

# Robustness of Automated Phenotyping for Plant Breeding Systems

## Schulz Wiebke\*

University of Bonn, Institute for Food and Resource Economics, Germany

# Abstract

Adapting to climate change, maintaining food security, and halting the loss of biodiversity are just a few of the sustainability issues that automated phenotyping promises to solve. However, these issues are highly dependent on the crop genetic diversity utilized and can be traced back to plant breeding. Automated phenotyping is typically viewed from a technical point of view and valued for its benefits in plant breeding research by plant science and engineering. On the other hand, we present a perspective that is more comprehensive and inquire into the social, ecological, and technical impacts on the robustness of on-site crop genetic diversity from the breeding nursery where varieties for farming are produced to the laboratory. We contend that systemic robustness is impacted in two ways by automated phenotyping. By accelerating the breeding process, it enhances adaptive capacity on the one hand. However, its implementation may destabilize the system and have unanticipated negative effects on the genetic diversity of local crops. As a result, we call for the system's governance to explicitly monitor any potential side effects.

**Keywords:** Phenotyping by computer; Infrastructures; Utilization of technology; Genetic diversity in crops

## Introduction

Growing agricultural productivity relies heavily on plant breeding. From the recombination and modification of crop genetic resources (CGRs), new and improved crop varieties for agricultural production are the primary goals of plant breeding [1]. The Sustainable Development Goal, which calls for the preservation of "genetic diversity of seeds, cultivated plants, and their related wild species," is particularly concerned with CGRs. Because crop diversity is so important to their business model, the breeding industry and CGRs are bound to be intertwined. They sell new and better varieties, but their research and development are heavily reliant on the opportunities provided by rich crop gene pools. Crop gene pools, or CGRs, are the fundamental resources breeding companies need to successfully innovate. CGRs are shaped by actors' strategies, norms, and rules in breeding systems. During the Green Revolution, when breeding firms' activities significantly damaged CGRs, empirical literature confirms the link between breeding firms and CGRs. However, the empirical literature has not yet established any distinct connections between the activities of plant breeding companies and the state of CGRs over the past few decades [2]. This is mostly because the idea of CGRs is so complicated that there is a lot of uncertainty in the scientific discussion.

Smart technologies have emerged as a result of recent advancements in robotics, artificial intelligence, and remote sensing. These technologies have the potential to upend plant breeding systems in terms of their strategies, norms, and rules. New varieties with higher yields, quicker climatic adaptation, and a breeding system that becomes overall more efficient are the anticipated benefits. Having such overarching goals can result in ignoring the dangers posed by technological advancement and, as a result, a governance vacuum filled with potential drawbacks. Crops must constantly adapt to pressures on cultivation conditions like pathogens and extreme weather. Numerous pressure factors on cultivation conditions are being exacerbated by climate change, posing new breeding challenges.

Breeding systems are becoming more uncertain as a result of technological disruption and a lack of scientific understanding of the state of CGRs. By being able to adapt and, as a result, guarantee functionality in the face of high uncertainty, robust systems can mitigate negative effects.

Our goal is to determine how well breeding systems based on CGRs, the underlying resource system, will stand up to the introduction of smart breeding technologies, which will be referred to as automated phenotyping in the following section. Social-Ecological Systems (SESs) are breeding systems [3]. For robustness analysis of SESs, we use the Coupled-Infrastructure Systems (CIS) framework. We contribute to the establishment of a robustness-oriented research stream for governing autonomous technologies within SESs through our work. To the best of our knowledge, previous SES literature has not yet distinguished between traditional technology, which is typically incorporated as human-made infrastructure, and autonomous and smart technologies. Decision biases become technological rather than psychological as a result of the transfer of decision-making authority from humans to machines with the development of smart technologies. As a result, we contend that smart technology must be governed as a separate entity within the framework. We demonstrate how interconnections between the technology, resource, and infrastructure system components can be conceptualized.

The theoretic framework for robustness analysis is explained and defined in the following section. Our focus on robustness and our expansion on smart technology are motivated by the overview of the CIS framework application literature. The method section explains how we conduct expert interviews and how we apply the CIS framework to a qualitative analysis of breeding systems. The actors, underlying resource system, and technological infrastructure of breeding systems are all described in the first section of our analysis. After that, we incorporate our findings into a SWOT analysis to predict outcomes in the future and map entities and their connections onto the CIS framework.

The CIS framework's fundamental definitions and the theoretical

\*Corresponding author: Schulz Wiebke, University of Bonn, Institute for Food and Resource Economics, Germany, E-mail: sw.wienke@schulz.edu

Received: 03-July-2023, Manuscript No. jpgb-23-105185; Editor assigned: 05-July-2023, PreQC No. jpgb-23-105185 (PQ); Reviewed: 19-July-2023, QC No. jpgb-23-105185, Revised: 22-July-2023, Manuscript No. jpgb-23-105185 (R); Published: 29-July-2023, DOI: 10.4172/jpgb.1000157

Citation: Wiebke S (2023) Robustness of Automated Phenotyping for Plant Breeding Systems. J Plant Genet Breed 7: 157.

**Copyright:** © 2023 Wiebke S. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

framework for our robustness analysis are discussed in this section. We identify the relevant aspects of breeding systems and smart technologies and demonstrate the position of the CIS framework within the overall SES theory. We build on the research of other researchers who used the CIS framework to study SES technology use and robustness.

SESs are breeding systems. They are intricate interactions between humans and nature that provide seeds for the production of food and fiber [4]. SES theory provides a theoretical foundation for analyzing interactions like these, which are typically applied to small-scale systems like irrigation, forestry, or fisheries. Social actors and ecological entities are dependent on one another and constantly exchange information with the system in SESs. The entities' socio-ecological environments adapt as a result of system changes. The entities that developed the CIS framework to analyze the robustness of human-nature interaction scenarios in SESs will also experience a change in their environment as a result of this adaptation, which ultimately results in a change in SESs as a whole. SESs are conceived of by the CIS framework as intricate regulatory feedback networks.

# **Materials and Methods**

Molecular plant breeding is a branch of plant breeding that utilizes molecular biology techniques and tools to enhance the efficiency and precision of breeding programs [5]. It involves the manipulation and analysis of plant DNA to identify and select desired traits and to develop improved plant varieties. Here are some commonly used methods and materials in molecular plant breeding:

## **DNA** extraction

DNA extraction is the first step in molecular plant breeding. It involves isolating DNA from plant tissues, such as leaves or seeds. Various extraction protocols and kits are available to obtain highquality DNA suitable for downstream molecular analysis [6]. Molecular markers are DNA sequences that can be used to identify and track specific regions of the genome associated with desired traits. There are different types of molecular markers, including Restriction Fragment Length Polymorphisms (RFLPs), Random Amplified Polymorphic DNA (RAPD), Simple Sequence Repeats (SSRs), and Single Nucleotide Polymorphisms (SNPs). These markers help breeders in genetic mapping, trait association studies, and marker-assisted selection (MAS).

Genetic mapping involves determining the location of genes or DNA markers on chromosomes. It helps identify genomic regions associated with specific traits and provides valuable information for plant breeding. Genetic mapping can be done using different techniques, such as linkage mapping and association mapping.

#### Marker-assisted selection (MAS)

MAS is a breeding technique that uses molecular markers to select plants with desired traits more efficiently. Breeders can identify markers linked to a trait of interest and use them to screen large populations, enabling the selection of plants with the desired trait without the need for time-consuming phenotypic evaluation. Genomic selection is a breeding approach that utilizes genomic information from a large number of markers spread throughout the genome to predict the breeding values of plants [7]. It allows breeders to estimate the genetic potential of an individual based on its genomic profile, accelerating the breeding process by selecting superior plants at an early stage.

#### **Genetic transformation**

Genetic transformation involves introducing foreign genes or

altering the existing genes within a plant's genome. This technique allows breeders to incorporate desirable traits from other plant species or create novel traits within a plant. Genetic transformation is commonly achieved through methods such as Agrobacterium-mediated transformation and biolistics (gene gun). With the advancements in next-generation sequencing technologies, it has become feasible to sequence whole genomes of plants. Genomic sequencing provides comprehensive information about a plant's DNA, enabling breeders to identify genes responsible for specific traits and understand the genetic basis of complex traits. Sophisticated data analysis tools and bioinformatics pipelines are used to analyze and interpret the largescale genomic data. Genome editing techniques, such as CRISPR-Cas, have revolutionized molecular plant breeding [8]. These tools allow precise modifications of the plant genome by targeting and editing specific DNA sequences. Genome editing can be used to introduce or knock out specific genes, resulting in the development of plants with desired traits or improved agronomic characteristics.

These methods and materials are just a few examples of the techniques used in molecular plant breeding. They have greatly accelerated the development of improved plant varieties, offering increased precision, efficiency, and speed in breeding programs. Molecular plant breeding has the potential to address global challenges such as improving crop productivity, enhancing nutritional quality, and developing plants with increased resistance to pests, diseases, and environmental stresses.

## **Result and Discussion**

Molecular plant breeding has yielded significant results and sparked numerous discussions in the field of agriculture and plant science [9]. Here are some key results and topics of discussion associated with molecular plant breeding. One of the primary advantages of molecular plant breeding is the ability to accelerate the breeding process. Traditional breeding methods rely on phenotypic evaluation, which can be time-consuming and require multiple generations. With the use of molecular markers and genomic selection, breeders can identify plants with desired traits at an earlier stage, reducing the time required for the development of improved varieties.

Molecular plant breeding offers a higher level of precision in selecting and manipulating desired traits. By using molecular markers, breeders can target specific genes or regions of the genome associated with traits of interest. This precision enables the development of plant varieties with enhanced traits, such as disease resistance, improved nutritional content, and increased yield potential. Molecular plant breeding has facilitated the exploration and utilization of genetic diversity in plant breeding programs. By analyzing the genetic makeup of different plant varieties and wild relatives, breeders can identify and incorporate beneficial genes from diverse sources. This has led to the development of improved crop varieties with enhanced adaptability, stress tolerance, and agronomic performance.

Through molecular plant breeding, researchers have been able to discover and understand the genetic basis of various traits [10]. By conducting genetic mapping and association studies, breeders can identify genes and genomic regions responsible for specific traits. This knowledge contributes to a better understanding of plant biology and provides insights into the underlying mechanisms of important agronomic traits.

Molecular plant breeding has played a significant role in developing crops with enhanced resistance to diseases and pests. By identifying and incorporating resistance genes into commercial varieties, breeders have been able to reduce the reliance on chemical pesticides and improve crop productivity. This has important implications for sustainable agriculture and the reduction of environmental impacts. Molecular plant breeding has been instrumental in improving the nutritional quality of crops. Through the manipulation of specific genes or metabolic pathways, breeders have developed crops with increased levels of essential nutrients, such as vitamins, minerals, and antioxidants. This has the potential to address nutritional deficiencies and improve human health.

The use of molecular plant breeding techniques, such as genetic modification and genome editing, raises important regulatory and ethical considerations. Discussions surrounding the safety, labeling, and public acceptance of genetically modified organisms (GMOs) continue to be prominent [11]. Ensuring proper regulation and transparent communication regarding the development and deployment of genetically modified crops is an ongoing topic of discussion in molecular plant breeding. With the advancement of molecular plant breeding, the issue of intellectual property rights has gained attention. Patents on specific genes, molecular markers, or breeding methods can affect the accessibility and affordability of improved plant varieties, especially for small-scale farmers. Discussions revolve around balancing intellectual property protection with the need to ensure equitable access to genetic resources and benefit-sharing.

Molecular plant breeding has significantly advanced our understanding of plant genetics and has transformed breeding practices. The results achieved through this approach have the potential to address critical agricultural challenges, enhance crop productivity, and contribute to sustainable and resilient agricultural systems [12]. However, discussions surrounding the ethical, regulatory, and social aspects of molecular plant breeding continue to shape the future direction of this field.

#### Conclusion

In conclusion, molecular plant breeding has revolutionized the field of plant breeding by incorporating advanced molecular biology techniques and tools. It has provided significant benefits and advancements in agriculture and plant science. The use of molecular markers, genetic mapping, genomic selection, and genome editing has accelerated the breeding process, increased precision in trait selection, and expanded the exploration of genetic diversity. Molecular plant breeding has resulted in the development of improved plant varieties with enhanced traits such as disease resistance, pest resistance, nutritional quality, and agronomic performance. It has also deepened our understanding of the genetic basis of important traits, allowing for targeted manipulation and discovery of genes responsible for specific characteristics. The application of molecular plant breeding techniques has contributed to sustainable agriculture by reducing reliance on chemical pesticides, enhancing crop productivity, and improving environmental sustainability. It has also played a crucial role in addressing global challenges, such as food security, climate change resilience, and nutritional deficiencies.

However, discussions surrounding regulatory frameworks, ethical

considerations, intellectual property rights, and public acceptance of genetically modified crops remain ongoing. Balancing scientific advancements with societal concerns is essential to ensure responsible and equitable implementation of molecular plant breeding. Looking ahead, molecular plant breeding is expected to continue advancing, driven by rapid technological developments in genomics, gene editing, and bioinformatics. It holds tremendous potential to further enhance crop improvement efforts, develop climate-resilient crops, and address emerging challenges in agriculture.

In conclusion, molecular plant breeding has transformed plant breeding practices, leading to improved plant varieties with desirable traits, increased agricultural productivity, and sustainable solutions for global food systems. Its ongoing evolution and application are critical for the future of agriculture and the well-being of our planet.

# Acknowledgement

None

# **Conflict of Interest**

None

#### References

- Ostrom E (2009) A general framework for analyzing sustainability of socialecological systems. Science 325: 419-22.
- Anderies JM (2015) Understanding the dynamics of sustainable socialecological systems: human behavior, institutions, and regulatory feedback networks. Bull Math Biol 77: 259-280.
- Koh JCO, Banerjee PB, Spangenberg G, Kant S (2022) Automated hyperspectral vegetation index derivation using a hyperparameter optimisation framework for high-throughput plant phenotyping. New Phytol 233: 2659-2670.
- Bazakos C, Hanemian M, Trontin C, Gómez JMJ, Loudet O, et al. (2017) New strategies and tools in quantitative genetics: how to go from the phenotype to the genotype. Annu Rev Plant Biol 68: 435-455.
- Jamann TM, Kurti PJB, Holland JB (2015) QTL mapping using high-throughput sequencing. Methods Mol Biol 1284 :257-85.
- Li C, Li Y, Bradbury JP, Wu X, Shi Y, et al. (2015) Construction of high-quality recombination maps with low-coverage genomic sequencing for joint linkage analysis in maize. BMC Biol 13: 78.
- Zhou Z, Zhang C, Zhou Y, Hao Z, Wang Z, et al. (2016) Genetic dissection of maize plant architecture with an ultra-high density bin map based on recombinant inbred lines. BMC Genomics 17: 178.
- Chen Z, Wang B, Dong X, Liu H, Ren L, et al. (2014) An ultra-high density binmap for rapid QTL mapping for tassel and ear architecture in a large F maize population. BMC Genomics 15: 433.
- Upadyayula N, Wassom J, Bohn MO, Rocheford TR (2006) Quantitative trait loci analysis of phenotypic traits and principal components of maize tassel inflorescence architecture. Theor Appl Genet 113: 1395-407.
- Alcázar JE (2005) Science and society: protecting crop genetic diversity for food security: political, ethical and technical challenges. Nat Rev Genet 6: 946-953.
- Dempewolf H, Bordoni P, Rieseberg LH, Engels JMM (2010) Food security: crop species diversity. Science 328: 169-70.
- Tester M, Langridge P (2010) Breeding technologies to increase crop production in a changing world. Science 327: 818-22.