

## Integrative and Inclusive Genomics to Underutilized Crops: Current Trends

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### Abstract

It is crucial to use underutilized crops to diversify food systems. Instead of being conducted in a vacuum, the genomics of these crops should be integrated with their breeding and capacity-building plans, capitalizing on advancements in big crops.

### Introduction

Humans regularly consumed around 7000 plant species before the invention of agriculture, but only about 250 of them have been fully domesticated, and just about 30 of these account for approximately 95% of the world's calorie consumption. Ecological and nutritional resilience have decreased as a result of investment in this limited range of crops. While vital locally, there are obstacles to their wider acceptance. A number of lesser-known domesticated or semi-domesticated crops have great promise to increase the diversity and resilience of our food systems. Instead of referring to these crops as "minor," "abandoned," or only coming from a certain location, we use the word "underutilised." While each of these titles would refer to a distinct crop category, we want to highlight the unrealized potential of these crops to support world nutrition by using the phrase "underutilised." Despite originally behind, the genomics of underutilized crops has accelerated because of advancements in genome assembly, sequencing, and annotation technologies. The accessibility of genetic resources is helping to clarify the history of underutilized crops, including as their artificial selection, domestication, and polyploidization. The genetic architecture of significant agronomic and end-use features, such as tuber quality in greater yam, and the distinct climatic resistance of crops, such as tepary

bean, which is suited to desert environments, have also been clarified by genomics. Advances in underutilized crop genomics are described in depth in recent reviews. A number of evaluations have also been conducted on the overall underutilization of underutilized crops as well as policy and ethical issues." We contend, however, that the creation of underutilized agricultural genetic resources must not to be carried out in a vacuum. Rather, by utilizing current advancements in key crops, such efforts should be in line with the overall breeding plans of the target crops as well as the requirements and perceptions of the populations who depend on these products.

### **Aligning the seed system and breeding strategies in Underutilized Crops Genomics:**

Improved seeds for most major crops are readily available through formal seed systems, which involve organized public and/or private sector breeding and distribution channels. However, underutilized crops are primarily shared among smallholder farmers through informal seed systems, which makes it more difficult to quickly adopt improved materials. Even while genomics might not have an immediate impact on all seed systems, early stakeholder involvement, especially during the breeding and germplasm evaluation phases, can greatly boost the allure, profitability, and adoption of underutilized crops. This is particularly true given that farmers' and end users' opinions of underutilized crops are occasionally founded on implicit traditional knowledge that is not always reflected in the quantitative features used in formal breeding. As shown by Woldeyohannes et al. and Gesesse et al, including this tacit knowledge into genomic screening will help advance our understanding of the adaptive potential and practical applications of the genetic variety that is already present in farmers' fields and preserved diversity in gene banks. With this knowledge, formal and farmer-participatory models may be integrated to identify, rank, or create farmer-preferred germplasm that is modified. Formal plant breeding is not necessary in this approach because, as the "Seeds for Needs" model suggests, integrated seed systems may be used to make important germplasm (landraces) discovered by genomic-assisted participatory screening broadly and easily available to farmers. The demand from the breeding and end-use communities should inform the choice of germplasm used to generate genomic resources to maximize the effect and relevance of underutilized crop genomics. This is especially crucial when choosing cultivars for reference genome assemblies, which should have demand-driven features that are



significant regionally, be representative of significant founder parents, or have abundant genetic resources (markers, genetic maps). For example, Bredeson et al. sequenced a breeding line that is commonly employed as a parent in the larger yam breeding program and that has a modest resistance to anthracnose, a significant disease in this crop, as part of their genome sequencing project for the greater yam.

#### **Promotion of use of underutilised crop genomes:**

Rich countries and institutions dominate the majority of genetic research on underutilized crops, as is the general trend in plant genomics. A few notable outliers include the recently sequenced lablab genome from East Africa, the Nigerian larger yam genome, the Colombian Lima bean genome, and the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) mandate crops, whose full genome sequencing was mostly directed from India. Genomic studies on underutilized crops should be used to strengthen research capabilities in these areas, considering the enormous importance of these crops to many indigenous communities. Just as vital as having access to a genome is the capacity to make use of it. To fully realize the promise of genetic data and technologies in underutilized crops, systems with overlapping knowledge and efficient communication chains among interest groups are required, while proficiency with genomic data is not a must for everyone. We contend that longer-term, hands-on, in-country trainings have a greater impact than short-term (days) capacity development initiatives, particularly when they are tailored to address shortages in the local environment. Rather than being an afterthought, these initiatives ought to be considered when genomics research on underutilized crops are first initiated. Genomic research on the target crops should be co-designed and co-led by researchers from communities that have a solid awareness of farmer and consumer preferences. Inclusion and capacity development in genomics research on underrepresented crops are now being promoted by an increasing number of international collaborations and consortia (e.g., Africa Bio Genome Project, African Orphan Crops Consortium, and CABANA/Capacity development for Bioinformatics in Latin America). The promotion of curiosity-driven research is aided by inclusivity and diversity, as local knowledge is integrated to enhance research questions. This results in more relevant, reliable, and translatable research outputs, improved adoption of recommendations, and greater ownership and stewardship of the resources that are produced.



### **Major crops should be used to fast-track underutilised crops genomics:**

The rate of genetic improvement in underutilized crops has to be accelerated. Numerous agriculturally significant features of key crops are well understood to be regulated by genes and molecular pathways. To enhance these crops, a variety of techniques, including transgenics, genome editing, genomic selection, and speed breeding, have been developed. These instruments have to be employed to disseminate expertise and expedite the process of domesticating and enhancing underutilized crops from scratch. Two of the most well-known breeding advances that drastically cut down on breeding time and expense are genomic selection and speed breeding. These instruments could be especially helpful in small breeding programs when resources are limited and genetic advances need to be accelerated. Crucially, fast breeding techniques and genomic selection that have been developed for several main crops might be effortlessly applied to closely related but underutilized crops to produce noticeable results right away. Dispensable areas may include adaptive variation, as in the case of foxtail millet, while core genome sections are present in all accessions but may comprise just half of the pangenome. Applying these methods to underutilised crops would provide a far more comprehensive view of genetic diversity. Unprecedented possibility to expedite domestication and development of underutilized crops is presented by gene editing. While keeping in mind that gene function is not necessarily conserved across species, knowledge about gene function from similar big crops may help choose prospective gene targets in underutilized crops. CRISPR/Cas systems have made gene editing more accessible and affordable. They have also shown promise in domesticating underutilized crops, such as groundcherry<sup>24</sup> and African rice, by focusing on genes that were initially researched in big crops. Despite this possibility, given the historic and cultural significance of these crops to indigenous populations, the application of gene editing, especially in underutilized crops, should be carefully evaluated. The widespread application of gene editing in several underutilized crops is impeded by the absence of effective transformation and regeneration techniques that are independent of genotype. Furthermore, a significant barrier to the use of CRISPR/Cas systems in varietal development remains licencing concerns. As a component of the above-mentioned capacity building endeavor, we support targeted projects and financial support to facilitate the transfer of technical know-how (in transformation and regeneration) and the creation of adequately resourced and licensed tissue culture laboratories for the



application of transformation-enhancing systems (such as morphogenic genes like WUSCHEL, BABY BOOM, and GRF-GIF) and gene editing in underutilized crop communities.

### **Linking genomics with physiology and biochemistry of underutilised crops:**

Numerous underutilized crops can withstand drought, cold, and heat stressors and are suited to degraded, marginal, or otherwise deficient soils. They have the reputation of being insurance or famine crops since they are frequently the only crops remaining after most staple crops have failed. Because underutilized foods have a high nutritional and nutraceutical content, many indigenous groups employ them to cure illnesses or encourage healthy living. Thus, crops that are underutilized are a source of unique adaptive genetic, physiological, and biochemical diversity. To construct a more comprehensive understanding of crop adaptability and metabolic phenotypes at the cell, organ, plant, and species levels, it is imperative to incorporate underutilized crop genomics with plant physiology and biochemistry. Research like those by Moghaddam et al. and Edwards et al. show how important it is to combine biochemistry, physiology, and genetics to find metabolic abnormalities and adaptability in underutilized crops. It has previously been demonstrated that several adaptive genes or alleles from underutilized crops provide climatic resilience in model plants or staple crops. In conclusion, crop genomics has been underutilized for a while, but it should not be used alone. It will be necessary to integrate various systems, participants (such as academics, breeders, and indigenous communities), tools (such as gene editing, genomic selection, and speed breeding), and disciplines (such as genomics, physiology, and biochemistry) to translate genomic advancements into feasible pathways towards food and nutritional security. Underutilized crops could help improve resilience and nutritional traits in major crops, and underutilized crops could benefit from knowledge gained in major crops in terms of domestication, yield, and agronomy improvements. Research on both major and underutilized crops would be beneficial to each other. To further research into underutilized crops, it is necessary to evaluate international rules on germplasm access and benefit sharing. It is also crucial to remember that sharing of germplasm and digital sequence information (DSI) is a component of this process.

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