



Short communication

New proposals to strengthen the boom of agriculture in Peru: massive use of genetic resources and development of modern breeding programs

Nuevas propuestas para fortalecer el boom de la agricultura en el Perú: uso masivo de recursos genéticos y desarrollo de programas modernos de mejoramiento

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Abstract

Peru is a place with abundant biological resources that should be employed for the benefit of society in general. However, to date, the use of Peruvian plant genetic resources was not fully exploited for the development of improved crops. This work was mostly conducted by the international private sector. The Climate Change Laboratory at Instituto Nacional de Innovación Agraria, and other laboratories at Universidad Nacional José Faustino Sánchez Carrión and Universidad Nacional Agraria La Molina together with other research programs of other institutions seek to promote the massive and sustainable use of plant genetic resources maintained in germplasm banks. It is planned to make use of modern molecular and morphological techniques. Moreover, infrastructure and human resources are being improved. As a result, we will be able to maintain the growth of the agricultural activity in Peru in terms of space and time.

Keywords: Plant genetic resources, genotype-phenotype association, molecular tools

Resumen

El Perú es un país con abundantes recursos biológicos que conviene emplear en beneficio de la sociedad en general. Sin embargo, hasta la fecha, el uso de los recursos fitogenéticos peruanos no se ha utilizado plenamente para el desarrollo de variedades mejoradas; este trabajo ha sido implementado principalmente por el sector privado a nivel internacional. El Laboratorio de Cambio Climático del Instituto Nacional de Innovación Agraria (INIA) y otros laboratorios de la Universidad Nacional José Faustino Sánchez Carrión (UNJFSC) y la Universidad Nacional Agraria La Molina (UNALM), junto a los programas de investigación de otros centros de investigación, buscan promover el uso masivo y sostenible de los recursos fitogenéticos mantenidos en los bancos de germoplasma; está previsto hacer uso de modernas técnicas moleculares y morfológicas, además que se está mejorando la infraestructura y los recursos humanos. Como resultado, podremos mantener el crecimiento de la actividad agrícola en el Perú en términos de espacio y tiempo.

Palabras clave: Recursos fitogenéticos, asociación fenotipo-genotipo, herramientas moleculares

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Introduction

The pandemic has marked a new stage in the world economy after the closure of many markets for agricultural products. There is sufficient evidence that the pandemic caused by the COVID-19 disease had an important effect on agriculture and the food supply chain, mainly affecting food demand and consequently food security (Siche, 2020). Recently, there is information that the world recovers significantly as many governments announced unprecedented economic rescue packages (Seven & Yilmaz, 2021). The prospects for an improvement in the global economy are revised upwards by the main multilateral organizations; this year we will have a 6% growth in the global economy according to the director of the Business and Economics Research Center of the Association of Exporters, world food imports will expand by 12% and will reach a global record level of 1.715 trillion dollars (Andina, 2021).

The rapid expansion of plant breeding during the second half of the 20th century brought the introduction of a big number of improved varieties, which progressively replaced old landraces, especially in developing countries. Not all the genes present in the farmers' varieties are also contained in modern varieties (Sonnino, 2017). Access to genetic and genomic resources can greatly facilitate the biological understanding of plant species leading to improved crop varieties. While model plant species such as *Arabidopsis* have had nearly two decades of genetic and genomic resource development, many major crop species have seen limited development of these resources due to the large, complex nature of their genomes (Hirsch et al. 2016). Gene banks play a crucial role in securing genetic diversity for research and breeding, now and in the future. The collection and correct classification of crop wild relatives is an important aspect of this work (van Bemmelen et al., 2021).

To date, Peruvian plant genetic resources have not been fully exploited for the development of improved crops. In this short communication, we discuss the importance and use of genetic resources for the establishment of modern plant breeding programs.

Peru, a center of domestication of important plants

Currently, in all scientific meetings and academic conversations about plants, it is almost impossible not to mention Peru when talking about domestication or centers of origin of crops that today feed the entire world. This is explained because Peru is one of the most important centers of plant domestication in the world, thanks to the work of ancient Peruvian farmers, who have cultivated and used more than 150 crops in the last 10,000 years such as aguaymanto (*Physalis peruviana*), caigua (*Cyclanthera pedata*), beans (*Phaseolus vulgaris*), potatoes (*Solanum* spp.), quinoa (*Chenopodium quinoa*), and many others. However, it is almost common to see in the news that our farmers obtain low yields or lose their crops due to frosts, droughts, pests and diseases, affecting their family income and placing them in conditions of risk and vulnerability. All these problems can be overcome by doing work similar to that carried out by Andean farmers during the last 10,000 years, that is, by breeding our crops complemented by efficient agronomic management of each one of them. The process of domestication of plants began using wild species -plants that grow freely in nature without needing the care of the farmer- (Martin & Sauerborn, 2013). For example, to the northeast of Camana in Arequipa (Peru), and other valleys of the Peruvian coast, there are wild tomatoes that coexist with other crops and plantations for human consumption. This wild tomato plant (*Solanum pennellii*) is small in size, with light green fruits and a sour taste. Recent research in tomato cultivation reports that many genes of these wild tomatoes are present in the crops that farmers grow in their fields (Bolger et al., 2014).

Agriculture has the potential to mitigate problems that Peru has dragged for decades, such as unemployment and poverty, and has the capacity to be an economic engine that drives the country on a sustained basis, in parallel with other economic sectors. For example, the agricultural sector comprises 30% of the EAP and 6% of the national GDP. Therefore, it is essential to continue supporting Peruvian agriculture making use of the richness in agricultural biodiversity,

through the study and genetic use of native and wild plants of Peru to later develop cultivars that help us face the problems in agriculture and maintain a robust sector in time and space.

To date, we consider that it is necessary to give greater importance to the development of modern breeding programs of key crops in our country. The Peruvian agro-export sector has been in constant growth in recent years, reaching an economic value of USD 7 billion annually. This boom is mainly explained by the use of greater agricultural technology, such as drip irrigation, fertigation, and pruning, among others. However, the genetic component has not yet been fully exploited. This is reflected in far below average yields for some crops.

For example, de Haan et al. (2010) showed that individual potato farm households in Peru maintain high levels of cultivar, morphological, and genetic diversity. Tetraploid native potatoes were most abundant, followed by diploids, triploids, and pentaploid potatoes. However, Peru has a national average yield of 16 t ha⁻¹, comparing to other countries where national averages of 40 t ha⁻¹ are reached. The big difference lies mainly in the use of higher quality seeds by farmers. This case is different for crops such as tomato, where hybrid seeds of very high genetic value are used, reaching averages very similar to those in the Netherlands in Peru, that is, 100 t ha⁻¹. Application of next-generation sequencing (NGS) technologies would accelerate germplasm enhancement, the evaluation of genetic diversity in situ and ex-situ, and conservation strategies of plant genetic resources (Machida-Hirano & Niino, 2017).

In order to support the rise of Peruvian agriculture, we have been executing research projects related to the massive use of Peruvian genetic resources in favor of Peruvian agriculture, focusing on the genetic improvement component of plants with the greatest national economic potential. Among the projects in execution and/or in the process of starting execution, garlic (*Allium sativum*), sweet cucumber (*Solanum muricatum*), carrot (*Daucus carota*), chilli peppers and hot peppers (*Capsicum* spp.), starchy corn (*Zea mays*) and onion (*Allium cepa*) are under consideration. At the same time, we invite

other research groups to join this initiative. In addition, it is helpful to interact more closely and constantly with the private agricultural sector. In this way, we can have a robust sector that works providing solutions to the constant challenges that arise in the agricultural sector.

It is very important that Peru maximizes the use of its great biodiversity, studying all the secrets maintained in the genes of native crops and their wild relatives that exist in the country. For example, wild tomato (*Solanum pennelli*) is native to Peru and has genes that give it tolerance to salinity (Peralta & Spooner, 2000). Making use of these genes present in this species will be of great importance to developing tomato cultivars with tolerance to salinity that can be cultivated in the desert and salty areas of the Peruvian coast.

Similarly, genes that improve the nutritional content of quinoa (*Chenopodium quinoa*), cañihua (*Chenopodium pallidicaule*) kiwicha (*Amaranthus caudatus*), arracacha (*Arracacia xanthorrhiza*), yacón (*Smallanthus sonchifolius*), maca (*Lepidium meyenii*), pepper, corn, among others, can be identified. The genetic improvement of these crops can be optimized thanks to the use of new technologies, such as the sequencing of whole genomes, which are highly reliable, fast to execute, and low cost. As a first step, we propose to know exactly what exists within germplasm banks at INIA and UNALM. This will be achieved through the characterization of germplasm. Therefore, the accessions will be genotyped to determine the genetic diversity and population structure.

Likewise, genotype-phenotype association studies can be carried out, thus identifying putative regions of the genome that code for regions of agronomic and/or economic interest. At the same time, it is necessary to know the genotype x environment (GxE) interaction. This will be achieved through the use of quantitative genetics tools. At the same time, in order to make the selection and obtain greater genetic gain in less time, the use of genomic selection will be performed. These jobs are focused mainly on pre-breeding work. The challenge for the next generation of quantitative geneticists and plant breeders is not only to understand the genetic basis of complex trait variation but also to use

that knowledge to efficiently synthesize twenty-first-century crop varieties (Cobb et al. 2013).

To date, we have a project underway regarding the improvement of starchy corn germplasm from ten Peruvian races. This work is conducted in collaboration with researchers from the Swedish University of Agricultural Sciences (SLU), Centro Internacional de Mejoramiento de Maíz y Trigo (CIMMYT) and North Carolina State University (NCSU). We genotyped 400 accessions of starchy maize. Likewise, the genome of “CUSCO Gigante” maize is being sequenced to generate molecular resources for subsequent genetic improvement and to understand more other biological aspects. On the other hand, we are working on developing molecular tools for the Peruvian national tree (quina, *Cinchona officinalis*), native chilli peppers (*Capsicum* spp.), sweet cucumber (*Solanum muricatum*), capirona (*Calycophyllum spruceanum*) and loche squash (*Cucurbita moschata*).

Likewise, we have two proposals for research projects still under evaluation. Finally, it should be noted that we are expanding our collaboration with different entities both nationally and internationally. This allows us not only to boost our scientific productivity but also to promote the academic exchange of the most valuable item in research, human resources.

Conclusions

As collections of crop wild relatives are increasingly genotyped and sequenced, this creates an excellent opportunity for gene banks to improve the quality of their documentation in several Peruvian food crops as potatoes, chilli peppers, quinoa, kiwicha, maize and others. Also, there are several studies focused on developing molecular tools to maximize tools in perennial species such as *Cinchona officinalis*, *Calycophyllum spruceanum*, and many other plant species, to maintain the growth of the agricultural activity in Peru.

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