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STUDY OF THE GENETIC DIVERSITY OF CROPS IN THE ERA OF MODERN PLANT BREEDING

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Abstract: *Modern plant breeding has transformed food production and will be essential to guaranteeing food security on a global scale. Striking a balance between increasing crop output in response to climate change and reducing crop failure in difficult conditions is crucial for sustainable agriculture. A fuller understanding of how plant breeding affects agricultural genetic diversity is necessary to make this trade-off. Molecular marker technology has been applied to research agricultural genetic diversity throughout the past three decades. Our results disproved our hypothesis that current plant breeding diminishes agricultural genetic diversity by revealing temporal patterns of genetic diversity. This review analyzed theoretical and empirical estimates of agricultural genetic variety, focusing on how genetic diversity varies in response to artificial selection through time, in an effort to understand these oscillations. Numerous studies on agricultural genetic diversity lacked sufficient experimental design, including technical biases related to cultivar and genome sampling, and were not intended to look at how certain plant breeding efforts affected diversity. Theoretical research on how plant breeding affects agricultural genetic diversity has received little attention. Computer simulations of five standard breeding strategies show that plant breeding has a considerable impact on the preservation of heterozygosity over generations. It is crucial that additional plant breeding research investigates the geographical and temporal diversity of agricultural genetics in order to achieve sustainable crop output.*

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Introduction

Plant breeding has had a substantial impact on food production since the early 1900s and will continue to be crucial to global food security. However, this has led to crop homogeneity across farmlands, making them genetically vulnerable to biotic and abiotic impacts. Since epidemics such as the Irish potato blight in the 1840s and the U.S. maize blight in the 1970s, the public has been made aware of such risks(Poland & Rife, 2012). The exceedingly dangerous new East African strain of stem rust, Ug99, poses a threat to wheat with a homogenous genetic makeup at now. Achieving a balance between maximizing crop yield under specified conditions and minimizing crop failure risk when those conditions change is essential, albeit challenging, for the development of effective solutions for sustainable agriculture. Understanding the effects of present plant breeding on agricultural genetic diversity is essential to achieving this accord(Rauf et al., 2010).

In the past three decades, molecular marker technology has been utilised to study agricultural genetic variation. These investigations have greatly improved our understanding of the types and quantities of genetic diversity present in agricultural germplasm that has been kept and/or is currently in use. In addition to supporting our efforts to preserve germplasm, these studies also provide recommendations for more efficient uses of germplasm in genetic advancement. Numerous studies have identified significant historical patterns of crop genetic diversity, generally contradicting the widely held belief that modern plant breeding reduces agricultural genetic diversity. A meta-analysis of 44 published diversity studies, for instance, revealed that the genetic origins of breeder-supplied types cannot be limited indefinitely(Cooper et al., 2014). Current plant breeding programmes would subject a small number of plant germplasm containing a few allele introgressions to strong selection, hence diminishing genetic diversity. In addition, freshly issued crop varieties are more uniform phenotypically and have less genetic diversity than previously published crop types. This mismatch demonstrates our poor grasp of the genetic diversity of modern plant breeding-produced crops(Turan et al., 2012).

To attempt to comprehend this discrepancy, we analysed both theoretical research on the evolution of genetic diversity under artificial selection and empirical estimates of crop genetic diversity. We intend to focus on the following concerns: (1) Why do most estimates of biodiversity fail to recognise the biodiversity loss caused by modern plant breeding? Is it true that plant breeding reduces agricultural genetic diversity? (3) How much theoretical study has been performed on the effects of artificial selection on genetic diversity? (4) What more research is necessary to fill the knowledge gap in this field? The goal of the evaluation was to provide explanations and recommendations regarding these issues.

Empirical analyses of the genetic diversity of crop species

In the past three decades, crop uniformity has been a cause for concern, and analyses of agricultural genetic varieties have been more prevalent. According to a prior study that analysed phenotypic and pedigree data, greater yield and other quality enhancements reduced the genetic diversity of the enhanced gene pools(Brown & Caligari, 2011). The discovery of molecular markers such as RAPDs, AFLPs, and SSRs has made crop diversity assessments more practicable and valuable than ever before. Despite the restricted use of genome-wide SNP markers, these molecular investigations have generated a wealth of information regarding the type and amount of genetic diversity observed in numerous crop species. These evaluations for marker application and agricultural genetic diversity have been investigated in detail. Here is a summary of the researchers' significant results(Gerald et al., 2013).

The context of contemporary plant breeding

By creating and utilising cutting-edge cultivars, plant breeding has had a significant impact on the world's food supply since the early 1900s. New cultivars have been produced using a number of effective breeding approaches, including marker-assisted selection for specific genes, controlled mating, phenotypic selection on natural variants, and importation. The two main components of plant breeding are: (1) the deliberate introduction of genetic diversity into breeding populations through intercrossing chosen plants with exceptional traits that complement one another; and (2) the selection of superior plants with genes for desired traits until higher levels of enhanced adaptation, genetic uniformity, and agronomic stability are attained. The most crucial aspects to take into account when choosing a breeding strategy are the crop reproductive mechanism (selfing or crossing) and the desired breeding outcomes(Forster & Thomas, 2010).

Increased yield, adaptability, resistance to biotic and abiotic stresses, and end-use quality have been the main goals of crop breeding activities. Breeding goals have changed throughout time in addition to increased output. Critical are new cultivars that can provide high yields with minimal chemical inputs, as well as the genetic variety necessary to preserve yield stability in the face of climatic change. Increased nutritional value, improved weed control, and optimised plant-soil microbial interactions are some of the distinguishing characteristics that have been upgraded for sustainable agriculture(Crossa et al., 2017). Conventional plant breeding has evolved to solve these challenges by incorporating ideas from other scientific domains, allowing breeders to better and more effectively manage genetic resources. Haplotype construction, the application of sterility procedures and transgenic technologies, apomixis, and processes supported by molecular markers are some of these cutting-edge operations(Smith et al., 2015). For a range of breeding objectives, molecular breeding has superseded conventional breeding in modern plant breeding, and several breeding methods have been used over time. As a result, for certain breeding programmes, selective pressure within breeding populations varies during different breeding phases, changing the genetic diversity of released crop cultivars. Self-pollinating plants will likely have more genetic variation than outcrossing ones (Crossa et al., 2010).

Differences in the ways genetic variation

Current understanding of genetic variation is limited. It is typically described as any change through time in the nucleotides, genes, chromosomes, or genomes of an individual, population, species, or region. Such a broad word always leads to misunderstandings and confusion. Therefore, its measurements are deceiving. Typically, the theta parameter, heterozygosity, and allelic polymorphism are employed to evaluate the genetic diversity of a population. It is standard practise to examine allele and genotype frequency differences in populations exhibiting genetic variation using a variety of distinct methods. Analogues, genetic segregation, and sequence divergence are the three. The management of these diversity programmes has been the subject of heated discussion(Tanksley & Orton, 2012).

In the past, morphological metrics, namely agro-morphological features of consumer value, have been utilised to analyse crop genetic diversity. Ultimately, biochemical techniques such as protein and isozyme electrophoresis were utilised to reduce the influence of ambient influences on the analysis. Since 1990, numerous molecular techniques, including RAPD, AFLP, and SSR, have been utilised to explore genetic diversity. These molecular markers can boost the resolution of genetic variation studies by removing environmental effects and giving plants with a more comprehensive genome sample. There are already over thirty distinct types of molecular markers that can be employed to evaluate genetic diversity. Using these genetic markers, which have been extensively used to characterise agricultural genetic variation, the genetic diversity of food plants has been analysed. Using genome-wide SNP markers and expanded plant genome collection, the genetic diversity of agriculture has not been exhaustively studied(Resende, 2016).

Due to the broad concept of genetic diversity, the variety of diversity metrics, and the extensive usage of molecular markers, published diversity evaluations vary substantially. Even for crop species, it is difficult to generalise and comprehend the conclusions of different variety indices based on various markers. For instance, the accuracy and precision of diverse genetic diversity assessments can vary, and not all genetic diversity measurements have consistently exhibited the same sensitivity in detecting changes in genetic variety brought about by plant breeding practises. As demonstrated with oat utilising AFLP and SSR markers, not all molecular markers utilised in the study of diversification are equally helpful. Consequently, differences are possible even when applying the same test but employing distinct variety elements (Lusser et al., 2012).

Importance of protecting plant and crop genetic material

What relevance does genetic diversity have? The two fundamental objectives of conservation genetics are the preservation of genetic variation at various scales and the creation of population monitoring and evaluation tools applicable to conservation planning. Each individual possesses genetic variety. Individuals are rarely the focus of conservation efforts or related research, despite the fact that genetic diversity is always measured at the level of the individual and can only be approximated for groups of individuals within a population or species(Breseghello & Coelho, 2013). In order to distinguish between phenotypic and genetic variation, traits can be categorised as discrete or quantitative, which are commonly referred to as qualitative traits. Defined characteristics are attributes that fall into discrete categories that are controlled by one or a limited number of dominant genes, such as the white, pink, or red petals of particular flowers. By analysing enzyme-level variation, protein electrophoresis can discover genetic diversity. The DNA nucleotide sequence can be utilised to study genetic differences(Jannink et al., 2010).

Loss of genetic diversity as a result of increasing size of the population

Inbreeding has been observed in cross-pollinated crops, resulting in negative consequences and decreased population fitness in tiny outcross groups due to recombination of unfavourable genes (recessive identical alleles)(Litrico & Violle, 2015). The crop in question faces extinction due to the so-called genetic bottleneck, which also impacts wild populations and causes dramatic population reductions, genetic variety loss, and increased susceptibility to infectious diseases and pests(Mammadov et al., 2012).

The effects of climate change on plant germplasm

Over the next ten to twenty years, the effects of climate change on agriculture and food security will probably be the most serious and immediate. Climate change's consequences will also be determined by the existing output status. Pollution is already an issue in the region, and climate change will almost surely exacerbate it(Xu et al., 2012). Food production systems rely on carefully selected cultivars in better-equipped habitats, but they may become more subject to the effects of climate change, such as the spread of pests and diseases(Hickey et al., 2017). If annual food production falls, there will be intense pressure to plant crops on marginal land or use unsustainable farming practises, which will deplete resources and destroy lands over time, have a negative impact on biodiversity in and around agricultural areas, and will also be under significant pressure(Savidan, 2010). In reality, the majority of emerging countries have encountered similar issues in the past. These modifications have been reported to lower the number of genetic loci (gene alleles) that control physical and phenotypic responses to climate change (Heslot et al., 2012). As a result, genetic diversity is critical for populations and species to persist across time in the face of changing environments. If this trend continues, no creature will be able to foretell its own future since evolutionary theory does not support it, and no species will be completely adapted to every imaginable environmental condition. Individuals of a crop species' adaptation to biotic and physical conditions, on the other hand, is governed by their genetic make-up(Brummer et al., 2011).

Evaluation of the genetic diversity in agricultural plants

Numerous techniques, including (I) morphological, (ii) biochemical characterization/evaluation (allozyme), and (iii) DNA (or molecular) marker examinations, particularly single nucleotide polymorphism (SNPs), are often used to study genetic variation within and between plant populations(Schaart et al., 2016). The same dominant/recessive or codominant inheritance patterns that apply to other qualities may also apply to markers. If a marker is codominant, it is possible to distinguish between the genetic make-up of homozygotes and heterozygotes. Codominant markers offer more information than dominant ones do(Poehlman, 2013).

Morphological markers

Despite the fact that morphological markers are based on traits that are visible to the naked eye, such as flower structure, fruit colour, plant growth habits, and pigmentation of flower, they frequently require large amounts of land for field experiments, making them potentially more expensive than molecular analysis in western (developed) countries and equally expensive in Asian and Middle Eastern (developing) countries when labour costs and availability are taken into account(Holland, 2010). Due to the phenotypic plasticity of these marker phenotypes, it is possible to evaluate diversity in the presence of both genotypic and environmental variation. Seeds with barbs, panicles with bristles, and unique flower/leaf colours are still essential for distinguishing adult plants in the field despite genetic interference (Ceccarelli, 2015).

Conclusion

Farmers have acknowledged the significance and irreplaceability of diverse plant genetic resources. To feed the world's constantly expanding population, there is a growing demand for these resources. It is essential for crop improvement that breeders have options for developing novel varieties and hybrids, which is provided by genetic diversity. This can be facilitated by phenotypic and molecular characterization of PGRs. Large gene pools can complicate reproduction.

Conflict of interest

The authors declared absence of conflict of interest.

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