stem, and leaves of *Ocimum americanum* were tested against seed germination and seedling growth of *Parthenium*. The inhibitory effects of the aqueous extract of *O. americanum* significantly inhibited the germination and seedling growth of *Parthenium*. Seed germination and seedling growth were significantly inhibited in the order of leaf > stem > root (Singh and Thapar, 2004). The allelochemicals present in *Azadirachta indica* have an inhibitory effect on the germination and seedling growth of *Parthenium* and *Amaranthus*. Due to the treatments, there was variability in germination (%) and shoot and root growth of seedlings. The degree of phytotoxicity of senescent leaves was higher than that of green leaves, and bark was more inhibitory to the germination of *Parthenium* and *Amaranthus*. The leachates of senescent leaves also reduced both the weeds' shoot length and root length (Sindhu et al., 2004).

Parthenium seed germination was inhibited in aqueous foliar extracts of *Cassia occidentalis*, *Andrographis paniculata*, *Abutilon indicum* and *Hyptis suaveolens*. There was no stimulatory effect of extracts on seed germination and seedling growth to test *P. hysterophorus*. All the species tested inhibited the seedling's early seedling growth and fresh weight. *Cassia sericea* recorded the highest reduction in seedling length, i.e.

87.66% and 87.31% by leaf and whole plant extract, respectively at 50% concentration, followed by *Hyptis suaveolens* (83.89% & 84.55%). These plants also caused a maximum reduction in the fresh weight of *Parthenium hysterophorus* in the seedlings (Senthil et al., 2004). Joshi and Mahadevappa (1986) reported that *Cassia occidentalis* has successfully displaced this weed in Dharwad and surrounding areas under natural course. Other species of *Cassia occidentalis* were found to be dominant and replaced *Parthenium* in patches in selected fields. The grazing animals dislike *Cassia* due to this pungent odour, considered a desirable trait, as it repelled the cattle and successfully replaced *Parthenium* even in unprotected land. Its rapid rate of growth, wide range of ecological adaptability, sufficient quantity of seed production and utility are also considered for its choice to suppress *Parthenium* weed. *Cassia* also has an allelopathic action that hampers the growth of *Parthenium*.

The competitive and/or allelopathic replacement of *P. hysterophorus* by native eco-friendly weeds such as *Croton bonplandianum* and *Amaranthus spinosus* have also been reported by Singh and Thaper (2002) and Swain et al. (2004), respectively.

References

1. Anaya, A.L.; Calera, M.R.; Mata, R. and Miranda, R.P. (1990). Allelopathic potential of compounds isolated from *Ipomea tricolor* Cav. (Convolvulaceae) *J. Chem. Ecol.* 16:2145-2152.
2. Aneja, A.K. (1991). Deadly weed *Parthenium hysterophorus* L. and its control – a review. In: Aery, N.C.; Chaudhary, B.L. (eds) *Botanical Researches in India*. Udaipur, India Himanshu Publications. 258-269.
3. Dhawan, S.R. and Dhawan, P. (1994). Congress grass. Effect of temperature and light on seed germination. *Adv. Plant Sci.* 7(1): 177-178.
4. Einhellig , F.A. (2002) . The physiology of allelochemical action: clues and views. In : *Allelopathy from Molecules to Ecosystem*, M. J.
5. Joshi, S. and Mahadevappa, M. (1986). *Cassia sericea* S. to fight *Parthenium hysterophorus* Linn. *Curr. Sci.* 55:261-262.
6. Kohli, R.K; Batish, D.R. and Singh, H.D., (1998). *Eucalyptus* oils for the control of *Parthenium* (*Parthenium hysterophorus* L.) s *Crop Prot.* 17: 119-122.
7. Lal, B. and Oudhia, P. (1999). Beneficial effects of Allelopathy: I. Crop Production, *Indian J. weed Sci.* 31(1 and 2): 103 –105.
8. Mahadevappa, M. and Ramaiah, H. (1988). Pattern of replacement of *Parthenium hysterophorus* plants by *Cassia sericea* in waste lands. *Indian Journal of Weed Science* 20, 83-85.
9. Mamatha, M. and Mahadevappa, M. (1992). Biological survey in relation to *Parthenium* control. *Adv. Plant Sci.* 1(2): 238-240.
10. Molisch , H. (1937). Der Enfusslinear Pflanze auf die andere-Allelopathic Fischer, Jena, GDR.
11. Naithani, H.B. (1987). *Parthenium hysterophorus* a pernicious weed in Arunanchal Pradesh and Nagaland. *Indian Forester* 113: 709-710.
12. Narwal, S.S. (1994). *Allelopathy in Crop Production*. Scientific Publishers, Jodhpur, 288.
13. Nath, R. (1988). *Parthenium hysterophorus* L. A general account *Agric. Rev.* 9:171-179.
14. Oudhia, P. and Tripathi, R.S. (1998). Allelopathic effects of *Parthenium hysterophorus* L. on Kodo mustard and problematic weeds. In: *Proceedings of the First International conference on Parthenium Management*. University of Agricultural Sciences, Dharwad, India. 6-8 Oct. 1997., 136-139.
15. Rice, E.L. (1984). Allelopathy second ed. Academic Press Inc. , Orlando, FL. 422.
16. Senthil, A.; Chinnusamy, C.; Shanmugasundaram, R. and Kandasamy, O.S. (2004) WM 20. Identification of competitive or allelopathic plant species for the management of *Parthenium hysterophorus*. Abstracts IVth International Conference Allelopathy in Sustainable Terrestrial and Aquatic Ecosystem. Ed., S.S. Narwal, Haryana Agri. University, Hisar, Aug. 23-25 p.24.

17. Sindhu, A.; Kumar , S.; Sindhu , G.; Ali, H. and Abdullah, M.K. (2004) WM 18. Allelopathic potential of neem (*Azadirachta indica* A. Juss)) on germination and seedling growth of weeds. Abstract IVth International Conference Allelopathy in Sustainable Terrestrial and Aquatic Ecosystem. Ed., S.S., Narwal , Haryana Agri. University Hisar, Aug. 23-25. p. 22.
18. Singh, N.B. and Thapar , R. (2004) WM 17. Allelopathic potential of *Ocimum americanum* on seed germination and seedling growth of *Parthenium hysterophorus* L.
19. Abstracts IVth International Conference Allelopathy in Sustainable Terrestrial and Aquatic Ecosystems. Ed., S.S. Narwal , Haryana Agri. University , Hisar Aug. 23-25. p. 21.
20. Singh, N.B. and Thaper, R. (2002). Allelopathic effect of *Croton bonplandianum* on *Parthenium hysterophorus*. *Allelopathy J.* 10:163-170.
21. Singh, N.P. (1983). Potential biological control of *Parthenium hysterophorus* L. *Current Science* 52, 644.
22. Swain, D.; Pandey , P.; Paroha, S., Singh, M. and Yaduraju, N.T.Y. (2004). Allelopathic effect of *Amaranthus spinosus* on *Parthenium hysterophorus*. *Ann. Pl. Prot. Sci.* 12 (2): 409-413.

CHAPTER – 10

INTRODUCTION TO BIOSTATISTICS: A BRIEF OVERVIEW

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Abstract

Biostatistics is the application of statistical methods to biological and health-related data. It involves collecting, analysing, interpreting, and presenting data in fields such as medicine, biology, public health, genetics, and environmental science. Biostatistics is a field that merges principles of statistics with biological sciences, aiming to apply statistical methods to analyze and interpret data related to living organisms. It is the implementation used in mathematical tools, biological sciences, and the field of medicine. This chapter explores the role of biostatistics and the application of advanced statistical methods to address key research questions.

10.1. Introduction

The role of biostatistics is widespread, impacting various aspects of scientific research and decision-making in healthcare, public health policy, genetics, environmental studies, and more. It's a critical tool for researchers and practitioners to make sense of complex biological and health-related data, leading to advancements in understanding diseases, developing treatments, and improving

overall health outcomes. Biostatistics is an integral part of the field of biology, enabling researchers to analyze and interpret data related to living organisms.

10.2. Applications of Biostatistics

Here are a few key applications of biostatistics across various areas:

a) *Clinical Trials and Epidemiology*

- **Drug Development:** Biostatistics plays a crucial role in designing and analyzing clinical trials for new drugs or treatments. It helps determine sample sizes, assess efficacy, and ensure statistical significance.
- **Epidemiological Studies:** Biostatistics aids in studying disease patterns, risk factors, and public health interventions. It helps epidemiologists analyze data to understand the spread and impact of diseases within populations.

b) *Genetics and Genomics*

Biostatistics is essential for designing experiments, analyzing genetic data, identifying genetic factors underlying traits or diseases, and making inferences about the inheritance and evolution of genetic traits. It's the backbone that enables researchers to navigate and understand the complexities within the genetic code. Here's how biostatistics is utilized in genetics.

- **Genetic Studies:** Biostatistics assists in analyzing genetic data, identifying genetic markers associated with diseases, and studying inheritance patterns.

- **Genomic Sequencing:** It helps in managing and analyzing large-scale genomic data to understand genetic variations and their implications in health and diseases.
- **Genetic Variation Analysis:** Biostatistical methods are used to analyze genetic variation within populations. This involves studying allele frequencies, genetic markers, linkage disequilibrium, and genetic diversity. These analyses help understand patterns of inheritance and genetic relationships among individuals or populations.
- **Genome-Wide Association Studies (GWAS):** Biostatistics is essential in GWAS, where researchers investigate the genetic basis of complex traits or diseases by analyzing genetic variations across the entire genome. Biostatistical tools help identify genetic variants associated with specific traits or diseases.
- **Quantitative Genetics:** Biostatistical methods are employed in quantitative genetics to study the inheritance of quantitative traits, such as height, weight, or blood pressure. These methods help estimate heritability, understand genetic and environmental influences, and predict phenotypic outcomes.
- **Population Genetics and Evolutionary Studies:** Biostatistics aids in studying evolutionary processes and population genetics by analyzing genetic data to infer

historical population dynamics, migration patterns, natural selection, and genetic adaptation.

- **Linkage and Association Analysis:** Biostatistical techniques are used to detect genetic markers linked to specific genes or traits. Linkage analysis identifies regions of the genome inherited together with a trait, while association analysis identifies correlations between genetic variations and traits in population-based studies.
- **Genomic Data Analysis:** With the advancement of high-throughput sequencing technologies, biostatistics plays a crucial role in analyzing vast amounts of genomic data, including whole-genome sequencing and transcriptomic data. These analyses help in identifying functional elements in the genome, gene expression patterns, and regulatory mechanisms.

c) ***Public Health***

- **Health Policy and Planning:** Biostatistics supports decision-making in public health policies by analyzing health-related data to formulate strategies and interventions.
- **Surveillance and Outbreak Analysis:** Monitoring disease outbreaks, tracking trends, and predicting future occurrences are done through statistical analysis in public health settings.
- **Healthcare Resource Allocation:** Biostatistics aids in assessing the cost-effectiveness of healthcare interventions and in understanding the economic impact of different health

policies. This information assists policymakers in allocating resources efficiently and prioritizing interventions that offer the most significant benefits for public health.

d) Environmental Health

- **Environmental Impact Studies:** Biostatistics aids in analyzing data related to the impact of environmental factors on human health, such as air and water quality assessments. Biostatistics is crucial in environmental studies as it facilitates the analysis of complex data related to environmental factors, ecosystems, and their impact on living organisms. Here's how biostatistics is applied in this field:
 - **Environmental Monitoring:** Biostatistics helps design sampling strategies and analyze data collected from environmental monitoring programs. It enables scientists to assess air and water quality, soil contamination, biodiversity, and other environmental factors.
 - **Ecological Studies:** Biostatistical methods are used to analyze ecological data, such as species abundance, diversity, distribution patterns, and interactions within ecosystems. These analyses aid in understanding ecosystem dynamics, species conservation, and the effects of environmental changes.
 - **Risk Assessment:** Biostatistics is employed in assessing risks associated with environmental pollutants, climate

change, and other factors affecting human and ecological health. It helps quantify exposure-response relationships and assess the potential impact on populations.

- **Spatial Analysis:** Biostatistics helps in analyzing spatial data related to environmental variables. Geostatistical methods are used to model spatial patterns, map environmental changes, and understand how geographical factors influence ecological systems.
- **Climate Studies:** Biostatistics is applied in climate research to analyze large datasets related to temperature changes, precipitation patterns, greenhouse gas concentrations, and their effects on ecosystems and biodiversity.
- **Environmental Epidemiology:** Biostatistics plays a role in environmental epidemiology, where it helps in studying the relationship between environmental exposures (like pollution or toxins) and health outcomes in human populations.
- **Conservation Biology:** Biostatistical tools aid in making informed decisions about conservation strategies. They help assess the effectiveness of conservation efforts, model population dynamics, and determine the impacts of habitat loss or fragmentation on species survival.

e) *Bioinformatics*

Biostatistics forms the backbone of bioinformatics, playing a pivotal role in the analysis, interpretation, and extraction of meaningful information from biological data, particularly in the realm of genomics, proteomics, and other -omics fields. Here's how biostatistics is applied in bioinformatics:

- **Sequence Analysis:** In fields like proteomics and bioinformatics, statistical methods help in analyzing biological sequences (DNA, RNA, proteins) to derive meaningful insights.
- **Data Mining and Analysis:** Biostatistics mines and interprets large biological datasets, extracting patterns and correlations for further research.
- **Interpretation:** Biostatisticians interpret the results of data analyses, determining the significance of findings and their implications for the specific field of study. They also communicate these findings to researchers, policymakers, and the broader scientific community.
- **Predictive Modeling:** Biostatisticians use statistical tools to develop models to predict outcomes or trends based on available data. These models can aid in understanding disease progression, forecasting public health trends, or optimizing treatment strategies.

f) Biomedical Research

- **Clinical Data Analysis:** Analyzing patient data, understanding disease progression, and predicting outcomes are essential aspects of biomedical research where biostatistics is applied. In biomedical research, rigorous statistical methods are essential to ensure that findings are reliable, reproducible, and applicable to the broader population. Biostatisticians collaborate closely with researchers, clinicians, and scientists to ensure that studies are well-designed, data analysis is robust, and accurate conclusions are drawn.

10.3. Experimental Design

Designing experiments, determining sample sizes, and ensuring statistical rigour are crucial in biomedical research to draw valid conclusions.

a) Agriculture and Veterinary Sciences

- **Crop and Animal Studies:** Biostatistics helps in analyzing agricultural and veterinary data to enhance productivity, understand diseases, and improve breeding programs. Biostatistics helps in the statistical analysis of evidence-based data of various diseases and disorders in animals, thus helping in tracking and interfering with the population and facilitating the testing of samples as well as diagnosis of diseases, thus helping greatly in health monitoring. It also has accuracy of sample testing and diagnosis, thus increasing

treatment accuracy. Statistical data helps us educate and provide information to various groups and organizations concerned with animal health and the common public.

- **Nutrition Studies:** Statistical methods are used to assess dietary patterns, nutritional impacts, and their effects on human and animal health outcomes. Biostatistics empowers researchers across diverse fields within biology, providing the tools and techniques necessary for sound data analysis and informed decision-making.
- **Anthropology:** Biostatistics plays a crucial role in anthropology by enabling researchers to analyze and interpret biological data related to human populations. Anthropologists often use biostatistical methods to study various aspects of human biology, evolution, and diversity.

Biostatistics is a branch of applied statistics, and it must be taught with a focus on its various applications in biomedical research (Paul E., 2017; Sami et al., 2010). It is essential for medical research, clinical decision-making, and health management (Adeleye OA, 2009).

10.4. Future of Biostatistics

Biostatistics plays a crucial role in designing experiments and clinical trials, ensuring that they are conducted in a manner that produces reliable and valid results.

The future of biostatistics is poised to be innovative and impactful, driven by advancements in technology, data collection, and computational methods. Here are some key areas that are expected to shape the future of biostatistics:

- a) **Big Data and Omics Integration:** Biostatisticians increasingly deal with massive datasets from various 'omics' technologies like genomics, proteomics, metabolomics, etc. The integration of these diverse datasets requires sophisticated statistical methods to extract meaningful insights and unravel complex biological processes.
- b) **Machine Learning and AI:** These technologies play a crucial role in predictive modelling, pattern recognition, and classification tasks in biostatistics. They aid in identifying correlations, making predictions, and optimizing treatment strategies by analyzing large volumes of data.
- c) **Personalized Medicine:** Biostatisticians are instrumental in developing statistical models that tailor medical treatment to individual characteristics, considering genetic, environmental, and lifestyle factors. This involves creating algorithms that can predict a patient's response to specific treatments or interventions.
- d) **Clinical Trial Design and Analysis:** Advancements in statistical methodologies are crucial in designing more efficient and adaptive clinical trials. This includes methods for smaller, targeted trials, incorporating real-world

evidence, and optimizing trial designs to accelerate the drug development process.

- e) **Data Privacy and Ethics:** With the increasing reliance on patient data for research, ensuring data privacy, maintaining confidentiality, and adhering to ethical standards are becoming central concerns. Biostatisticians play a role in developing protocols and methods that protect patient privacy while enabling valuable research.
- f) **Interdisciplinary Collaboration:** Collaboration between biostatisticians and researchers from other fields, such as biology, medicine, computer science, and engineering, will continue to grow. This collaboration fosters the development of new methodologies more attuned to biological and medical data complexities.
- g) **Remote Monitoring and Real-Time Data Analysis:** With the rise of wearable devices and telehealth, a wealth of real-time health data is available. Biostatisticians are developing methods to process and analyze this continuous stream of data to monitor health conditions, detect anomalies, and provide timely interventions.
- h) **Data Collection:** Biostatistics will help design experiments and studies to gather data to ensure accuracy and relevance to the research questions being asked. This includes determining sample sizes, data collection methods, and protocols. Biostatisticians use various statistical software

like R, SAS, SPSS, and Python, along with a range of statistical tests and models tailored to different types of data (e.g., categorical, continuous, and survival data).

10.5. Conclusion

Overall, biostatistics is the ultimate goal of advanced statistics that will help to solve problems of human health and diseases as well as in the fields of agriculture, biochemistry, and biology. Epidemiology, anthropology, genetics, pharma industry and many more. For a better future as a biostatistician, we need to communicate our professional roles and goals, be scientifically responsible, and promote top-quality statistical designs and analyses. At its core, biostatistics is a powerful tool to unravel complex biological phenomena by employing statistical methods. Through rigorous analysis of data sets, biostatisticians draw conclusions that can impact healthcare policies, treatment effectiveness, disease prevention strategies, and our overall understanding of biological systems. These conclusions help researchers and practitioners make informed decisions, improve patient outcomes, and drive advancements in the field of life sciences.

10.6. References

1. Paul E. Leaverton. Biostatistics, 2017. <https://www.sciencedirect.com/topics/medicine-and-dentistry/biostatistics>
2. Sami W. Biostatistics education for undergraduate medical students. *Biomedica* 2010;26:80-4
3. Adeleye OA, Offili AN. Difficulty in understanding statistics: Medical students' perspectives in a Nigerian University. *Int J Health Res* 2009;2:233-4