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Spatial Analysis for Crop Genetic Resources Conservation

Selected Approaches for *In* and *Ex Situ* Efforts

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Abstract

In and *ex situ* conservation are two approaches that can support each other and benefit from spatial analysis to inform about genetic resources distribution, change dynamics, and conservation priorities. This chapter reviews approaches that integrate spatial analysis to support *in* and *ex situ* conservation and their linkages; specifically, the mapping of crop diversity patterns at various scales, identification of conservation gaps, modeling to reveal unique or uncovered diversity, participatory cartography, and the identification of candidate sites for establishing conservation networks. It highlights areas for future research and action, which include improving data quality and availability, establishing baselines of the spatial distribution of intraspecific diversity, experimenting with remote sensing tools and citizen science, as well as further work needed to explain spatial patterns in crop diversity and develop models to elucidate how crop diversity responds to different drivers of change. Finally, it argues that integrating different spatial scales, such as field, local, regional, and global is a major challenge that requires attention.

Introduction

Crop genetic diversity consists of plants that have sprung from domestication and selection trajectories (Leclerc and d'Eeckenbrugge 2012b) and their wild and weedy cousins (i.e., crop wild relatives). Crop genetic resources are the raw materials for crop breeding that have supported the rapid increase in agricultural productivity over the past 50 years. Breeding programs have produced high-yielding hybrids and varieties that, for many crops and regions, have

resulted in the replacement of local traditional varieties (i.e., landraces). This loss of crop genetic diversity, or "genetic erosion" diminishes the options for future crop improvement and may affect resilience of farming systems (Harlan 1975). The concern about genetic erosion has led to the further support and creation of new crop genetic resources conservation programs. Nonetheless, high levels of crop genetic diversity still persist on farms globally, particularly in rainfed, marginal, and complex environments within smallholder systems and family farms (Brush 1995; Brush et al. 2003; Jarvis et al. 2008b). What is unclear, however, is how much genetic diversity actually exists, its past and current spatial distribution, and the degree to which it continues to change.

Two main approaches have been established to address the risk of crop genetic diversity loss. The first, and dominant approach, involves the creation of *ex situ* collections or gene banks. Most countries in the world have gene banks, and a collection of major food crops is maintained in international gene banks (e.g., by the Consultative Group on International Agricultural Research, or CGIAR). The second approach is *in situ* conservation, which consists of conserving landraces on farm and crop wild relatives in their natural habitats.

In this chapter, we begin with a review of these two approaches. We discuss selected examples of how spatial data analysis has been used to support these conservation efforts and highlight linkages between them. We conclude by looking at some of the current challenges and benefits of using spatial analysis as an element to enhance the integrated conservation of crop genetic resources.

In Situ and *Ex Situ* Conservation

Since the late nineteenth century crop genetic resources have been formally collected for introduction into new areas, use in crop improvement programs, and conservation. After the 1960s, the notion of rapid genetic erosion in areas of high crop diversity fueled an increased interest in conserving crop genetic resources in *ex situ* collections (Gepts 2006b; Harlan 1975; Pistorius 1997). In *ex situ* collections, samples of crop wild relatives and crops are maintained and stored alive, be it as plants, seeds, or in tissue or cryopreserved cultures. A stated ideal is that gene banks conserve 95% of the rarest 5% of alleles (Oka 1969), but it is not known how much genetic diversity is actually conserved. More than 7 million samples are conserved globally, but it is estimated that 65–70% might be duplicates (FAO 2010b) as samples are exchanged and a sample may end up in multiple gene banks, or because essentially the same genotypes are collected multiple times. To evaluate the effectiveness of conservation programs, it is important to estimate the difference between the genetic diversity that exists, or used to exist, and what is conserved. Such "gap analysis" can be used to plan additional collection efforts to improve the coverage of *ex situ* collections, or to prioritize *in situ* conservation efforts. *Ex situ* conservation largely occurs through formal institutions, including public organizations and

the private sector. Gene banks conserve a snapshot of crop diversity, maintain it through time, and provide access to crop genetic resources. These collections are largely used by researchers, yet may be unknown to potential other users, particularly farmers (Bjørnstad et al. 2013).

In situ conservation of crop landraces occurs at the farm level, where conservation is not the ultimate goal. Instead, conservation may be an emergent property of farming systems in which seed is generated locally and there is no demand for product uniformity. There can also be explicit demand for varietal diversity for a number of reasons, including local cuisine, risk management, identity, and prestige. From a global perspective, there is an interest in the persistence or creation of farming systems that maintain landraces or traditional animal breeds to permit their evolution through anthropogenic and natural selection. The idea is that high levels of crop genetic diversity at farm and community levels can enable adaptive evolution in response to changing pests, disease, climate, and consumption patterns (Bellon et al. 2017).

In situ conservation is thus mostly an outcome of autonomous smallholder farmers' decision making. A number of intervention approaches has been created to promote *in situ* conservation among farmers, such as seed fairs (FAO 2006; Tapia and Rosas 1993a), development of value chains to commercialize specialty landraces (see PapaAndina in Devaux et al. 2016; Gonsalves 2013), community seeds banks (Vernooy et al. 2017), organization of agritourism routes and park systems (e.g., the Potato Park in Peru: Argumedo 2008; Shepherd 2017), adult education programs (e.g., in pest and disease management), and youth engagement plans as well as direct payments to farmers (Wale et al. 2011). Little is known about the effect of such interventions, and more research is needed to evaluate their effectiveness (see also Chapter 2). The following examples of work by the International Potato Center and others on Andean potatoes illustrate the diversity of *in situ* conservation approaches and how they can be linked with *ex situ* conservation:

- The establishment of community gene banks (Huamán 2002)
- A park model linking accumulated repatriated diversity with tourism (Argumedo 2008; Shepherd 2017)
- Development of value chains that connect varietal diversity to urban markets (Ordinola et al. 2007b; Tobin et al. 2016)
- Long-term systematic crop diversity monitoring (de Haan et al. 2016)

The first three of these examples have introduced potato landraces from a gene bank to farms without baseline inventories or monitoring of local landrace populations. The fourth strategy established an *in situ* baseline of farmer-managed landrace diversity and had the goal to explore gaps in gene bank collections. This gap analysis was not successful due to methodological challenges (i.e., the relatively high cost and turnover of genetic marker systems to compare sizeable populations).

Ideally, *ex situ* and *in situ* approaches would act in a complementary fashion, such as establishing sites for *in situ* conservation while collecting the target genetic resources for storage in a gene bank (*ex situ* conservation). Permanent monitoring of the crop diversity targeted for conservation in such a site, as part of the *in situ* conservation strategy, can produce relevant information about shifts (i.e., loss or enrichment) in *in situ* populations. It can also help identify new alleles or genotypes which, in turn, can be conserved in gene banks (for further discussion, see Chapter 3).

In reality, *in situ* and *ex situ* approaches are often not fully integrated or linked, as the objectives, mechanisms, institutions, and actors involved are very different (Chapter 2). Important reasons for this disconnect include:

- The institutional setup underlying each conservation approach differs. *In situ* conservation tends to be decentralized and follow more informal dynamics, whereas *ex situ* conservation is governed by formal structures and institutions. Both domains are governed by different norms and dynamics that need to be reconciled for complementary conservation action.
- Paradigms and objectives of the conservation communities are seldom aligned. While gene banks focus on maintaining a snapshot of genetic diversity that is accessible to users, stakeholders involved in *in situ* conservation stimulate the evolution of gene pools and their activities support primarily local use, benefits, and rights.
- Global and national legal frameworks discourage the connection between *in situ* and *ex situ* conservation: Collecting new crop diversity to conserve in gene banks can result in lengthy bureaucratic processes, depending on the policies established at the national or even regional level, where material is planned to be collected. Conversely, the lack of documented and practical benefit-sharing schemes that should accompany complementary efforts may discourage participation by smallholder and traditional farmers (Chapter 14).

Putting aside the conservation strategy to be implemented, baseline information and analytical tools are necessary to support decisions needed to maintain and increase crop diversity efficiently. Spatial and genetic analyses are increasingly being used to understand patterns of crop diversity at different temporal and spatial scales. Such approaches can help prioritize species, landraces, or gene pools requiring conservation action. In addition, they can set priorities for complementary *in situ* or *ex situ* conservation while adequately allocating the resources available. A main advantage of using spatial data analysis for informing conservation planning of crop genetic resources resides in the possibility of revealing diversity patterns at different scales. These patterns can be combined with other spatial data to study the processes that affect genetic diversity (e.g., isolation, and environmental and cultural variability) and how

these may affect the composition and distribution of landraces and crop wild relatives in the future.

Diversity Distribution Patterns

A number of studies focused on the diversity patterns of crop wild relatives have been used to collect local data on herbarium specimens and gene bank accessions for wild potatoes (*Solanum* section *Petota*: Solanaceae; Hijmans and Spooner 2001; Hijmans et al. 2002), wild groundnuts (*Arachis* spp., Jarvis et al. 2003), and wild vignas (*Vigna* spp., Maxted et al. 2004). Generally of a descriptive nature, these studies provide a good starting point to understand the evolutionary and biogeographical history of a group, to assess the environmental conditions in which the group occurs, to identify highly diverse areas where reserves could be established for *in situ* conservation, to prioritize areas favorable for the collection of samples for *ex situ* conservation or for *in situ* monitoring, and to identify areas where crop landraces and their wild relatives overlap, making evolutionary changes in the genetic composition of such populations more likely to occur.

There are only a few examples of studies mapping intraspecific diversity of cultivated species. Perales and Golicher (2014) and Orozco-Ramirez et al. (2017) mapped maize race diversity in Mexico. Their analyses were enabled by the CONABIO database on maize landraces. This unique database includes gene bank records but mostly consists of a nation-wide survey. The maize diversity patterns show clear geographic variation; most diversity is found in the highlands, which are more isolated, less market oriented, and have a large Indigenous population. While there is insufficient historical data to allow for a very rigorous evaluation of changes in race diversity, Perales and Golicher (2014a) concluded that there was no evidence for substantial genetic erosion. Their analysis was done using vernacular nomenclature of maize races as a unit of analysis. In contrast, Dyer et al. (2014) reported loss of maize diversity in Mexico at the farm level based on household surveys between 2002 and 2007.

Genetic data has also been used extensively to increase understanding of the geographic origin of a crop, its dispersal, and the structure that crop diversity may have over a delimited geographic area (e.g., Bradbury et al. 2013; Rabbi et al. 2015; Vigouroux et al. 2008). Combining both genetic data and spatial analyses has proven useful to determine priorities for *in situ* and *ex situ* conservation (van Zonneveld et al. 2012). Producing large data sets of genetic data has become relatively cheap and we expect that the use of such data for mapping crop diversity will become more common.

Over the last decade, an increased number of landrace catalogues have been prepared to record the landrace diversity found in *in situ* hotspots at different geospatial scales. These catalogues, which often contain ploidy, nutritional,

and phenotypic information, document diversity from the village to the provincial level. One example is the large number of Andean potato catalogues that has been released over the last two decades (MINAGRI 2017). They contain spatially explicit, time-tagged, and genetic data that offers the possibility to elucidate the spatial patterns of crop diversity in the center of origin. To date, however, no efforts have been made to consolidate the information using spatial modeling tools.

Gap Analysis

Over the past decade, several studies have attempted to assess the degree to which *ex situ* collections represent the diversity within crop wild relatives (Castañeda-Álvarez et al. 2015; Khoury et al. 2015a, b; Ramírez-Villegas et al. 2010; Syfert 2016). The studies cited estimated the entire geographic range of species with species distribution models. Such models use occurrence (locality) data from herbaria and environmental predictor variables to identify geographic areas with similar environmental conditions where the species may be presumed to be present (Elith and Leathwick 2009b). The predicted potential distribution of a species was compared with the observed range of the species from the gene bank samples using the circular area method (Hijmans and Spooner 2001). This comparison can be done in terms of area covered and in terms of environmental diversity covered, and combined with other indicators to determine the extent of representativeness of each taxon in *ex situ* holdings and identify geographic regions where further germplasm collecting missions can be prioritized. The data collected in these studies can also serve to derive information about regions where multiple crop wild relatives are likely to be found, and thus their viability as candidate sites for *in situ* conservation for multiple species (Castañeda-Álvarez et al. 2016; Hijmans and Spooner 2001).

Fielder (2015) conducted a study to identify candidate sites for *in situ* conservation of crop wild relatives in the United Kingdom. She compiled georeferenced records of crop wild relatives and used an iterative method to identify a network of complementary sites for conservation in their natural habitats (Rebelo 1994). The network consists of 15 sites and includes populations for 148 priority crop wild relatives. Further refinements included field visits and molecular analysis performed for a range of crop wild relatives populations. These refinements indicate that the priority species are geographically structured, suggesting that conservation efforts for crop wild relatives in the United Kingdom need to involve a network of conservation sites to conserve wild relatives in their habitats, rather than focus on a single site. Complementary conservation strategies (e.g., *ex situ*) can benefit from this approach, as it reveals patterns of richness and sites where multiple species occur, thus allowing for collections to be assembled more efficiently. Molecular characterization

and diversity analysis revealed the structure of populations in their habitats and thus provided intelligence for the gene bank minimum sampling size required for effective collections of seeds and propagules. Future work on gap analysis methodology could investigate

- the coverage of crop wild relatives rich areas within the network of established protected areas,
- the level of coincidence with global biodiverse hotspots to identify regions where there is a potential to conserve crop wild relatives together with other species (Myers et al. 2000),
- the likely vulnerability of crop wild relatives due to land-use change (Watson et al. 2016), and
- the expected impact of climate change on the future spatial distribution or survival of crop wild relatives (Jarvis et al. 2008a).

A weakness of the gap analysis methods employed so far is that there is no distinction made between species; that is, there has been no attempt to adjust for phylogenetic diversity, or the known usability of species. There has also been a strong reliance on the probably weak assumption that a large range implies a large infraspecific diversity. Ideally, infraspecific diversity should be estimated and taken into account to set conservation priorities (e.g., Camadro 2012; Camadro et al. 2012).

The species level is not a very relevant unit of comparison for cultivated species. For crops we need to consider intraspecific diversity (i.e., races in maize, landraces of cassava). One plausible approach is to model premodern patterns of diversity and then to check if it has been sampled appropriately. For the Americas, van Etten and Hijmans (2010) present a spatially explicit model of maize dispersal that can be used to determine the geographic distribution of maize genetic diversity. Thus, this model provides elements for a gap analysis in crops to set priorities for *in situ* and *ex situ* conservation.

Modeling to Find Novel Genetic Resources

The use of geographic analyses as data support tools for the conservation of crop genetic resources is not restricted to the definition of highly diverse hotspots or species-rich areas. Spatial models can also be used as an input for more efficient germplasm-collecting missions to complete *ex situ* holdings. This was done for a rare chili pepper in Paraguay (Jarvis et al. 2005), for lupins that displayed particular adaptations to microclimates along the Iberian Peninsula (Parra-Quijano et al. 2011), and to research forages in Russia (Greene et al. 1999). In addition, spatial models can be used as a tool to discover new species (Särkinen et al. 2013). Of course, the same tools simultaneously draw attention to unique locations that can be considered as *in situ* conservation sites. Other studies have focused on the distribution of traits of interest. For example, Hijmans et al. (2003) mapped the distribution

of frost tolerance in potatoes and Bonman et al. (2007) mapped the distribution of stem rust resistance in wheat. Insight into the distribution of particular traits of interest can be of use as a guide for further screening, but also for targeted collection and conservation.

Local-Level Studies

Research on local-level (e.g., community) diversity can capture the spatial distribution of intraspecific diversity at a very high resolution (e.g., field level or within fields). Such studies have associated diversity with social variables (e.g., ethnicity, culture, social organization, language) and other variables associated with on-farm management of intraspecific diversity (Delêtre et al. 2011; Labeyrie et al. 2014, 2016). Local-level data collection can enable communities to participate in the research process and the establishment of observatories for systematic monitoring (see Chapter 2).

Since 2012, the International Potato Center has conducted baseline studies and *in situ* monitoring of potato landrace diversity in the Peruvian and Bolivian Andes at the community level (de Haan et al. 2016; Polreich et al. 2014). This is an effort to compile high-resolution information on the current spatial distribution of landraces managed by local communities. The communities are involved through participatory cartography and this has been instrumental in systematically capturing detailed spatial data at the landrace level (Juarez et al. 2011). This high-resolution information is valuable as a baseline to characterize the genetic and spatial distribution of landraces at sites of high landrace diversity (de Haan et al. 2010). Furthermore, field-level mapping and sampling with farmers allows quantification of the relative abundance of specific landraces, which in turn can be used to construct indicators of risk of extinction (e.g., Red List) of rare landraces. This approach can be replicated to track spatial shifts and changes in the conservation status of landraces for other crops as well, and this is currently being promoted for banana, cassava, and yam by partners of the CGIAR Research Program on Roots, Tubers, and Bananas. Systematic monitoring of agrobiodiversity at benchmark sites allows researchers to better understand change dynamics in time and space. This approach offers potential ways to connect conservation strategies:

- It provides information about resemblances between *in situ* and *ex situ* populations.
- It enables the detection of specific landraces that may be rare and possibly warrant an *ex situ* backup.
- It provides gap analysis at the cultivar level and the possibility to enhance gene bank coverage through the addition of uncovered landraces to the collection.

Satellite Image Analysis and Modeling Approaches

Remote sensed images together with survey data are also used to understand and model the dynamics of agrobiodiversity. Processes of interest include decision making and management choices of farmers and communities regarding the cultivation of crops and cropping systems in the context of global change (Meles 2011; Rostami et al. 2016; Zimmerer 2013). For instance, satellite images have been used to estimate landscape-scale attributes related to the management of both the diverse maize crop and the market-driven expansion of peach growing in Bolivia (Zimmerer 2013). These estimates were incorporated into a model illustrating the trajectories of agrobiodiversity between 2000 and 2010 in the context of global change drivers related to environmental factors (water availability) and socioeconomic conditions (market change). Additional farmer and land-use surveys were used to determine how agrobiodiversity use and *in situ* conservation can be compatible with agricultural intensification under conditions of favorable markets, the continued cultural valuation of agrobiodiversity, and generally adequate availability of water resources. Zimmerer and Rojas Vaca (2016) used joint count statistics to demonstrate high levels of spatial clustering of highly diverse maize fields. Remote sensing can also be used to infer upon the fine-grained, field-level dynamics of agrobiodiversity. One approach focuses on field-level interactions involving the spatial externalities of short-distance spillover processes (e.g., information sharing, coordination of labor, seed exchanges). This approach has been used to evaluate organic and high-agrobiodiversity farming through the incorporation of econometric modeling and farm surveys (Lewis et al. 2008; Zimmerer and Rojas Vaca 2016). Satellite images have also been used to differentiate tree species assemblages and cultivars (Turner et al. 2003), but more attempts are needed to use images to disaggregate landrace assemblages, particularly for annual crops.

Future Challenges and Opportunities

To inform conservation action, we need to understand both the challenges and opportunities of using spatial analysis to anticipate future spatial changes in agrobiodiversity. Global environmental change, including climate change, urbanization, and land-use intensification, are likely to affect the distribution of crop genetic resources (Chapter 8); in particular, the distribution and relative abundance of species and intraspecific diversity at the landscape level. Spatial shifts that result from climate change have been demonstrated for wild flora and fauna (e.g., Bodin 2010b; Morueta-Holme et al. 2015; Seimon et al. 2007), and have been predicted for crops (e.g., Hannah et al. 2013) but have only rarely been documented for agrobiodiversity (cf. Skarbø and VanderMolen 2015). In addition, high spatial resolution and regularly updated distribution

maps of agrobiodiversity at intraspecific levels are still rare, but when available, they prove useful for conservation action (Pacicco et al. 2018). Thus, systematic approaches are needed to link scales and cluster interactions among landscapes (including different environments and production zones), species (including subspecies), cultivars (including races, cultivar groups, landraces, and bred varieties), and genetic diversity (including genes and alleles).

Data availability, completeness, and quality are important challenges for spatial analysis of crop diversity. Several of the studies presented in this chapter relied on gene bank collection locality data. There has been enormous progress in the availability of such data over the past twenty years or so, thanks to an expanding culture of open data access for public institutions, such as gene banks, albeit mostly in Europe, the United States, and international institutions; much less so in national-level gene banks in other countries. Thus, despite heroic global efforts to digitize and publish biological-related data, notably through the Global Biodiversity Information Facility, Plants JSTOR, Eurisco, and Genesys, a large share of global crop collection records are not digitally and publicly available (FAO 2010b). The reluctance by some to share locality data, especially when coordinates or detailed geographic descriptions are available, remains a major obstacle to research in this field. While spatial modeling can be used to estimate distribution patterns based on small samples, as has been done in the gap analysis work we described, this method will likely not perform well if there are major geographic gaps in the sample that the model is based on.

Nomenclatural identity (i.e., scientific name) and sampling bias are key elements that determine the quality of crop genetic resources collection data, and thus directly affect the consistency of spatial analyses. Plant taxonomy is dynamic and changes over time. Keeping accessions properly identified and updating taxonomical classification is crucial to knowing what crop wild relatives and cultivated (sub)species are being conserved (see Syfert 2016). Continuous updates require verification (i.e., whether a species name has changed according to the taxonomic consensus of the moment). Of course, lack of consensus can further complicate matters (Oliveira et al. 2012). Herbarium specimens are often subject to updates, yet this rarely happens for crop genetic resources in gene banks. In addition, spatial bias is a result of the patterns followed by germplasm-collecting missions. Most georeferenced, *ex situ* collections targeted fields next to roads, rural markets, and locations where collections could quickly be made (Hijmans et al. 2000); often the frequency of collecting missions spanned numerous years and different lengths of time. In an effort to overcome such biases, several questions have emerged:

- Are areas rich in crop genetic diversity actually properly sampled?
- Is the information we can access enough for studying the dynamics of crop diversity?
- What is the status of the crop diversity in understudied areas?

An additional challenge emerges in relation to the management of duplicated accessions in *ex situ* collections and its effect on collection data. Duplicated accessions have been removed from *ex situ* collections (a) to reduce overrepresentation of widespread landraces (i.e., those with a wide distribution range) and (b) to lower the cost of the management of collections. Such rationalization has led to landraces represented by a single representative accession with a single geographical coordinate. These factors, among others, may limit the value of gene bank collection data to elucidate spatial patterns beyond species and ploidy distributions (Spooner et al. 2010). Understanding the spatial distribution patterns of crop diversity at the intraspecific level (for cultivar groups and landraces) often requires a sufficient number of samples, together with prolonged and fine-grained mapping efforts. Several questions for future action can be posed:

- How can we create solid baselines of spatial distribution at the intraspecific level?
- How should we address this at multiple scales, given that varietal nomenclature changes rapidly, due to local and genetic marker systems?

It is important to note that spatial analysis can provide tools to identify environmentally homologous sites where landraces could be established, used, maintained, and therefore conserved. The intent of such an approach can have completely different outcomes: it can result in the conservation of landraces with farmers willing to manage and maintain landraces over time, but with farms located outside the centers of origin of the crop (Bazile et al. 2016; Ríos et al. 2007). It can also result in the diversification of agricultural production systems, which may lead to improved sustainability and ability of the systems to respond to extreme climatic and economic events (Kahiluoto et al. 2014).

An ultimate challenge is to expand spatial analyses so that patterns of crop diversity can be converted into models that elucidate how crop diversity is affected (positively or negatively) by different drivers and change scenarios. Such models would be useful to predict responses to human intervention and environmental events (e.g., floods, drought spells, variable rainfalls, land use change).

The use of spatial analysis in plant genetic resource collection and conservation has been broadly reviewed (Guarino 1995; Guarino et al. 2002; van Zonneveld et al. 2011). Over this twenty-year period, tremendous progress has been made in data availability (including location, environmental, and genetic data), analytical methods, and diversity of applications. Another clear change is that we have moved from paper-based computation (Guarino 1995), to specialized "GIS" software (Guarino et al. 2002), to the current situation where spatial data is no longer special and analysis is primarily done in a general data analysis environment such as "R."[1]

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[1] For information on R, a free software environment for statistical computing and graphic, see https://www.r-project.org/ (accessed Sept. 12, 2018).

We expect that spatial methods using genetic data ("landscape genetics") will become more common and provide new insights about the dynamics of crop diversity. Using genetic data together with archeobotanical data, environmental, and other data sources may provide additional insights into the study of crop diversity (see Kraft et al. 2014; van Etten and Hijmans 2010).

In terms of *in situ* monitoring, data capture can be improved by using remotely sensed data from satellites and "drones," crowdsourcing, and citizen science. Crowdsourcing techniques and citizen science (e.g., mobile technologies) offer the potential to involve local communities in the monitoring of crop diversity and the mapping of on-farm conserved crop genetic resources in real time. This could result in greater local community engagement and more frequent production of fine-scale georeferenced data.