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Strengthening national genebanks through genomics and regional collaboration: Lessons from Latin America and the Caribbean

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ABSTRACT

Latin America and the Caribbean (LAC) is a center of origin and domestication for globally important crops such as cassava, common bean, maize, and potato, all of which are key to food and nutrition security worldwide. Despite this strategic role, many national genebanks in the region face technical, financial, and policy barriers that limit the use of genomic tools for characterization and conservation. These genebanks safeguard the genetic diversity needed to enhance crop yields, climate-change resilience, nutritional quality, and pest and disease resistance. In 2022, CGIAR Centers and partners established the "Community of Practice (CoP) of national genebanks in LAC" to strengthen regional capacity for generating and interpreting digital sequence information (DSI), facilitate collaboration, and promote sustainable management of plant genetic resources. Through coordinated capacity-building activities, joint crop-based analyses, and shared learning, the CoP has connected 17 institutions across 13 countries. Members have begun generating and interpreting DSI for common bean, maize, and potato, while addressing gaps in data sharing, interoperability, and policy frameworks. Looking ahead, the CoP seeks to conduct diversity analysis, establish regional core collections, integrate existing global data portals, and advocate for policy alignment to sustain genomic characterization and access to diversity. This CoP initiative provides a model applicable in other regions to strengthen genebank operations through collaborative innovation and coordinated action, contributing to resilient and equitable global food systems.

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1. Introduction

Latin America and the Caribbean (LAC) is a primary center of domestication for staple crops, including cassava, common bean, maize, and potato, that are vital to global food security, and sustain a significant portion of the world's population (De Jong, 2016; Gaut, 2014; Pickersgill, 2007). Among these, the common bean was domesticated independently in Central and South America, maize originated in Mesoamerica, and the potato in the Andes. These widely distributed crops remain essential for both local livelihoods and global food systems. In 2022, global production of dry beans (28.34 million metric tons), maize (1.16 billion metric tons), and potatoes (374.78 million metric tons) highlighted their importance for food security (FAOSTAT, 2022).

Since the 1960s, concerns over genetic erosion, driven by agricultural intensification, environmental pressures, and socioeconomic changes, have led to coordinated efforts to collect and conserve traditional landraces and crop wild relatives (Khoury et al., 2022). Today, over 1750 genebanks worldwide safeguard most of this diversity, including more than 200 genebanks in LAC, which conserve over 5000 cultivated and wild crop species, and close to half a million accessions (Diulgheroff et al., 2025). These ex situ collections potentially play a crucial role in providing the genetic diversity needed to enhance crop yields, nutritional characteristics, resistance to pests and diseases, and climate-adaptation capacity. This makes them essential to agricultural innovation and crop breeding, food and nutrition security, and sustainable livelihoods in LAC and globally (Baptista et al., 2022; Campbell et al., 2025; Sheat et al., 2019).

Despite advances in genomics, digital phenotyping, and information systems, national genebanks in low- and middle-income countries (LMICs) face persistent barriers to effectively applying these tools. While DNA sequencing costs have decreased dramatically with new technologies, phenotyping has become the main bottleneck, constrained by high labor and equipment costs, and the time-intensive evaluation of large numbers of plants under diverse conditions. Importantly, the two approaches are complementary rather than interchangeable, as accurate interpretation of diversity and trait data requires integrating both genetic and phenotypic information. However, once genomic data are available, even limited phenotypic datasets can be used in trait association analyses to predict traits in unphenotyped materials, thereby extending the utility of the available data (Ospina et al., 2024).

National genebanks in LMICs also face practical and systemic challenges that limit their ability to use these technologies effectively. These include sample handling issues, limited capacity for data analysis, high costs for reagents and equipment, procurement difficulties, quality assurance constraints, shipment fees, and regulatory uncertainties. Broader systemic obstacles, such as insufficient funding, weak policy support, shifting government priorities, and institutional bureaucracy, further undermine efforts to maintain and characterize collections (Table 1). Although comprehensive genomic characterization is essential for optimizing the management and use of ex situ collections and for promoting their application in breeding and research, it remains underdeveloped. Such characterization supports regeneration planning, diversity analysis, identification of duplicates, improved storage strategies, and facilitates identifying traits relevant to global agricultural challenges. At the same time, recent uncertainty surrounding the conservation and accessibility of major accessible germplasm collections, particularly within the U.S. Department of Agriculture (USDA), which safeguards an extensive diversity of LAC crops, underscores the urgency of strengthening regional collaboration and self-reliance. Reports of staff cuts and administrative instability within the USDA's National Plant Germplasm System have raised concerns about the long-term continuity of this globally important collection (Charles, 2025).

Past regional initiatives, such as REGENSUR and REMERFI in LAC, sought to strengthen regional conservation efforts but lacked a focus on genomics and became inactive due to resource constraints, highlighting the need for renewed, sustainable, and regionally coordinated approaches (Ferrer et al., 2007). Complementary regional tools and frameworks, such as CAPFITOGEN, DIVA-GIS, and gap analysis methodologies, could also serve as useful references for revisiting and improving data management and analysis across genebanks, particularly regarding the use of GIS and passport data for conservation planning (Maxted et al., 2020).

Countries have sovereign control over their genetic resources, a principle stated in the Convention on Biological Diversity (CBD)*[1] and underlined in the Nagoya Protocol on Access and Benefit Sharing*.[2] The Nagoya Protocol is a supplementary international agreement to the CBD, stating member countries' core obligations and compliance measures for using genetic resources and sharing the benefits arising from their use. Further, in exercising their sovereignty, more than 150 countries have ratified the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA, also referred to as the "Plant Treaty"), which has established a multilateral system of access and benefit sharing (ABS) for selected crops, to facilitate their access and use for crop research and breeding. At the same time, global food security depends on a high degree of interdependence among countries. The genetic foundations of major crops, such as common bean, maize, and potato, are the result of centuries of exchange and breeding that transcend national borders. Commercial varieties cultivated across LAC often trace their pedigrees to germplasm originating from multiple countries within and beyond the region. This interdependence underscores a shared responsibility among genebanks worldwide to ensure the continued exchange and availability of genetic resources, particularly as climate change, pests, and diseases intensify pressures on agriculture.

Strengthening cooperation on emerging technologies for the characterization and conservation of plant genetic resources (PGR) can significantly enhance the effectiveness and use of national ex situ collections. By improving the availability, quality, and interoperability of genetic data, such efforts make it easier for breeders, researchers, and growers to identify and access materials with desirable traits for crop improvement and adaptation. Genebanks thus act as bridges between genetic resources conservation and use, playing a pivotal role in ensuring both current and future food security by safeguarding the genetic diversity that underpins crop improvement, resilience, and adaptation to climate change. One way to reinforce this role is through a sustained regional Community of Practice (CoP) that provides a strategic platform for genebank personnel to exchange knowledge, strengthen technical capacity, and coordinate action. We present the case of a regional CoP of national genebanks in LAC that is leveraging genomics and digital tools to improve the conservation, characterization, and accessibility of crop diversity. The CoP focuses on strengthening institutional collaboration and national capacities to generate and interpret DSI. Through joint crop-based analyses, participating genebanks are developing the technical, organizational, and policy foundations required for the sustainable and equitable use of genomic tools across the region. This initiative not only enhances the contribution of genebanks to food and nutrition security today, but also prepares them to contribute solutions to the agricultural challenges of tomorrow. It serves as a model for fostering regional collaboration and may inform similar efforts in other parts of the world, particularly in Asia and Africa.

[1] The Convention on Biological Diversity has been in force since 13 December 1993. https://www.cbd.int/convention.

[2] The Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization (ABS) to the Convention on Biological Diversity—referred to as the Nagoya Protocol or Nagoya Protocol on Access and Benefit Sharing—entered into force on 12 October 2014. As of May 2025, 142 countries are parties to the Nagoya Protocol. https://www.cbd.int/abs/nagoya-protocol/signatories.

Table 1
Key constraints reported by national genebanks participating in the Community of Practice (CoP), associated impacts on genebank functionality, and collective actions undertaken by the CoP to mitigate these challenges.

Constraint Category	Description of Limitations	Impact on Genebank Functionality	CoP Actions to Address the Challenge
Technical and Laboratory Capacity	Limited access to equipment, reagents, and trained personnel for DNA extraction, as well as limited experience with DNA sequencing or with procedures for preparing and shipping samples to service providers.	Inconsistent or low-quality DSI generation prevents full genomic characterization or incorrect interpretations. Reduced capacity to produce genomic data and integrate molecular information into genebank management.	Provide virtual and hands-on training and facilitate peer learning on DNA extraction, including sharing protocols and troubleshooting across institutions. Share standardized protocols for tissue collection and shipment as cost-effective alternatives to outsourcing through service providers. Facilitate theoretical and practical experience in genotyping.
Data Management and Analysis Capacity	Limited computational infrastructure and/or expertise to curate, analyze, store, and interpret genomic data.	Underutilization of generated DSI, with challenges in integrating results with phenotypic or passport data. Low-quality samples and markers can hinder accurate interpretation.	Organize virtual and in-person hands-on training sessions on bioinformatics and biostatistics pipelines; provide access to available software and packages; and facilitate both individual and collaborative DSI interpretation through crop-based analyses.
Data Sharing and Interoperability	Lack of a common regional portal or standardized database for managing and sharing passport data, along with limited knowledge of permit and agreement requirements, data volume management, intellectual property issues, and inter-institutional trust.	Fragmented and inaccessible data hinder regional collaboration, limit comparative analyses, and reduce the visibility and use of collections. Restricts germplasm and DSI exchange among national genebanks.	Promotes the adoption of existing global portals (e.g., GENESYS) rather than developing new platforms and supports data harmonization and training on metadata standards. Facilitates training on policy frameworks regulating the use, access to, and benefit-sharing (ABS) of genomic data linked to genebank collections. Provides a neutral dialogue space for understanding national frameworks; aligns practices with international agreements (Plant Treaty, Nagoya Protocol).
Institutional and Financial Constraints	Insufficient funding, procurement barriers, institutional bureaucracy, and shifting government priorities.	Limits long-term planning, delays research activities, and reduces the continuity of genebank operations. Hinders the sustainability of genotyping and training initiatives.	Advocates for long-term CoP recognition and funding at the regional and global levels.
Collaboration and Knowledge Exchange	Genebanks traditionally worked in isolation with little coordination across countries.	Missed opportunities for shared learning, joint analyses, and resource optimization.	Established crop-based working groups (e.g., bean, maize, potato) and initiated regional core collection development for joint evaluations.

2. Roadmap for advancing the LAC genebanks community of practice

In 2021, CGIAR Centers*[3] operating or based in LAC–the Alliance of Bioversity International and CIAT in Colombia, and CIMMYT in Mexico–conducted a regional survey involving 48 genebank scientists and managers from 33 institutions, including national and university genebanks, across 14 countries. The survey assessed capacities, needs, and interests related to applying genomics in ex situ conservation and characterization. It revealed highly variable collection sizes, with most institutions maintaining between 1000 and 10,000 accessions, and limited use of genomic tools, typically applied to 0−20 percent of collections for studies on diversity, trait discovery, association analysis, and germplasm characterization. Key barriers to data sharing included inter-institutional trust, intellectual property concerns, data volume, legal restrictions, and policy constraints.

In response, a regional CoP of national genebanks was established in 2022 to promote knowledge exchange and capacity building around the use of genomics in ex situ conservation. The CoP, known in English as the "Community of Practice of National Genebanks for Latin America and the Caribbean", and in Spanish–the CoP's working language–as the "Comunidad de Práctica de Bancos de Germoplasma para América Latina y el Caribe", was catalyzed by DivSeek International and supported by the two CGIAR Centers. It now brings together 17 organizations across 13 countries: Argentina, Brazil, Chile, Colombia, Costa Rica, Cuba, El Salvador, Guatemala, Honduras, Mexico, Paraguay, Peru, and Uruguay. Focusing on crops native to the region, such as common bean, maize, and potato, which are central to both regional diets and global food systems, the CoP seeks to link the conservation and characterization of genetic diversity with countries' capacity to respond to current and future food security challenges.

Based on the initial survey results, capacity-building priorities were identified and addressed through a combination of virtual and in-person meetings held between 2022 and 2025. The first focus area was strengthening technical expertise in core processes such as sample

[3] "Centers" refers to the research organizations that are recognized as CGIAR Research Centers contributing knowledge, technical expertise, and resources in support of the CGIAR Strategy and Results Framework. Each organization is an independent legal entity with its own governing board, governing instruments, and host country agreements. As of this Framework's agreement date, the following 14 research organizations are recognized as CGIAR Research Centers: Africa Rice Center, also known as AfricaRice, the Alliance of Bioversity International and the International Center for Tropical Agriculture (CIAT), Center for International Forestry Research (CIFOR), International Center for Agricultural Research in the Dry Areas (ICARDA), International Centre for Research in Agroforestry (ICRAF), also known as World Agroforestry Centre, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), International Food Policy Research Institute (IFPRI), International Institute of Tropical Agriculture (IITA), International Livestock Research Institute (ILRI), International Maize and Wheat Improvement Center (CIMMYT), International Potato Center (CIP), International Rice Research Institute (IRRI), International Water Management Institute (IWMI), and International Center for Living Aquatic Resources Management (ICLARM), also known as WorldFish.

tracking, DNA extraction, and the use of genotyping platforms for generating DSI. The second priority centered on building and strengthening genebank capacity to analyze and interpret genotypic data derived from genebank collections. Another focus area aims to foster genebank collaboration through jointly selected annual topics of focus (e.g., genebank collection gap analysis, regeneration and post-harvest practices in seed collections, and core collections), and enhancing regional cooperation while navigating the policy framework governing the use, access to, and benefit-sharing of DSI from ex situ collections. By addressing these technical and policy gaps, the CoP is not only improving national genebank efficiency in the region but also directly enhancing their ability to mobilize genetic diversity for crop improvement. This, in turn, strengthens national food security strategies and contributes to global efforts to develop more resilient, nutritious, and climate-adapted crops (Fig. 1).

3. Knowledge sharing, capacity building, and DSI generation

During virtual and in-person meetings, CoP members shared their expertise and experience in sample tracking for recording, monitoring, characterizing, and managing biological samples for large collections, sequencing and genotyping platforms, and for data management and analysis (Table 1). A key aspect of fostering deeper engagement in collaboration, while advancing hands-on training, was the CoP members' active participation in generating and analyzing genotypic data for commonly conserved crops in national ex situ collections. To ensure consistency and comparability across collections, CoP members first prioritized cassava, common bean, maize, potato, and wheat, and used a common genotyping platform. This facilitated collaboration among genebank scientists, strengthened crop-based working groups, and enabled both individual and collective analyses across institutions and countries. However, since only one institution expressed an interest in wheat, which is not native to the LAC region, the CoP did not establish a dedicated crop-based working group for this crop.

Not all institutions and countries were able to contribute samples for genomic data generation due to persisting challenges. These included technical limitations such as a lack of equipment, reagents, or lab capacity, as well as low-quality DNA samples that yielded suboptimal results (Table 1). This was particularly the case for genebanks interested in working on cassava, where DNA extraction presented technical challenges in obtaining good-quality samples. Moreover, national regulations continue to restrict some institutions' ability to exchange samples across borders within the region. Although among the 155 Contracting Parties of the Plant Treaty, all CoP participating countries (except Mexico) have either ratified or acceded to it (FAO Legal Office, 2025), the extent and consistency of national implementation remain limited and uneven. The CoP provides a neutral platform for dialogue and collective learning, helping members navigate these regulatory frameworks and align their practices with international agreements. Within the CoP, these challenges have been considered to identify country-specific constraints affecting the use of genetic sequencing and to introduce practical solutions. Despite these limitations, all CoP participants remained actively engaged. They contributed to data interpretation, learning from peers who progressed in the process, and identifying opportunities to apply DSI for comparing, interpreting, and curating ex situ crop diversity conserved in national genebanks.

Through these coordinated efforts, the CoP is generating new forms of institutional, scientific, and social knowledge by connecting national genebanks that had previously worked in isolation through shared DSI interpretation. This regional integration enables comparative analyses across environmental gradients and supports the joint development of regional core collections that can later be evaluated under contrasting climatic conditions. These provide insights relevant to climate-change adaptation, conservation planning, and using crop diversity to

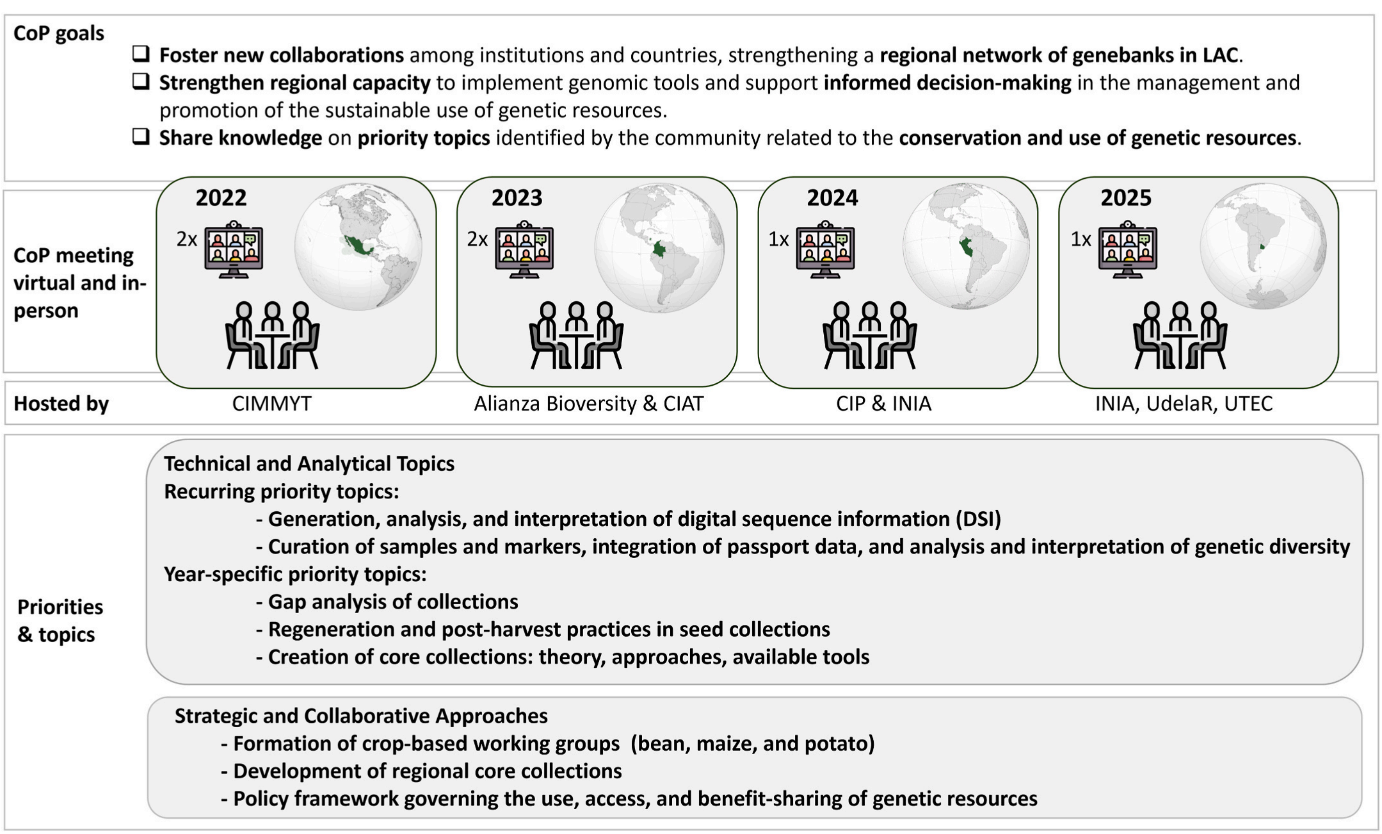

Fig. 1. Roadmap and evolving priorities of the Community of Practice (CoP) of national genebanks in Latin America and the Caribbean, summarizing the CoP's overarching goals, annual meetings (virtual and in-person), host institutions, and key priority topics addressed between 2022 and 2025.

improve food security.

Data obtained through preliminary CoP-led crop-specific analyses, conducted jointly by national genebanks, have provided valuable insights into the potential use of the data for exploring their collections' composition compared to that of other institutions and countries. Although only a small subset of accessions was provided by each genebank, the preliminary analyses enabled both intra- and inter-collection comparison exercises, contributing to a broader understanding of the region's genetic diversity (Fig. 2). These initial findings, led by CoP crop-specific working groups, are being further developed into research publications. In parallel, the working groups have begun reviewing existing passport data and discussing best practices for data management, including the use of standardized descriptors and improved data storage methods. Some crop-specific working groups are using genotypic data to search for associations with climatic conditions or the seeds' phenotypic traits, which could inform breeding programs. These studies are particularly relevant to pre-breeding efforts because better characterization of germplasm expands the pool of useful landraces or wild relatives available for crop improvement. This, in turn, enables developing varieties that support food security in LAC and contributes to more resilient and sustainable food systems globally.

Notably, our assessment revealed that institutions and countries across LAC do not use a common platform or portal for sharing PGRFA information, which limits data accessibility among genebanks and constrains regional and global collaboration. This contrasts with other regions that use well-established platforms such as GRIN-Global (Germplasm Resources Information Network), developed jointly by USDA and Bioversity International; EURISCO (European Search Catalogue for Plant Genetic Resources); and the global GENESYS-PGR portal, which are more widely adopted, particularly across Africa and Europe. While recognizing the importance of working through a shared platform, CoP members also acknowledge that developing a new, ad hoc regional platform is unnecessary. Hence, they are exploring the option of collaboration through existing global portals, particularly GENESYS, to enhance data sharing and ensure interoperability, and to address capacity gaps among national genebanks. Some institutions have already begun implementing these platforms, while others are seeking guidance on their technical, legal, and procedural requirements for data upload.

4. LAC community of practice foresight strategy

In 2024 and 2025, the CoP outlined key action points for 2026 and beyond, aimed at strengthening collaboration and improving genebank operations in LAC, going beyond simply building capacity on DSI. These priorities include: (i) addressing the absence of a common, standardized platform for managing and registering passport and characterization data across national genebanks, by promoting the adoption of existing global platforms such as GENESYS; (ii) exploring the establishment of regional core collections of selected crops to facilitate seed exchange and multi-environment evaluations within appropriate legal frameworks; (iii) finalizing diversity analysis within crop-specific working groups focused on the initial case studies (common bean, maize, and potato; Fig. 3), and forming new groups for additional priority crops belonging to the genera *Capsicum, Cucurbita, and Chenopodium*, as selected by CoP members during the October 2025 CoP meeting held in Montevideo, Uruguay; (iv) advocating CoP recognition and support at the Eleventh Session of the Governing Body of the Plant Treaty, to be held in Peru in November 2025, and engaging with GRULAC (Latin America and the Caribbean Group, known by its Spanish acronym), a non-binding dialogue and consultation group representing LAC countries, to enhance national policy implementation through technical guidance and follow-up; and (v) identifying funding opportunities to support and sustain these initiatives.

Importantly, initiatives such as creating regional core collections and active policy advocacy are not only operational milestones but also strategic steps toward strengthening food systems (Fig. 1). A precedent for this type of coordinated effort can be traced to 1989, when an international network developed the International Barley Core Collection based on European genebank collections documented in the European Barley Database (Knupffer and van Hintum, 2003). This initiative exemplifies the interest of international collaboration to make the management, research, and use of genetic resources more efficient. Establishing regional core collections can streamline access to well-characterized germplasm for breeding, while policy engagement ensures that supportive legal and institutional frameworks are in place for their responsible use. Together, these actions can help secure long-term regional food security and strengthen the contribution of LAC germplasm to global efforts for resilient and sustainable agriculture. Here, we have presented the origins, structure, activities, and future plans of the CoP of national genebanks in LAC, highlighting its role as a

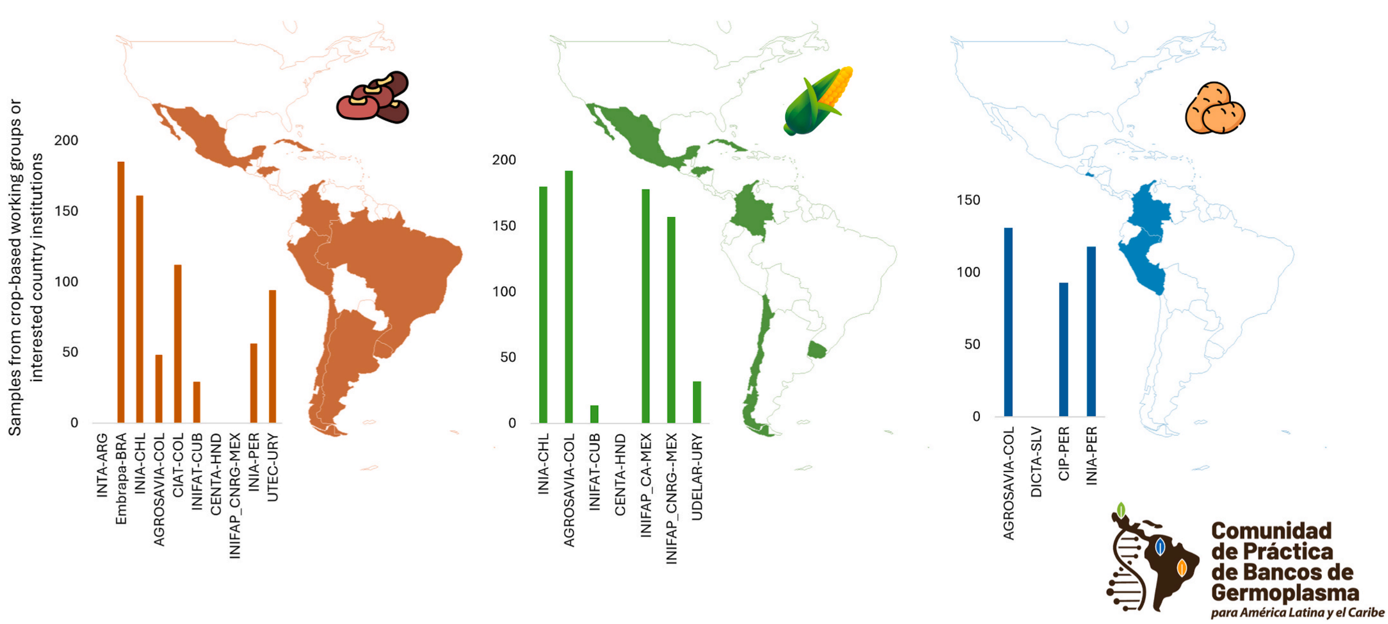

Fig. 2. Maps summarizing institutional and country contributions to the three crop-based working groups of the LAC regional genebanks' Community of Practice.

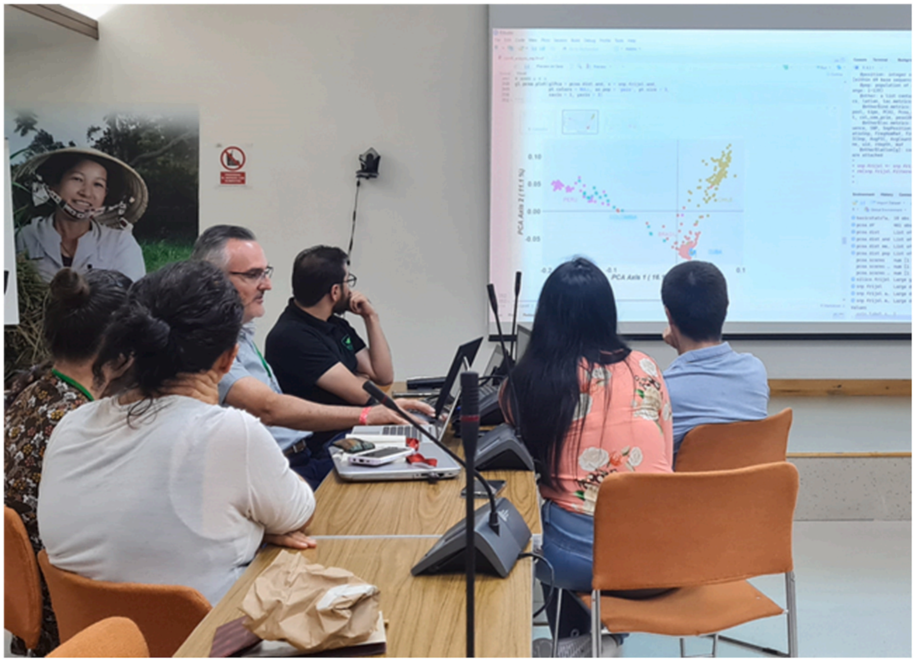

Fig. 3. Members of the Bean Working Group CoP during an in-person annual meeting, analyzing genotypic data from national collections from Brazil, Chile, Colombia, Cuba, and Peru (2023, *photo credit: Monica Carvajal-Yepes)*.

regional platform for building technical capacity, enabling cost-effective use of advanced sequencing technologies, and developing coordinated regional conservation strategies. Beyond these operational benefits, the CoP also serves as an advocate for regional policies that reinforce capacity building, reduce technology access inequalities among countries, and foster collaboration to address shared challenges for the conservation, characterization, and sustainable use of genetic resources.

Drawing from practical experiences, such as genotyping, and sharing DSI for genetic diversity analysis and developing regional core collections, the CoP has identified critical technical and logistical gaps related to applying genomics, and promoting data sharing and ABS. It has also contributed to regional and global dialogue, notably supporting the adoption of ITPGRFA Resolution 16/2023, which emphasizes the need for capacity building, funding, and technology transfer to ensure equitable access to DSI tools (FAO, 2023). By enhancing collaboration and innovation in genebank operations, breeding programs worldwide can build more sustainable and resilient food systems that are capable of adapting to climate change, pest and disease pressures, and evolving dietary demands. LAC genebanks are taking a leading role in collaborating to better assess the diversity of globally important crops conserved in the region, many of which are also conserved in genebanks worldwide. Encouraged by this progress, and with CGIAR support, other regions are beginning to explore the adoption of the LAC CoP model, particularly for globally significant crops, with the strategic foresight that these CoPs may eventually evolve into a coordinated global initiative for conserving and using plant genetic resources. To guide these efforts, we propose three priorities: (i) Supporting regional platforms for sharing and managing information on PGRFA to foster transparency and collaboration; (ii) Strengthening national genebanks' capacity to generate and use DSI, and apply genomic tools in conservation for breeding purposes; and (iii) Embedding regional CoPs into national agricultural research agendas to ensure continuity, policy alignment, and institutional sustainability.

By safeguarding and expanding access to crop diversity, CoPs, such as the one presented in this paper, enhance regional food security and contribute to global food system resilience, since many crops originating in the region remain central to diets worldwide.

CRediT authorship contribution statement

M. Carvajal-Yepes: Conceptualization, Methodology, Writing – original draft. **C. Petroli:** Conceptualization, Writing – review & editing. **M. Correa:** Formal analysis, Methodology, Writing – review & editing. **F. Breseghello:** Conceptualization, Formal analysis, Writing – review & editing. **G. Tapia:** Formal analysis, Writing – review & editing. **E. Salazar:** Conceptualization, Formal analysis, Writing – review & editing. **A. Chassaigne:** Conceptualization, Resources, Writing – review & editing. **M. Ferreyra:** Conceptualization, Methodology, Writing – review & editing. **P.H. Reyes-Herrera:** Conceptualization, Formal analysis, Writing – review & editing. **M. Guzmán:** Formal analysis, Writing – review & editing. **A. Mendoza:** Conceptualization, Methodology, Writing – review & editing. **R. Vidal:** Conceptualization, Methodology, Writing – review & editing. **F. Condón:** Conceptualization, Writing – review & editing. **N. de Almeida:** Conceptualization, Formal analysis, Writing – review & editing. **E. Fernandez:** Conceptualization, Formal analysis, Writing – review & editing. **L. Rodríguez:** Conceptualization, Formal analysis, Writing – review & editing. **W. Solano:** Conceptualization, Writing – review & editing. **A.J. Morales:** Conceptualization, Writing – review & editing. **B.L. Velásquez-Flores:** Conceptualization, Writing – review & editing. **J. Soto:** Conceptualization, Formal analysis, Writing – review & editing. **R. Robles:** Conceptualization, Writing – review & editing. **A. Ledesma:** Conceptualization, Formal analysis, Writing – review & editing. **M. Aragón:** Conceptualization, Writing – review & editing. **D. Castillo:** Writing – review & editing. **C. Roa:** Conceptualization, Writing – review & editing. **I. López Noriega:** Conceptualization, Writing – review & editing. **P. Wenzl:** Conceptualization, Resources, Writing – review & editing. **C. Sansaloni:** Conceptualization, Resources, Writing – review & editing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Data availability

Data will be made available on request.

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