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THOMAS REVIEW

# Past, present and future of local crop evolution

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**Societal Impact Statement**

Promoting agrobiodiversity is a promising strategy for mitigating the negative effects of climate change on global food security. We highlight the central role evolutionary processes play in harnessing the potential of local crops by integrating genomics, archaeology, ethnobotany and traditional ecological knowledge (TEK). Our aim is to empower Indigenous peoples and local communities as key actors in agrobiodiversity and crop innovations, fostering ethical and active collaborations. Local contributions to diversifying the global food system will enhance climate resilience and ensure that the benefits of agricultural innovation are shared more broadly and justly across peoples.

**Summary**

Strengthening diverse agricultural systems can mitigate the effects of accelerated climate change on crop production. Unlocking local crops' potential requires understanding their origins, domestication, fundamental attributes and uses. Here, we review the role of genomics, archaeology and ethnobotany that increased our understanding of crop evolution. We highlight biases in data availability towards globally commercial crops and chart pathways to develop baseline knowledge for local crops. We propose integrating these fields with traditional knowledge to illuminate how cultivation and uses have shaped, and will continue to shape, local crops and promote ethical collaborations. The lessons learnt from the past can help us chart the future of sustainable and climate-resilient agriculture. Supported with evidence from recent research and traditional knowledge, we propose to orient seed conservation, breeding and accelerated domestication around Indigenous peoples and local communities.

> These, then, are yours—grains of maize, chili pepper seeds, beans, pataxte, and cacao, this is yours, and if something is stored or forgotten it is yours too, eat it.
>
> Popol Vuh

## 1 | INTRODUCTION

Concerns are growing over disruptions to Earth's regulatory systems governing cycles and processes at a planetary scale

(Intergovernmental Panel on Climate Change [IPCC], 2022). Industrial food systems, although high yielding, are sensitive in the Global South to the increased risk of the emergence of pests and pathogens in monoculture while simultaneously exerting detrimental impacts on ecosystems, human nutrition and traditional ecological knowledge (TEK) (Headey & Hoddinott, 2016; Hultgren et al., 2025; Khoury et al., 2014; Thrupp, 2000). TEK is understood as knowledge and beliefs on species relationships, natural features and phenomena and agriculture, transmitted through generations by Indigenous peoples and local communities (IP&LC). They are defined as people who maintain an intergenerational connection to their land and nature through their way of life, cultural identity, languages, worldviews, institutions and ecological knowledge.

Although we have knowledge of approximately 7000 edible plants, only a few hundred are domesticated, and from those, 15 crops constituted 90% of the total food consumed globally in 2022 (FAO, 2020). Edible plant species are highly diverse and can become a reservoir of micronutrients for future generations (Cantwell-Jones et al., 2022) and environmental adaptations, while many are associated with multiple uses/services and sustainable farming practices (Ulian et al., 2020). They are a source of stress resilience genes (Kumar et al., 2022) and are promising candidates for development into climate-smart crops (Gutaker et al., 2022) with vast potential to increase agrobiodiversity. Diversification represents a ‘high confidence’ strategy to enrich the resilience of food systems and strengthen food security based on a 2022 IPCC report (Intergovernmental Panel on Climate Change, 2023). Crop diversity also increases the stability of food production at a national level through spatial and temporal (rotations) heterogeneity (Marini et al., 2020; Renard & Tilman, 2019). Agrobiodiversity can positively impact local environmental integrity: ecosystem functions, soil health and carbon sequestration while benefiting IP&LC livelihoods (United Nations, 2024; Zimmerer, 2010).

Previous research suggests that so-called ‘under-utilised’, ‘minor’, ‘orphan’ or ‘neglected’ crops from locally important food systems, which are globally under-utilised (hereafter ‘local crops’), are essential to global food systems as supplements to ‘common’, ‘major’ crops, which are globally important (hereafter ‘global crops’), or as sources of traits for breeding (Mabhaudhi et al., 2019). Although many species exist on the spectrum between local and global crops, we use these categories to illustrate the disparity in our understanding of their evolutionary histories (Figure 1), differences in current evolutionary processes and, in consequence, possible alternative pathways for their conservation and utilisation. Ethically investigating the substantial yet under-explored potential of local crops, particularly integrating genomic evidence with archaeology, TEK and ethnobotany, is a promising way to study their evolution and pave the way to unlock their benefits, as well as to bolster resilience in IP&LC who depend on them (Jennings et al., 2023; Muñoz-García et al., 2025; Tadele, 2019; Ye & Fan, 2021).

Crop evolutionary processes are central in shaping global agriculture and our understanding of general evolutionary mechanisms, echoing Darwin's foundational insights into domestication. Crops offer a tangible narrative of evolutionary processes through centuries of cultivation, showcasing the complex interplay between environmental pressures and the selective forces influenced by human practices (Verhoeven, 2004). *Environmental factors*, such as climate, soil geochemical characteristics, pest and disease pressures and interspecies interactions, shape plants' adaptive responses (Bar-Yosef, 2011), manifested as changes in phenotypes that enhance survival and/or reproductive success. These forces drive the evolution of crops through positive selection, adapting to specific environments, for example, making them resistant to drought or herbivory (Bowles et al., 2021; Chaudhary, 2013; Koziol et al., 2012). Diverse local crops, cultivated in a very broad range of environmental gradients, including under extremely dry or hot conditions, provide insights into their adaptive mechanisms that can be translated into other crops under similar conditions (Figure 1a). They also serve as pre-adapted species that can be deployed into regions of the world where climate is predicted to be more restrictive for current global crops.

Concurrently, *cultural influences* profoundly impact crop evolution, encompassing agricultural techniques, harvesting and propagation practices and reasons for species or varietal selection (Maeda et al., 2016). These forces shaped dietary characteristics and adaptation to cultivation practices. Agronomic traits, such as non-shattering, yield and coordinated phenology, are the evolutionary responses to human agrarian practices. Culinary properties, including flavour, texture and cooking characteristics, reflect human cultural preferences and dietary habits, influencing the selection and propagation of specific crop varieties (Brown et al., 2009). Additionally, sociocultural identity influences crop cultivation and high-diversity maintenance, as seen by how Quechua communities manage potato varieties within polyculture fields (Velásquez-Milla et al., 2011; Zimmerer, 1991), simultaneously growing different varieties or several species, conducive to a sustainable way of agriculture. Propagation methods and seed distribution systems have a profound effect on the pace and intensity of local adaptation. Furthermore, cultural associations extend beyond agronomic practices to encompass broader sociocultural dimensions, including spiritual beliefs, ritual practices and symbolic meanings attributed to crops within IP&LC.

Despite the central role of local crops in sustaining agrobiodiversity and food sovereignty, their domestication and adaptation histories remain largely under-explored. We argue that a holistic, culturally grounded perspective is essential for understanding the coevolution of people and crops and for ethically revitalising the appreciation of long-standing TEK in modern agricultural systems. We review the genomic, archaeological and TEK evidence, including ethnobotanical data and IP&LC oral histories, and highlight how their integration illuminates lesser-known domestication narratives of local crops. We propose to orient new agricultural innovations around local crops, TEK and local farmers. These innovations include coupling of the in situ seed maintenance and accelerated crop development with cutting-edge approaches in molecular biology and big data analysis. With that, we strive to increase the visibility of TEK as a source of efficient ideas for sustainable and climate-resilient agriculture, which would best be utilised in situ.

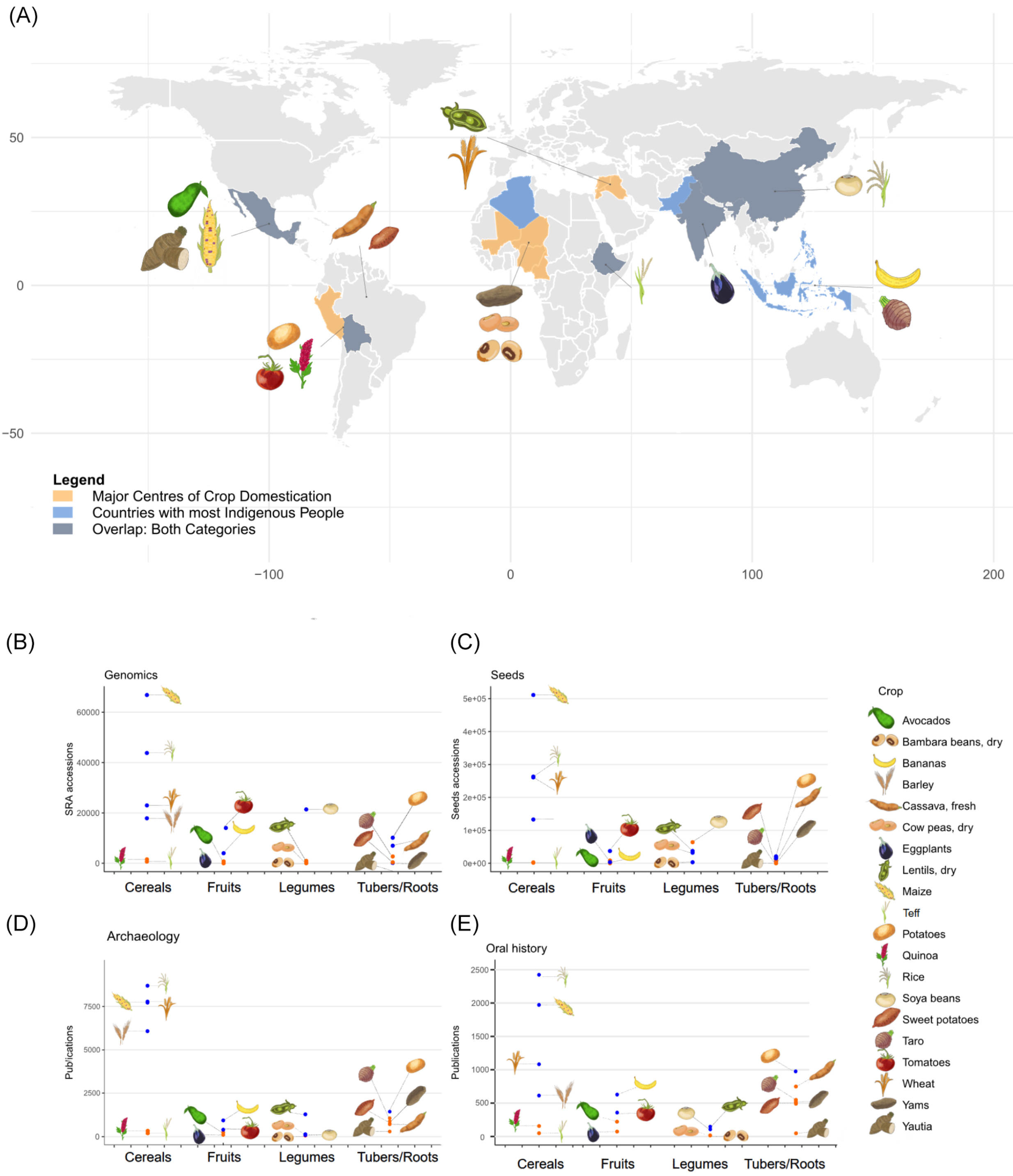

**FIGURE 1** Distribution and data available for global and local crops. Local crops are represented by 10 food species with high production in countries with the high proportion of Indigenous peoples in different regions (International Working Group for Indigenous Affairs, more on Data S1). Global crops are the 10 most produced crops globally (FAO statistics). (a) Approximate areas of origin of local and global crops. (b) Comparison of data available for local and global food crops (Data S1). Available genomic data are measured by the number of genome submissions in short read archive (top left). (c) Seed availability for local and global crops is measured by accessions registered in GeneSys (top right). (d) Number of publications within the field of archaeology, with keyword 'archaeology' (bottom left). (e) For indigenous knowledge, we used the terms 'ethnobotany', 'oral histories' and 'indigenous knowledge' (bottom right) as listed in JSTOR (journals and books; https://www.jstor.org/). Global crops are represented by blue dots and local crops by orange dots. Crops are grouped in four categories: cereals, fruits, legumes and roots and tubers.

## 2 | THE PAST EVOLUTIONARY PROCESSES OF DOMESTICATION

### 2.1 | Genetic evidence

Genomic studies of local crops not only accelerate the identification of functional genes and improve our understanding of species' evolution but also help facilitate the improvement of crops undergoing domestication (Gutaker et al., 2022; Lemmon et al., 2018; Satterlee et al., 2024). Multiple prominent approaches are being utilised to further our understanding of crop evolution: (i) forward genetics, which uses the diversity in known domestication traits to map underlying genetic elements; (ii) comparative genomics, which contrast genetic variants between domesticated and wild forms; and (iii) ortholog search, which uses domestication genes in model crops as a template to find their counterparts in newly sequenced species. Each approach requires specific types of data and experimentation, which vary in the skills and resources demanded.

Large genomic datasets generated through population re-sequencing of crops can aid the identification of genes that underlie key agronomic traits, either through genome-wide association studies (GWAS) to identify genotype–phenotype associations or through detecting molecular signatures of selection in genomes. This approach has already been adopted for local crops, and GWAS has identified several known domestication traits (Wu et al., 2020), for example, in rice beans (Guan et al., 2022) and finger millet (Tiwari et al., 2020). Notably, GWAS analyses have unveiled genes linked to agronomic traits absent in staple cereal crops, such as genes associated with storage root development in cassava (Zhang et al., 2018). Similarly, a GWAS on 600 wild green foxtail accessions revealed a novel domestication gene involved in seed shattering (Mamidi et al., 2020). Guan et al. (2022) identified a gene associated with seed yield traits in rice beans. SNP datasets can also be useful for identifying and circumscribing discrete units of genetic variation in crop plants, including those associated with key agronomic traits (Davis et al., 2025).

Re-sequencing of wild relatives can provide a contrasting historical reference point to identify genes undergoing selection during crop domestication. Researchers speculated domestication in an ancient barnyard grass (*Echinochloa crus-galli* var. *oryzoides*) distributed in China, due to the large grain size and non-shattering spikelets. Re-sequencing data for wild and cultivation forms revealed significant differentiation (attributed to selection) in genes that could be linked to domestication (Wu et al., 2022). Many local crops demonstrate weak selection on traditional domestication syndrome traits, mainly due to incomplete fixation, genetic constraints or pervasive gene flow. For example, the South American grain amaranth was subject to weak selection for grain size and seed colour (Stetter et al., 2017). So far, selection analyses on fonio millet have only identified two major domestication traits: seed shattering and grain weight (Abrouk et al., 2020). *Echinochloa* is also characterised by weak selection in key domestication traits (Wu et al., 2022). Weak domestication in local crops could be explained by the trade-off between retaining the genetic diversity advantageous in diverse environments and the selection for improving yield in optimal conditions (Yu et al., 2021).

Weak selection under domestication in local crops can be counterbalanced by prior knowledge of target genes. This knowledge gained from the decades of global crop research enables science to capitalise on and enhance our understanding of genes that control key agronomic traits in local crops. Primarily, shared traits related to ‘domestication syndrome’ (Hammer, 1984; Harlan et al., 1973), which enhance yield and facilitate harvest, are commonly examined for homology. At the gene level, convergence is apparent in cereals for traits such as seed shattering (Abrouk et al., 2020; Hammer, 1984; Lin et al., 2012; Wu et al., 2022), dormancy (Wang et al., 2018), stem branching (Remigereau et al., 2011) and grain size increase (Meyer & Purugganan, 2013). Phylogenomic studies identify genes conserved in multiple plant species, linked to crop domestication, pointing to promising candidates for accelerated improvement of under-developed crops through so-called neodomestication (Di Vittori et al., 2021; Guan et al., 2022; Wang et al., 2021; Wu et al., 2022). However, the molecular underpinning of various domestication syndrome phenotypic traits can vary. For instance, Doust et al. (2004) identified novel genes controlling branching in foxtail millet, while the major branching gene in maize had a minor effect. Therefore, genomic studies employing re-sequencing datasets, in addition to a reference genome, are needed to provide a more extensive understanding of the molecular underpinnings of the domestication of local crops.

With approximately 7000 plant species that are edible to humans (Diazgranados et al., 2020), the genomics of food plants is still in its infancy. While the number of local crops with reference genomes (high-quality, complete genetic information for a single specimen chosen as a representative of a species) is dynamically growing, it was less than 100 in 2022 (Chapman, 2022). In contrast, within global crops, rice presently has 49 reference genomes and an additional 10,000 domesticated and wild rice accessions with re-sequenced genomic data (Figure 1b) (Wing et al., 2018). Notable funded initiatives are improving representation (e.g., The African Orphan Crops Consortium) (Hendre et al., 2019; Jamnadass et al., 2020). However, most genomic investigations into local crops rely mainly on cheaper and more readily available techniques, thus limiting progress in assembling complex genomes. Significant advancements in sequencing technologies have markedly enhanced the ability of assembling large and polyploid plant genomes (Marks et al., 2021). Although these approaches necessitate complex bioinformatic procedures and fine-tuning for non-model species, chromosome-level reference genomes for complex local crop species are emerging, for example, *Echinochloa* species (Wu et al., 2022) and fonio millet, *Digitaria exilis* (Abrouk et al., 2020).

A significant disparity is evident in the availability of genomic data for local crops compared to global crops, the latter being researched more widely (Figure 1b). Additionally, plant genome sequencing projects are generally led and conducted almost exclusively in China, Europe and the United States, which enforces biases among global crops and further decreases the representation of local crops (Marks et al., 2021). As such, local crop genomics often depends on identifying domestication traits through ortholog searches based on model species, exploiting apparent parallelism in evolution under domestication. However, the absence of classical genetic studies poses a significant setback, particularly in comprehending the genetic architectures governing stress resistance and species-specific domestication traits in these local crops. Basic knowledge about agrarian practices and uses derived from TEK is key to identifying domestication phenotypes for genetic studies. Hence, the progress in domestication studies on local crops is reliant on allocating resources to both genomics and TEK disciplines.

## 2.2 | Archaeological evidence

Archaeological data provide empirical evidence for crop domestication and diffusion histories and have helped to identify at least 20 regions of crop origins (Fuller et al., 2014). It provides the context and stratigraphy for the archaeobotanical record, linking it to timelines and cultural influences in the region. Macrobotanical remains, such as seeds or vegetative tissue fragments, are very valuable. They can evidence the presence of a given crop in the area and, coupled with direct radiocarbon dating, can provide a timestamp, often with precision to the decade or century. Microremains, including phytoliths and starch granules, have more limitations and are more difficult to identify and date but have superior preservation and can provide a very much needed breadth of evidence where macroremains are missing.

The timing and geography of domestication histories are more refined when there are enough excavations from the relevant time periods and spatially across regions (Fuller et al., 2014, 2023). For example, wild-to-domestic transitions have been possible to examine for wheat and barley in the Fertile Crescent, sorghum in east Sudan and maize in Mexico. Macrobotanical remains of seed crops are mostly preserved through charring and are often identifiable to species. The changing appearance of cereal rachis attachment scars reflecting the shift from shattering to non-shattering seed dispersal is the most identifiable trait. Seed size, especially for most cereals, pulses and fruits, and sometimes features like seed coat thickness can also be measured (Fuller et al., 2014). Combined, these data provide accurate spatial information for crop emergence.

Characteristics of macrobotanical remains coupled with radiocarbon dating can inform us about the onset of domestication and its dynamics. Large enough datasets now exist for a few global crops to show how phenotypic changes could span millennia, shifting ideas away from domestication ‘events’ to processes (Bogaard et al., 2021; Fuller et al., 2023). The most robust datasets originate from Fertile Crescent domesticates (wheat and barley) and Eastern Asian crops (rice) owing to the heavy concentration of archaeological excavations. In contrast to global grains, data for millets, a group of stress-tolerant small-seeded cereal species mostly from West and East Africa as well as South and East Asia, are patchier due to a limited number of archaeological excavations (Figure 1d) and more difficult to obtain due to the small size of their seeds. Archaeological records for millets are often sufficient to highlight their long-term regional importance, but for several species insufficient to elucidate the timing and precise geography of their domestications.

There are also many other local crops still grown in local food systems today that have little or no archaeological record, especially from Africa and Southern Asia (Fuks et al., 2024). Crops like roots and tubers that are vegetatively propagated can be less well known than seed crops, archaeologically and agronomically. Generally, roots and tubers leave fragmentary, occasional and hard-to-identify remains (Figure 1d). Starch identification by itself is not enough to conclude species presence, while phytoliths (silica bodies) form in only a few species (Ryan, 2018). An exception is bananas, which form phytoliths in leaves and seeds and thus have a better understood archaeological record (Denham et al., 2020). Additionally, identification criteria for charred parenchyma are still advancing and could improve the identification of crops like yams and taro in the future (Barron et al., 2022).

Overall, global seed-producing crops (such as maize, rice and wheat) tend to be the best known because of superior preservation, identifiability and research focus (Fuller et al., 2014). Additionally, the possible selection pressures related to, for example, harvesting are well known for many cereals and pulses, providing context for crop evolution under domestication. In contrast, vegetatively propagated species like roots and tubers leave fewer traces and have more diverse modes of propagation and domestication traits. Multiple lines of archaeobotanical, archaeological and ethnoecological evidence have built up information for several important species (Figure 1d) (Denham et al., 2020). Progress in understanding local crop evolution can be made given more excavations and research focus, as well as the integration of experimental archaeology with research on plant uses from TEK. Especially the latter can inform the identification of traits characteristic for local crop domestication.

## 2.3 | Local and indigenous knowledge evidence

Studying plant use, cultivation and management practices through the lens of local indigenous knowledge (LIK), especially in regions of primary crop diversity, can improve the understanding of domestication histories of crops alongside genomics and archaeology, as well as informing decision-making processes when planning sustainable agriculture solutions (Cleveland & Soleri, 2022). TEK is a vital, scientific field that provides deep, place-based understanding of ecosystems, complementing and informing Western science. Ethnosciences as a way of analysing TEK have the potential to provide insights into cultivation practices and, thus, possible selection pressures on local crops, including relationships with people (ethnobotany) and environment (ethnoecology) (Albuquerque et al., 2018; Hildebrand, 2009; Nyerges, 2016). Additional insights come from LIK cosmologies, which provide evidence for crop origins, domestication and agroecology, while the analysis of vernacular names and varietal groupings can help elucidate migration patterns of crops, their uses and characteristics.

In general, traditional modes of cultivation, harvesting and processing practices are best documented for seed crops and especially the global cereals and pulses, where common trends are noticeable (e.g. the harvest of non-shattering seeds). By contrast, locally cultivated small-seeded millets, teff and fonio, are not subject to strong selection for non-shattering. While less common, documentation for local crops, especially vegetatively propagated species, can bring important insights into non-canonical domestication processes. For example, Guinea yam (*Dioscorea cayenensis* ssp. *rotundata*) is a rare case due to the ongoing practice of 'ennoblement', where wild yams are brought into cultivation to create new cultivars. This practice occurs in both West and East Africa, introducing novel diversity and illustrating the alternative domestication pathways to cereals (Condé et al., 2024; Hildebrand, 2003, 2009). The cultivation of Guinea yams varies across communities and local environments, implying the importance of diverse local practices. For cassava, there is a cosmological tradition called kukurro where people include new volunteer plants in selection trials, resulting with diversity increase (Freitas & Zarur, 2007). However, a comparison with enset in Ethiopia emphasises that vegetative crops follow more species-specific domestication pathways compared to most cereals and are harder to generalise (Fuller et al., 2023; Hildebrand, 2016; White et al., 2023).

Ethnobotany can provide insights into contemporary varietal groupings, for example, through documenting their names, uses and recent histories (Burton et al., 2024; Gros-Balthazard et al., 2023). Such an approach can elucidate the meaning of local crop names (based for example on use, phenotypic traits or area of cultivation). Interviews about crop uses can also investigate the reasons why different varieties are maintained, for example, for certain foods, fodder or resilience (Shewayrga & Sopade, 2011), and can shed light on changing local crop diversity. Some historically oriented anthropological and ethnobotanical studies also examine how varieties have been exchanged or translocated. For example, maroon women from Suriname and French Guiana, while fleeing enslavement, brought rice varieties to their communities. The diverse maroon rice varieties can carry the names of the female ancestors or tribes or other ethnic minorities which they came from. Rice and cassava varieties were secretly transported in women's hair and are commemorated with traditional braiding (van Andel et al., 2024). Overall, ethnobotanical research sheds light onto crop diversification processes, including dispersals and selection for local uses.

Many IP&LCs have agrarian practices rooted in a profound relationship with the natural environment that can illuminate crop origins, domestication and adaptation. Their traditional sustainable farming practices encompassing environmental, cultural and socio-economic elements of an overall knowledge, in which TEK is included, can be integrated with a holistic cosmological understanding sometimes known as cosmovision (Pierotti, 2010). This TEK, often not recorded in writing, can be passed as oral histories and art, describing crop origins and selection in local environments (Berkes, 2017; Fuller et al., 2023). For example, the Central Amazonian Sateré-Maué people have a story about wild and cultivated guaraná (*Paullinia cupana* or 'eyes of the gods'), which stemmed from the two eyes of a murdered child, from which trees the Sateré-Maué peoples descended (Prance, 1997). Through their cosmovision, both cultivated and non-cultivated guaraná are revered, while the presence of both suggests that the domestication of guaraná likely occurred in the Sateré-Maué lands. Similarly, K'iche' people (in today's Guatemala) recorded orally and later in Popol Vuh (*The Book of Events*) the creation of the universe, including crop plants, which played a fundamental role in creating people (Christenson, 2012). The sacred epic features cotton (*Gossypium hirsutum*), chia (*Salvia hispanica*), maguey (*Agave americana*) and other local species.

Overall, the number of publications recording indigenous knowledge once again favour in number global cereal crops, as well as fruits and legumes (Figure 1e). Oral traditions, however, can significantly improve our understanding of local crops' origins and agroecologies, providing a great starting point for elucidating crop evolutions, like in the examples of guarana, chia or maguey. Additionally, Popol Vuh includes a multi-species traditional Mesoamerican agricultural ecosystem (*milpa*) practised by the gods and followed by people until now owing to its ecological efficiency (Christenson, 2012; Pérez-Martin et al., 2022). The most well-known *milpa* was created by Haudenosaunee people, which include three species, such as squash, beans and maize, whose complementary roles in the field co-evolved to increase collective fitness. Polycultures are thought to be very efficient systems, and integrating TEK with genomic evidence would bring novel insights into the co-evolution of plants in multicropping environments (Liebman, 2018; Ricciardi et al., 2021).

## 2.4 | Integrating evidence

Domestication and dispersal histories of global crops are comparatively well known through multidisciplinary approaches spanning genomics, archaeology, anthropology, ethnobotany and historical resources (Figure 2). Cases in which these distinct disciplines are congruent are reasonably common. Perhaps the best example is the completely independent dating of maize domestication through archaeology and genetics (Matsuoka et al., 2002), both pointing at the ninth millennium BP. In some cases, however, the evidence of crop dispersal and adaptation is discordant. By combining linguistic data and oral history, researchers showed that sweet potatoes, originally from the tropical Americas, could have reached the Pacific during ~1300 or ~1600 AD (Wiessner, 2005). The heterogeneous geography of New Guinea, as well as the rituals and TEK the local communities developed around sweet potatoes, translated into the high diversity of this species (Roullier et al., 2013). Genetic data, relying on a few loci, also confirmed the American origin of Pacific sweet potatoes in pre-Columbian times. However, the hypothesis that sweet potatoes were spread by human agency has been contested using genomic data, concluding this crop arrived in Polynesia through naturally occurring long-distance dispersal more than 100,000 years ago (Muñoz-Rodríguez et al., 2018). Similarly, based on linguistics alone, rice was assumed to be introduced to the Philippines and Austronesian Archipelago from Taiwan. However, genetic evidence suggests introduction through the Malay Peninsula (Alam et al., 2021). These examples show that a single line of evidence might not be sufficient to resolve complex evolutionary histories.

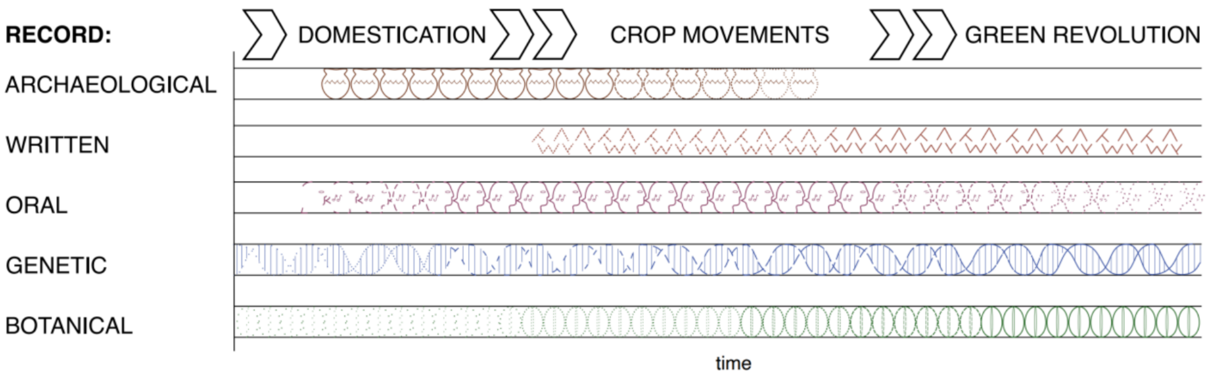

**FIGURE 2** Evidence available for research on crop evolution is multidisciplinary, complementary and integrable. Fields of archaeology, written and oral histories, genomics and botany complement one another on a temporal scale. Interdisciplinary records span key agricultural transition periods that substantially affected crop evolution, such as domestication and crop global movement, including ancient dispersals and the forced Columbian exchange, as well as the Green Revolution.

Careful synthesis, through an interdisciplinary approach, promises to recover an accurate picture of crop evolution and bring completely new insights. Perhaps the best example is a recently published work on cassava, where a combination of genomics, archaeology and ethnobotany led to novel insights into the domestication and dispersal of vegetatively reproduced clonal crops (Kistler et al., 2025). TEK explained the unusual signatures of kinship and selection in a global set of cassava clones. Similarly, interdisciplinary research brings exciting new insights into the mechanisms of early crop dispersals. Archaeogenomics (applying a genomic approach to archaeological materials), ethnobotany and morphological studies were combined, revealing multiple migration waves of maize between the South and Central American varieties (Kistler et al., 2018, 2020). The pathways of rice dispersal throughout Asia have been reconstructed using the combination of archaeology, palaeoenvironmental reconstruction and genomic associations with linguistics and culinary data (Gutaker et al., 2020). Beyond Asia, a fine-scale regional dispersal process can be investigated by a mix of genomic and historical evidence alongside more occasional archaeobotanical finds (Gutaker & Purugganan, 2024). For example, rice introduction to the northern part of South America from multiple sources based on historical records and varietal naming was confirmed by the analysis of genomic ancestry from West Africa, North America and Southeast Asia (van de Loosdrecht et al., 2024). In another example, banana domestication and dispersal from Papua New Guinea were evidenced in archaeological microremains, evidence for agricultural fields, linguistics and genomics (Perrier et al., 2011). Such interdisciplinary analyses are particularly valuable for local crops, where oral histories can be used as a solid starting point for investigating domestication, evolution of use and crop dispersals (Figure 3).

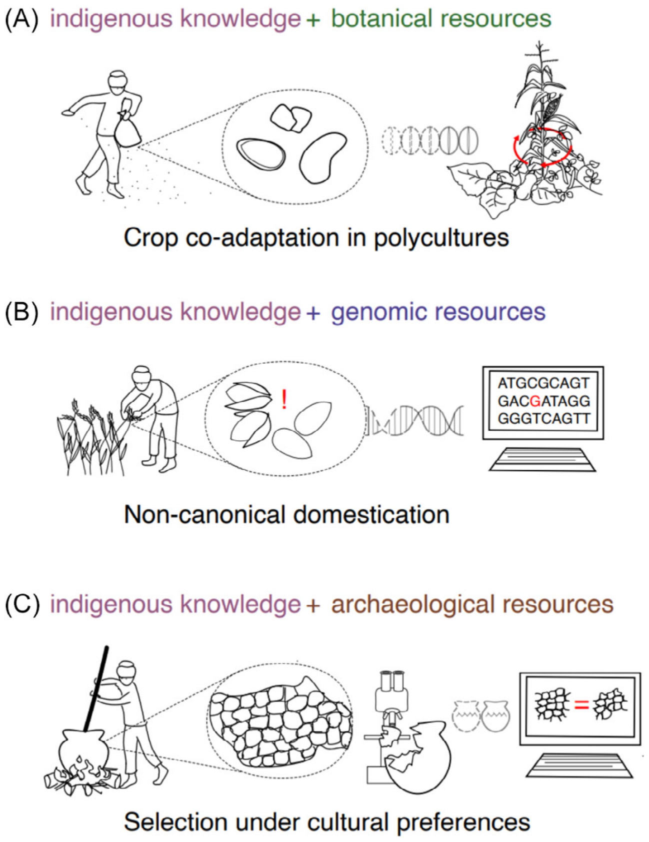

**FIGURE 3** Local indigenous knowledge can be a starting point for novel investigations into crop plant evolution. (a) The highlighted example includes combining traditional ecological knowledge (TEK) with botanical resources to understand co-adaptation of multiple crops in polycultures. (b) Combining it with genomics to elucidate genetic basis of non-canonical domestication traits. (c) Inspiring processing experiments that will allow comparisons with archaeological record.

The aim of this review is not to list comprehensively cases of interdisciplinary research for local crops but to inspire future interdisciplinary research, reaching beyond 'Western science'. In the above sections, we have exemplified how integrating TEK with genomics and archaeology could yield novel insights into the domestication, diversification and adaptation processes. Examples include using TEK for in depth understanding of selective forces (resultant from propagation practices and cultural preferences) to elucidate their climatic and biotic suitability and domestication phenotypes in local crops and underlying genetic architectures (Figure 3). TEK can also help in interpreting archaeological remains, for example, by informing how crops have been traditionally processed into food products (Figure 3). Finally, we suggest that the TEK of milpas could benefit from genomic evidence to help in understanding crop adaptation to multicropping environments (Figure 3). Bringing TEK forward can empower IP&LC by acknowledging their ancestral role in domesticating and diversifying crops, as well as leading efforts within agrobiodiversity to achieve food sovereignty, which is the right of peoples to healthy and culturally appropriate food produced through ecologically sound and sustainable methods. All generated data and associated knowledge managed by IP&LC should be carefully handled to adhere to the Access Benefit Sharing framework of the Convention of Biological Diversity and the communities' preferences, especially if the aim is to diversify the global food systems (Jennings et al., 2023; Muñoz-García et al., 2025).

## 2.5 | Evolutionary processes in current system

Various agricultural transformations started at the beginning of the 20th century with the aim of increasing yields of staple crops. The global movement called 'the Green Revolution' (GR) was rooted in major improvements in wheat production in Mexico since the 1940s and in rice production in the Philippines and India since the 1960s. During that period, the introduction of high-yielding crop varieties (HYVs) as well as the implementation of modern agricultural practices, prominently synthetic fertilisers, led to a rapid increase in crop yields with only a modest increase in areas under cultivation (Athwal, 1971; Pingali, 2012). In 1965, more than 800,000 ha of wheat-growing land in Mexico (∼95%) was occupied by HYV supplied by the International Centre for Wheat and Maize Improvement in Mexico (CIMMYT) (Athwal, 1971). Similarly, high-performing rice varieties developed by the International Rice Research Institute (IRRI) were planted on approximately 2.7 million ha in the Philippines (77.4%) by 1980–1981 (Herdt & Capule, 1983). The rapid spread of these HYVs in the Global South increased yield by ∼50% and production by 40% during 1980–2000 (Evenson & Gollin, 2003), dominating the global calorie uptake. After the success of rice and wheat HYVs, breeding programmes aimed at developing improved varieties in other crops. The development of HYVs for maize, sorghum, pearl millet, barley, common beans, lentils, groundnuts, potatoes and cassava was much slower with only a few modern varieties until the 1980s. By 2000, there were more than 8000 modern varieties of these 11 crops released globally (Evenson & Gollin, 2003).

The impact of GR on the global crop evolution has been fundamental. Firstly, it led to the reduction in both genetic and phenotypic variations. In wheat, domestication together with modern breeding programmes caused ∼84% and 69% reductions in the genetic diversity of tetraploid durum wheat and hexaploid bread wheat, respectively (Peng et al., 2011). Currently, over 70% of cultivated wheat varieties have semi-dwarf characteristics (Evans, 1998). In India, over 100,000 local rice varieties have disappeared post-GR (Eliazer Nelson et al., 2019). Secondly, GR crops were initially bred for optimal conditions in breeding stations, supplemented with irrigation and agrochemicals. Many abiotic stress resilience traits have been lost in this process. Recent breeding efforts aim to reintroduce those resilience traits, but with limited success owing to complex genetic architectures and background-dependent efficiency (McCouch et al., 2020; Westengen et al., 2023). Finally, centralised seed systems associated with GR crops drastically limit crop ability to adapt to local conditions (Mastretta-Yanes et al., 2024; Mercer & Perales, 2010). An alternative that has been explored for some crops is subjecting evolutionary populations to natural selection in field trials (Döring et al., 2011). In one well-researched case in a single barley field, this process has led to a substantial decrease in genetic diversity nonetheless (Landis et al., 2024). In multi-site evolutionary breeding experiments, divergent selection on grain size and plant height has been observed with general yield increase, suggesting adaptation to local environmental conditions (Bocci et al., 2020).

Conversely, there has been a general lack of global investment for a vast range of local crops. Many local cereals, legumes, tubers, fruits and root crops are mainly limited to local breeding efforts, and progress in improving them is understandably lagging. Traditionally, IP&LC and smallholder farmers (small-scale farmers who manage 1–10 ha of land and are family-focused) cultivate multiple crop species for local markets and self-consumption (Jarvis et al., 2011), and within those, multiple varieties, maintaining and promoting genetic variation leading to better resilience and lower environmental impact (Zhu et al., 2000). Local crops are propagated and selected in situ, promoting adaptation to local conditions, which are often not well represented in breeding stations. This process, included in the concept of evosystem services, brings attention to the importance of traditional seed systems as a source of diverse and adapted local varieties and species (Mastretta-Yanes et al., 2024).

Changes in agriculture in the last century have led to diversity loss, the magnitude of which varies by species, taxonomic and geographic scale and region (Khoury et al., 2022). Past focus on global crops was at odds with promoting highly resilient locally adapted crops. While it was unlikely the aim of the GR, it had a detrimental effect on conserving and developing genetic diversity for local crops by neglecting local crops' ex situ collections and promoting global crops for in situ replacement (Figure 1b). For example, intensive rice cultivation in the Philippines led to the loss of leafy vegetables grown in paddy fields (Pingali & Roger, 1995). Approximately 6 million ex situ plant accessions are conserved in gene banks all over the world, mainly as seeds under long-term or medium-term storage conditions, with only three global cereal crops (wheat, rice and maize) comprising about 30% of the collections, and local crops significantly under-represented or undocumented (ITPGR PubStat). The gradual replacement of farmers' seed systems by a centralised system since the GR, in conjunction with the modernisation of agriculture, continues to pose a threat to the conservation of local crops at the farm level (Khoury et al., 2014; Westengen et al., 2013).

## 2.6 | The perspectives of future local crop evolution

### 2.6.1 | In situ conservation and adaptation

Ex situ seed banks for global cereals have been established to conserve native genetic diversity off-site and increase research access for their improvement. However, substantial global agrobiodiversity remains in the diversity of local crops, which tends to be undercollected and for some crops, conservation may be best achieved using different approaches. Since the mid-20th century, the global decay and loss of regional germplasm centres represent a major issue. In the tropics, many local crops are clonally propagated, requiring either living collections or tissue banks (e.g. Banana, via the International Musa Germplasm Transit Centre, which facilities are rare and expensive to run). Ex situ conservation may require complex agreements, specialised material export, shipment and funding for continued maintenance. Investigating the areas of domestication and modelling distribution of local crops will enable us to predict spatial and taxonomic priorities for research, use and in situ conservation. As local crops are often range-restricted they are likely to occur close to their areas of origin. Vavilov already proposed that those areas like the Andes, Ethiopian Highlands or Fertile Crescent, are also centres of genetic, trait and use diversity, as well as the richness of associated knowledge (Pingali & Roger, 1995). Some research suggests that regions such as Ethiopian Highlands successfully maintained local crop diversity despite wide spread adoption of introduced global crops (Rampersad et al., 2023).

For most local crops, millions of IP&LC and smallholder farmers currently provide in situ conservation, maintaining considerable TEK in the process, while enabling continued adaptive evolution through selection (Mastretta-Yanes et al., 2024). Smallholder farmers and IP&LC using their traditional farming systems illustrate the advantages of agrobiodiversity by selecting crop species and local varieties that meet their needs. For example, in Ethiopia, farmers increase the area cultivated for the local perennial food security crop enset during periods of drought as a resilience strategy (Chase et al., 2023). Intraspecific crop diversity within sweet potato encompasses traits useful to tolerate warming under climate crisis (Heider et al., 2021). Similarly, Quechua families in the Peruvian Andes manage hundreds of traditional oca varieties (*Oxalis tuberosa*) through seed banks and community *chakra* (arable plots), continuously selecting for stress tolerance traits and adapting them to microclimates across the rugged Andean landscape (Velásquez-Milla et al., 2011). While local crops are generally well adapted to current conditions, anticipating future climate scenarios may require introducing additional germplasm. Hence, there is an urgent need for local farming communities to be better connected.

Currently, smallholder conservation of agrobiodiversity is largely motivated by self-sufficient resilience and cultural value. Approaches prioritising biological and cultural values have been developed over recent decades, including expansion of community-based conservation efforts, networks of farmers and local seed banks. Another approach is to adapt Payments for Ecosystem Services models to smallholder farmers, compensating them for conserving agrobiodiversity, which was successfully piloted in several countries on crops including quinoa and potato (Jago et al., 2024). For this, a priority is to understand the competing incentives for farmer crop choice (e.g. subsidies for global crops) and develop mechanisms to support in situ maintenance of agrobiodiversity. In some scenarios, high agrobiodiversity systems may be less productive, or profitable, than cultivating global crops, but on the other hand, they provide conservation services of value for global agriculture. More immediate local realisation of the benefits of crop development may demonstrate the value of agrobiodiversity conservation to local stakeholders.

### 2.6.2 | Prospects for TEK-inspired crop development

In the past, colonial practice was to introduce globally desirable or familiar crops into new land without the consideration for local environmental conditions, local people's preferences, experiences and skills. A good example of this was an attempt to replace locally cultivated robusta coffee in Uganda with Arabica. Despite initial success, Arabica has been abandoned, and local farmers reverted to robusta cultivation, where TEK-supported selection process resulted with export of high-quality coffee (Davis et al., 2023). Allocating resources into local efforts will allow IP&LC and smallholder farmers to further innovate their crops, traditionally or by collaborating with local researchers and institutions. Argument has been made that IP&LCs' practices can be theorised and incorporate in collaborative plant breeding (Soleri & Cleveland, 2001). Such collaborations would be mutually beneficial. An example of that is the decentralised, so-called tricot breeding (Dawson et al., 2008) (also known as tricot approach) that has been applied, for example, to wheat breeding in Ethiopia and common bean breeding in Nicaragua (van Etten et al., 2019), where IP&LCs evaluated the varieties themselves. Neodomestication, achieved through traditional selection practices or accelerated with genome editing, should be the next frontier for the collaboration between IP&LCs and 'Western' scientists.

Neodomestication or de novo domestication achieved through genome editing demonstrated that wild or semi-domesticated species can be rapidly reshaped into more productive crops through targeted gene editing. In wild tomato *Solanum pimpinellifolium*, CRISPR–Cas9 was used to enhance fruit size, yield and nutritional content while preserving traits like stress tolerance that are often lost in conventional breeding (Zsögön et al., 2018). Similarly, in wild allotetraploid rice (*Oryza alta*), researchers established an editing platform, enabling the improvement of key agronomic traits and laying the foundation for a novel staple crop adapted to the current climate crises (Yu et al., 2021). The breakthroughs in crop wild relatives offer a compelling framework for extending genome editing to local crops. Genome editing in foxtail millet species accelerated their domestication through improvement of plant stature and seed non-shattering (Yu et al., 2023; Zhang et al., 2025).

Currently, the motivations for crop neodomestication have aggregated around converging pressures on global food systems, such as soil deterioration, limited space and climate change adaptation. Neodomestication opens possibilities for the development of perennial alternatives to annual cereals that are healthy for the soil, like *Thinopyrum intermedium*, a grass relative of wheat that can withstand environmental stresses while reducing soil erosion (DeHaan et al., 2020). Diversification through neodomestication extends beyond rural agriculture to urban settings, where space constraints require crops specifically tailored for vertical farming and controlled environments (Kwon et al., 2020). Changes in temperatures and precipitation that are associated with climate change, combined with the challenging nature of the genetic mechanisms underlying resilience in certain crops, motivate the identification of edible plants that can already withstand climate disruption and prioritisation to neodomesticate them (Gutaker et al., 2022).

While these are all noble and timely motivations, they overlook the critical aspect of human agency. Neodomestication of local crops becomes especially critical in regions where climate change will impact agricultural systems the most, particularly in the Tropics (Hultgren et al., 2025). This is compounded by the fact that the traditional farming systems in the Global South face economic pressures from global crop subsidies and shifting market forces that favour industrial agriculture over local varieties and crop species. Research on local crops (drawing from evolutionary history, archaeological records and TEK) provides critical insights for building the genetic and cultural foundations for neodomestication. Integrating cutting-edge genomic tools with TEK and participatory research models opens a pathway to ethically neodomesticate these species. In doing so, we not only enhance the adaptive capacity of local food systems but also reaffirm the cultural and ecological knowledge systems that sustain them. Ultimately, neodomestication of local crops can represent more than technological innovation offering a pathway to rebuilding the fundamental relationships between researchers, local communities, their crops and their landscapes.

Furthermore, neodomestication could and should draw inspirations from TEK. In this section, we propose a few TEK-inspired ideas for neodomestication (Figure 3). One approach includes the neodomestication centred around ecological and cultural parameters. Considering ecological interactions opens the possibility of selecting multiple plant species that support each other in a polyculture arrangement, akin to the famous ‘three sisters’ previously mentioned. Building on this scheme, researchers could pick a new adapted cereal, legume and cucurbit species to support each other in different climatic and cultural environments. The *milpa* system in Mesoamerica offers a framework for identifying candidate species for neodomestication. By focusing on crops that already complement each other, researchers and farmers can prioritise species that are ecologically viable, ensuring the future of crop evolution remains compatible with agrobiodiversity practices. Another idea would be to select agroforestry species with TEK criteria for neodomestication.

It is also important to consider traits that are compatible with local processing technologies and culinary practices. For example, we can focus on reducing bitterness in tubers that are becoming less cultivated due to changing frost patterns (which is otherwise necessary for processing bitterness) in the Andean Altiplano or improving husk removal in fonio millet to reduce labour intensity in West Africa (which currently requires laborious cycles of pounding, winnowing and flotation). Similarly, traits that suit regional cooking styles should be considered when selecting species for neodomestication, like favouring amylopectin-rich starches (sticky) in grains for Northeast Asia and starchy crops in West Africa that would be easy to make into dough balls. By allowing local needs to shape the traits of interest, we ensure that genomic innovations remain culturally important and are supporting instead of replacing TEK systems.

Neodomestication process should be conducted ethically and with the prior informed consent and active participation of IPLC. Understanding the cultural roles of local crops helps to ensure that neodomestication approaches align with IPLC values, helping their acceptance and long-term sustainability. Field trials should be conducted in collaboration with local farmers under relevant environmental conditions. Feedback from these trials can inform iterative improvements, making the new crops scientifically sound and culturally and ecologically grounded.

### 2.6.3 | Local crops and the value chain

Most IP&LC and smallholder farmers are part of a value chain of some description, from the local to the global scale. Local and national value chains are usually biased towards food crops, both fresh and storable, and at the international level towards cash crops, such as bananas, coffee, cocoa and cashew. The development of numerous value chain crops has occurred at the local level, including the development of ‘indigenous varieties’, ‘farmer's lines’ and ‘heirloom varieties’. Well-known examples include coffee (Bekele & Hill, 2018; Davis et al., 2023). Short value chains, such as those involving merchandising at local and national marketplaces, are less complex, with immediate or short-term feedback cycles invoked when crops are altered, either via external forces such as climate change or by purposeful intervention by the farmer. Longer value chains, involving internationally traded crops, with numerous value chain stakeholder, and consumers based outside the country of origin, are multifaceted. Crops developed by IP&LCs must suit the farmer and their communities, and the processors, exporters, importers and consumers, over the entirety of the value chain.

In response to growing market demand and supply sustainability, coffee has witnessed some recent noteworthy changes. For example, in some areas of Uganda, local farmers (∼350 farms) have shifted from traditional and indigenous robusta coffee (*Coffea canephora*) cultivation to mixed farms incorporating non-traditional but indigenous excelsa coffee (*Coffea dewevrei*) with robusta, in response to worsening climate for robusta (Davis et al., 2022; Davis et al., 2022; Davis et al., 2023). In most cases, the farms grow roughly equal quantities of both species, but on many farms, excelsa now dominates. These transitions were undertaken without or only with minimal consultation with value chain representatives. A similar transition involving these two species has occurred at smaller scale in South Sudan, initiated and guided by TEK (Davis, Kiwuka, Faruk, Walubiri, & Kalema, 2022). In India, excelsa coffee is being upscaled at the local level to diversify traditional Arabica (*Coffea arabica*) and robusta productions systems, also in response to climate change (Davis, Kiwuka, Faruk, Walubiri, & Kalema, 2022). In India, these three coffee species were introduced to India in the recent past, that is, are non-indigenous. In Southeast Asia, and notably Malaysia, Liberica coffee (which was introduced at the end of the 20th century) is re-emerging at the local level, as a culturally and economically important crop (Davis, Kiwuka, Faruk, Walubiri, & Kalema, 2022).

These local-led initiatives provide proof of concept for the potential of TEK and local biodiversity (whether indigenous or introduced) in the global value chain. To achieve the best possible outcomes for these and similar activities, stakeholder involvement and research is required to direct further crop development of under-utilised and neglected crops, ensuring food safety, profitability and sustainability. For example, whereas Liberica coffee may suit local use and short national value chains, low outturn values (i.e. the conversion of fresh fruit to clean, exportable coffee) due to the thick, tough pulp, thick endocarp (parchment layer) and low seed density drastically reduce profitability (Davis, Kiwuka, Faruk, Walubiri, & Kalema, 2022). These same characteristics, in combination with large fruit and large seed size, mean that extended drying times are required (compared to other coffee crop species) and the development of the use of specialised equipment for drying, pulping and hulling (Davis, Kiwuka, Faruk, Walubiri, & Kalema, 2022). In such an example, genomics and neodomestication approaches can play a pivotal role in guiding selection and breeding programmes for crop improvement (Davis et al., 2025).

## 3 | CONCLUSIONS

Growing evidence illustrates the benefits of agrobiodiversity in meeting our current and future crop needs. For example, national crop diversity (and harvest asynchrony) stabilises food production (Renard & Tilman, 2019), but global analyses show that agrobiodiversity remains dramatically under-utilised (Jones et al., 2021). We argue that understanding evolutionary histories of local crops, including adaptations to myriad uses, cultivation practices and environments, provide a basis for sustainable utilisation of agrobiodiversity enhancing the benefits we derive from agriculture. In this paper, we have discussed the heavy bias in data availability for evolutionary research on global ('commercial', 'major') crops versus local ('orphan', 'minor', 'neglected') crops. We also illustrated that data derived from genomics, archaeology, ethnobotany and LIK are useful in investigating crop histories, adaptation and uses and work much better in a combination than separately. By integrating cultural and natural sciences, we can better understand patterns of crop diversity (at genomic and on-farm levels), traits, evolutionary processes and the mechanisms that create and sustain in situ diversity. Given new and increasingly accessible tools, genomic approaches are becoming democratised and achievable in smaller research groups with more limited funding. This therefore represents an opportunity for a larger part of the research cycle to be undertaken in situ, where crops originate, have the most TEK and LIK, and the research stands to most directly benefit the crops' custodians. Leveraging international finance to accelerate this process is likely to achieve both local and global benefits in an increasingly global food system. Encouragingly, this represents an opportunity to sustainably diversify our narrow basket of global crops increasing the resilience of recent food security gains, as well as achieving this through a more equitable network of stakeholders and beneficiaries.

### AUTHOR CONTRIBUTIONS

Nataly Allasi Canales and Rafal M. Gutaker conceptualised the idea. Nataly Allasi Canales, Rafal M. Gutaker, Philippa Ryan, Amy Jackson, James Borrell, Aaron Davis and Hong Phuong Le wrote the manuscript. Rafal M. Gutaker, Nataly Allasi Canales, Philippa Ryan, James Borrell and Aaron Davis edited the manuscript. Nataly Allasi Canales prepared Figure 1, and Rafal M. Gutaker prepared Figures 2 and 3.

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### CONFLICT OF INTEREST STATEMENT

The authors declare no competing interests.

### DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available in JSTOR at https://www.jstor.org/, NCBI at https://www.ncbi.nlm.nih.gov/ and GENESYS at https://www.genesys-pgr.org/.

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## SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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